ISOLATION, IDENTIFICATION AND CHARACTERIZATION OF NON-*SACCHAROMYCES* AND *SACCHAROMYCES* YEASTS IN TRADITIONAL WINES MADE FROM FIVE DIFFERENT NATIONAL GRAPES IN TURKEY

A THESIS SUBMITTED TO
THE GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
OF
MIDDLE EAST TECHNICAL UNIVERSITY

BY

İPEK AKTUNA

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR
THE DEGREE OF MASTER OF SCIENCE
IN
BIOTECHNOLOGY

JULY 2019

Approval of the thesis:

ISOLATION, IDENTIFICATION AND CHARACTERIZATION OF NON-*SACCHAROMYCES* AND *SACCHAROMYCES* YEASTS IN TRADITIONAL WINES MADE FROM FIVE DIFFERENT NATIONAL GRAPES IN TURKEY

submitted by **İPEK AKTUNA** in partial fulfillment of the requirements for the degree of **Master of Science in Biotechnology Department, Middle East Technical University** by,

Prof. Dr. Halil Kalıpçılar
Dean, Graduate School of **Natural and Applied Sciences** _____

Assoc. Prof. Dr. Can Özen
Head of Department, **Biotechnology** _____

Prof. Dr. G. Candan Gürakan
Supervisor, **Biotechnology, METU** _____

Prof. Dr. Ayşegül Çetin Gözen
Co-Supervisor, **Biological Science, METU** _____

Examining Committee Members:

Prof. Dr. Alev Bayındırlı
Food Engineering, METU _____

Prof. Dr. G. Candan Gürakan
Biotechnology, METU _____

Assoc. Prof. Dr. Remziye Yılmaz
Food Engineering, Hacettepe University _____

Assist. Prof. Dr. Aysun Cebeci Aydın
Food Engineering, Abdullah Gül University _____

Assist. Prof. Dr. Asya Çetinkaya
Food Engineering, Kafkas University _____

Date: 26.07.2019

I hereby declare that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. I also declare that, as required by these rules and conduct, I have fully cited and referenced all material and results that are not original to this work.

Name, Surname: İpek Aktuna

Signature :

ABSTRACT

ISOLATION, IDENTIFICATION AND CHARACTERIZATION OF NON-*SACCHAROMYCES* AND *SACCHAROMYCES* YEASTS IN TRADITIONAL WINES MADE FROM FIVE DIFFERENT NATIONAL GRAPES IN TURKEY

Aktuna, İpek
Master of Science, Biotechnology
Supervisor: Prof. Dr. G. Candan Gürakan
Co-Supervisor: Prof. Dr. Ayşegül Çetin Gözen

July 2019, 315 pages

Kalecik Karası, Öküzgözü, Dimrit and Boğazkere are local red grapes in Ankara, Elazığ, Cappadocia and Elazığ, respectively. Moreover, Emir is a local white grape grown in Cappadocia. Yeast populations are different in various types of grapes due to the unique properties of these grapes. In this study, 104 non-*Saccharomyces* and 293 *Saccharomyces* yeasts were isolated at different maceration and fermentation times from the grape's musts and wines made of these grapes. All 104 non-*Saccharomyces* isolates were sequenced. 29 (among 77 sequenced isolates) out of 293 total *Saccharomyces* yeasts were selected as those with high technological properties. Among all 181 (104 non-*Saccharomyces* and 77 *Saccharomyces*) yeast isolates, 16 different species of yeasts were identified by DNA sequencing of internal transcribed spacer (ITS) region and/or D1/D2 domain of large subunit ribosomal DNA as: *Hanseniaspora guilliermondii*, *Hanseniaspora opuntiae*, *Hanseniaspora uvarum*, *Rhodotorula mucilaginosa*, *Wickerhamomyces anomalus*, *Metschnikowia aff. fructicola*, *Metschnikowia fructicola*, *Lachancea thermotolerans*, *Solicoccozyma aeria*, *Metschnikowia aff. pulcherrima*, *Metschnikowia pulcherrima*, *Metschnikowia*

sinensis, *Metschnikowia chrysoperlae*, *Starmerella bacillaris, Saccharomyces cerevisiae* and *Saccharomyces cf. cerevisiae/paradoxus*. Selected non-*Saccharomyces* isolates were tested for some phenotypic properties such as alcohol tolerance, SO_2 tolerance and H_2S production. In addition, selected *Lachancea thermotolerans* and *Saccharomyces cerevisiae* were used as starter cultures for sequential inoculation to produce Emir wine. Moreover, *Hanseniaspora uvarum* and *Saccharomyces cerevisiae* were added as a single starter culture separately for wine making from Kalecik Karası grapes. Volatile compounds of these wines were analyzed by gas chromatography-mass spectrometry (GS-MS). According to flavour profiles and amounts of volatile compounds, Emir wines with sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains were found successful.

Keywords: Non-*Saccharomyces*, *Saccharomyces,* wines starter cultures, identification, aroma compounds

ÖZ

TÜRKİYE'DEKİ BEŞ FARKLI YEREL ÜZÜMDEN YAPILAN GELENEKSEL ŞARAPLARDAN NON-*SACCHAROMYCES* VE *SACCHAROMYCES* MAYALARIN İZOLE EDİLMESİ, TANIMLANMASI VE KARAKTERİZASYONU

Aktuna, İpek
Yüksek Lisans, Biyoteknoloji
Tez Danışmanı: Prof. Dr. G. Candan Gürakan
Ortak Tez Danışmanı: Prof. Dr. Ayşegül Çetin Gözen

Temmuz 2019, 315 sayfa

Kalecik Karası, Öküzgözü, Dimrit ve Boğazkere sırasıyla Ankara, Elazığ, Kapadokya ve Elazığ'ın yerel kırmızı üzümleridir. Buna ek olarak, Emir, Kapadokya'da yetişen yerel beyaz üzümdür. Bu üzümler kendilerine özgü özelliklere sahip oldukları için bu üzümlerdeki maya popülasyonu birbirlerinden farklıdır. Bu çalışmada, bu üzümlerin şıralarından ve şaraplarından değişik maserasyon ve fermantasyon zamanlarında 104 non-*Saccharomyces* ve 293 *Saccharomyces* maya izole edilmiştir. 104 non-*Saccharomyces* mayanın hepsi sekanslanmıştır. Toplam 293 *Saccharomyces* mayadan (77 sekanslanmış izolat arasından) 29 tanesi yüksek teknolojik özellik taşıyanlar olarak seçilmiştir. Tamamı 181 maya izolatı arasından (104 non-*Saccharomyces* ve 77 *Saccharomyces*) ITS bölgesine ve ribosomal DNA'nın büyük alt ünitesindeki D1/D2 domainindeki DNA dizilimine göre 16 farklı maya türü tanımlanmıştır: *Hanseniaspora guilliermondii*, *Hanseniaspora opuntiae*, *Hanseniaspora uvarum*, *Rhodotorula mucilaginosa*, *Wickerhamomyces anomalus*, *Metschnikowia aff. fructicola*, *Metschnikowia fructicola*, *Lachancea thermotolerans*, *Solicoccozyma aeria*, *Metschnikowia aff. pulcherrima*, *Metschnikowia pulcherrima*, *Metschnikowia*

sinensis, Metschnikowia chrysoperlae, *Starmerella bacillaris, Saccharomyces cerevisiae* ve *Saccharomyces cf. cerevisiae/paradoxus*. Seçilen non-*Saccharomyces* izolatların alkol direnci, SO_2 direnci ve H_2S üretimi gibi bazı fenotipik özellikleri test edilmiştir. Buna ek olarak seçilen *Lachancea thermotolerans* ve *Saccharomyces cerevisiae,* Emir şarabına starter kültür olarak sıralı inoküle edilmiştir. Bununla beraber, *Hanseniaspora uvarum* ve *Saccharomyces cerevisiae,* Kalecik Karası üzümünden şarap yapımı için tek starter kültür olarak kullanılmıştır. Bu şarapların aroma bileşikleri gaz kromatografisi-kütle spektrometresi ile analiz edilmiştir. Aroma profillerine ve miktarlarına göre *Lachancea thermotolerans* ve *Saccharomyces cerevisiae* suşlarımızla sıralı aşılama yöntemiyle yapılan Emir şarapları başarılı bulunmuştur.

Anahtar Kelimeler: Non-*Saccharomyces*, *Saccharomyces*, şarap starter kültürü, tanılama, aroma bileşikleri

To My Beloved Family…

ACKNOWLEDGEMENTS

I would like to thank The Scientific and Technological Research Council of Turkey (TUBITAK) for funding through the support program for scientific and technological research projects (1001) with the project number 116O521. This study is a part of this project.

I would like to express my sincere gratitude to my supervisor, Prof. Dr. G. Candan Gürakan for her continuous patience, guidance, encouragements and endless support. It has been an honor and a great pleasure to be the part of this project under her valuable guidance. I would also like to thank my co-advisor, Prof. Dr. Ayşegül Çetin Gözen. I would like to thank Prof. Dr. Serkan Selli for the analysis part of volatile compounds. I would express my thankfulness to Assist. Prof. Dr. Asya Çetinkaya for critically reading evaluation of the analysis of volatile compounds and Assist. Prof. Dr. Aysun Cebeci Aydın for her suggestions.

I would like to thank Dr. Houman Jabbarifarhoud for the support of DNA sequencing at BM Laboratory Systems. I would express my thankfulness to Mehmet Başkaya, Zafer Oylan and Özlem Özarda for sensory analysis of produced wines. I also would like to thank Faruk Kaya at Kavaklıdere Winery for chemical analysis of produced wines and Sercan Pekel from Chr. Hansen for providing commercial strain reference. I am also thankful to Turasan Winery for providing commercial strain references.

I would like to thank Elnaz Seyed Monir, my team-mate, for her endless help and friendship during my studies. I am grateful to my laboratory friends Çağrı Çavdaroğlu, Sefa Ulutaş, Manal Sami, Gizem Arslan, Nasim Allahyari for their motivations and deepest supports throughout this study. I also thank Duygu Çiftçi, Serkan Söylenmez, Dilber Mazanli, Aida Mahboubi and my friends Ezgi Oğuz, Ceyda Duman, Sacide Aydın, İlhami Okur, Aylin Cesur, Şahin Namlı, Barış Özel, Özge Yamaner for their

friendship and support. I would like to express my special gratitude to Merve Seda Yaşar for her endless help and friendship throughout my university life and during my studies.

I would like to express my sincerest and deepest gratitude to my lovely parents, Çiçek Aktuna and Halit Aktuna. They always support and trust in me in every part of my life.

TABLE OF CONTENTS

LIST OF TABLES

TABLES

LIST OF FIGURES

FIGURES

LIST OF ABBREVIATIONS

NS: Non-*Saccharomyces*

S: *Saccharomyces*

YPG: Yeast extract-peptone-glucose

ESA: Ethanol sulfate agar

v/v: Volume per volume

CM: Cold maceration

NM: Normal maceration

E-LT-SC: Wine made by sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains in Emir grapes

E-SC: Wine made by inoculation of our *Saccharomyces cerevisiae* strain in Emir grapes

E-WA-SC: Wine made by sequential inoculation of our *Wickerhamomyces anomalus* and *Saccharomyces cerevisiae* strains in Emir grapes

E-A: Traditional wine made from emir grapes (A-Parallel)

E-B: Traditional wine made from emir grapes (B-Parallel)

E-Laff: Wine made by inoculation of commercial *Saccharomyces cerevisiae* strain (Laffort) in Kalecik Karası grapes

K-13: Wine made by inoculation of our *Saccharomyces cerevisiae* strain in Kalecik Karası grapes

K-HU: Wine made by inoculation of our *Hanseniaspora uvarum* strain in Kalecik Karası grapes

K-SC: Wine made by inoculation of commercial *Saccharomyces cerevisiae* strain (Chr. Hansen) in Kalecik Karası grapes

K-A: Traditional wine made from Kalecik Karası grapes

O-LT-SC: Wine made by sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes

O-HO-SC: Wine made by sequential inoculation of our *Hanseniaspora opuntiae* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes

O-HG-SC: Wine made by sequential inoculation of our *Hanseniaspora guilliermondii* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes

O-SC: Wine made by inoculation of our *Saccharomyces cerevisiae* strain in Öküzgözü grapes

O-A: Traditional wine made from Öküzgözü grapes

O-CH: Wine made by inoculation of commercial *Saccharomyces cerevisiae* strain (Chr. Hansen) in Öküzgözü grapes

CHAPTER 1

INTRODUCTION

1.1. Grape Varieties

1.1.1. Grape Varieties in The World

Vineyards include 75% of the world area. According to the research for 44 countries at 2000, these areas are much more than 65,000 hectares for 10 main diversity.

There are three type of grapes with respect to usage area: table grapes (fresh grapes), dried grapes and wine grapes (Figure 1.1). According to this usage area, vineyards are taken forms. Production of grape wine becomes prominent in France and Spain while production of table and wine grapes comes to the forefront in Italy. In addition, production of three types grapes (fresh, dried and wine) come to the forefront in China and USA whereas production of table and dried grape becomes prominent in Turkey (Karabat, 2014).

In the world, there is 10000 known grape diversity and 13 of them encompass more than 33% of all vineyard field (Table 1.1).

According to the international catalogue of *Vitis* genus, there are 21045 names, and this includes 12250 for *Vitis vinifera*. However, this covers excessively synonyms and homonyms (Maul & Topfer, 2015). Indeed, the number of *Vitis vinifera* species is predicted as 6000 in the world (Lacombe, 2012).

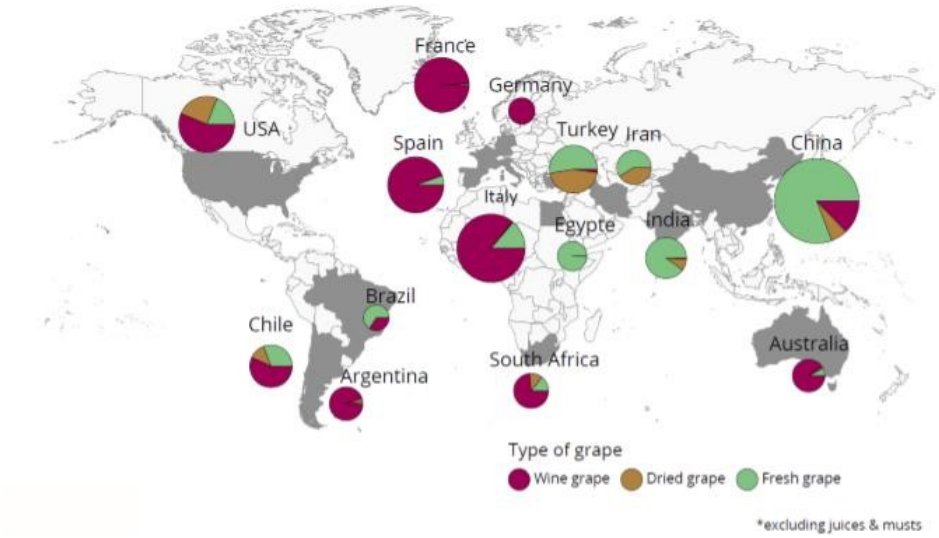


Figure 1.1. Grape Varieties in The World ("International Organisation of Vine and Wine", 2017)

Table 1.1. Distribution of Grape Variety in The World ("International Organisation of Vine and Wine", 2017)

Grape Variety	*Grape Colour*	*Usage Area*	*Field (Hectares)*
Kyoho	Black	Table	365000
Cabernet Sauvignon	Black	Wine	341000
Sultanina	White	Table, Drying and Wine	273000
Merlot	Black	Wine	266000
Tempranillo	Black	Wine	231000
Airen	White	Wine, Brandy	218000
Chardonnay	White	Wine	210000
Syrah	Black	Wine	190000
Red Globe	Black	Table	159000
Garnacha Tinta/ Grenache Noir	Black	Wine	163000
Sauvignon Blanc	White	Wine	123000
Pinot Noir / Blauer Burgunder	Black	Wine	112000
Trebbiano Toscano / Ugni Blanc	White	Wine, Brandy	111000

1.1.1.1. Kyoho

Kyoho is main grape in China. China has more than 90% vines all over the world. Moreover, it has been produced in Japan since 1994 (Morinaga, 2001).

Kyoho has big purple grape including high sugar concentration. This brix value is between 18 and 20. It has nice foxy aroma. The shelf life of this grape is very short and the property of resistance of disease is medium level. It gives 12-15 tons per hectare product (Morinaga, 2001).

1.1.1.2. Cabernet Sauvignon

Cabernet Sauvignon comprises of Cabernet Franc and Sauvignon Blanc. The origin is Bordeaux. It has small grape with long ripeness period. It gives 2-14 tons per hectare product (Galet, 2015).

Wines with these grapes typically have violet and bell pepper aroma. They have high tannin content. Because of the high tannin content and color, these grapes are blended with other grapes such as Merlot, Cabernet Franc, Malbec and/or Petit Verdot. In addition, their wines are suitable for ageing. During ageing process, vegetal aroma has lost gradationally and develop more complex aroma.

Cabernet Sauvignon is the most cultivated grapes all over the world. It covers 341,000 hectares in the world (4% of the vineyards in the world). It is also mentioned an international variety. It produces in France, Argentina, United States, Italy, Spain, China, Australia, Chile and South Africa ("International Organisation of Vine and Wine", 2017).

1.1.1.3. Sultanina

The origin of Sultanina is Afghanistan. It is white seedless grape. Because of small grape, it is suitable for raisin. Moreover, it is used for table grape and wine grape especially in Turkey and The United States of America. Moreover, it can also be used for production of raki.

The production is 273,000 hectares approximately. It produces mainly in the Middle East such as Turkey, Pakistan, Iraq, Afghanistan and Iran, and Central Asia such as Tajikistan, Turkmenistan and Uzbekistan ("International Organisation of Vine and Wine", 2017).

1.1.1.4. Merlot

The origin of Merlot is Bordeaux, France. It has average ripeness time with early flowering. Moreover, it has small berries. Its wines have deep colour, round and structural properties. Because high tannin properties, they can be blended with other grapes.

It can be produced in 37 counties, and the production area is 266,000 hectares. This means 3% of vineyard in the world.

1.1.1.5. Tempranillo

The origin of Tempranillo is Spain. The production area is 231,000 hectares. It gives 2-10 tons per hectare product (Hidalgo, 2002).

Its wine has deep colour, high alcohol concentration and low acidity properties (Galet, 1990).

1.1.1.6. Airen

The origin of Airen is Spain. It is a white grape. Its wine has light color, distinctively fragrance and low acidity properties. It can be blended with other grapes frequently. Moreover, it can be used for making a red wine and spirit. It gives 5-20 tons per hectare product.

1.1.1.7. Chardonnay

The origin of Chardonnay is Burgundy. It is a white wine. It comprises of Gouais Blanc and Pinot (Bowers et al., 1999).

It has small berries and its wine has outstanding flavour. For example, its dry and sparkling wine with adding spirit, it gives dried fruit, walnuts or butter flavours. In addition, it is suitable for ageing process. It gives between 3 and 10 tons per hectare product (Galet, 2015).

It is most international white grapes all over the world. The production area is 210,000 hectares. It produces in Italy, France, Spain, Chile, The United States, and Australia.

1.1.1.8. Syrah

The origin of Syrah is France. It comprises of Mondeuse Blanche and Dureza (Meredith & Boursiquot, 2008).

It has a short ripening time and a late harvesting period. Size of berries changes between small and medium. Its wine has deep colour and high tannin content. It gives between 3 and 8 tons per hectare product.

The production area is 190,000 hectares. It is produced in The United States, Australia, Chile, South Africa and Argentina.

1.1.1.9. Red Globe

Red globe is the second produced table grape all over the world. 91% of total production area is China. The rest of producers are in Spain, Italy, Turkey, Portugal, Chile, The United States, Argentina, and South Africa. It gives between 8 and 30 tons per hectare product.

It can be used for addition of salads (Galet, 2015).

1.1.1.10. Garnacha Tinta (Grenache Noir)

The origin of this grape is Spain and its producers are mainly in Spain and France. It gives 2-8 tons per hectare product.

Its wine has deep colour and high alcohol concentration. Therefore, it can be blended with other grapes.

1.1.1.11. Sauvignon Blanc

The origin of Sauvignon Blanc is France. It is an international white variety. Total production area is 123,000 hectares and 20,500 of them is in New Zealand. It gives 5-10 tons per hectare product.

Its wine has thiol aroma such as exotic fruit, blackcurrant and boxwood. It can be used for producing young white wine. In addition, its dessert wine has high quality.

1.1.1.12. Pinot Noir (Blauer Burgunder)

The origin of Pinot Noir is Burguny. It has small black berries. It has high sugar content and partially acidic properties. In addition, its skin has high polyphenol concentration. Its wine has a light colour and is suitable for ageing in barrels. Moreover, it can be blended with Chardonnay for making sparkling wines.

It produces in Romania, Spain, Italy, Germany, Hungary, Switzerland, Argentina, New Zealand, Chile, Australia, South Africa and the United States. Therefore, it is the fourth most produced grape type.

1.1.1.13. Trebbiano Toscano (Ugni Blanc)

The origin of this grape is Italy. Its producers are in Italy, France, and Portugal.

It is a white grape. Its wine has low alcohol content and high acidity properties. It can be blended with other grape varieties because of balancing neutral aroma. Therefore, it is used for making dry wines, liqueurs and sparkling wines. In addition, this grape is one of the main sources of ice wine (D'Agata, 2014).

According to distribution of grape varieties, the following figures are generated with most 5 grape producer countries (Figure 1.2-1.6):

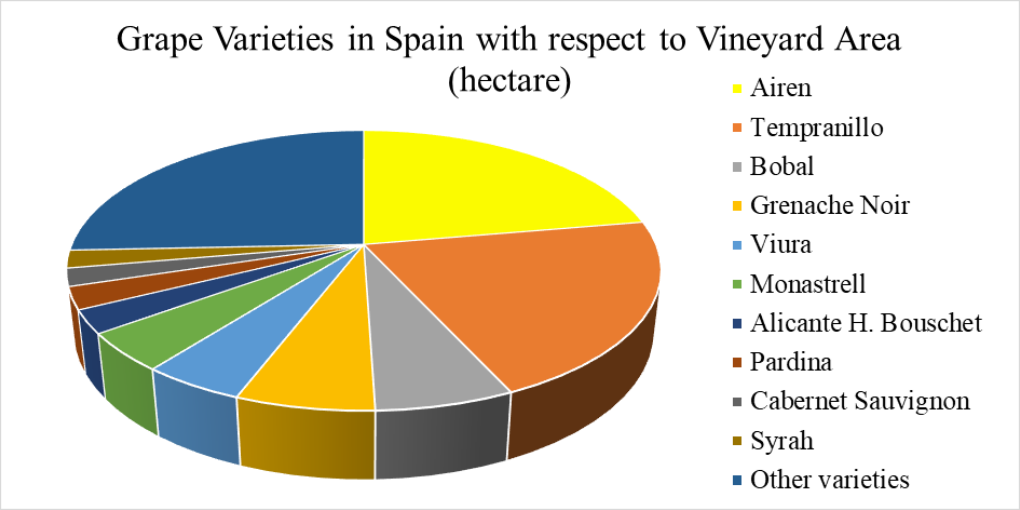


Figure 1.2. Grape Varieties in Spain ("International Organisation of Vine and Wine", 2017*)*

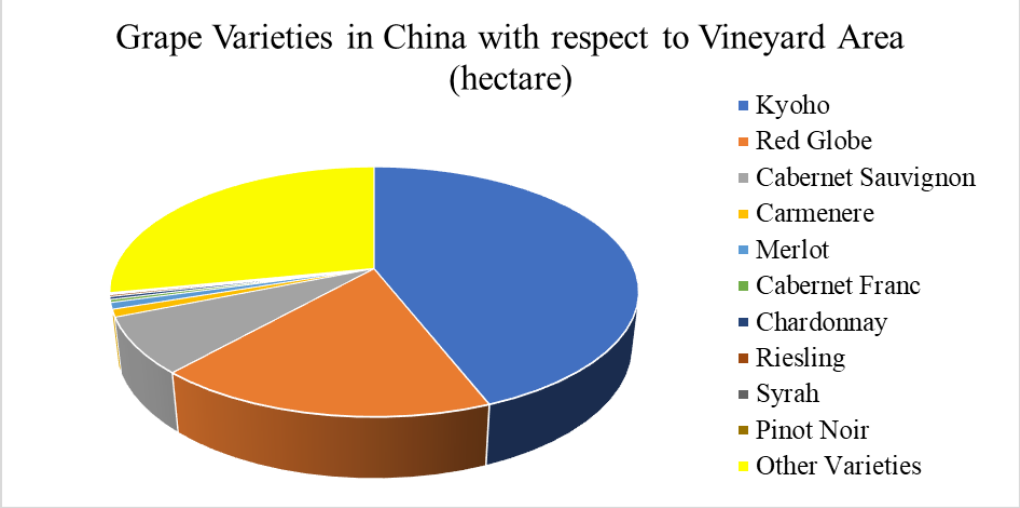


Figure 1.3. Grape Varieties in China ("International Organisation of Vine and Wine", 2017)

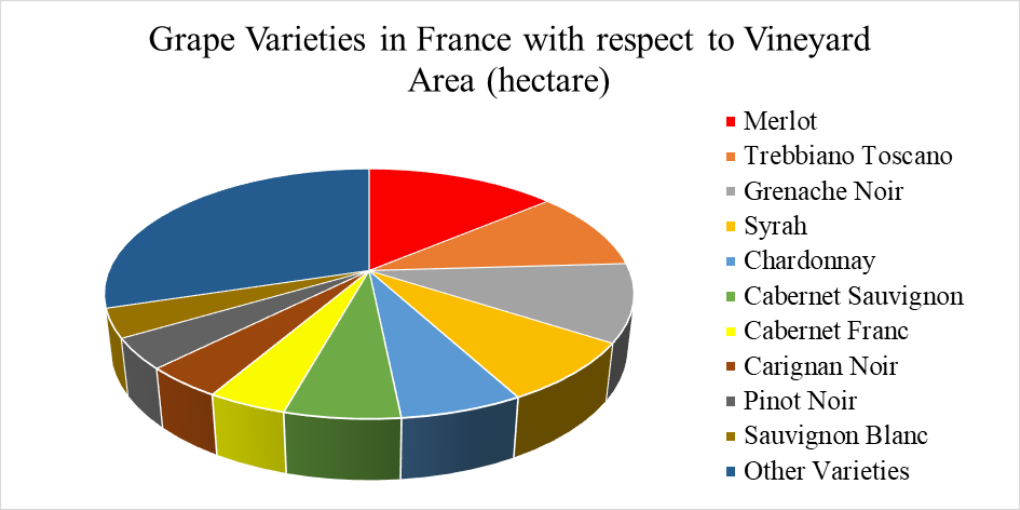


Figure 1.4. Grape Varieties in France ("International Organisation of Vine and Wine", 2017)

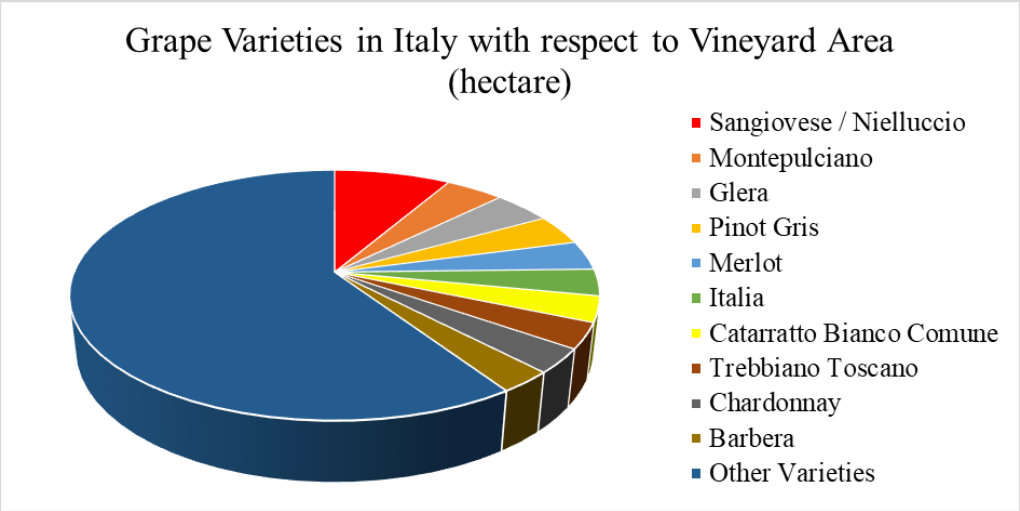


Figure 1.5. Grape Varieties in Italy ("International Organisation of Vine and Wine", 2017)

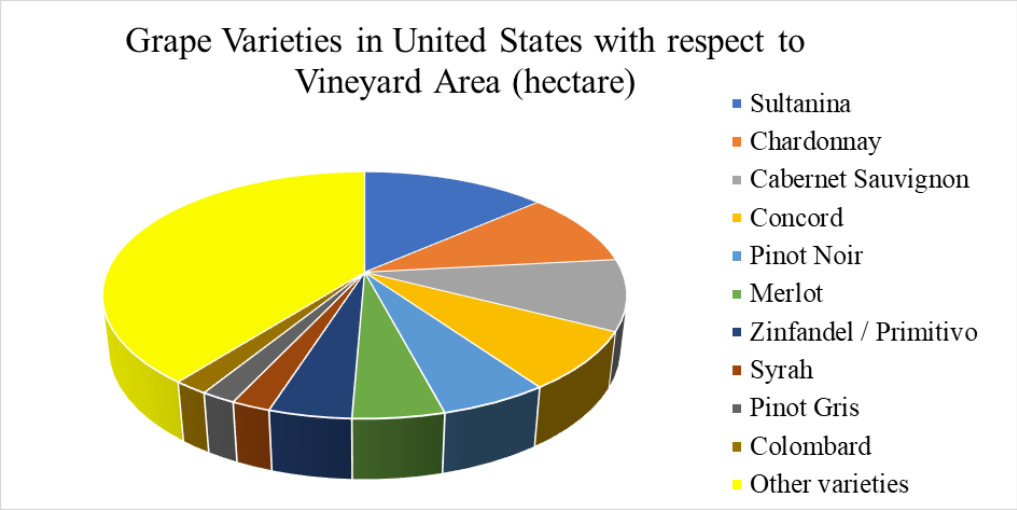


Figure 1.6. Grape Varieties in United States ("International Organisation of Vine and Wine", 2017)

1.1.2. Grape Varieties in Turkey

According to statistic information in 2011, vineyard area is 7,098,755 hectares in the world and 472,545 hectares in Turkey. The capacity of fresh grape is 4,296,351 tons in Turkey while this number is 69,093,293 tons all over the world (FAO, 2012).

According to production area, Turkey is the fifth major producing country (Spain, France, Italy, China, Turkey and USA). In addition, Turkey is the sixth country with respect to the amount of grape production (China, Italy, USA, France, Spain, and Turkey).

Grapes in Turkey separate three parts: fresh (table), dried and wine grapes. The percentages of total grape production are 52.8% for fresh grape, 36.4% for dried grape, and 10.8% of must-wine grape (Karabat, 2014).

There are more than 1200-1500 grape varieties. 600-800 of them are genetically different from each other in Turkey. The number of produced wine grape varieties is around 30: Adakarası, Alicante Bouchet, Boğazkere, Bornova Misketi, Cabernet Franc, Cabernet Sauvignon, Carignan, Chardonnay, Cinsault, Çalkarasi, Çavuş,

Dimrit, Emir, Gamay, Grenache, Kalecik Karası, Karalahana, Kuntra (Karasakız), Malbec, Merlot, Narince, Öküzgözü, Papazkarası, Petit Verdot, Pinot Noir, Riesling, Sangiovese, Sauvignon Blanc, Semillon, Shiraz, Sultaniye, Tempranillo, Vasilaki, Viognier. 15 of them are Turkey's native grapes: Adakarasi, Boğazkere, Bornova Misketi, Çalkarasi, Çavuş, Dimrit, Emir, Kalecik Karası, Karalahana, Kuntra (Karasakiz), Narince, Öküzgözü, Papazkarası, Sultaniye, Vasilaki. ("Wines of Turkey", 2019). These wine grape varieties and their production areas are shown in Figure 1.7.

Figure 1.7. Grape Varieties in Turkey ("Balkan Pazar", n.d.)

1.1.2.1. Sultaniye

It grows in Denizli and Manisa. It is used for table grape and wine-making. Its wine has light colour and fresh fruity aroma. In addition, it can be made dry or semi-dry wine.

The aroma profile is asparagus, pineapple, mango, pear, floral, lemon, hay, golden and green apples.

1.1.2.2. Öküzgözü

The origin is Elazığ. It also grows in Cappadocia, Ankara and Uşak. It is medium bodied, producing round and fruity wines with tannin and high acidity property. The alcohol range changes between 12.5% to 13.5%. Its wine has floral and fruity aroma.

Therefore, its wine can be drunk easily and also suitable for ageing due to high acidity property. The color of Its wine is light red. It can be blended with Boğazkere grapes.

The aroma profile is raspberry, mint, sour cherry, dark cherry, pomegranate, chocolate, ripe plum, eucalyptus, cardamom.

1.1.2.3. Boğazkere

The origin is Diyarbakır. It also grows in Elazığ, Ankara, Uşak, Manisa, Denizli, and Elmalı. Its wine is full bodied, dense tannin with complex aroma profiles and medium acidity. Its wine reaches balance with ageing.

The aroma profile is raspberry, black cherry, blackberry, pepper, eucalyptus, leather, tobacco, dark chocolate, pine forest, clove, liquor ice.

1.1.2.4. Kalecik Karası

The origin is Ankara. It also grows in Denizli, Manisa, Uşak, Elmalı, and Cappadocia. Its wine has dried red rose colour and a sugar candy flavour. It also has moderate bodies on the palate with low tannins and crunch acidity properties. Its alcohol level is 14% (v/v).

The aroma profile is cherry, red berries, cotton candy, raspberry and strawberry.

1.1.2.5. Narince

The origin is Tokat. It also grows in Cappadocia. It is consumed both table and wine grape. It is suitable for dry or semi-dry wines. Its wine has yellow colour and citrus and fruity flavour. In addition, it has round, moderate to high body properties with balanced acidity. It is suitable for ageing with oak. This ageing process gives a complex flavour in this wine.

The aroma profile is grapefruit, white pineapple, orange, floral, acacia, ripe green apple, quince, walnut, plumeria, lime, basil, fruit blossom.

1.1.2.6. Emir

The origin is Cappadocia. It is used for sparkling and dry wines. Its wine has yellow colour with lively crunch flavour. It has light to moderate bodies with high fragile acidity. It is not suitable for ageing with oak. In addition, it is not designed to malolactic fermentation. It has been drunk within 1 or 2 years.

The aroma profile is pineapple, apple, lemon, kiwi, white rose, blood orange.

1.1.2.7. Çalkarası

The origin is Denizli. It is used for rosé wine. Its wine has lightly fruit red colour with high acidity. It has lively and balanced aroma. The alcohol level changes between 12% and 13.5% (v/v).

The aroma profile is strawberry, peaches, ripe white fruits, fresh red fruits.

1.1.2.8. Bornova Misketi

The origin is İzmir. It also grows in Manisa. Its wine has muscat flavour. It has light golden colour with lively aroma. It can be drunk easily. In addition, it can be suitable for dry and sweet wine.

The aroma profile is flowers, tropical fruits, citrus, bay leaves, thyme ("Wine of Turkey", 2019).

The following tables and figure show distribution of the mentioned grape varieties with production capacity and national grape types with their origin and producers (Table 1.2 & 1.3 and Figure 1.8):

Table 1.2. Distribution of Grape Variety in Turkey

Grape Variety	*Grape Colour*	*Usage Area*	*Output (Tons)*
Sultaniye	White	Table and Wine	14000
Shiraz (Syrah)	Black	Wine	11932
Öküzgözü	Black	Wine	11830
Boğazkere	Black	Wine	8850
Kalecik Karası	Black	Wine	6885
Narince	White	Table and Wine	6150
Emir	White	Wine	5500
Çalkarası	Black	Wine	5000
Cabernet Sauvignon	Black	Wine	3125
Merlot	Black	Wine	2840
Sauvignon Blanc	White	Wine	1165
Chardonnay	White	Wine	1135
Bornova Misketi	White	Wine	910

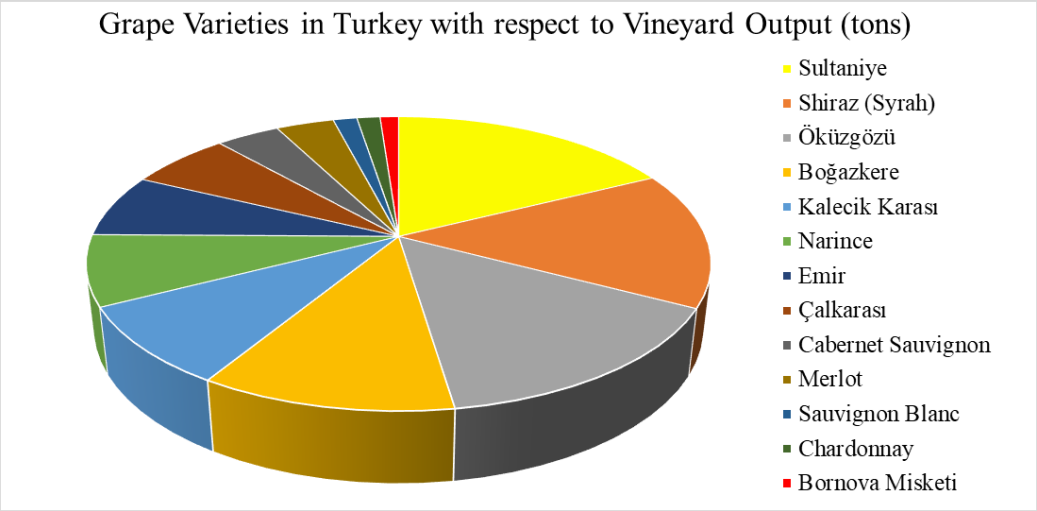


Figure 1.8. Grape Varieties in Turkey

Table 1.3. Origin of Grapes and Winemakers in Turkey

Grape Type	*Origin*	*Winemaker**
Adakarası	Avşa	Büyülübağ
Boğazkere	Diyarbakır	Kavaklıdere, Suvla, Kayra, Doluca, Sevilen, Likya, Turasan, Buzbağ
Bornova Misketi	İzmir	Sevilen, Corvus Vineyards, Kavaklıdere, Nif
Çalkarası	Denizli	Sava, Kavaklıdere
Çavuş	Bozcaada	Corvus Vineyards, Talay Vinification
Dimrit	Kapadokya	Turasan, İllegüp
Emir	Kapadokya	Turasan, Kavaklıdere, Vinolus, Doluca, Kocabağ,Gilamada, Corvus, Yazgan
Kalecik Karası	Ankara	Kavaklıdere, Diren, Vinkara, Kayra, Doluca, Sevilen
Karalahana	Çanakkale	Corvus, Çamlıbağ
Karasakız (Kuntra)	Çanakkale	Suvla, Kocadere, Paşaeli
Narince	Tokat	Kavaklıdere, Doluca, Buzbağ, Kayra, Diren, Vinkara, Sava, Vinolus, Sevilen
Öküzgözü	Elazığ	Kavaklıdere, Diren, Suvla, Doluca, Vinkara, Kayra, Vinolus, Kuzeybağ, Corvus, Kocabağ, Buzbağ
Papazkarası	Tekirdağ	Melen, Chamlija
Sultaniye	Denizli	Kavaklıdere, Doluca, Sevilen,Yazgan, Nif
Vasilaki	Bozcaada	Talay, Çamlıbağ, Corvus

*Winery A.Ş.

1.2. **Wine Yeasts**

1.2.1. Definition of Yeasts

Yeast is a eukaryotic microorganism categorized as fungi in the kingdom and described as single cell fungi which predominantly reproduced by budding or fission. According to type of reproduction, it is classified as ascomycetes (budding), basidiomycetes (fission), and imperfect fungi (Deuteromycetes).

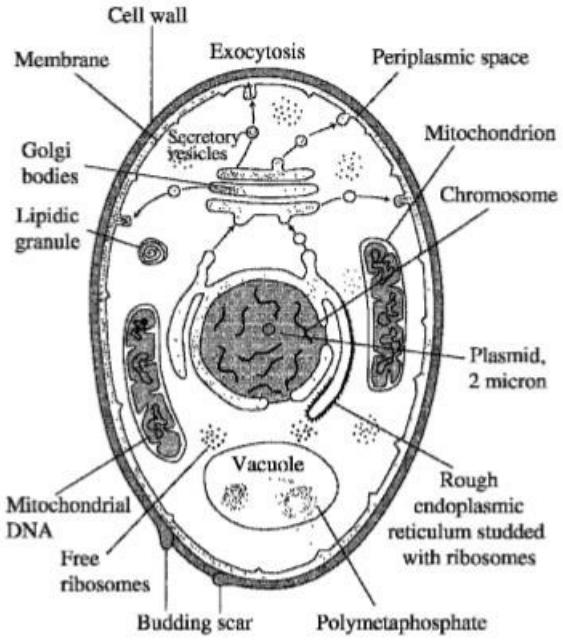


Figure 1.9. Yeast Cell (Gaillardin & Heslot, 1987)

Yeast cell includes cell envelopes, a cytoplasm with different organelles, and a nucleus encompassed by a membrane. Cellular envelope of yeast has a critical role. This is to provide alcohol fermentation successfully and release some components which contribute composition of final wine (Don, 2006).

1.2.2. Taxonomy of Wine Yeasts

Taxonomy of yeast contains classification and identification. Classification refers to indicate similarity or difference with ancestors. Identification demonstrates unknown microorganisms and put it to a group which has similar properties.

Taxonomy categorizes the microorganisms with respect to morphological, physiological, genetic and biochemical properties. The phenotypic properties of yeasts base on spore formation, size and shape of cell, ethnical characters, assimilation and fermentation of sugars and nitrogen sources, cycloheximide resistance (Don, 2006).

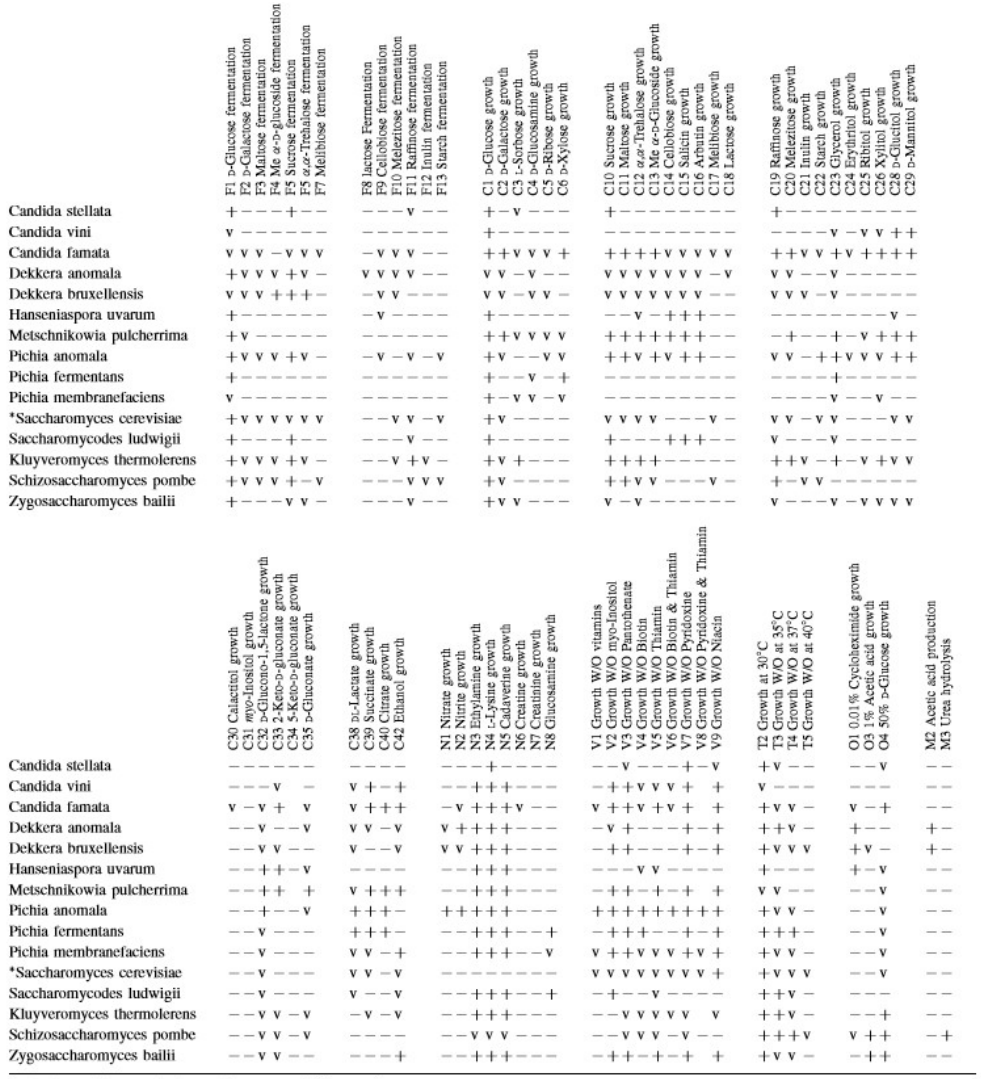


Figure 1.10. Physiological Properties of Wine Yeasts (Barnett et al., 2000)

1.2.2.1. Candida

Candida, represents a very large group in wine, is an anamorphic genus. Its cell appears spherical, ellipsoidal or elongate under the microscope (Meyer et al., 1998).

Reproduction property of this genus is multilateral budding (Fugelsang & Edwards, 2007).

According to the species, sugars and nitrogen sources can be fermented or assimilated. For example, *Candida stellata* can use glucose, raffinose, and sucrose for fermentation and assimilation (Figure 1.10). However, *Candida pulcherrima* can ferment glucose, but assimilate galactose, sucrose, glucose, melezitose, mannitol, maltose (Meyer et al., 1998).

1.2.2.2. Dekkera

The other name is *Brettanomyces.* It is a spoilage microorganism for wine. There are a lot of species such as *D.anomala (B. anomala)*, *D. bruxellensis (B. bruxellensis)*, *B. custersianus*, *B. naardenensis*, and *B. nanus* (Smith, 1998).

Cell shape of *Brettanomyces* is boat-shaped or ogival. In addition, colour of colony in the agar is white to yellowish. This agar can be seen moist, straight, dull or glistening.

According to strains, they can ferment most sugars such as glucose, maltose, sucrose, galactose. *D. anomala* can ferment lactose with respect to strains while *D. bruxellensis* cannot use. This property can be used for identification of species.

1.2.2.3. Hanseniaspora

Cell shape of *Hanseniaspora* is spherical or ovoid for a young microorganism and lemon-shaped or apiculate for an older microorganism (Fugelsang & Edwards, 2007).

There are a lot of species in wine such as *H. uvarum*, *H. guillermondii*, *H. opuntiae.* For example, *H. uvarum* ferments only glucose, but it assimilates glucose, salicin and cellobiose. In addition, *Hanseniaspora* prefers to use fructose instead of glucose (Ciani and Fatichenti, 1999).

1.2.2.4. Metschnikowia

Reproduction property of *Metschnikowia* is multilateral budding. Generally, *Metschnikowia pulcherrima* found in the wine. It ferments glucose while galactose fermentation changes with strain to strain. In addition, it assimilates other sugars such as maltose, galactose, sucrose and lactose. Moreover, this species produces a brown or red pigment in the agar (Pallmann et al., 2001).

1.2.2.5. Pichia

Two species of *Pichia* found in wine: *P.anomala* and *P.membranifaciens*. *P.guilliermondii* found only in must or wine equipment (Dias et al., 2003).

The cell shape appears cylindrical, ovoid or ellipsoidal under the microscopy. In addition, reproduction property of this genus is multilateral budding. Colonies are seen cream or white, wrinkled, and dull on the agar (Fugelsang & Edwards, 2007).

P.anomala and *P. fermentans* ferment glucose while *P.membranifaciens* cannot ferment with respect to strains.

1.2.2.6. Saccharomyces

The cell shape appears ovoid under the microscopy. In addition, reproduction property of this genus is multilateral budding. Colonies are seen smooth on the agar.

Two species of *Saccharomyces* found in wine: *S. cerevisiae* and *S. bayanus. S. cerevisiae* ferments sucrose, glucose and raffinose. In addition, it assimilates glucose, maltose, sucrose, raffinose, but it doesn't utilize lactose. It can also not use five carbon sugars such as pentoses (Fugelsang & Edwards, 2007).

1.2.2.7. Saccharomycodes

The cell shape appears lemon-shaped under the microscopy. In addition, reproduction property of this genus is bipolar budding.

Saccharomycodes ludwigii ferments and assimilates sucrose and glucose.

1.2.2.8. Schizosaccharomyces

The cell shape appears ovoid and cylindrical under the microscopy. In addition, reproduction property of this genus is fission.

S. pombe ferments sucrose, maltose and glucose. In addition, it assimilates maltose, glucose, raffinose, and sucrose. However, it cannot use ethanol and nitrate.

1.2.2.9. Zygosaccharomyces

The cell shape of *Z. bailii* appears cylindrical and ovoid under the microscopy. In addition, reproduction property of this species is bipolar budding.

Z. bailii has alcohol tolerant property. It grows 18% (v/v) ethanol concentration (Thomas and Davenport, 1985).

1.2.3. Isolation of Yeasts

Bacteria and molds grow easily with yeast on standard medium. Therefore, some special mediums are used for isolation of yeasts. In these mediums, bacteria and molds don't grow. Generally, pH level, water activity, antibiotic or fungistatic addition are used for this purpose.

Generally, yeasts grow about 3.7 pH, but they don't resist high pH (4.5-5.0). However, *Schizosaccharomyces* only resist this pH ranges.

Usually, yeasts grow in high sugar concentration (30-50%), but bacteria don't grow in this medium. However, osmotolerant molds grow in this medium. There can be used with a rotary shaker in incubation time to inhibit molds.

A few media containing anti-microbials have been depicted which can be utilized to stifle co-occuring microorganisms. Tetracycline (50 mg/L), chloramphenicol (100-300 mg/L) or a combination of streptomycin sulfate and penicillin G (150-500 mg/L) are most used antibiotics to inhibition. Moreover, biphenyl (150 mg/L), cycloheximide (100-500 mg/L), pimaricin (5-100 mg/L) or cyclosporin A (4-10 mg/L)

can be used for inhibition of fungal (Kurtzman, 2011; Zott, Miot-Sertier, Claisse, Lonvaud-Funel, & Masneuf-Pomarede, 2008).

Selective media can also be used for specific yeast isolation. For example, the media including cycloheximide and sorbic acid (pH 4.8) can be used for *Dekkera* (Van der Walt and Van Kerken, 1961). Moreover, the medium including methanol, cycloserine and penicillin G can be utilized for inhibition of bacteria and isolation of yeast which use methanol (Van Dijken and Harder, 1974). In addition, lysine medium can be used for isolation of non-*Saccharomyces* (van der Aa Kühle & Jespersen, 1998), and ethanol sulfate agar (ESA) which containing 10 % (v/v) ethanol and SO_2 can be utilized for isolation of *Saccharomyces* (Kish, Sharf, & Margalith, 1983).

In our study, yeast isolation methods were used according to according to Zott et al., Kish et al., and van der Aa Kühle et al. as described in detail in part 2.2.2.

1.2.4. Identification of Yeasts

There are two type methods for identification of yeast: phenotypic identification and genotypic identification.

1.2.4.1. Phenotypic Identification

Phenotypic identification bases on morphological, physiological and biochemical tests. In morphological test, isolated yeasts are looked at the microscope. A yeast can be identified with respect to cell shape. For example, *Saccharomyces cerevisiae* has ovoid cell shape while *Hanseniaspora uvarum* has lemon-shape.

Physiological test bases on carbohydrate fermentation or assimilation properties (Figure 1.10), utilization of nitrogen sources, growth temperature, growth in high sugar concentration, and antibiotic resistances.

In addition, there are some automated systems such as API System, Biolog or Vitek. For example, API system kits provide 20-32 test for growing in wells. Time of reading is approximately between 18 and 24 hours. It can be identified between 42 and 63 species with respect to coding system (Kurtzman, Fell, Boekhout, & Robert, 2011).

1.2.4.2. Genotypic Identification

There are some genotypic identification methods:

- 5.8S- ITS Region Sequencing of Ribosomal DNA
- 5.8S- ITS Region Restriction Fragment Length Polymorphism (RFLP)
- D1/D2 Domain Sequencing of Ribosomal DNA
- Restriction Analysis of Mitochondrial DNA (mtDNA)
- Random Amplification of Polymorphic DNA (RAPD)
- Polymerase Chain Reaction (PCR) Amplification of Variable Regions of the Genome (Microsatellites and Minisatellites)
- Real-Time Polymerase Chain Reaction (q-PCR)
- Polymerase Chain Reaction Denaturing Gradient Gel Electrophoresis (PCR-DGGE)
- Pulsed-Field Gel Electrophoresis (PFGE)
- Amplified Fragment Length Polymorphism (AFLP)

1.2.4.2.1. 5.8S- ITS Region Sequencing of Ribosomal DNA

The ITS region contains the 5.8 rRNA gene coding and the two flanking non-coding and variable transcribed inner spacers (Figure 1.11). ITS1 and ITS2 demonstrate highly variability of interspecific size. However, their intraspecific polymorphism is low. In addition, the extremely conserved sequences of rRNA genes with ITS region enable universal primers to be used for fungi. Therefore, RFLP analysis of 5.8S ITS region is used for identification of *Saccharomyces* and non-*Saccharomyces* yeasts (Guillamön et al., 1998, Esteve-Zarzoso et al., 2009). In addition, the differences between sequencing of ITS regions in rDNA were utilized to identify species of yeast (Christoph & Thomas, 2001; Villa-Carvajal, Querol, & Belloch, 2006). The research study by Chavan et al. (2009), has demonstrated that *Saccharomyces* and non-*Saccharomyces* yeasts were identified by 5.8S ITS sequencing of rDNA.

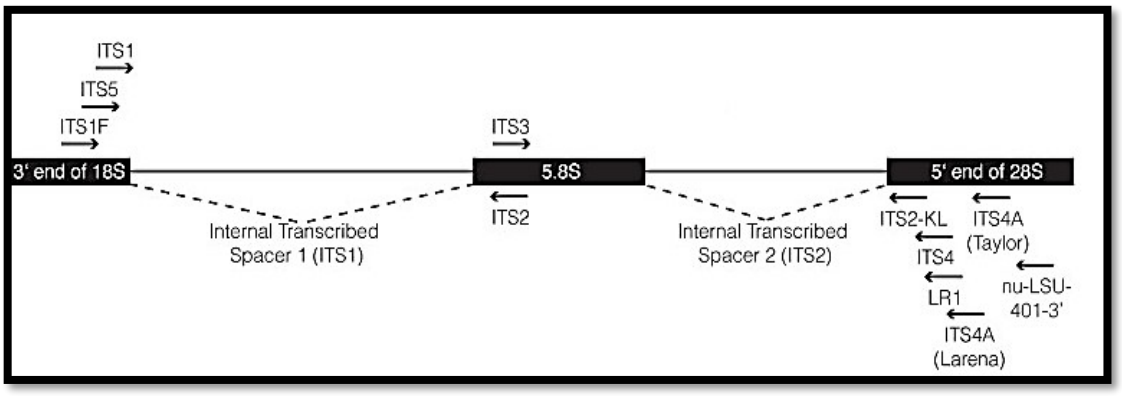


Figure 1.11. Primers of Internal Transcribed Spacer (ITS) Regions. SSU, small subunit (18 S); LSU, large subunit (25-28 S) (Nelsen, M. P., 2018)

The following sequences show the used ITS1 and ITS4 primers:

ITS1 5' TCCGTAGGTGAACCTGCGG 3'

ITS4 5' TCCTCCGCTTTATTGATATGC 3' (Chavan et al., 2009; White et al., 1990)

PCR amplicons with respect to ITS1-5.8S rDNA-ITS2 are different for each species. The following table shows amplicons of some wine yeasts (Table 1.4):

Table 1.4. The ITS1-5.8 rDNA-ITS2 PCR Amplicons of Yeasts (Ghosh, 2017; Pham et al., 2011).

Yeasts	*ITS1-5.8 rDNA-ITS2 PCR Amplicons (bp)*
Metschnikowia pulcherrima	390
Metschnikowia aff. pulcherrima	390
Pichia fermentans	445
Starmerella bacillaris	475
Dekkera bruxellensis	468
Dekkera anomala	540
Wickerhamomyces anomalus	600
Rhodotorula mucilaginosa	610
Lanchancea thermotolerans	675
Kluyveromyces marxianus	720
Kluyveromyces lactis	740
Hanseniaspora uvarum	747
Hanseniaspora guilliermondii	749
Torulaspora delbreuckii	798
Saccharomyces cerevisiae	842

1.2.4.2.2. D1/D2 Domain Sequencing of Ribosomal DNA

D1/D2 domain covers 600 nucleotides in the sequence (Guadet et al., 1989). According to this domain, *Saccharomyces* and non-*Saccharomyces* can be identified (Kurtzman & Robnett, 1998). The research studies by Baleiras-Couto et al. (2006, 2010), demonstrated that wine yeast species were examined by restriction profiles of D1/D2 domain in the large unit of ribosomal DNA. In addition, sequencing of this domain has facilitated identification of species accurately and rapidly (Hesham et al., 2014). This identification method was used for *Saccharomyces* (Hesham et al., 2011), *Kluyveromyces* (Belloch, Barrio, Garcia, & Querol, 1998), and other wine yeast species (Guillamon, Sabate, Barrio, Cano, & Querol, 1998) (Table 1.5).

The following sequences show the used NL1 and NL4 primers (Figure 1.12):

NL-1 5' GCATATCAATAAGCGGAGGAAAAG 3'

NL-4 5' GGTCCGTGTTTCAAGACGG 3' (O'Donnell, 1993).

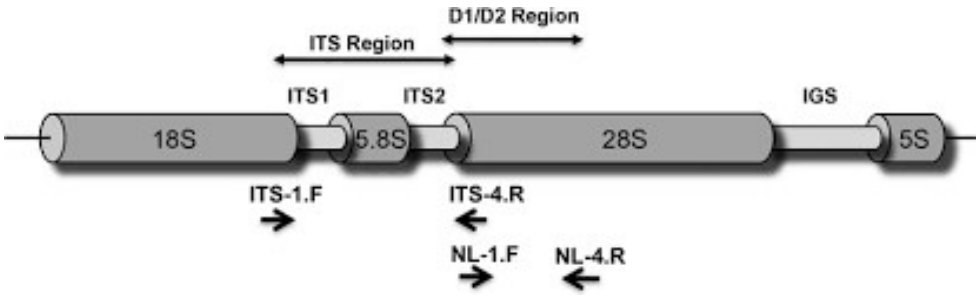


Figure 1.12. ITS Region and D1/D2 Domains of rRNA (Romanelli, Fu, Herrera, & Wickes, 2014)

Table 1.5. Used Identification Methods in the Literature (Fernandez-Espinar, Llopis, Querol, & Barrio, 2011)

Studies	*Used Methods*	*References*
NS and S	ITS Region and D1/D2 Domain	Tofalo et al. (2009)
NS	ITS Region	Zott et al. (2008)
NS	D1/D2 Domain	Romancino et al. (2008)
NS and S	ITS Region	Rodriguez et al. (2004)
NS and S	ITS Region	Esteve-Zarzoso et al. (2001)
S	ITS Region	Fernández-Espinar et al. (2000)
NS and S	ITS Region	Guillamon et al. (1998)

NS: Non-*Saccharomyces;* S: *Saccharomyces.*

1.2.5. Diversity of Indigenous Non-*Saccharomyces* Yeasts Isolated from Musts of Grapes

Indigenous non-*Saccharomyces* yeasts play role in wine quality due to metabolites they produced (Jolly, Augustyn, & Pretorius, 2006). These yeast strains indicate differences in their desirable characteristics according to regions from which they are isolated. The following table shows diversity of indigenous non-*Saccharomyces* yeasts according to regions from which they are isolated (Table 1.6):

Table 1.6. Diversity of Indigenous Non-*Saccharomyces* Yeasts According to Regions (Jolly et al., 2006)

Name of Isolated Yeast	*Region or Country*	*Grape Variety*
Brettanomyces bruxellensis (D. bruxellensis)	Tenerife	White Listan
Candida colliculosa (T. delbrueckii)	Catalonia	Macabeo and Grenache
Candida guilliermondii (P. guilliermondii)	Israel	Cabernet Sauvignon
Candida krusei (I. orientalis)	Argentina	Malbec
Candida pulcherrima (M. pulcherrima)	Israel	Cabernet Sauvignon and Muscat d' Alexandrie
	Argentina	Malbec
Candida stellata	Argentina	Malbec
Candida valida (P. membranifaciens)	Argentina	Malbec
Kloeckera apiculata (H. uvarum)	California	Vineyard
	Australia	Riesling, Semillon, Malbec and Hermitage
	Bordeaux	Semillon and Merlot
	Argentina	Malbec
Kloeckera apis (H. guilliermondii)	Spain	Abarino, Godello and Mencia
Kluyveromyces thermotolerans (L. thermotolerans)	Catalonia	Macabeo and Grenache
	Tenerife	White Listan
Rhodotorula mucilaginosa	Western Cape	Grapes
	Spain	Abarino, Godello and Mencia
Pichia anomala (W. anomalus)	Majorca	Chenin blanc
Saccharomycodes ludwigii	Spain	Ribeiro
Zygosaccharomyces bailii	Spain	White and red varieties

In addition to this table, non-*Saccharomyces* yeasts were isolated from different regions recently. In India, 10 different non-*Saccharomyces* yeasts (*Candida quercitrusa, Candida azyma, Hanseniaspora guilliermondii, Hanseniaspora uvarum, Hanseniaspora viniae, Issatchenkia terricola, Issatchenkia orientalis, Pichia membranifaciens, Zygoascus steatolyticus*) were isolated from Bangalore Blue, Cabernet, Zinfandel, Sauvignon Blanc, Chenin Blanc and Shiraz grape varieties (Chavan et al., 2009) while 17 yeast species (*Candida bombi, Candida inconpicua, Candida zemplinina, Candida quercitrusa, Cryptococcus carnescens, Cryptococcus flavescens, Cryptococcus magnus, Hanseniaspora guilliermondii, Hanseniaspora uvarum, Issatchenkia terricola, Issatchenkia orientalis, Metschnikowia pulcherrima, Pichia fermentans, Pichia guilliermondii, Sporidiobolus pararoseus, Zygosaccharomyces bailii, Zygosaccharomyces fermentati*) were identified from Chardonnay, Cabernet Sauvignon, and Merlot grape varieties in China (Li et al., 2010).

Lately, few studies have been carried out to study the non-*Saccharomyces* yeasts isolated from grape and grape must of vineyards in Turkey. Çelik et al. (2017) found 8 different non-*Saccharomyces* yeasts species (*Candida zemplinina, Hansenispora guilliermondii, Hanseniaspora uvarum, Metschnikowia* spp.*, Lachancea thermotolerance, Pichia kluyveri, Pichia occidentalis, Torulaspora delbrueckii*) in Narince grapes from the region Tokat. In addition, 18 non-*Saccharomyces* (*Debaryomyces hansenii, Hanseniaspora guilliermondii, Hanseniaspora uvarum, Hanseniaspora opuntiae, Kluyveromyces marxianus, Metschnikowia chrysoperlae, Metschnikowia fructicola, Metschnikowia pulcherrima, Pichia anomala, Pichia kudriavzevii, Pichia sporocuriosa, Rhodotorula mucilaginosa, Pichia guilliermondii, Pichia sporocuriosa, Issatchenkia terricola, Issatchenkia terricola, Zygoascus hellenicus, Zygoascus meyerae*) species were isolated from grapes which were harvested from Adana, Urla, and Tekirdağ (Ükelgi, 2011). Moreover, Nurgel et al. (2005) found dominant non-*Saccharomyces* yeasts (*Kloeckera apiculate*, *Lachancea thermotolerance*, *Candida pulcherrima*) during fermentation of Emir grapes and

isolated non-*Saccharomyces* yeasts (*Kloeckera apiculata*, *Metschnikowia pulcherrima*, *Candida holmii*, *Candida valida*, *Candida guillermondii* and *Candida sp.*) during alcoholic fermentation of Kalecik Karası grapes. Although this study of yeast flora for Kalecik Karası and Emir grape varieties in the Anatolia region was carried out, a study of yeast populations for five different grape varieties (Kalecik Karası, Öküzgözü, Boğazkere, Dimrit, Emir) taken from three different regions (Ankara, Elazığ and Cappadocia) in Turkey hasn't been conducted yet.

1.2.6. Non-*Saccharomyces* Yeasts Used as a Starter Culture

1.2.6.1. Hanseniaspora guilliermondii

Hanseniaspora genera comes to the forefront of acetate ester producer. A study was carried out by Viana et al. (2008), that 11027 and 11102 strains of *Hanseniaspora guilliermondii* were selected as a starter culture due to ester profile for enological characterization. In addition, different strains of *Hanseniaspora guilliermondii* strongly produce ethyl acetate and 2-phenylethyl acetate which give flowery and fruity aroma in must (Nathalie Moreira, Mendes, Hogg, & Vasconcelos, 2005; Rojas, Gil, Piñaga, & Manzanares, 2003). In addition, some strains of this microorganism have ethanol tolerance like *Saccharomyces cerevisiae*. This microorganism resists up to 25% (v/v) ethanol level (Pina, Santos, Couto, & Hogg, 2004).

1.2.6.2. Hanseniaspora opuntiae

Hanseniaspora opuntiae affects positively wine aroma, especially sensory of wines. this microorganism with inoculation of *Saccharomyces cerevisiae* increases aroma of the wines and gains specific profile in to the wine. A study showed that usage of *Hanseniaspora opuntiae* and *Saccharomyces cerevisiae* var. *bayanus* in Cabernet sauvignon, Chenin Blanc, Rose grapes gave a typical wine flavour. These wines were preferred by consumers due to positive sensory qualities (Assis et al., 2014).

1.2.6.3. Hanseniaspora uvarum

Hanseniaspora uvarum is used microorganism as a starter culture for winemaking process. Although this microorganism causes stuck fermentation, some researchers used this microorganism with sequential or co-inoculation with *Saccharomyces cerevisiae* to use industrial production of wine. This usage decreases volatile acidity component of a wine and gives organoleptic quality to the wine (Tristezza et al., 2016).

1.2.6.4. Rhodotorula mucilaginosa

A study in China showed that *Rhodotorula mucilaginosa* which has a high level of β-glucosidase gave fruity and floral aroma in the wine due to glycosides of C_{13}-norisoprenoids and benzenic compounds (Hu et al., 2016). In addition, *Rhodotorula mucilaginosa* and *Saccharomyces cerevisiae* were used with sequential inoculation in dry white wine to enhance aroma profile. Nerol oxide, certain ethyl and acetates compounds and (Z)-3-hexene-1-ol were found in this mixed fermentation. They gave berry, citrus, floral, sweet and acid fruit aroma in this wine (Wang et al., 2017).

1.2.6.5. Wickerhamomyces anomalus (*Pichia anomala*)

A study of the mixed culture of *Saccharomyces cerevisiae* and *Wickerhamomyces anomalus* showed that this co-inoculation affects quality of cider positively. In addition, it reached same ethanol level as monoculture of *Saccharomyces cerevisiae*. This mixed culture enhanced remarkably higher alcohols, ethyl esters, acetate esters, ketones and aldehydes than pure culture fermentation. It found more desirable than the product of monoculture fermentation (Ye, Yue, & Yuan, 2014).

1.2.6.6. Metschnikowia spp.

Metschnikowia pulcherrima is very use species in this genus. It significantly reduces volatile and total acidity of the wines. This usage of mixed inoculation with *Saccharomyces cerevisiae* affect isoamyl acetate, 2-phenyl ethanol, and medium-chain fatty acids production positively. It also increases polysaccharides content in the wine (Comitini et al., 2011).

1.2.6.7. *Lachancea thermotolerans* (*Kluyveromyces thermotolerans*)

Lachancea thermotolerans and *Saccharomyces cerevisiae* are used for enhancement of acidity and wine quality improvement by simultaneous and sequential fermentation. A study has shown that glycerol and 2-phenylethanol enhanced with co-inoculation of these microorganisms. In addition, spicy aroma and total acidity increased with these two microorganisms using starter cultures (Gobbi et al., 2013).

Lachancea thermotolerans is used a commercial starter culture by Chr. Hansen (Viniflora® SYMPHONY). It is used for improving aroma in white (Riesling, Pinot Blanc, Chardonnay and Pinot Gris) and red (Pinot Noir, Shiraz, Cabernet Sauvignon and Merlot) grapes. It gives tropical fruit and floral aroma (Jolly et al., 2006).

1.2.6.8. *Starmerella bacillaris* (*Candida zemplinina*)

A study was carried out to the molecular and physiological characterization of *Starmerella bacillaris* yeasts isolated from grapes in Italy. This study has shown as this microorganism produced a low amount of acetic acid and ethanol as a high level of glycerol. Therefore, this microorganism is suitable for application of mixed fermentation with *Saccharomyces cerevisiae* for winemaking. In addition, this mixed culture can be used for reduction of ethanol in wine (Englezos et al., 2015).

1.2.6.9. Williopsis saturnus

Williopsis saturnus (*Hansenula saturnus*) produces a significant level of volatile esters, particularly isoamyl acetate and ethyl acetate. Isoamyl acetate gives banana-like aroma in the wine (Wang et al., 2017). Although this non-*Saccharomyces* yeast does not found grapes surfaces and equipment of winery, it produces desirable flavour. *Williopsis saturnus* potentially enhances fruity aroma in the wines which were obtained from characteristics of neutral cultivar. Therefore, *Williopsis saturnus* was used as a starter culture with *Saccharomyces cerevisiae* to produce the wine. Erten and Tanguler (2010) carried out the study of mixed inoculation of *Williopsis saturnus* and *Saccharomyces cerevisiae* in Emir wine.

1.2.7. *Saccharomyces* Yeasts Used as a Starter Culture

Saccharomyces cerevisiae is known as the wine yeast due to an important species in alcoholic fermentation (Tofalo et al., 2013). It converts all sugars in the grapes to ethanol and CO_2 during fermentation process due to ethanol resistance. Therefore, it is an indispensable species for wine-making.

1.2.8. Characterization of Yeasts and Selected Yeasts for Starter Culture

Isolated yeasts should be characterized to be selected as a starter culture for wine-making. The followings show the features of a starter culture:

- Having high alcohol tolerance
- Having SO_2 tolerance
- Having temperature tolerance
- Having pH tolerance
- Producing low level H_2S
- Producing low volatile acid
- Converting sugars to ethanol at suitable rate in the must
- Fermenting all sugars
- Having high fermentation speed
- Producing low level of sulphur dioxide
- Producing low foam
- Having a killer property
- Producing low level of acetaldehyde
- Producing enough level of glycerol
- Settling easily after fermentation (Bağder, 2008; Nikolaou, Soufleros, Bouloumpasi, & Tzanetakis, 2006)

1.3. Fermentation Process

Wine is the result of a complicated biochemical and biological interaction between grapes and various microorganisms such as non-*Saccharomyces* and *Saccharomyces*

yeasts, acetic acid and lactic acid bacteria, other fungi (Fleet, 2003). This process begins to a vineyard and moving through fermentation and ageing.

Yeasts have a critical role in this process because they convert sugar grape to ethanol and carbon dioxide (CO_2). In addition, even though flavour and quality of the wine depend on grape variety directly and other factors such as weather, soil structure, wine making practices, it affects yeasts with products of metabolisms through growth and autolysis (Fleet, 2003; Jolly et al., 2006; Swiegers & Pretorius, 2005). Moreover, maceration process is important for yeasts especially cold maceration. *Saccharomyces* yeasts stand at stationary phase, non-*Saccharomyces* yeasts grow at 4˚C. Therefore, cold maceration provides to flavour improvement and colour extraction (Hierro, González, Mas, & Guillamón, 2006).

Fermentation process occurs by two ways: spontaneous (traditional) or inoculation way.

1.3.1. Spontaneous Fermentation

Spontaneous fermentation occurs without addition of yeasts. It is a traditional method. Yeasts which locate on the grapes or wine equipment's start fermentation process. Therefore, this wine has a unique property. Aroma profile of this wine doesn't appear similar the other parallel wines. Sometimes, it has high quality. However, it can be bad because of dominant spoilage yeasts such as *Dekkera bruxellensis.* In addition, stuck fermentation can occur in this fermentation (Jolly et al., 2006).

This method is not preferable in Turkey excluding homemade wine while this is used by commercially producers in Europe (Pretorius, 2000).

1.3.2. Inoculated Fermentation

Inoculated fermentation is a more reliable method than spontaneous fermentation because the wine can have the wanted properties such as alcohol level or H_2S production level. This quality of wine doesn't change year by year with the help of the used commercial strain.

1.3.2.1. Inoculation of Non-*Saccharomyces* Yeasts

Many studies have shown that non-*Saccharomyces* yeasts contribute to a more complicated aroma and enhanced quality of wine (Maurizio Ciani, Beco, & Comitini, 2006; Henick-Kling, Edinger, Daniel, & Monk, 1998; Romano, Suzzi, Comi, Zironi, & Maifreni, 1997).

A lot of studies have indicated that using non-*Saccharomyces* starter cultures improve the quality of wine especially in a controlled manner (Maurizio Ciani et al., 2006; Erten, 2002; Toro & Vazquez, 2002).

1.3.2.2. Inoculation of *Saccharomyces* Yeasts

Although non-*Saccharomyces* yeasts improve wine quality, generally, they don't complete fermentation because of low level of alcohol tolerance. In other words, non-*Saccharomyces* yeast are not able to convert all sugar in the grapes to ethanol. Therefore, usage of *Saccharomyces* yeast is needed. In addition, *Saccharomyces* plays an important role for final quality and bouquet of the wine (Cocolin, Pepe, Comitini, Comi, & Ciani, 2004).

There are three type of inoculation: pure, sequential or co-inoculation. In pure fermentation, a yeast is added as a starter culture purely. In sequential inoculation, firstly, a non-*Saccharomyces* yeast is added, then, *Saccharomyces cerevisiae* can be added after 4-7 days later with respect to fermentation temperature (Maurizio Ciani et al., 2006). In co-inoculation, non-*Saccharomyces* and *Saccharomyces cerevisiae* are added in the must at the same time (Padilla, Gil, & Manzanares, 2016).

1.3.2.3. Mixed Inoculation

Selected non-*Saccharomyces* and *Saccharomyces cerevisiae* are combined with respect to abilities. These combinations have unique aromatic properties. According to their ability to generate enzymes that improve flavor or alter secondary metabolites concentration, various combinations of mixed starter cultures have been created and analyzed to improve wine quality (Padilla et al., 2016).

There are two mixed inoculation methods: sequential or co-inoculation. These two methods are used by researchers and winemakers. The following table was shown inoculation types and effects of the wine quality for using non-*Saccharomyces* and *Saccharomyces* mixed culture (Table 1.7).

Table 1.7. Effects of Mixed Inoculations (Padilla et al., 2016)

Mixed Inoculation	*Effects*	*Type of Inoculation*	*References*
C. zemplinina & S. cerevisiae	Decreasing acetic acid	Sequential, co-inoculation	(M. Ciani & Ferraro, 1998; Rantsiou et al., 2012)
H. guilliermondii & S. cerevisiae	Increasing acetate ester and sulphur compound	Co-inoculation	(Moreira et al, 2008)
H. uvarum & S. cerevisiae	Increasing acetate ester	Co-inoculation	(Andorrà et al., 2010)
H. vineae & S. cerevisiae	Increasing ethyl ester and acetate	Sequential, co-inoculation	(Medina et al., 2013)
I.orientalis & S. cerevisiae	Deacidification of wine	Co-inoculation	(Kim, Hong, & Park, 2008)
L. thermotolerans & S. cerevisiae	Acidification of wine	Sequential, co-inoculation	(Gobbi et al., 2013b)
M. pulcherrima & S. cerevisiae	Decreasing acetic acid and increasing α-terpineol, ethyl ester, alcohol level	Sequential, co-inoculation	(Comitini et al., 2011; Zohre & Erten, 2002)
P. fermentans & S. cerevisiae	Decreasing acetic acid and increasing alcohol level	Sequential, co-inoculation	(Clemente-Jimenez, et al, 2005; Comitini et al., 2011)
T. delbrueckii & S. cerevisiae	Decreasing acetic acid and increasing alcohol level, ethyl ester, acetate, linalool and α-terpineol	Sequential, co-inoculation	(Azzolini et al, 2015; Comitini et al., 2011)
W. anomalus & S. cerevisiae	Increasing ethyl ester and acetate	Sequential	(Cañas, García, & Romero, 2011)
W. saturnus & S. cerevisiae	Increasing acetate ester	Co-inoculation	(Erten & Tanguler, 2010)
Z. bailii & S. cerevisiae	Increasing ethyl ester	Co-inoculation	(Garavaglia et al., 2015)

1.4. **Aroma Profiles of Wine**

Aroma profile plays an important role in the wine quality. Wine aroma consists of 100s of various compounds with levels varying from 10^{-1} to 10^{-10} g/kg (Rapp & Mandery, 1986). Interaction and balance of these compounds affect quality of wine aroma.

There are three type of wine aroma: primary (varietal) aroma, secondary (fermentation) aroma, and tertiary (bouquet) aroma (Padilla et al., 2016).

1.4.1. Primary Aroma

Primary aroma relates to variety of grape. It affects ripeness of grapes. Primary aroma includes C_{13}-norisoprenoids, terpenes, methoxypyrazines, and volatile sulfur compounds (Ebeler & Thorngate, 2009). Carotenoids is derived by C_{13}-norisoprenoids. Non-floral aroma is given by C_{13}-norisoprenoids, especially β-damascenone and β-ionone (Fang & Qian, 2016). Terpenes found all grape varieties, but especially, it is high level in Muscat and Rhine Riesling (King & Dickinson, 2000). 70 terpenes found in the grape and their wines such as monoterpenoid alcohols (Mateo & Jimenez, 2000). They are α-terpineol, linalool, citronellol, geraniol, and nerol which are widest and stronger participators to aroma of wines (Carrau et al., 2005). In addition, they have low value of thresholds and give floral aroma (Zalacain, Marin, Alonso, & Salinas, 2007). Methoxypyrazines are produced by metabolism of amino acids. They give green, vegetal, and herbaceous aroma in wine (Sidhu et al., 2015). Volatile sulfur compounds also give aromatic thiols in the wine. Especially, it is important for Sauvignon Blanc wine (Bouchilloux, Darriet, & Henry, 1998).

1.4.2. Secondary Aroma

Secondary aroma relates to yeasts and conditions of fermentation. Secondary aroma includes high levels of alcohols, volatile fatty acids, esters, and low level of aldehydes (Rapp & Versini, 1995). In addition, compounds containing sulfur or nitrogen contribute wine aroma.

1.4.2.1. Higher Alcohols

Most aromatic compounds are higher alcohols. They give complex aroma under 300 mg/L concentration level. On the contrary, above 400 mg/L concentration level, they give negative effect on wine (Rapp & Mandery, 1986).

Pure *Hanseniaspora* species produce higher alcohol than its mixed inoculation with *S. cerevisiae* during must fermentation. Moreover, *Zygosaccharomyces* produces low level of high alcohols while *C. zemplinina* produces high level of these alcohols and it exceeds 400 mg/L (Andorrà et al., 2010; Romano et al., 1993).

2-phenylethyl alcohol, especially, gives pleasant aroma in wines and it is a characteristic's property of some non-*Saccharomyces* such as *M. pulcherrima*, *L. thermotolerans*, *C. zemplinina* (Andorrà et al., 2010; Beckner et al., 2015; Josefa María Clemente-Jimenez, Mingorance-Cazorla, Martínez-Rodríguez, Las Heras-Vázquez, & Rodríguez-Vico, 2004).

1.4.2.2. Volatile Fatty Acids

The majority (90%) of volatile fatty acids in wines is acetic acid. The rest of them are butanoic and propanoic acids. Acetic acid gives unpleasant flavour between 0.7 and 1.1 g/L range while 0.2-0.7 g/L is optimal range (Lambrechts & Pretorius, 2000).

Some non-*Saccharomyces* yeasts produce high amount of acetic acids such as *Hanseniaspora*, *Zygosaccharomyces*, and *Schizosaccharomyces pombe* (Mendoza, De Nadra, & Farias, 2007; Snow and Gallander, 1979). However, this property can change strain to strain. For example, strains of *H. uvarum* produce between 0.6 g/L and 3.4 g/L acetic acid (Romano, Fiore, Paraggio, Caruso, & Capece, 2003a). On the other hand, the other non-*Saccharomyces* have a property of low acetic acid production such as *T. delbrueckii*, *L. thermotolerans* and *C. zemplinina* (Comitini et al., 2011). *L. thermotolerans* produces low acetic acid whereas high L-lactic acid. *C. zemplinina* also produces low acetic acid and ethanol whereas high glycerol (Englezos et al., 2015; Rantsiou et al., 2012).

1.4.2.3. Esters

Esters consist of isoamyl acetate, 2-phenylethyl acetate, ethyl acetate, isobutyl acetate, deriving from acetic acid, and ethyl caprylate, ethyl butanoate, ethyl caprate, ethyl caproate, originating from saturated fatty acids of esters. Ethyl acetate is primary ester and has negative effect at 150-200 mg/L concentration (Lambrechts & Pretorius, 2000).

Some non-*Saccharomyces* have capacity of high level of ethyl acetate production such as *Candida*, *Pichia*, and *Hanseniaspora*. *Pichia* and *Hanseniaspora* have similar ethyl acetate production level. In addition, *Hanseniaspora* produces isoamyl acetate and 2-phenylethyl acetate which are esters of fruity acetate. In the species level, *H. uvarum* is generally a successful producer of esters while *H. osmophila* and *H. guilliermondii* give 2-phenylethyl acetate. Moreover, *Rhodotorula* and *Pichia* give isoamyl acetate significantly (Romano et al., 1997; Viana et al.,2008).

1.4.2.4. Aldehydes

Aldehydes give apple-like flavour and their thresholds values are low. The concentration level in the wines changes between 10 mg/L and 300 mg/L (Lambrechts & Pretorius, 2000).

Usually, *Saccharomyces cerevisiae* generates greater concentrations of acetaldehyde (5-120 mg/L) than non-*Saccharomyces* (max 40 mg/L) such as *M. pulcherrima*, *C. krusei*, *H. anomala*, *C. stellate* . *H. uvarum* can produce 25 mg/L acetaldehyde with respect to the strains (Romano, Fiore, Paraggio, Caruso, & Capece, 2003).

1.4.2.5. Phenols

Vinylphenols and ethylphenols are very important compounds for white and red wines, respectively. *p*-coumaric and ferulic acid produce these phenols. They give an undesirable flavour in wines. *Brettanomyces* produces ethylphenol (Lambrechts & Pretorius, 2000). On the other hand, *H. osmophila*, *H. guilliermondii*, and *P.*

membranifaciens produce neither ferulic nor *p*-coumaric acids (Padilla et al., 2016; Viana et al., 2008).

1.5. **The Objectives of the Study**

Starter cultures are the microorganisms used for the production of bakery and dairy products such as cheese and yogurt or fermented alcoholic beverages such as beer and wine. The following table shows international starter culture producers and their products (Table 1.8):

Table 1.8. International Starter Culture Producers

Company Name	*Products*
AB Mauri Food Inc. (Fleischmann)	Baker's yeast
Chr. Hansen A/S	Cheese and dairy products and alcoholic beverages' cultures
LAFFORT® Company	Wine yeast
Lesaffre Yeast Corporation (Red Star)	Wine and baker's yeast
Lallemand Inc.(Lalvin, Anchor)	Beer and wine yeasts
Mangrove Jack's, BSGi NZ Ltd	Beer, cider and wine yeasts
Bio Sunkeen Co., Ltd.	Beer, wine and baker's yeasts
Martin Vialatte	Wine yeast
Angel Yeast Co., Ltd. Gloripan	Baker's yeast
Koninklijke DSM N.V.	Cheese and dairy products and alcoholic beverages' cultures
Dow Inc. (DuPont (Danisco, Holdback))	Cheese and dairy products' cultures
Biolacter Inc	Cheese and dairy products' cultures
Proxis Développement Sas (Bioprox)	Lactic starter cultures for cheese, yogurt, fermented milk, butter, bakery and oenology

On the other hand, there is only one starter culture producer in Turkey. Pak Food Production and Marketing Inc. (Pakmaya) produces bakery yeasts. However, there are no starter culture producers for winemaking in Turkey.

Traditional wine is the product of spontaneous fermentation by indigenous yeasts in the grapes. Although this wine process doesn't achieve standard properties of wine due to changes in climate, regions and years, starter culture addition in the wine is preferred. However, technology with starter cultures provides standard and ordinary products. Thus, researchers and winemakers have begun to prefer using native strains as starter cultures to adapt in the native grape must easily and give specific odour properties in this wine (Capece et al., 2010; Cocolin et al., 2004). Native non-*Saccharomyces* species produce authentic wines because they impart significant regional and desirable properties (Jolly et al., 2006). In addition, native *Saccharomyces cerevisiae* strains yield easily in native grape types due to high adaptation properties (Cappello, Bleve, Grieco, Dellaglio, & Zacheo, 2004).

The objectives of this study are:

- To learn about non-*Saccharomyces* and *Saccharomyces* yeast populations in local grapes at different maceration and fermentation times in Turkey
- To isolate non-*Saccharomyces* and *Saccharomyces* yeasts in local microflora of the grapes
- To identify and characterize the isolates
- To select high properties yeasts as starter culture
- To make wine with using selected yeasts and analyze volatile compounds of these wines.

Therefore, this study can provide to encourage using these selected native strains as a starter culture for boutique or industrial wine-making production of native grapes in Turkey.

CHAPTER 2

MATERIALS AND METHODS

2.1. Materials

Commercial *Saccharomyces cerevisiae* starter cultures were Chr. Hansen: Viniflora® Merit and Laffort: Zymoflore VL1 Vin Blanc, used for making commercial red and white wines, respectively.

Yeast extract, peptone from casein (tryptone), lysine agar, lactose, mannitol, maltose, sucrose were purchased from Lab M Limited. Moreover, D-(+)-glucose monohydrate, Biggy agar, agar-agar, cycloheximide were bought from Sigma-Aldrich Chemical Co. In addition, the brand of chloramphenicol and buffered peptone water was VWR International Company.

2.2. **Methods**

2.2.1. Winemaking

2.2.1.1. Source of Grapes and Production

Wines were produced with the traditional method and the commercial method by the using commercial strain. Using different *Saccharomyces cerevisiae* strains cause different taste and aroma profile (Bisson, 2012).

5 different wines were produced from 5 different kinds of grapes: Kalecik Karası, Öküzgözü, Boğazkere, Dimrit and Emir (Figure 2.1). These grapes were gathered different time and provinces as shown in Table 2.1.

Table *2.1.* Grape Variety Collected from Three Different Region from Turkey

Grape Variety	*Region*	*Time*
Kalecik Karası	Ankara (Kalecik)	11.09.2017
Dimrit	Kapadokya, Ürgüp	19.09.2017
Emir	Kapadokya, Ürgüp	29.09.2017
Öküzgözü	Elazığ	01.10.2017
Boğazkere	Elazığ	01.10.2017
Emir	Kapadokya, Ürgüp	19.09.2018
Öküzgözü	Elazığ	21.09.2019

The grapes mentioned in the Table 2.1 could reach Ankara under 24 hours.

Figure 2.1. Grape Varieties Collected from Three Different Region of Turkey

2.2.1.2. Separation of Grapes from Stems and Crushing

Incoming grapes were separated from the stalks and detonated. At this stage, attention was given to blowing the seeds without damaging them. In this way, the bitterness of grape seed was prevented from getting into the must.

Each grape was broken down to 3 immediately after the explosion and the wine production process begun. The first two parallel were used for traditional wine production, the last parallel was used for commercial wine production. In this commercial wine production, concentration of SO_2 was calculated 30 mg/L for adding potassium metabisulphite (Fugelsang & Edwards, 2007). In addition to traditional wines, commercial wines have been obtained with the use of commercial strains. The use of two parallel runs in this phase was intended to prevent any possible

contamination. The purpose of doing commercial wine was to provide positive control. At this stage, samples were taken from each grape variety for measuring specific gravity, pH, temperature, brix, dry matter and isolating yeast.

After crushing of grapes, specific gravity of grapes varies between 1100 and 1090 showed the amount of sugar content of grapes. This refers the potential of alcohol content at the final wine. In addition, pH can be changed between 3.3 and 3.7 (Baker, J. & Clarke, 2012).

2.2.1.3. Maceration

There were two types of maceration in wine making: one was cold maceration and the other was normal maceration. The application of cold maceration is not obligatory, but it applies to enrich the aroma of wine (Hierro et al., 2006).

Therefore, the musts were first kept at 4 °C for 4 days and the specific weights were measured every day by hydrometer. At the end of the 4th day, the specific weights were measured, and after the samples were taken, they were left at the normal maceration stage at 20°C. During this process, the temperature was stabilized at 20°C by help of air conditioner.

In both stages of the maceration, the musts were mixed twice a day in order to get oxygen and prevent growing molds (Figure 2.2).

Figure 2.2. Mixing Process of Must Grapes in The Maceration Stage

2.2.1.4. Inoculation of Commercial Yeast, Fermentation Process, Removal of Pulp

In the traditional wine making process, any inoculation method was not applied. Only in the commercial wine making process, the commercial strain was used for positive control. The brand name of this commercial strain was Viniflora® Merit of Chr. Hansen which is a pure *Saccharomyces cerevisiae* starter culture (Figure 2.3).

Firstly, this starter culture, which had been waiting at 4°C, was weighed according to 1 g yeast/4 L must and secondly, activated with pure water for 10 minutes at 35°C. After that, a little bit must be taken and added this activated culture. Then, it was kept at 35°C for 20 minutes in order to adapt this yeast in must. Finally, this mix was added in the must.

When the red grapes reach the specific gravity between 1010 and 1020, the stage of maceration was terminated, and the must was squeezed with the help of a cheesecloth (Hyma et al., 2011). The must which was removed from the pulp was taken into glass jars and the mouth of the vessel was closed with an airlock to prevent oxygen ingress. Thereafter, alcoholic fermentation started in an anaerobic environment and continued at room temperature of 25 °C until specific gravity reaches 990 which refers to 15% (v/v) and 12% (w/w) alcohol content (Baker, J. & Clarke, 2012).

The first measurements of white grapes were made and after the sample was taken, it was squeezed with the help of a cheesecloth and the mouths were closed with air locks in glass jars to start alcoholic fermentation for an anaerobic environment. Alcoholic fermentation continued at 18°C due to the improvement of specific aroma components of white wines (Çelik et al., 2017). For commercial white wine, Laffort: Zymoflore VL1 Vin Blanc *Saccharomyces cerevisiae* culture was used (Figure 2.4).

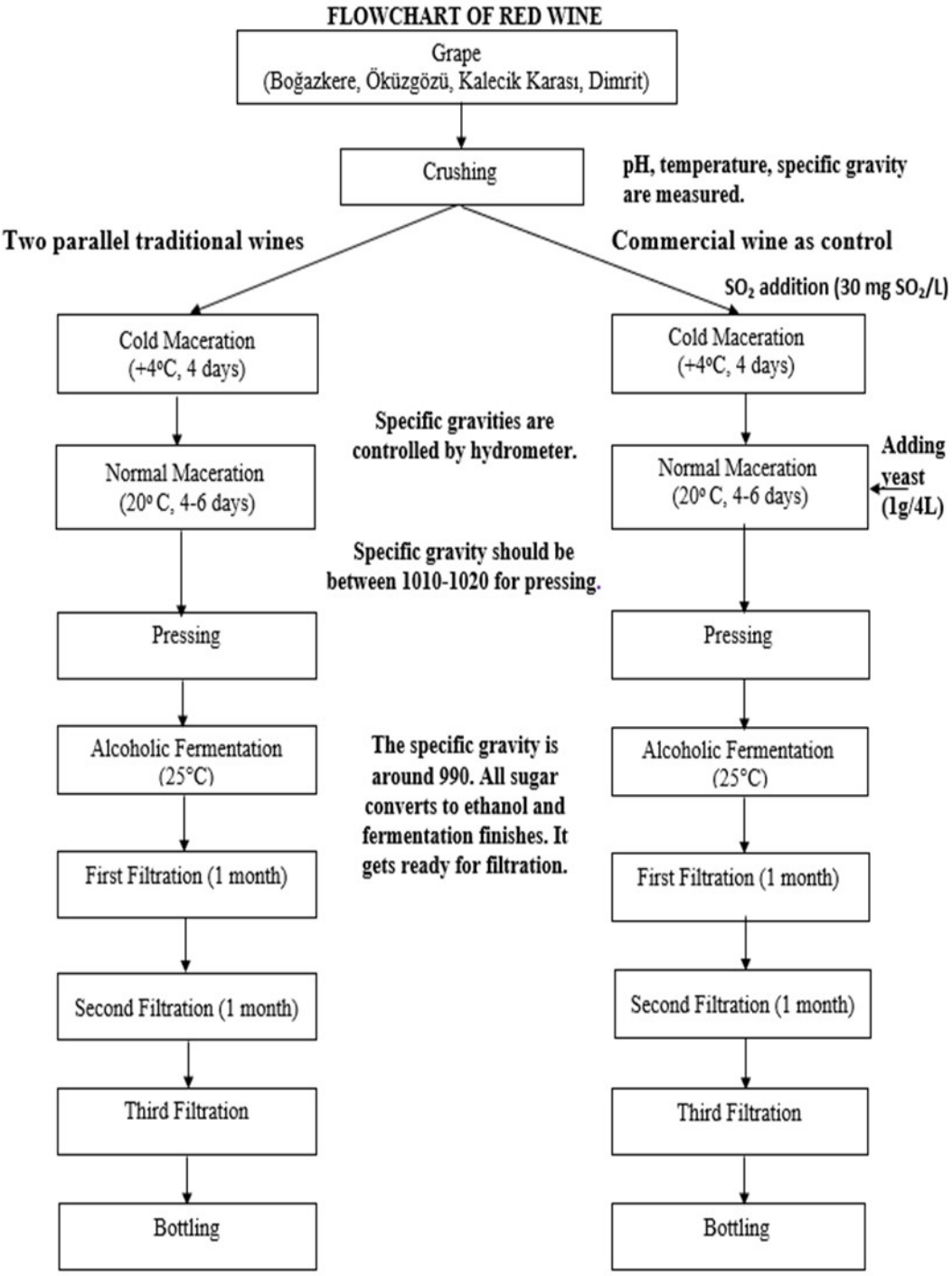


Figure 2.3. Flowchart of Red Wine Making

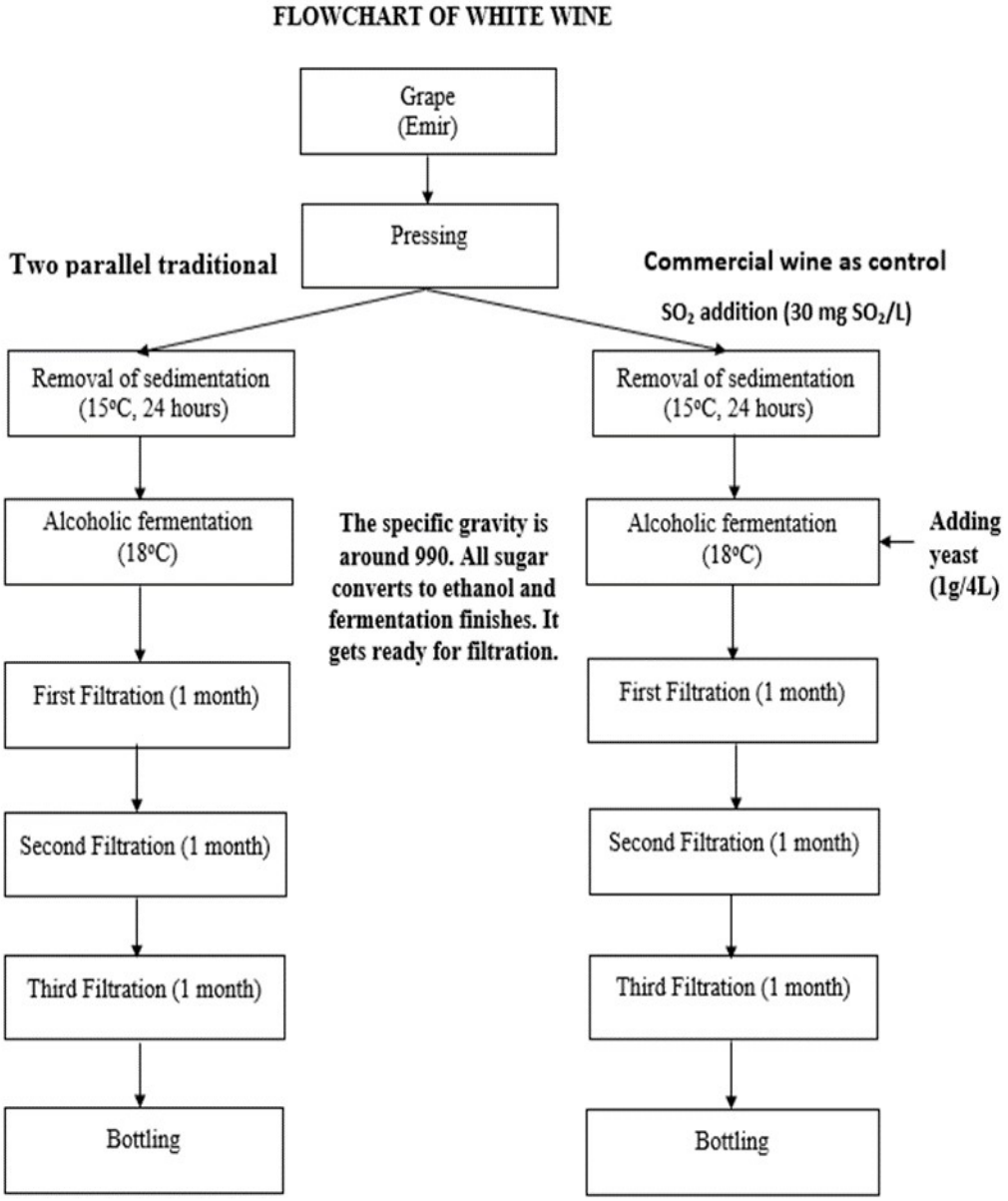


Figure 2.4. Flowchart of White Wine Making

2.2.1.5. Filtration and Bottling

Filtration was applied by siphonage method with 3 times totally in order to clarify the wine. After the filtration process, the wines were taken in green bottles with the help of siphonage method and the cork caps were attached (Figure 2.5).

Figure 2.5. Bottling

2.2.2. Isolation of Non-*Saccharomyces* and *Saccharomyces* Yeasts

The samples were taken at the specified times and diluted with peptone water. In this isolation process, two different media were used for non-*Saccharomyces* and *Saccharomyces* yeasts. The first one was selective mediums for non-*Saccharomyces* yeast. One of the selective mediums non-*Saccharomyces* yeast was yeast extract-peptone-glucose (YPG) agar (10 g/L yeast extract, 10 g/L peptone from casein (tryptone), 20 g/L glucose, 20 g/L agar) supplemented with cycloheximide (1 µg/mL), biphenyl (0.15 g/L of a 7.5 g/L stock solution), and chloramphenicol (0.1 g/L of a 5 g/L stock solution) (Zott et al., 2010). The other medium was lysine agar containing 66 g/L lysine agar, 1 ml potassium lactate, and 0.1 ml of 10% lactic acid (Van Der Aa Kühle & Jespersen, 1998).

The selective medium which was used for *Saccharomyces* was ethanol sulfate agar (ESA) containing 20 g/L glucose, 5 g/L yeast extract, 5 g/L yeast extract, 20 g/L agar, 0.15 g/L sodium metabisulfite, and 10% (v/v) ethanol. (Kish et al., 1983; Heard et al., 1985). Growing microorganisms on these mediums were subjected to purification twice in YPG agar. At the last stage, a single colony was obtained and inoculated on

the liquid medium. Thereafter, stock cultures were made to be 15% glycerol solution and put at -80 ° C (Figure 2.6).

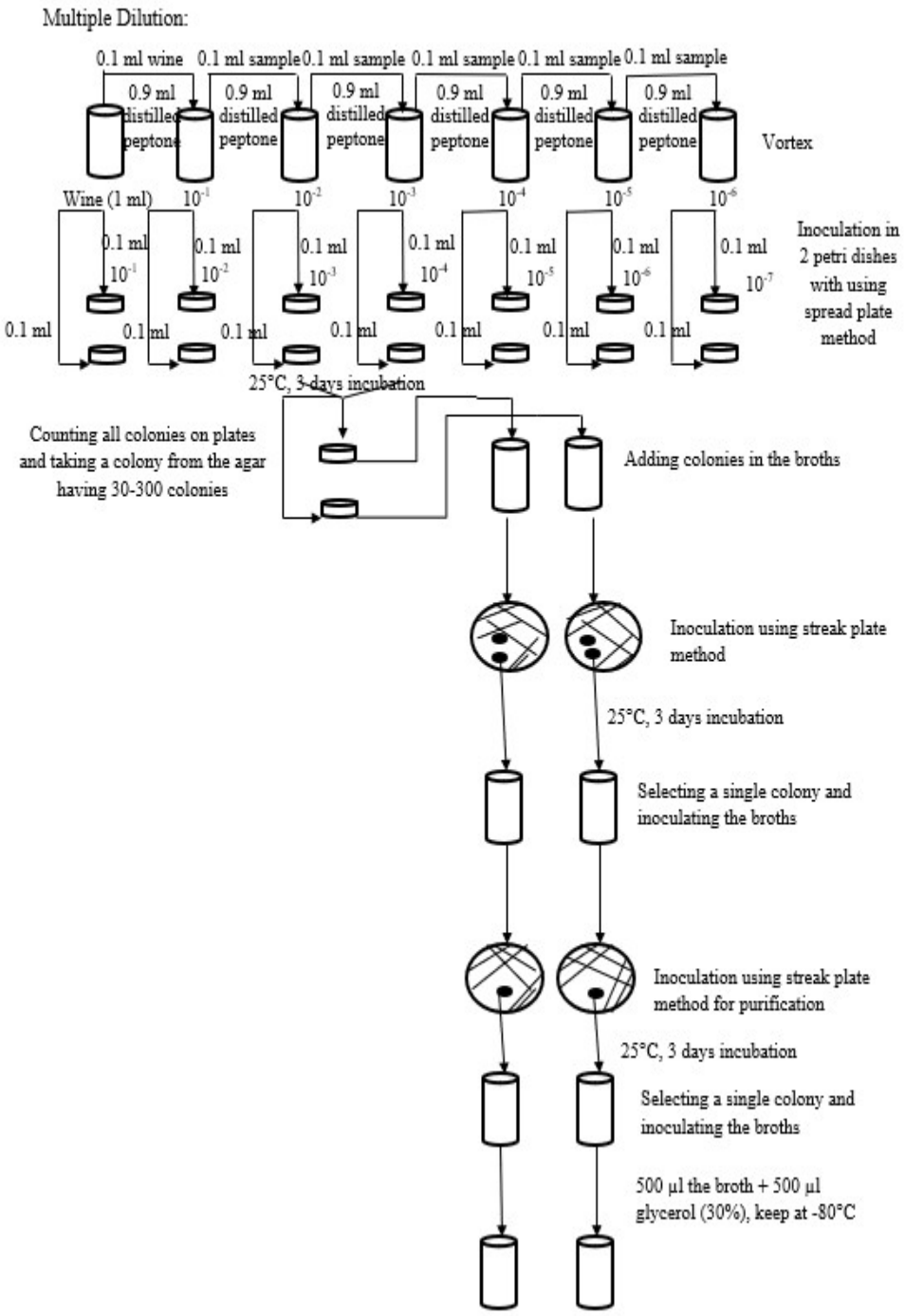


Figure 2.6. Isolation Method of *Saccharomyces* and Non-*Saccharomyces* Yeasts

2.2.3. Identification of Non-*Saccharomyces* and *Saccharomyces* with Molecular and Biochemical Techniques

2.2.3.1. Identification with Molecular Technique

EurX Gene Matrix Bacterial & Yeast DNA isolation kit (E3580) was used for DNA isolation according to the instruction. Spectrophotometric measurements were made on a Thermo Scientific Nanodrop 2000 (USA) instrument in order to check the amount of the DNA and purity. The ratio of absorbance at 260 nm and 280 nm was used to assess the purity of DNA. Approximately, a ratio of 1.8 was accepted as pure for DNA. PCR amplifications were performed using universal primers ITS1 and ITS4 primers. NL-1 and NL-4 primers were used for identification of repeated yeasts.

The following sequences were the used primers for ITS region and D1/D2 domain, respectively:

ITS1 5’ TCCGTAGGTGAACCTGCGG 3’

ITS4 5’ TCCTCCGCTTTATTGATATGC 3’ (Chavan et al., 2009; White et al., 1990)

NL-1 5' GCATATCAATAAGCGGAGGAAAAG 3'

NL-4 5' GGTCCGTGTTTCAAGACGG 3' (O’Donnell, 1993).

The PCR conditions were as follows:

- Initial denaturation at 95 ° C for 5 minutes
- During 35 cycles
  - Denaturation at 95 ° C for 45 seconds
  - Annealing at 57 ° C for 45 seconds
  - Extension at 72 ° C for 60 seconds
- Final extension for 5 minutes at 72 ° C
- The temperature was reduced to 4 ° C and the PCR was completed.

PCR reaction was performed with Solis Biodyne (Estonia) FIREPol® DNA Polymerase, Taq polymerase enzyme. After PCR, Kyratec SuperCycler Trinity (Australia) was used. In agarose gel electrophoresis, a single band was obtained for our samples and PCR was successful. The marker was a 100 bp Solis Biodyne (Estonia) DNA ladder Ready to Load.

In order to purify PCR products, ExoSAP-IT™ PCR Product Cleanup Reagent (ThermoFisher Scientific, USA) was used. Purified PCR products were sequenced with the aid of forward and reverse primers. After gel electrophoresis, sequencing of PCR products was commercially provided by BM Laboratory Systems.

2.2.3.2. Identification with Biochemical Technique

2.2.3.2.1. Carbohydrate Fermentation Test

Isolates were subjected to the test for the property of carbohydrate fermentation. In this test, firstly, isolates were grown in 15 ml YPG (10 g/L yeast extract, 10 g/L peptone from casein (tryptone), 20 g/L glucose) broths at 28˚C. The amounts of cells in the broths were measured in the spectrometer at 600 NM. When OD reached 1 in spectrometer, it refers to 10^6 CFU/ml in the broths. After the number of microorganisms reached 10^6 CFU/ml, they were centrifuged. They were washed twice with autoclaved distilled water in order to get rid of the medium especially glucose.

Moreover, 4.5 g/L yeast extract and 7.5 g/L peptone were dissolved in distilled water and bromothymol blue was added in order to give adequately green color. Bromothymol blue stock solution was prepared 50 mg/ 75 ml with distilled water, and 4 ml of this stock solution was added for 100 ml the medium. After autoclaving, 7.8 g/L glucose, sucrose, maltose, mannitol and lactose were added in each medium separately with filter sterilization.

10 µl microorganism was added in 100 µl medium containing a sugar which was tested in a well. This microtiter plate was incubated at 25 ˚C for 3 days.

Each sugar was tested in duplicate. Positive control contained glucose as a carbon source, while negative control did not contain any carbon sources.

If the microorganism uses the sugar, the color of medium will change from green to yellow at the end of the incubation time as shown in Figure 2.7 and 2.8. (Kurtzman, Fell, Boekhout, & Robert, 2011; Ru, Bernal-grande, Cordero-bueso, & Hughes-herrera, 2017).

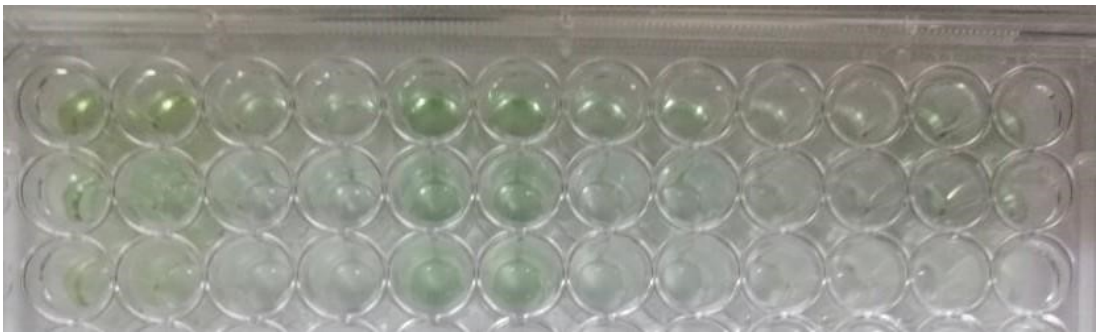


Figure 2.7. Carbohydrate Fermentation Test on Microplate Before Adding the Microorganisms (right to left: positive control, sucrose, maltose, mannitol, lactose, negative control)

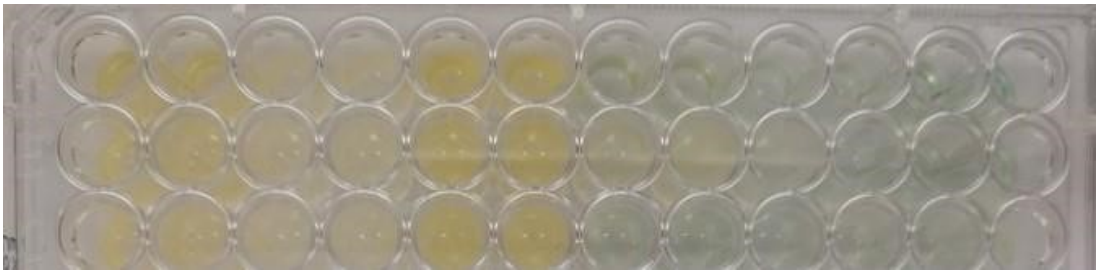


Figure 2.8. Carbohydrate Fermentation Test on Microplate After 3 Days (right to left: positive control, sucrose, maltose, mannitol, lactose, negative control)

2.2.4. Characterization of Non-*Saccharomyces* and *Saccharomyces*

2.2.4.1. Ethanol Tolerance Test

In order to observe alcohol tolerance, firstly, the isolates were grown in the YPG broth for 24 hours at 25°C. After 24 hours, the amounts of cells in the broths were measured in the spectrometer at 600 NM. When OD reached 1 in spectrometer, it refers to 10^6 CFU/ml in the broths. After measuring, 0.1 ml of each having microorganism broth

was added to the YPG broth which contains different ethanol concentrations. These new YPG broths were prepared at 0, 10, 13 and 15% (v/v) ethanol concentrations respectively. Moreover, this test was occurred duplicate. After inoculation, these broths incubated for 3 days at 30°C (Guimarães et al, 2006).

2.2.4.2. Sulfur Dioxide Resistant Test

In order to observe sulfur dioxide resistance, firstly, the isolates were grown in the YPG broth for 24 hours at 25°C. After 24 hours, the amounts of cells in the broths were measured in the spectrometer at 600 NM. After reaching 10^6 CFU/ml in the broths, 0.1 ml of each having microorganism broth was added to the YPG broth which contains different concentration of SO_2. These concentrations are 0, 50, 100, 150, 200 mg/L, respectively. Moreover, this test was occurred duplicate. After inoculation, these broths incubated for 3 days at 30°C (Bağder, 2008).

2.2.4.3. Hydrogen Sulfide Production Test

The isolates were grown in the YPG broth for 24 hours at 25°C. After 24 hours, the samples in broths were inoculated on BIGGY (Bismuth Sulfite Glucose Glycine Yeast) agar (1 g/L yeast extract, 3 g/L sodium sulfite, 10 g/L glycine, 10 g/L dextrose, 5 g/L bismuth ammonium citrate, 16 g/L agar). After inoculation, these broths incubated for 3 days at 30°C (Vicente et al, 2006). The characteristics of H_2S production of the strains were determined according to the colors of the colonies formed on the BIGGY agar; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark-brown, 6: black (Sipiczki et al, 2001). In addition, *Candida* spp. was used for a positive control on the BIGGY agar.

2.2.5. Sequential Inoculation of Non-*Saccharomyces* and *Saccharomyces cerevisiae* in the Wines

2.2.5.1. Sequential Inoculation of *Lachancea thermotolerans*, *Wickerhamomyces anomalus* and *Saccharomyces cerevisiae* in Emir Grapes

Emir grapes were taken from Cappadocia at 2018. These grapes were separated three parts for sequential inoculation our non-*Saccharomyces* and *Saccharomyces cerevisiae* strains, and pure inoculation of our *Saccharomyces cerevisiae* strain. They were added 30 mg/L SO_2 in order to kill all indigenous yeasts and molds. After 24 hours, selected yeasts were inoculated in these grapes.

For sequential inoculation, the microorganisms were grown in the YPG broth at 25°C. After reaching 10^6 cells/ml, our *Lachancea thermotolerans* strain (OB 4.CM NS4) was inoculated for sequential inoculation with respect to the flowchart of white wine (Figure 2.4). After 7 days, our *Saccharomyces cerevisiae* strain (OB 4.CM S1) was added in this Emir must. (Maurizio Ciani et al., 2006). In addition, our *Wickerhamomyces anomalus* strain (KA 0.CM S1) was added with *Saccharomyces cerevisiae* strain in the same way.

For single *Saccharomyces cerevisiae* inoculation, our *Saccharomyces cerevisiae* strain (OB 4CM S1) was inoculated as a single culture after 24 hours of SO_2 treatment.

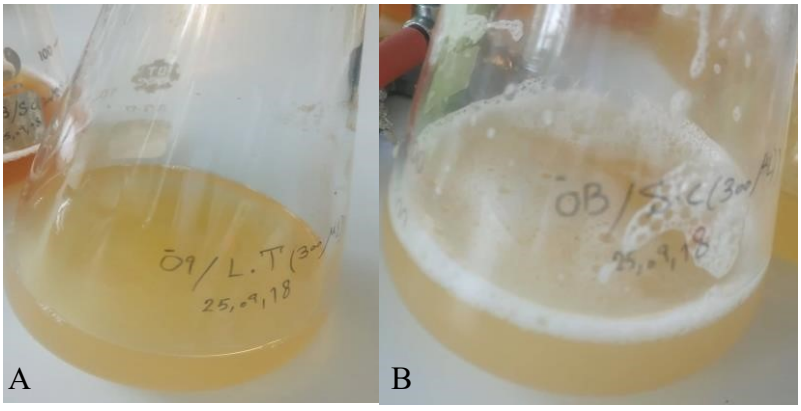


Figure 2.9. YPG Broths with the Selected Yeasts (A: *Lachancea thermotolerans* strain (OB 4.CM NS4, B: *Saccharomyces cerevisiae* strain (OB 4CM S1))

2.2.5.2. Inoculation of *Hanseniaspora uvarum* and *Saccharomyces cerevisiae* in Kalecik Karası Grapes

Kalecik Karası grapes were taken from Ankara at 2017. These grapes were separated into two parts for pure non-*Saccharomyces* (*Hanseniaspora uvarum*) and pure *Saccharomyces cerevisiae* inoculation. These two grapes were added 30 mg/L SO_2 in order to destroy all indigenous yeasts and molds. After 24 hours, selected yeasts were inoculated in these grapes.

The microorganisms were grown in the YPG broth at 25°C. After reaching 10^6 cells/ml, our *Hanseniaspora uvarum* (Strain 1) and *Saccharomyces cerevisiae* (Strain 13) strains were added in Kalecik Karası musts, separately, with respect to the flowchart of red wine (Figure 2.3).

2.2.5.3. Inoculation of *Hanseniaspora guilliermondii*, *Hanseniaspora opuntiae Lachancea thermotolerans* and *Saccharomyces cerevisiae* in Öküzgözü Grapes

Öküzgözü grapes were taken from Elazığ at 2018. These grapes were separated into four parts for sequential inoculation our non-*Saccharomyces* and *Saccharomyces cerevisiae* strains, and pure inoculation of our *Saccharomyces cerevisiae* strain (Table 2.2). They were added 30 mg/L SO_2 in order to kill all indigenous yeasts and molds. After 24 hours, selected yeasts were inoculated in these grapes.

For sequential inoculation, the microorganisms were grown in the YPG broth at 25°C. After reaching 10^6 cells/ml, our *Lachancea thermotolerans* strain (OB 4.CM NS4) was inoculated for sequential inoculation with respect to the flowchart of red wine (Figure 2.3). After 4 days, *Saccharomyces cerevisiae* strain was added in this Öküzgözü must. (Maurizio Ciani et al., 2006). In addition, our *Hanseniaspora guilliermondii* (KA 0.CM NS1) and *Hanseniaspora opuntiae* (KA 0.CM NS2) strains were separately added with *Saccharomyces cerevisiae* strain in the same way.

For single *Saccharomyces cerevisiae* inoculation, our *Saccharomyces cerevisiae* strain (OB 4.CM S1) was inoculated after 24 hours.

Table 2.2. Inoculation of Microorganisms

Microorganisms	*Grapes*	*Inoculation Type*
L. thermotolerans & *S. cerevisiae*	Emir	Sequential Inoculation
W. anomalus & *S. cerevisiae*	Emir	Sequential Inoculation
S. cerevisiae	Emir	Pure Inoculation
H. uvarum	Kalecik Karası	Pure Inoculation
S. cerevisiae	Kalecik Karası	Pure Inoculation
L. thermotolerans & *S. cerevisiae*	Öküzgözü	Sequential Inoculation
H. guilliermondii & *S. cerevisiae*	Öküzgözü	Sequential Inoculation
H. opuntiae & *S. cerevisiae*	Öküzgözü	Sequential Inoculation
S. cerevisiae	Öküzgözü	Pure Inoculation

2.2.6. Wine Analysis

2.2.6.1. Determination of Alcohol, Acid, pH, Volatile Acid, Reducing Sugar and Malic Acid Content

Ethanol, total acidity, pH, volatile acid, reducing sugar and malic acid contents of wine samples were measured with Foss WineScan™ Auto Equipment (Type 79067, Denmark) at Kavaklıdere Winery A.Ş. WineScan™ composes of the analyzer and Foss Integrator software (Figure 2.10 and 2.11).

10 mL of wine samples was put in standard tubes of instrument and analysis of samples started by immersing the specific probe in each sample. Ethanol, total acidity, pH, volatile acid, reducing sugar and malic acid measurement of wine samples were obtained by Foss Integrator software.

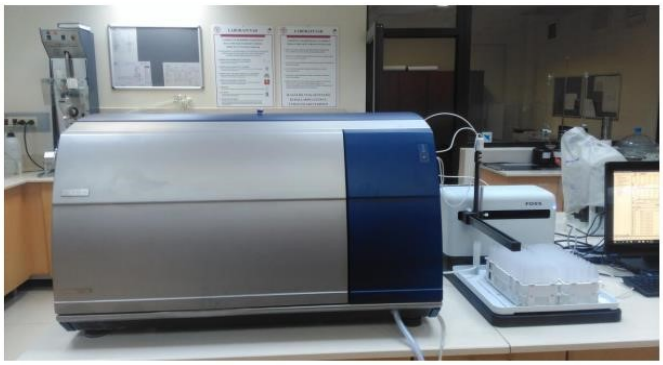


Figure 2.10. Foss WineScan™ Auto Equipment

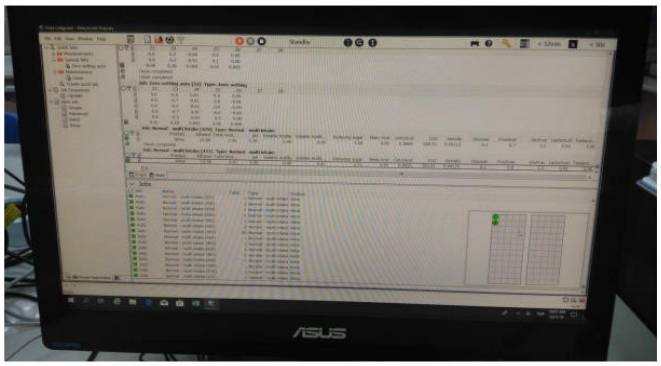


Figure 2.11. Foss Integrator Software

2.2.6.2. Determination of Free and Total Sulphur Dioxide

The amounts of free and total SO_2 were measured by Flastar 5000 Analyzer (Figure 2.12). There were 5 solution boxes in this analyzer. These boxes were dinitro benzoic acid, two buffer solution, diluted HCl, distilled water.

0.74 g sodium disulfide and 50 ml ethanol were mixed, and it covered 500 ml with distilled water to prepare mixture 1.

1, 2, 4, 8, 14 and 20 ml mixture 1 were covered 100 ml with distilled water in volumetric flasks to prepare 10, 20, 40, 80, 140, and 200% SO_2. These volumetric flasks were put in the machine with wine samples.

The program ("Sofia") was opened and total SO_2 graph was drawn (r=0.99).

The references volumetric flashes of 140% and 200% SO_2 were taken off the machine due to measurement of free SO_2. Then, free SO_2 graph was drawn with this software (r=0.99). The results denominated as mg/L.

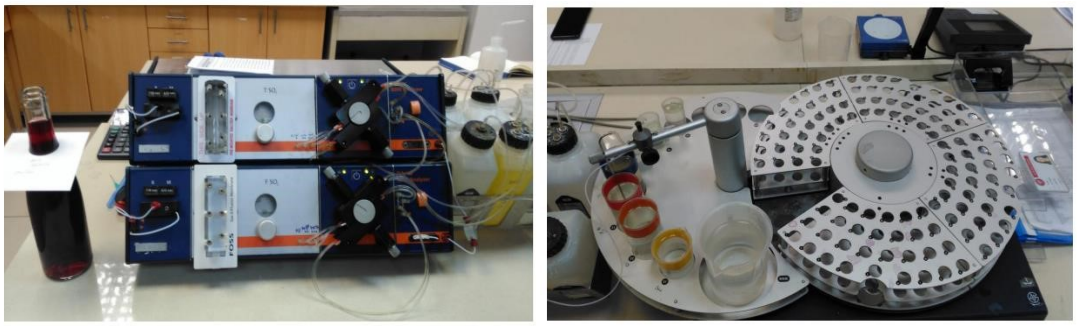


Figure 2.12. Flastar 5000 Analyzer for Determination of Free and Total SO_2

2.2.7. Volatile Compounds and Sensory Analysis of Wines

2.2.7.1. Volatile Compounds

Analysis of volatile compounds was carried out at Prof. Dr. Serkan Selli's Laboratory in Cukurova University.

2.2.7.1.1. Extraction of Volatile Compounds in Wine Samples

Volatile compounds of wine samples were obtained with liquid-liquid extraction method and defined with gas chromatography and mass spectrometry whose brand names are Agilent 6890 GC and 5973 MSD. Extraction was carried out by mixing 45 ml of the sample in a 500 ml Erlene with 40 µg of 4-nonanol (internal standard) and 50 ml of a high purity dichloromethane solvent in a magnetic stirrer at 4-5 ° C for 45 minutes under nitrogen gas. After extraction, the samples were centrifuged at 0°C 5500 rpm for 15 minutes. After centrifugation, water which may be present in dichloromethane and aromatic extract was separated by separatory funnel. It was removed with sodium sulfate and this mixture was concentrated to 1 mL at 40°C in a distillation column of Vigreux. The aromatic extracts were concentrated again to 0.5 ml under nitrogen gas and directly injected into GC-FID, GC-MS systems to

determine the flavoring agents. Extraction was done with three replications (Selli et al., 2007) (Figure 2.13).

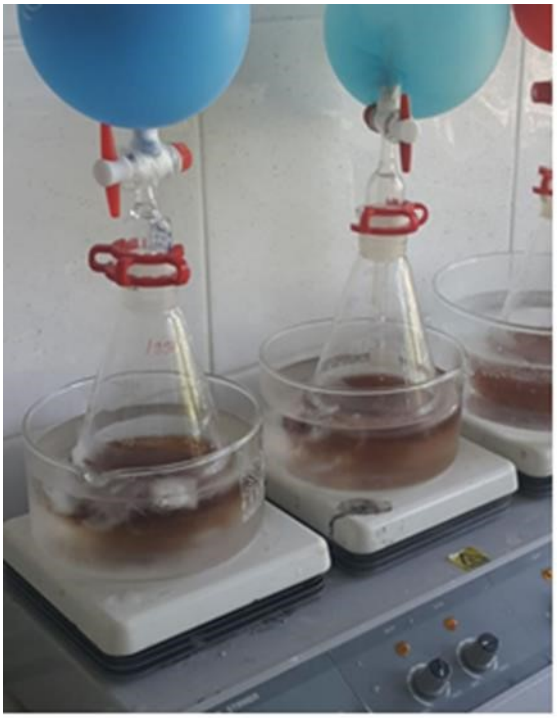


Figure 2.13. Extraction of Volatile Compounds in Wine Samples (Provided kindly by Prof. Dr. Serkan Selli)

2.2.7.1.2. Identification and Quantification of Volatile Compounds

For identification of volatile compounds, Agilent 6890N gas chromatography and Agilent 5975B VL MSD mass spectrometry were used simultaneously. In addition, Agilent 6890N flame ionization detector (FID) gas chromatography was used for quantification of volatile compounds. The separation of the aromatics was carried out using DB-WAX capillary column (60 m x 0.25 mm x 0.4 µm). The injector temperature was at 220°C, detector temperature was 250°C, column temperature was 60°C for 3 minutes. Then, column temperature was increased by 2°C per minute to 220°C and then 3°C per minute to 245°C. This temperature was remained constant for 20 minutes by a program. The amount injected into the device was 3 µl. Helium was

used as the carrier gas and the flow rate was fixed at 1.5 ml/min. Temperatures of detector and injector were 250°C.

For identification of volatile compounds, Agilent 5975B VL MSD mass spectrometry was used. Injector type and temperature program had the same conditions as gas chromatography. The speed of helium used as carrier gas was 1.5 ml/min. The ionization energy of the mass spectrometer was screened at 70 eV, the ion source temperature was 250°C, the quadrupole temperature was 120°C, and it was scanned between 29-350 mass /load (m/e) at the intervals of one second. The peak diagnosis was made by comparing the mass spectrum for the non-standard compounds to the standard mass spectra in the libraries of the aroma substances in the computer memory (Wiley 9.0, NIST-11, and Flavor.2L) and for the standard solution to the standard of for the compounds. After the diagnosis of peaks, concentrations of flavoring substances were calculated according to the following formula according to the internal standard method (Selli et al., 2007). Each analysis was performed with 3 replications.

$$C_i=(A_i/A_{st})\times C_{st}\times RF\times HF$$

C_i: Concentration of the compound

A_i: Peak area of the compound

A_{st}: Peak area of internal standard

C_{st}: Concentration of internal standard (40 µg/50 mL)

RF: Answer factor

HF: Calculation factor (factor for converting the sample amount to L).

2.2.7.2. Statistical Analysis

According to GS-MS results, statistical analyses of volatile compounds in wine were made with the help of MiniTab. The results were evaluated with ANOVA and Tukey's multiple range test. In these tests, the significant level was chosen $P < 0.05$.

2.2.7.3. Sensory Analysis of Wine

Sensory analyses of wines were realized with four degustators. In these analyses, there were 9 criteria: color, flavor, fullness, sweetness, acidness, bitterness, astringency, final astringency, and overall impression. Degustators were graded from 1 (weak) to 5 (strong) with respect to these criteria. Sensory profile was formed in radar charts by Excel Office 365.

CHAPTER 3

RESULTS AND DISCUSSION

3.1. Isolation of Microorganisms

469 microorganisms were obtained with the isolation method. It was thought that 204 of these yeast isolates belong to non-*Saccharomyces*, 265 belong to *Saccharomyces* yeasts. Figure 3.1 showed yeast colonies grown on selective mediums. Non-*Saccharomyces* yeast colonies were grown on lysine agar (A), YPG agar containing cycloheximide, biphenyl, and chloramphenicol (B) and *Saccharomyces* yeast colonies on the ethanol sulfate agar (C). Each colony was randomly picked from these specific agars (Figure 3.2) and streaked on YPG agar for purification (Figure 3.3.).

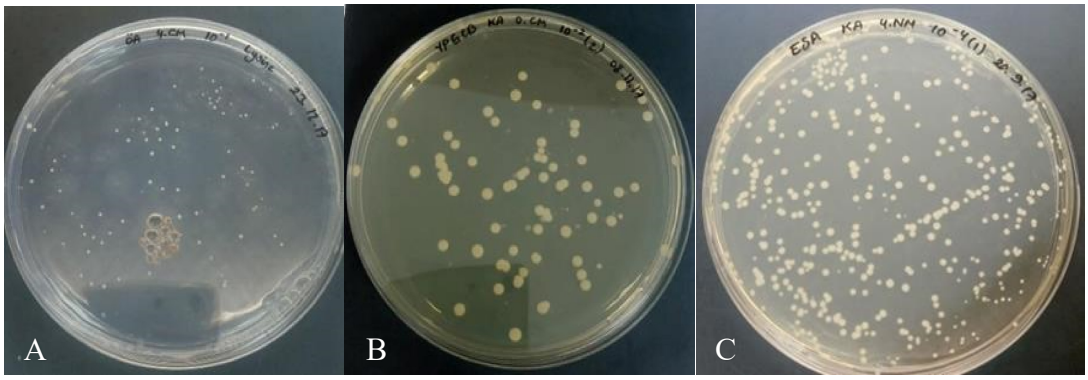


Figure 3.1. Yeast Colonies Grown on Selected Agars (A, lysine agar; B, YPG agar containing cycloheximide, biphenyl, and chloramphenicol; C, ESA)

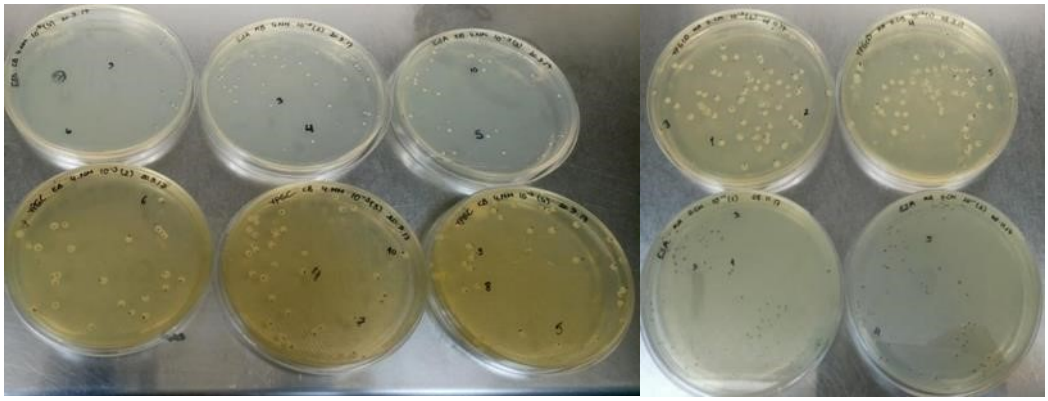


Figure 3.2. Selection and Isolation of Growing Microorganisms in Selective Agars

Figure 3.3. Purification Method of Selected Colonies on YPG Agar

469 microorganisms were obtained with the isolation method. It was thought that 204 of these yeast isolates belong to non-*Saccharomyces*, 265 belong to *Saccharomyces* yeasts (Figure 3.4). The number of isolated *Saccharomyces* and non-*Saccharomyces* yeasts from five different grape varieties of Turkey with using selective mediums (ESA, lysine agar and YPG agar containing cycloheximide, biphenyl, and chloramphenicol) were depicted in Figure 3.5.

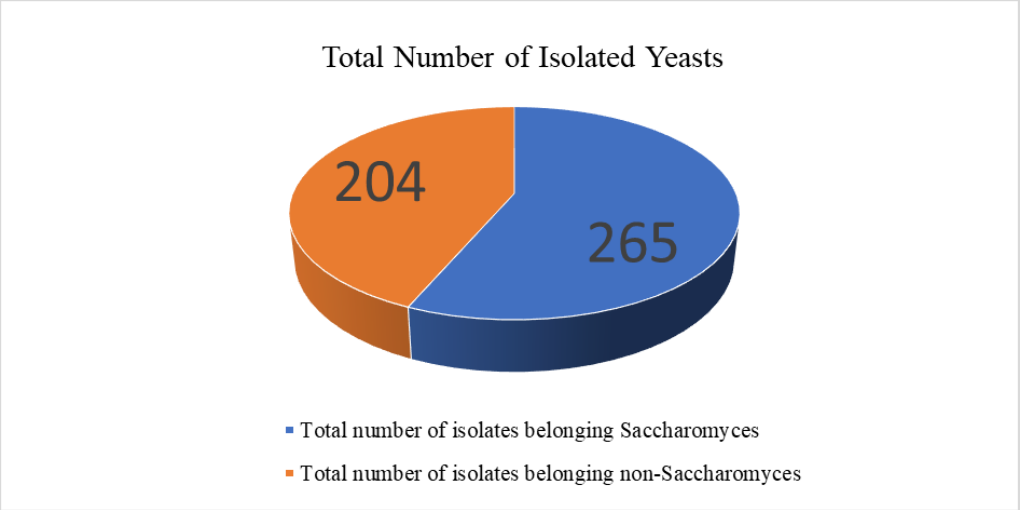


Figure 3.4. Total Number of Isolated Yeasts

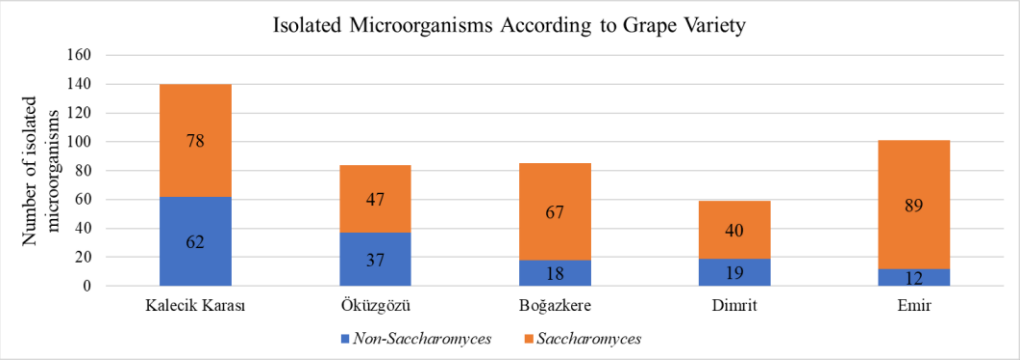


Figure 3.5. Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Yeast According to Grape Variety

Total number of isolated microorganisms were 140 from Kalecik Karası grape. 60 were considered as non-*Saccharomyces*, while 80 as *Saccharomyces* according to isolates from selective agars (YPG agar containing cycloheximide, biphenyl, chloramphenicol, and ESA, respectively) (Figure 3.6.).

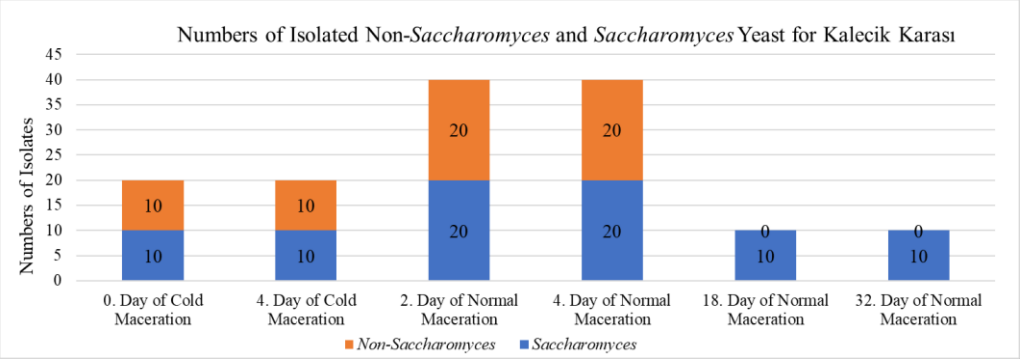


Figure 3.6. Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Y*easts* for Kalecik Karası Grape

Total number of isolated microorganisms were 84 from Öküzgözü grape. 40 were considered as non-*Saccharomyces,* while 44 as *Saccharomyces* yeasts according to isolates from lysine agar and ESA, respectively (Figure 3.7).

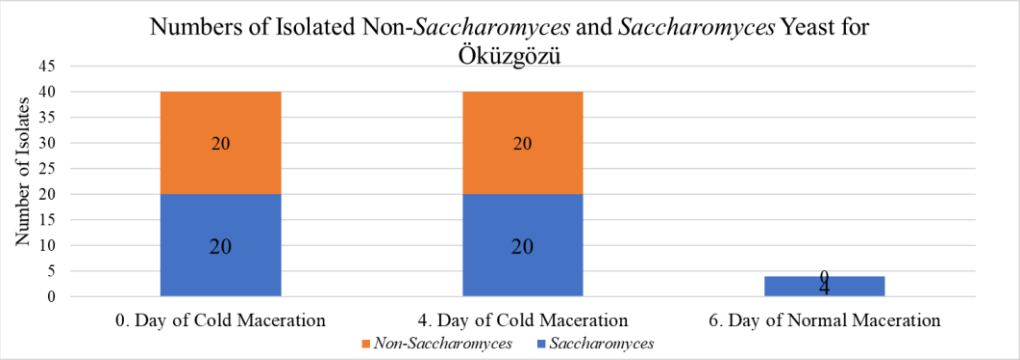


Figure 3.7. Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Yeast for Öküzgözü Grape

Total number of isolated microorganisms were 85 from Boğazkere grape. 41 were considered as non-*Saccharomyces*, while 44 as *Saccharomyces* according to isolates from selective agars (lysine agar and ESA) as depicted in Figure 3.8.

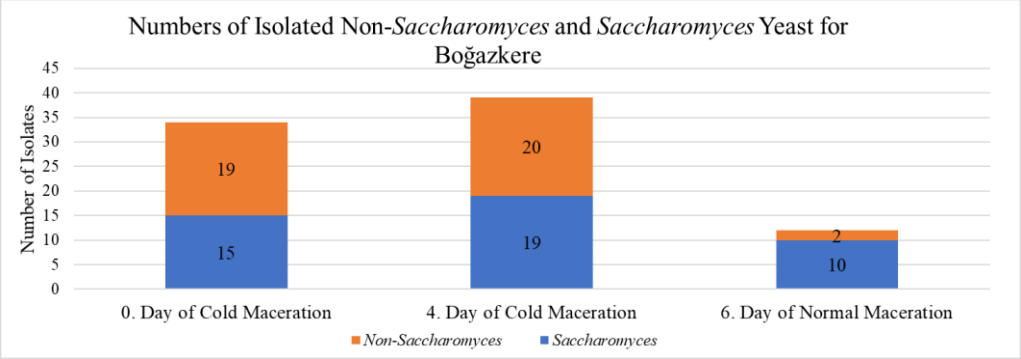


Figure 3.8. Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Yeasts for Boğazkere Grape

Total number of isolated microorganisms were 59 from Dimrit grape. 19 were considered as non-*Saccharomyces*, while 40 as *Saccharomyces* according to isolates from selective agars (lysine agar and ESA) (Figure 3.9).

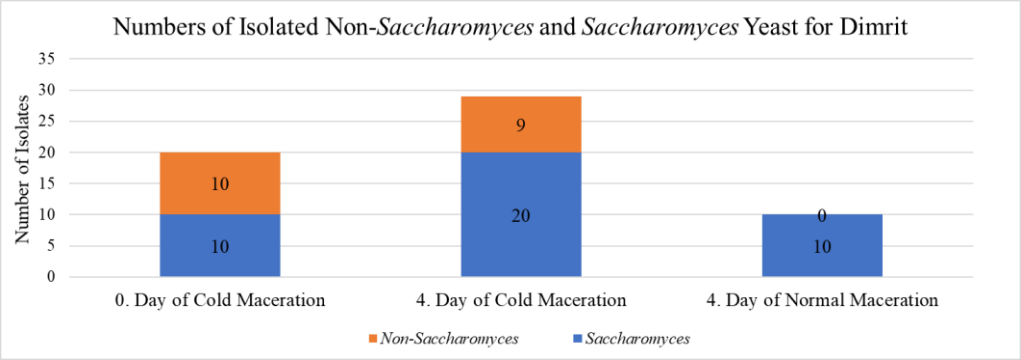


Figure 3.9. Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Yeasts for Dimrit Grape

Total number of isolated microorganisms were 101 from Emir grape. 44 were considered as non-*Saccharomyces*, while 57 as *Saccharomyces* according to isolates from lysine agar and ESA, respectively (Figure 3.10).

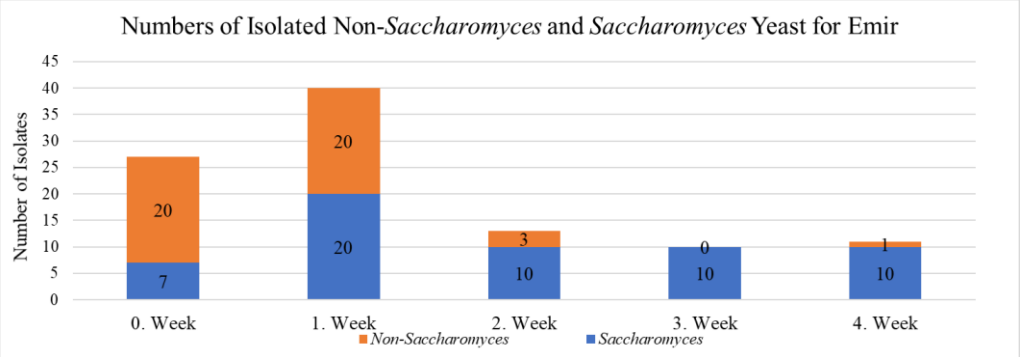


Figure 3.10. Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Yeasts for Emir Grape

3.2. **Phenotypic Characterization of *Saccharomyces* Yeasts**

Firstly, H_2S production test was applied. Biggy agar was used to test of hydrogen sulfide production. Production of H_2S was indicated by the intensity of colours. Low H_2S production was observed for the isolate DA 4.NM S1 (Figure 3.11.A). Another isolate (OB 4.CM S2) from Öküzgözü grape produced intermediate H_2S amount (Figure 3.11.B). Moreover, the commercial *Saccharomyces cerevisiae* was used in order to compare strains. The level of H_2S production of this strain was intermediate (3) (Figure 3.11.C). On the other hand, *Candida* spp. was used as positive control, and the level of H_2S production is high (4) on Figure 3.11.C.

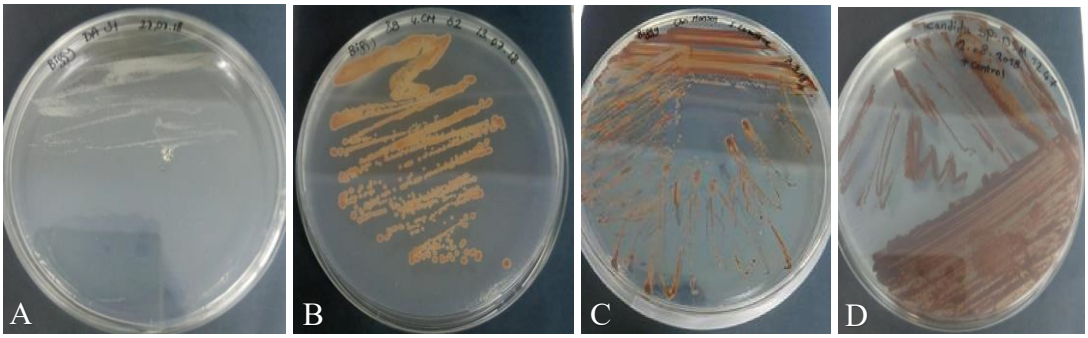


Figure 3.11. Biggy Agars (From left to right these isolates are given 1, 3, 3 and 4 of H_2S production.)

Secondly, test of alcohol tolerance was applied. The results of isolates from Dimrit were given as an example (Table 3.1). The other results of isolates from Kalecik karası, Öküzgözü, Boğazkere and Emir were given in Appendix C.

Table 3.1. The Alcohol Tolerance and H_2S Production Results of *Saccharomyces* Isolates from Dimrit

Name	*Alcohol Tolerance (%)*				*H_2S Production*
	0	10	13	15	
DA 0CM S2	+	+	+	+	3
DA 0CM S3	+	+	+	+	3
DA 0CM S4	+	+	-	-	2
DA 0CM S5	+	+	w	w	2
DA 4CM S1	+	+	+	-	2
DA 4CM S2	+	+	+	w	2
DA 4CM S3	+	+	w	w	2
DA 4CM S4	+	+	+	+	2
DA 4CM S5	+	+	w	w	3
DA 4CM S6	+	w	-	-	2
DA 4CM S7	+	+	w	-	2
DA 4CM S8	+	+	+	w	2
DA 4CM S9	+	w	-	-	2
DA 4CMS10	+	w	-	-	ng
DA 4NM S1	+	+	+	w	1
DA 4NM S2	+	+	+	w	3
DA 4NM S3	+	+	-	-	3
DA 4NM S4	+	+	w	-	3
DB 0CM S1	+	w	w	-	3
DB 0CM S2	+	+	w	-	3
DB 0CM S3	+	+	w	w	4
DB 0CM S4	+	+	+	+	2
DB 0CM S5	+	+	+	w	3
DB 4CM S1	+	+	w	-	3
DB 4CM S2	+	+	-	-	3
DB 4CM S3	+	+	w	-	2
DB 4CM S4	+	+	w	w	3
DB 4CM S5	+	+	w	w	4
DB 4CM S6	+	+	w	w	3
DB 4CM S7	+	+	-	-	2
DB 4CM S8	+	+	w	w	4
DB 4CM S9	+	+	+	w	3
DB 4CMS10	+	+	+	-	3
DB 4NM S1	+	+	w	w	3
DB 4NM S2	+	+	w	w	3
DB 4NM S3	+	+	w	w	4
DB 4NM S4	+	-	-	-	ng
DB 4NM S5	+	+	+	w	3
DB 4NMS6	+	+	w	w	4

DA: A Parallel of Wine Made from Dimrit Grape, DB: B Parallel of Wine Made from Dimrit Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 4NM: 4. Day of Normal Maceration; S: *Saccharomyces*; +: positive growth, w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; ng: not growth.

According to H_2S production, some strains were eliminated. Strains with low level H_2S production were selected for the following tables (Table 3.2-3.6). However, isolates of Öküzgözü were chosen among intermediate level (3) H_2S producing strains due to the lack of low level (1 and/or 2) H_2S producing strains. Then, SO_2, temperature, pH tolerances, and carbohydrate fermentation tests were performed for these low level H_2S producing strains.

In addition, phenotypic properties of all *Saccharomyces* yeasts were given Appendix C.

The number of low H_2S producing *Saccharomyces* strains isolated from Kalecik Karası must and wine was 10 (Table 3.2).

Table 3.2. Phenotypic Characterization and Carbohydrate Fermentation Test Results of S*accharomyces* Strains Isolated from Kalecik Karası Must and Wine

Name	*Alcohol Tolerance (%)*				*SO_2 Tolerance (mg/L)*			*Temperature Tolerance (°C)*				*pH Tolerance*			*Carbohydrate Assimilaton Test*				*H_2S Product*
	0	*10*	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*	
KB 2NM S4	+	+	-	-	+	+	+	+	+	+	w	+	+	+	+	+	-	-	1
KB 4NM S2	+	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
KA 32NM S2	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	1
KA 4NM S8	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
KB 4NM S10	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
KA 4NM S2	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
KA 18NM S2	+	-	-	-	+	+	+	+	-	+	-	-	-	-	+	+	-	-	2
KB 18NM S1	+	-	-	-	w	w	w	+	-	+	-	-	-	-	-	+	-	-	2
KB 18NM S3	+	w	+	+	+	+	+	+	+	+	-	w	w	-	-	+	-	-	2
KB 18NM S4	+	-	-	-	+	w	+	+	+	+	-	w	-	-	-	+	-	-	2

KA: A Parallel of Wine Made from Kalecik Karası Grape, KB: B Parallel of Wine Made from Kalecik Karası Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 2NM: 2. Day of Normal Maceration, 4NM: 4. Day of Normal Maceration, 18NM: 18. Day of Normal Maceration (Middle of the fermentation), 32NM: 32. Day of Normal Maceration (End of the fermentation); S: *Saccharomyces*; +: positive growth, w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black.

The only one strain isolated from Öküzgözü must and wine had low H_2S production (2). Therefore, isolates with intermediate level of H_2S production were added to the following table (Table 3.3). Moreover, the level of H_2S production of commercial *Saccharomyces* strain was also 3.

Table 3.3. Phenotypic Characterization and Carbohydrate Fermentation Test Results of *Saccharomyces* Strains Isolated from Öküzgözü Must and Wine

Name	*Alcohol Tolerance(%)*				*SO_2 Tolerance (mg/L)*				*Temperature Tolerance(°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*
	0	*10*	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*	
OA 0CM NS3	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
OB 0CM S6	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	w	w	3
OA 0CM S10	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3
OB 0CM S5	+	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3
OB 4CM S2	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3
OB 4CM S1	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4

OA: A Parallel of Wine Made from Öküzgözü Grape, OB: B Parallel of Wine Made from Öküzgözü Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration; S: *Saccharomyces*; +: positive growth, w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black.

The low level of producing H_2S *Saccharomyces* strains isolated from Boğazkere and Dimrit musts and wines was represented in Table 3.4 and Table 3.5, respectively.

Table 3.4. Phenotypic Characterization and Carbohydrate Fermentation Test Results of S*accharomyces* strains Isolated from Boğazkere Must and Wine

Name	*Alcohol Tolerance(%)*				*SO_2 Tolerance (mg/L)*				*Temperature Tolerance(°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*
	0	*10*	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*	
BA 0CM NS3	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
BA 0CM NS5	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
BB 0CM NS6	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
BA 4CM NS6	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
BB 4CM S10	+	+	+	w	+	+	+	+	+	+	-	+	+	+	+	w	-	-	2

BA: A Parallel of Wine Made from Boğazkere Grape, BB: B Parallel of Wine Made from Boğazkere Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 6NM: 6. Day of Normal Maceration; S: *Saccharomyces*; +: positive growth, w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black.

Table 3.5. Phenotypic Characterization and Carbohydrate Fermentation Test Results of *Saccharomyces* Strains Isolated from Dimrit Must and Wine

Name	*Alcohol Tolerance(%)*				*SO_2 Tolerance (mg/L)*				*Temperature Tolerance(°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Production*
	0	*10*	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*	
DA 4NM S1	+	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
DA 4CM S3	+	+	w	w	+	+	+	+	+	+	-	w	w	-	+	+	w	w	2
DA 4CM S1	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2
DA 4CM S4	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	w	w	2
DA 4CM S9	+	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
DA 4CM S2	+	+	+	w	+	+	+	+	+	w	-	w	w	-	-	+	w	-	2
DA 4CM S8	+	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
DA 0CM S5	+	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
DA 0CM S4	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	2
DA 4CM S7	+	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2
DA 4CM S6	+	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	2
DB 4CM S7	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2
DB 0CM S4	+	+	+	+	+	+	+	+	+	+	w	+	+	+	-	+	-	-	2
DB 4CM S3	+	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2

DA: A Parallel of Wine Made from Dimrit Grape, DB: B Parallel of Wine Made from Dimrit Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration 4NM: 4. Day of Normal Maceration; S: *Saccharomyces*; +: positive growth, w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black.

The number of low H_2S producing *Saccharomyces* strains isolated from Emir must and wine was 24 (Table 3.6). The highest number of low H_2S producing *Saccharomyces* isolates were obtained from Emir must and wine.

Table 3.6. Phenotypic Characterization and Carbohydrate Fermentation Test Results of S*accharomyces* Strains Isolated from Emir Must and Wine

Name	*Alcohol Tolerance(%)*				*SO_2 Tolerance (mg/L)*				*Temperature Tolerance(°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*
	0	*10*	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*	
EA 3W S4	+	+	-	-	+	+	+	+	+	+	-	+	+	+	-	-	w	w	1
EB 3W S5	+	+	+	w	+	+	+	+	+	+	-	w	+	w	+	+	-	-	1
EA 4W S5	+	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
EA 1W NS5	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
EA 1W NS6	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
EB 1W NS1	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
EB 1W NS7	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1
EA 0W NS5	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 0W NS1	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EA1WNS10	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	-	-	2
EB 1W NS2	+	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 1W NS3	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 1W NS9	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EA 2W NS1	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EA 0W NS9	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EA 3W S2	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2
EA 3W S5	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 2W S5	+	+	+	w	+	+	+	+	+	+	-	+	+	+	-	-	w	w	2
EB 3W S1	+	+	-	-	+	+	+	+	+	+	-	+	+	+	-	+	-	-	2
EB 4W S1	+	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 0W S2	+	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 1W S3	+	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2
EB 1W S5	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	-	-	-	2
EA 3W S3	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	-	-	-	2

EA: A Parallel of Wine Made from Emir Grape, EB: B Parallel of Wine Made from Emir Grape; 0W: 0. Week, 1W: 1.Week, 2W: 2. Week; S: *Saccharomyces*; +: positive growth, w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black.

3.3. **Identification of *Saccharomyces* Yeasts by DNA-Sequencing Methods**

3.3.1. Identification of *Saccharomyces* Yeasts by Sequencing of ITS Region

According to phenotypic properties, selected *Saccharomyces* isolates were identified by sequencing of ITS1-5.8S-ITS2 regions.

The following figure (Figure 3.12) showed PCR products of isolated *Saccharomyces* strains amplified by ITS1 and ITS4 primers. The results of DNA-sequencing for all strains were given in Appendix A.

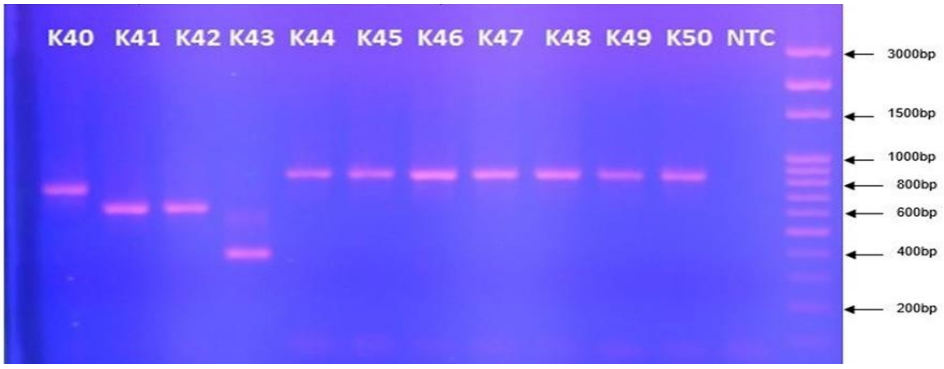


Figure 3.12. PCR Products of *Saccharomyces* Yeasts Amplified by ITS1 and ITS4 Primers. K40, *Hanseniaspora opuntiae*; K41-42, *Wickerhamomyces anomalus* (600 bp); K43, *Metschnikowia* spp.; K44-47, *Saccharomyces cerevisiae* (842 bp); K48-K50, *Saccharomyces cerevisiae* (K, isolates from Kalecik Karası grapes).

3.3.2. Identification of *Saccharomyces* Yeasts by Sequencing of D1/D2 Domain

Contradictory results were obtained for few isolates using the ITS and D1/D2 domain (Table 3.7).

Table 3.7. The Results of Sequencing with respect to ITS Region and D1/D2 Domain

Name	*Region*	*Similarity*	*BLAST Result*	*Name*	*Region*	*Similarity*	*BLAST Result*
K48	ITS	100%	*Saccharomyces cf. cerevisiae/paradoxus*	K48	D1/D2 Domain	100%	*Saccharomyces cerevisiae*
B35	ITS	100%	*Saccharomyces cf. cerevisiae/paradoxus*	B35	D1/D2 Domain	100%	*Saccharomyces cerevisiae*

Fernández-Espinar et al. (2000) has reported that ITS1-5.8S-ITS2 region showed greater interspecific differences than genes of 18S and 26S rRNA. Therefore, ITS region often allowed the differentiation of closely related species. Moreover, ITS region simplified the methodology due to the smaller size compared to D1/D2 domain. It was stated that this situation was also related to *Saccharomyces* genus (Fernandez-Espinar, Esteve-Zarzoso, Querol, & Barrio, 2000).

It was decided to determine the identity of these strains with further identification studies in the future.

3.4. **High Technological Properties of *Saccharomyces* Strains**

According to phenotypic properties, selected isolates of *Saccharomyces* were identified by DNA sequencing methods. Table 3.8 showed these selected isolates with high technological properties (high alcohol tolerance and low hydrogen sulfur production except OB 4 CM S1). OB 4 CM S1 was randomly chosen as *Saccharomyces cerevisiae* strain before phenotypic characterization. It was used for wine production. Although it produced relatively high H_2S (3) product, it has 13% alcohol resistance and high aroma quality was obtained in the wines produced with this microorganism.

Table 3.8. Selected Isolates of *Saccharomyces* with High Technological Properties

Name	*Alcohol Tolerance (%)*			*SO_2 Tolerance(mg/L)*				*Temperature Tolerance(°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*			*H_2S Production*		*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
KA 32NM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	1	Nd	+
KB 4NM S2	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
KB 4NMS10	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
KA 4NM S2	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	Nd	+
EA 1W NS5	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
EA 1W NS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
EB 1W NS1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
EB 1W NS7	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
EB 3W S5	+	+	w	+	+	+	+	+	+	-	w	+	w	+	+	-	-	1	Nd	+
EA 0W NS5	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
EB 0W NS1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
EA 1W NS10	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	-	-	2	+	Nd
EB 1W NS2	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
EB 1W NS3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
EB 1W NS9	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
EA 2W NS1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
EA 0W NS9	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
OA 0CM NS3	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
OB 4CM S1*	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	Nd	+
OB 4CM S2	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	Nd	Nd
BA 0CM NS3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
BA 0CM NS5	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
BB 4CM S10	+	+	w	+	+	+	+	+	+	-	+	+	+	+	w	-	-	2	Nd	+
BB 0CM NS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
BA 4CM NS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
DA 4NM S1	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	Nd	+
DA 4CM S1	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2	Nd	+
DA 4CM S3	+	w	w	+	+	+	+	+	+	-	w	w	-	+	+	w	w	2	Nd	+
DA 4CM S8	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	Nd	+
Commercial	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	Nd	+

KA: Kalecik Karası grape wines A parallel, KB: Kalecik Karası grape wines B parallel; EA: Emir grape wine A parallel, EB: Emir grape wine B parallel; OA: Öküzgözü grape wines A parallel, OB: Öküzgözü grape wines B Parallel; BA: Boğazkere grape wines A parallel, BB: Boğazkere grape wines B parallel; DA: Dimrit grape wines A Parallel, DB: Dimrit grape wines B parallel; 0CM: 0. day of cold maceration, 4CM: 4. day of cold maceration, 4NM: 4. day of normal maceration, 32NM: 32. day of normal maceration (end of the fermentation), 1W: 1. Week, 2W: 2. Week, 3W: 3. Week; S: *Saccharomyces*; +: positive growth , w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; Nd: not determined; *: Randomly chosen *Saccharomyces cerevisiae* was used for wine production, Commercial: Commercial *Saccharomyces cerevisiae* strain.

According to literature, *Saccharomyces cerevisiae* ferments glucose, sucrose and maltose as carbohydrate. On the other hand, it doesn't use mannitol and lactose (Kurtzman *et al.*, 2011.) Although Kurtzman et al. (2011) have reported that *Saccharomyces cerevisiae* ferments sucrose, some of our strains did not utilize sucrose. Moreover, they were identified as *Saccharomyces cerevisiae* by DNA sequencing method. On the other hand, although Guimarães isolated sucrose negative strains, they eliminated these strains (Guimaraes *et al.*, 2006). Similarly, Barnett et al. (2000) emphasized that sucrose, mannitol and maltose may vary from strain to strain. In the light of the contradictory results in the literature, sucrose negative isolates were not selected in Table 3.8 and, strains which have high alcohol tolerance (13% and above 13%) and low H_2S production (1 and 2) were chosen. Ethyl alcohol tolerance higher than 12-13% (v/v) is a desirable technological property for yeasts used as fermentation starters (Vaughan-Martini & Martini, 1998). 29 strains with high technological properties were shown in Table 3.8 and identified by ITS region and/or D1/D2 domain of rDNA sequencing. Therefore, the desired number of yeasts was reached to be used as starter cultures for winemaking.

In addition, isolates with the highest technological characteristics were selected from each type of grapes, and if possible, 2 isolates were selected from these grapes (Table 3.9). Only one isolate from Öküzgözü grape produced a low amount of H_2S and this isolate was selected from this grape variety. Grape varieties of the cultures of this grape, the region-specific characters and authentic features are added to the wine. In addition, it is thought that they will maintain the fermentation process more effectively by being superior to climate and environmental conditions (Jolly et al., 2005). As a result, these isolates will be the strains which can be suggested for the wines to be prepared from the grapes.

The commercial *Saccharomyces cerevisiae* strain was added in Table 3.8 and 3.9 as a reference strain to compare the results.

Table 3.9. Selected High Technological Properties of *Saccharomyces* Strains

Name	*Alcohol Tolerance (%)*				*SO_2 Tolerance (mg/L)*		*Temperature Tolerance (°C)*				*pH Tolerance*			*Carbohydrate Fermentation Test*			*H_2S Production*		*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
KA 32NM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	1	Nd	+
KB 4NM S2	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
EA 1W NS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
EB 1W NS1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
OA 0CM NS3	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	Nd
BA 0CM NS3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	Nd
BB 4CM S10	+	+	w	+	+	+	+	+	+	-	+	+	+	+	w	-	-	2	Nd	+
DA 4NM S1	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	Nd	+
DA 4CM S3	+	w	w	+	+	+	+	+	+	-	w	w	-	+	+	w	w	2	Nd	+
Commercial	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	Nd	+

KA: Kalecik Karası grape wines A parallel, KB: Kalecik Karası grape wines B parallel; EA: Emir grape wine A parallel, EB: Emir grape wine B parallel; OA: Öküzgözü grape wines A parallel, OB: Öküzgözü grape wines B Parallel; BA: Boğazkere grape wines A parallel, BB: Boğazkere grape wines B parallel; DA: Dimrit grape wines A Parallel, DB: Dimrit grape wines B parallel; 0CM: 0. day of cold maceration, 4CM: 4. day of cold maceration, 4NM: 4. day of normal maceration, 32NM: 32. day of normal maceration (end of the fermentation) 1W: 1. Week; S: *Saccharomyces*; +: positive growth , w: weak growth, -: negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; Nd: not determined; *: Randomly chosen *Saccharomyces cerevisiae* was used for wine production, Commercial: Commercial *Saccharomyces cerevisiae* strain.

.

3.5. **Identification of Non-*Saccharomyces* Yeasts by DNA-Sequencing Methods**

3.5.1. Identification of Non-*Saccharomyces* Yeasts by Sequencing of ITS Region

Isolated non-*Saccharomyces* yeasts can be identified by sequencing of ITS1-5.8S-ITS2 regions.

The following figures (Figure 3.13, 3.14, 3.15, 3.16) showed PCR products of isolated non-*Saccharomyces* strains amplified by ITS1 and ITS4 primers.

The results of DNA-sequencing for all non-*Saccharomyces* strains were given in Appendix A.

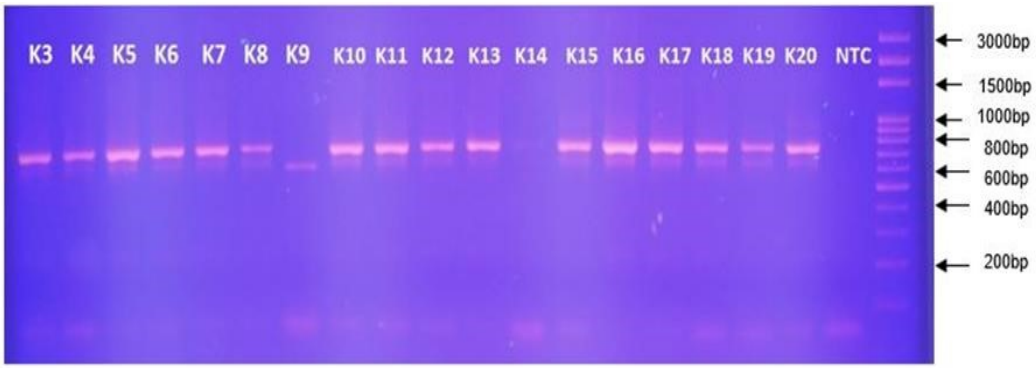


Figure 3.13. PCR Products of Non-*Saccharomyces* Yeasts Amplified by ITS1 and ITS4 Primers. K3, *Hanseniaspora uvarum* (747bp); K4, not identified; K5, *Hanseniaspora guilliermondii* (749 bp); K6, not identified; K7-8, *Hanseniaspora opuntiae*; K9, *Rhodotorula mucilaginosa* (610 bp); K10-12, *Hanseniaspora opuntiae*; K13, *Hanseniaspora uvarum* (747 bp); K14, not identified; K15-20, *Hanseniaspora opuntiae* (K, yeast isolates from Kalecik Karası grapes).

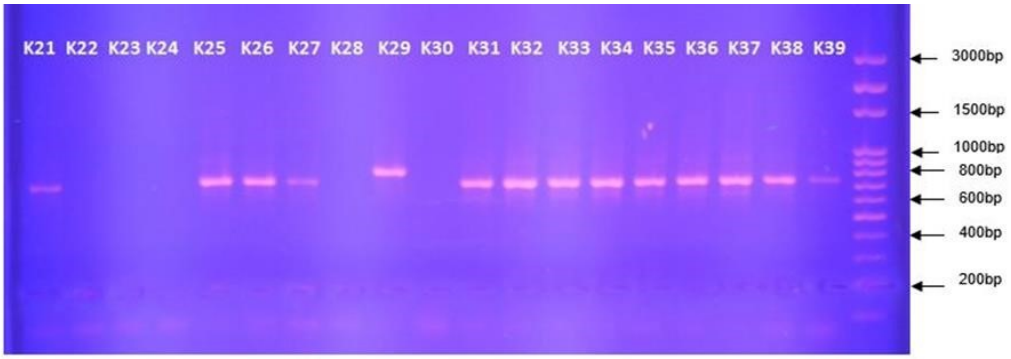


Figure 3.14. PCR Products of Non-*Saccharomyces* and *Saccharomyces* Yeasts Amplified by ITS1 and ITS4 Primers. K21, *Hanseniaspora opuntiae*; K22-24, not identified; K25-26, *Hanseniaspora uvarum* (747 bp); K27, *Hanseniaspora opuntiae*; K28, not identified; K29, *Saccharomyces cerevisiae* (842 bp); K30, not identified; K31, *Hanseniaspora guillermondii* (749 bp); K32, *Hanseniaspora opuntiae*; K33, *Hanseniaspora guillermondii* (749 bp); K34-35, *Hanseniaspora opuntiae*; K36, *Hanseniaspora guillermondii* (749 bp); K37-38, *Hanseniaspora opuntiae*; K39, *Hanseniaspora guillermondii* (749 bp). (K, yeast isolates from Kalecik Karası grapes)

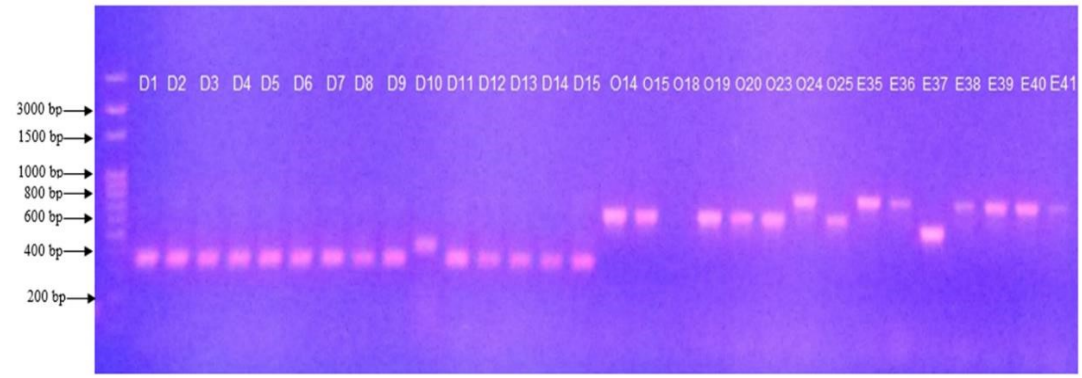


Figure 3.15. PCR Products of Non-*Saccharomyces* and *Saccharomyces* Yeasts Amplified by ITS1 and ITS4 Primers. D1, not identified; D2*, *Metschnikowia* spp.; D3*, *Metschnikowia sinensis*; D4, *Metschnikowia pulcherrima* (390 bp); D5, not identified; D6, *Metschnikowia chrysoperlae*; D7, not identified; D8*, *Metschnikowia* spp.; D9, not identified; D10, *Starmerella bacillaris* (475 bp); D11-14, *Metschnikowia pulcherrima*; D15*, *Metschnikowia* spp.; O14-23, *Lachancea thermotolerans*; O24, *Saccharomyces cerevisiae*; O25, *Lachancea thermotolerans* (675 bp); E35-36, *Saccharomyces cerevisiae* (842 bp); E37, *Wickerhamomyces anomalus* (600 bp); E38-41, *Saccharomyces cerevisiae* (D, yeast isolates from Dimrit grapes; O, yeast isolates from Öküzgözü grapes; E, yeast isolates from Emir grapes).

(*) These microorganisms are identified accurately according to D1/D2 Domain.

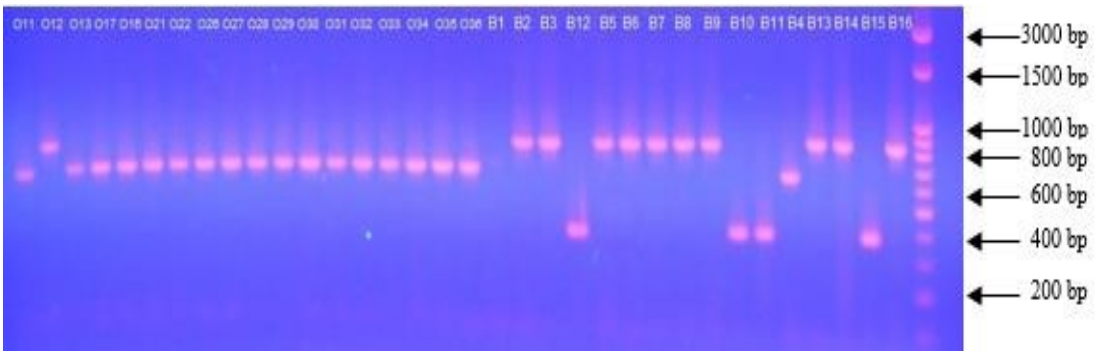


Figure 3.16. PCR Products of Non-*Saccharomyces* and *Saccharomyces* Yeasts Amplified by ITS1 and ITS4 Primers. O11, *Lachancea thermotolerans* (675 bp); O12, *Saccharomyces cerevisiae* (842 bp); O13-36, *Lachancea thermotolerans*; B1, not identified; B2-3, *Saccharomyces cerevisiae*; B12, *Metschnikowia pulcherrima* (390 bp); B5-9, *Saccharomyces cerevisiae*; B10, *Metschnikowia pulcherrima*; B11*, *Metschnikowia* spp.; B4, *Solicoccozyma aeria*; B13-14, *Saccharomyces cerevisiae*; B15, *Metschnikowia pulcherrima*; B16, *Saccharomyces cerevisiae* (O, yeast isolates from Öküzgözü grapes; B, yeast isolates from Boğazkere grapes).

(*) These microorganisms are identified accurately according to D1/D2 Domain.

Table 3.10 showed PCR amplicons of non-*Saccharomyces* and *Saccharomyces* yeasts by using ITS1 and ITS4 primers (Ghosh, 2017; Pham et al., 2011).

Table 3.10. The ITS1-5.8 rDNA-ITS2 PCR Amplicons of Yeasts (Ghosh, 2017; Pham et al., 2011)

Yeasts	*ITS1-5.8 rDNA-ITS2 PCR Amplicons (bp)*
Metschnikowia pulcherrima	390
Metschnikowia aff. pulcherrima	390
Starmerella bacillaris	475
Wickerhamomyces anomalus	600
Rhodotorula mucilaginosa	610
Lanchancae thermotolerans	675
Kluyveromyces marxianus	720
Kluyveromyces lactis	740
Hanseniaspora uvarum	747
Hanseniaspora guilliermondii	749
Saccharomyces cerevisiae	842

According to the results of our PCR products, *Hanseniaspora uvarum* strains gave 747 bp while *Rhodotorula mucilaginosa* gave 610 bp in size (Figure 3.13). In addition, isolates of *Hanseniaspora* spp. utilized nearly the same band size in Figure 3.14. On the other hand, *Metschnikowia pulcherrima* gave 390 bp in size while *Starmerella bacillaris* utilized 475 bp in Figure 3.15. *Lachancea thermotolerans* isolates also gave 675 bp in Figure 3.16.

The result of our PCR products (bp) of non-*Saccharomyces* and *Saccharomyces* yeasts amplified by ITS1 and ITS4 primers were similar to amplicons (bp) of Ghosh (2017) as shown in Table 3.10.

3.5.2. Identification of Non-*Saccharomyces* Yeasts by Sequencing of D1/D2 Domain

Basic Local Alignment Search Tool (BLAST) results for identification of yeasts by ITS sequencing (Appendix A) were contradictory for few yeast isolates. Therefore, it was decided to carry out sequencing of 26/28S rDNA D1/D2 domain for these isolates. PCR amplicon of these isolates were displayed in Figure 3.17.

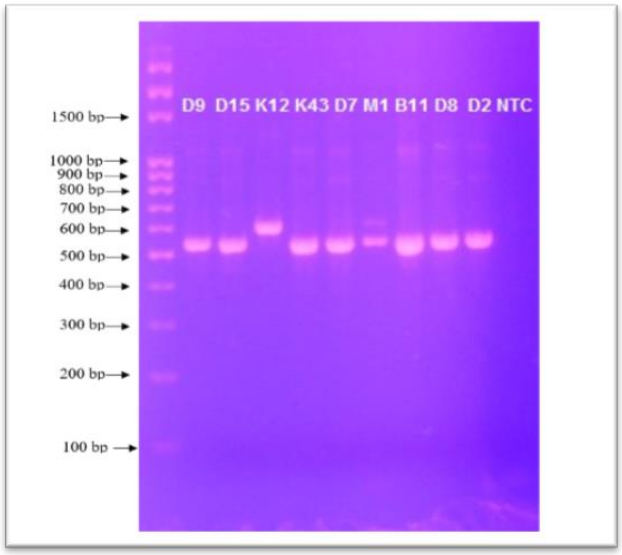


Figure 3.17. PCR Amplicon of Non-*Saccharomyces* Yeasts Amplified by NL1 and NL4 Primers. D9, not identified; D15, *Metschnikowia fructicola*; K12, *Hanseniaspora opuntiae*; K43, *Metschnikowia aff. fructicola*; D7, not identified; M1, *Metschnikowia aff. fructicola*; B11, *Metschnikowia aff. pulcherrima*; D8, *Metschnikowia pulcherrima*; D2, *Metschnikowia aff. pulcherrima*

These results of D1/D2 domain sequencing were compared with those obtained for ITS region sequencing. Contradictory results were obtained particularly for *Metschnikowia* spp. by two identification methods while the other yeast isolates gave the same identification results (Table 3.11). Table 3.12 showed also differences between yeasts identified by ITS region and D1/D2 domain sequencing.

Table 3.11. The Results of Sequencing with respect to ITS Region and D1/D2 Domain

Name	*Region*	*Similarity*	*BLAST Result*	*Name*	*Region*	*Similarity*	*BLAST Result*
K5	ITS	100%	*Hanseniaspora guilliermondii*	K5	D1/D2 Domain	100%	*Hanseniaspora guilliermondii*
K12	ITS	100%	*Hanseniaspora opuntiae*	K12	D1/D2 Domain	100%	*Hanseniaspora opuntiae*
K25	ITS	100%	*Hanseniaspora uvarum*	K25	D1/D2 Domain	100%	*Hanseniaspora uvarum*
K35	ITS	99%	*Hanseniaspora opuntiae*	K35	D1/D2 Domain	100%	*Hanseniaspora opuntiae*
K43	ITS		Not identified	K43	D1/D2 Domain	99%	*Metschnikowia aff. fructicola*
K62	ITS	100%	*Hanseniaspora opuntiae*	K62	D1/D2 Domain	100%	*Hanseniaspora opuntiae*
K65	ITS	99%	*Hanseniaspora opuntiae*	K65	D1/D2 Domain	99%	*Hanseniaspora opuntiae*
K70	ITS	98%	*Hanseniaspora uvarum*	K70	D1/D2 Domain	98%	*Hanseniaspora uvarum*
O1	ITS	99%	*Lachancea thermotolerans*	O1	D1/D2 Domain	99&	*Lachancea thermotolerans*
O7	ITS	100%	*Hanseniaspora opuntiae*	O7	D1/D2 Domain	100%	*Hanseniaspora opuntiae*
B4	ITS	100%	*Solicoccozyma aeria*	B4	D1/D2 Domain	99%	*Solicoccozyma aeria*
B11	ITS	98%	*Metschnikowia pulcherrima*	B11	D1/D2 Domain	99%	*Metschnikowia aff. pulcherrima*
B33	ITS	99%	*Metschnikowia pulcherrima*	B33	D1/D2 Domain	100%	*Metschnikowia aff. fructicola*
D2	ITS	100%	*Metschnikowia chrysoperlae*	D2	D1/D2 Domain	99%	*Metschnikowia aff. pulcherrima*
D3	ITS	94%	*Metschnikowia sinensis*	D3	D1/D2 Domain	99%	*Metschnikowia pulcherrima*
D8	ITS	95%	*Metschnikowia chrysoperlae*	D8	D1/D2 Domain	99%	*Metschnikowia pulcherrima*
D10	ITS	100%	*Starmerella bacillaris*	D10	D1/D2 Domain	100%	*Starmerella bacillaris*
D15	ITS	97%	*Metschnikowia aff. chrysoperlae*	D15	D1/D2 Domain	99%	*Metschnikowia fructicola*

K, Yeast isolates from Kalecik Karası; O,Yeast isolates from Öküzgözü; B, Yeast isolates from Boğazkere; D, Yeast isolates from Dimrit grapes.

Table 3.12. The Microorganisms Shown Different Results with respect to ITS Region and D1/D2 Domain Sequencing

Name	*Region*	*Similarity*	*BLAST Result*	*Name*	*Region*	*Similarity*	*BLAST Result*
K43	ITS		*Not identified*	K43	D1/D2 Domain	99%	*Metschnikowia aff. fructicola*
B11	ITS	98%	*Metschnikowia pulcherrima*	B11	D1/D2 Domain	99%	*Metschnikowia aff. pulcherrima*
B33	ITS	99%	*Metschnikowia pulcherrima*	B33	D1/D2 Domain	100%	*Metschnikowia aff. fructicola*
D2	ITS	100%	*Metschnikowia chrysoperlae*	D2	D1/D2 Domain	99%	*Metschnikowia aff. pulcherrima*
D3	ITS	94%	*Metschnikowia sinensis*	D3	D1/D2 Domain	99%	*Metschnikowia pulcherrima*
D8	ITS	95%	*Metschnikowia chrysoperlae*	D8	D1/D2 Domain	99%	*Metschnikowia pulcherrima*
D15	ITS	97%	*Metschnikowia aff. chrysoperlae*	D15	D1/D2 Domain	99%	*Metschnikowia fructicola*

K: Isolates from Kalecik Karası, B: Isolates from Boğazkere, D: Isolates from Dimrit.

Cordero-Bueso et al. and García et al. (2017) reported the difficulty of distinguishing Metschnikowia fructicola species from Metschnikowia pulcherrima species. Moreover, Hesham et al. at 2014 performed researches about the identification of biofuel yeast by sequencing of ITS region and D1/D2 domain. According to this study, the sequencing of D1/D2 domain of 26S ribosomal DNA was accepted as an accurate identification method for the unknown yeast species. Therefore, accurate results for our strains were also obtained by this method for non-Saccharomyces yeasts shown contradictory result respect to ITS region sequencing. Although K43 was not identified according to the ITS region sequencing, it was defined as *Metschnikowia aff fructicola* by the sequencing of the D1/D2 domain.

Moreover, Boekhout et al. (2014) reported that PCR products of D1/D2 domain of yeast rDNA changing between 600 and 650 bp in size. In our study, *Hanseniaspora* spp. gave the same results within 600-650 bp in size, while *Metschnikowia* spp. gave different pattern with 520 bp in size (Figure 3.18) as Goldhawke et al (2016) mentioned in their studies (Figure 3.18).

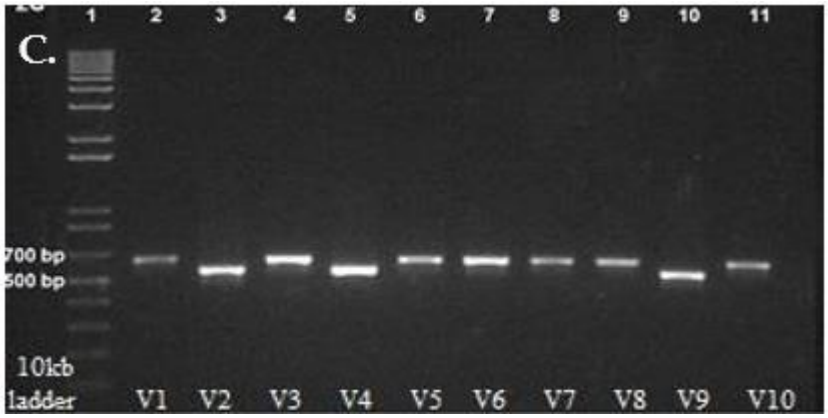


Figure 3.18. PCR Products of D1/D2 Domain. V1, V3, V5, V6, V7, V8, V10, *Hanseniaspora uvarum*; V2, V4, *Metschnikowia fructicola*; V9, *Metschnikowia* spp. (Goldhawke et al., 2016)

The D1/D2 nucleotide sequence of isolate (D3 strain) which was identified as *Metschnikowia sinensis* by ITS sequencing was compared with D1/D2 sequence of *Metschnikowia pulcherrima*. Only four nucleotide difference was observed according to alignment (Figure 3.19). However, ITS sequences of these two species were highly different (Figure 3.20). Therefore, further studies will be performed to clarify this confusing issue in the future.

Figure 3.19. Alignment of D3 strain (Query) and *Metschnikowia pulcherrima* (Sbjct) according to D1/D2 Domain

Figure 3.20. Alignment of *Metschnikowia sinensis* (D3 strain)(Query) and *Metschnikowia pulcherrima* (Sbjct) according to ITS Region

Finally, 16 species were identified according to ITS region and/or D1/D2 domain sequencing results. 14 out of 16 yeast species were non-*Saccharomyces* as following: *Hanseniaspora guilliermondii*, *Hanseniaspora opuntiae*, *Hanseniaspora uvarum*, *Rhodotorula mucilaginosa*, *Wickerhamomyces anomalus*, *Metschnikowia aff. fructicola*, *Metschnikowia fructicola*, *Lachancea thermotolerans*, *Solicoccozyma aeria*, *Metschnikowia aff. pulcherrima*, *Metschnikowia pulcherrima*, *Metschnikowia sinensis, Metschnikowia chrysoperlae*, *Starmerella bacillaris*. The others were *Saccharomyces cerevisiae* and *Saccharomyces cf. cerevisiae/paradoxus.* However, *Metschnikowia sinensis* was identified as *Metschnikowia pulcherrima* and *Saccharomyces cf. cerevisiae/paradoxus* as *Saccharomyces cerevisiae* by D1/D2 sequencing. The results of *Metschnikowia* spp. were given according to D1/D2 domain in Figure 3.21-3.25.

Hanseniaspora spp. (*Hanseniaspora guilliermondii*, *Hanseniaspora opuntiae*, *Hanseniaspora uvarum*) was found predominant species in must of Kalecik Karası grapes. Moreover, *Rhodotorula mucilaginosa*, *Wickerhamomyces anomalus*, *Metschnikowia aff. fructicola* were also isolated and identified from Kalecik Karası grapes. Kalecik Karası had rich microflora according to isolated non-*Saccharomyces* yeast species. On the other hand, *Lachancea thermotolerans*, *Hanseniaspora opuntiae,* and *Wickerhamomyces anomalus* were isolated from Öküzgözü while *Solicoccozyma aeria*, *Metschnikowia aff. pulcherrima*, *Metschnikowia pulcherrima* were found in must of Boğazkere although Öküzgözü and Boğazkere grapes were taken from the same region (Elazığ). Emir grapes had less rich microflora than the others because *Hanseniaspora uvarum* and *Wickerhamomyces anomalus* were just isolated. On the other hand, *Metschnikowia* spp. and *Starmerella bacillaris* were isolated from Dimrit must although Emir and Dimrit grapes were taken from the same region (Cappadocia). In addition, *Metschnikowia* spp. (*Metschnikowia fructicola, Metschnikowia aff. pulcherrima*, *Metschnikowia pulcherrima*, *Metschnikowia chrysoperlae*) was found remarkably in Dimrit's must (Figure 3.21).

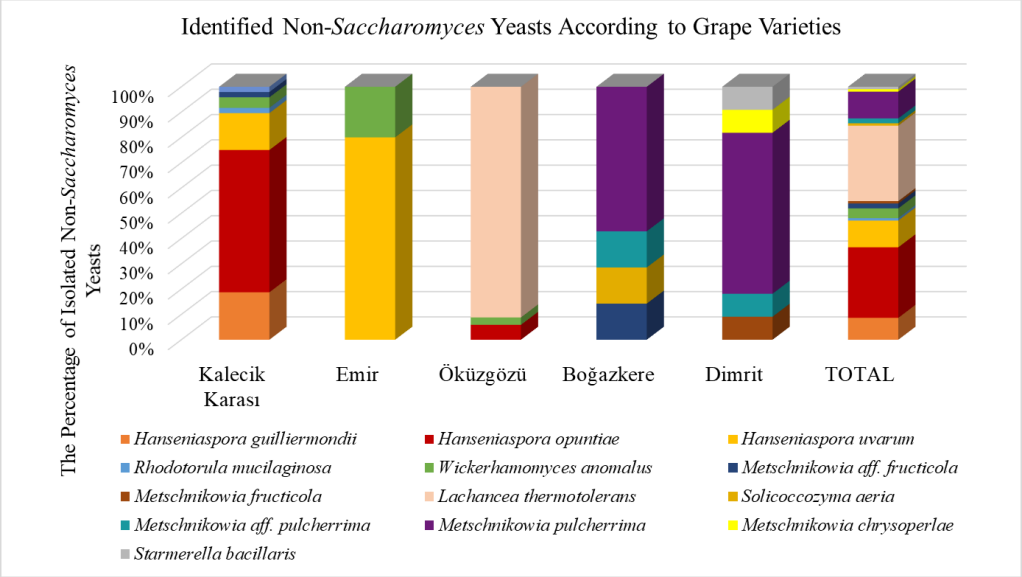


Figure 3.21. Identified Non-*Saccharomyces* Yeasts According to Grape Varieties

Hanseniaspora uvarum and *Hanseniaspora opuntiae* species were isolated from must and on the fourth day of cold maceration, the second and fourth day of normal maceration while *Hanseniaspora guilliermondii* were detected in the must and the fourth day of maceration. Moreover, *Rhodotorula mucilaginosa* and *Wickerhamomyces anomalus* species were only isolated from the must and *Metschnikowia aff. fructicola* during the fourth day of cold maceration of Kalecik Karası grapes (Figure 3.22).

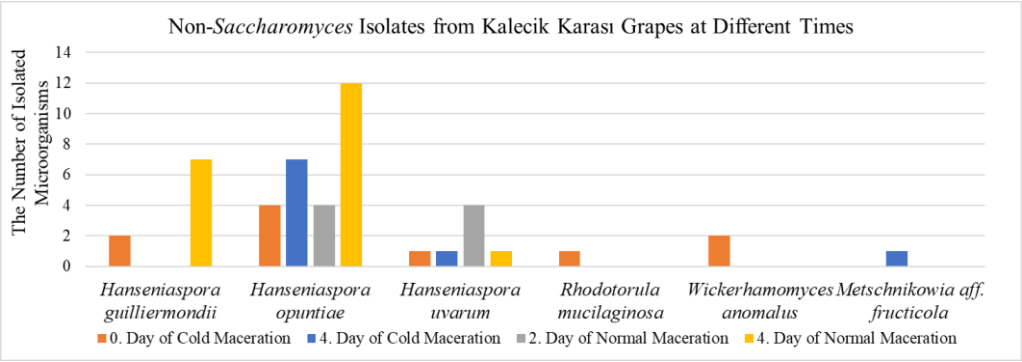


Figure 3.22. Non-*Saccharomyces* Yeast Isolates from Kalecik Karası Grapes at Different Time

Non-*Saccharomyces* yeasts were only isolated during cold maceration for Öküzgözü, Boğazkere and Dimrit musts. *Lachancea thermotolerans* can be obtained during cold maceration while *Hanseniaspora opuntiae* and *Wickerhamomyces anomalus* were isolated on the fourth day of cold maceration from the Öküzgözü must (Figure 3.23).

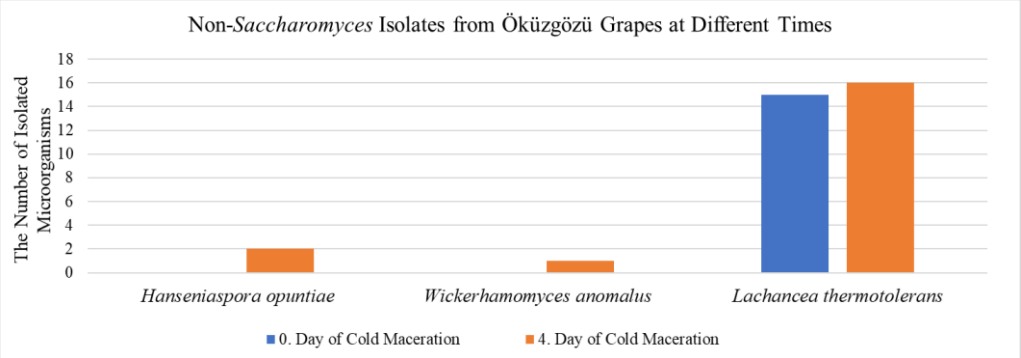


Figure 3.23. Non-*Saccharomyces* Yeast Isolates from Öküzgözü Grapes at Different Time

Metschnikowia pulcherrima species was isolated from must and during the fourth day of cold maceration while *Solicoccozyma aeria* and *Metschnikowia aff. pulcherrima* were only isolated from must grapes of Boğazkere. In addition, *Metschnikowia aff. fructicola* was isolated during the fourth day of cold maceration (Figure 3.24).

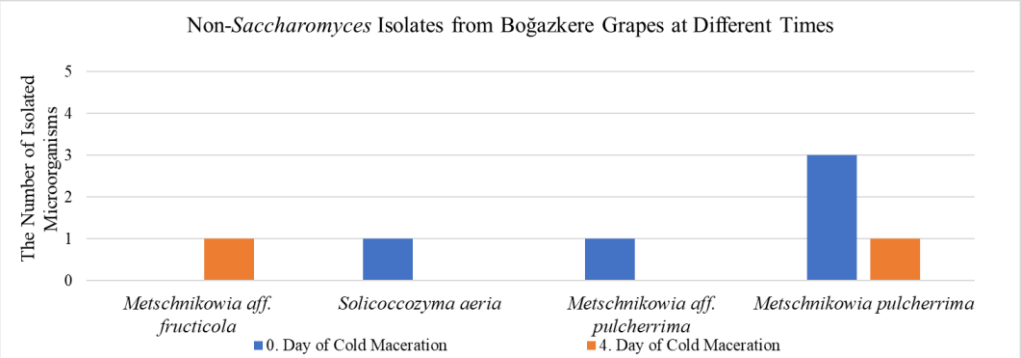


Figure 3.24. Non-*Saccharomyces* Yeast Isolates from Boğazkere Grapes at Different Time

Metschnikowia pulcherrima species were isolated from must and the fourth day of cold maceration of Dimrit grapes. *Metschnikowia aff. pulcherrima,* and *Metschnikowia chrysoperlae* were only isolated from must while *Starmerella bacillaris* during the fourth day of cold maceration (Figure 3.25).

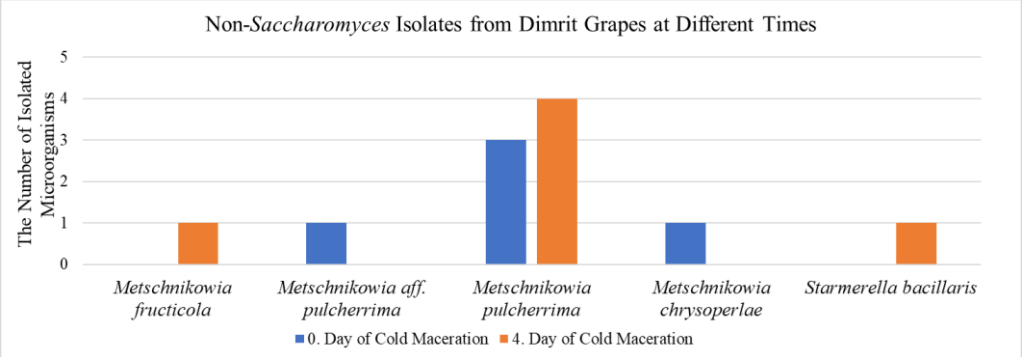


Figure 3.25. Non-*Saccharomyces* Yeast Isolates from Dimrit Grapes at Different Time

Wickerhamomyces anomalus was isolated after pressing of Emir grapes while *Hanseniaspora uvarum* species were only isolated at the end of first week of fermentation (Figure 3.26).

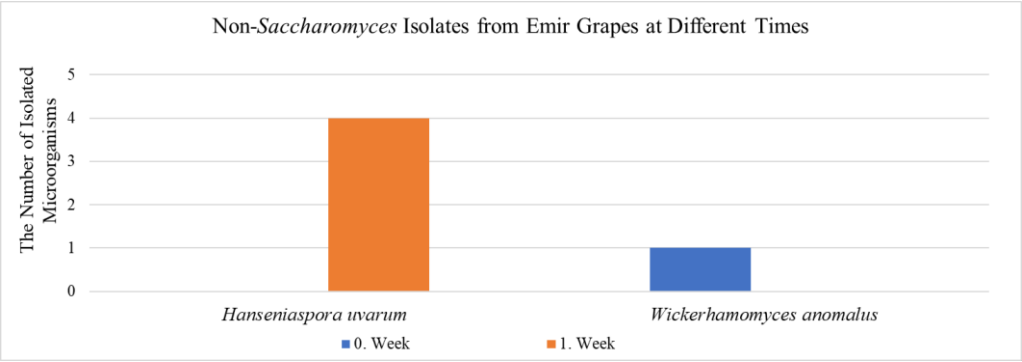


Figure 3.26. Non-*Saccharomyces* Yeast Isolates from Emir Grapes at Different Time

These microorganisms were generally isolated in cold and/or normal maceration times. Zott et al. (2008) also found non-*Saccharomyces* species, especially *Hanseniaspora uvarum* and *Starmeralla bacillaris* at the end of the cold maceration and early stage of fermentation process. Moreover, Çelik et al. (2017) isolated 8 different non-*Saccharomyces* yeasts species (*Candida zemplinina, Hanseniспora guilliermondii, Hanseniaspora uvarum, Metschnikowia* spp., *Lachancea thermotolerance, Pichia kluyveri, Pichia occidentalis, Torulaspora delbrueckii*) at the early stage of fermentation in Narince grapes from the Tokat region. In addition,

Nurgel et al. (2005) isolated *Lachancea thermotolerance* and *Kloeckera apiculate* species at the beginning of the fermentation in Emir must. In our study, similarly, 14 non-*Saccharomyces* species were isolated during cold maceration and early stage of fermentation. It is a predictable result because these yeasts are dominant in early stage of fermentation. After increasing ethanol level, these yeasts die, and *Saccharomyces cerevisiae* is a dominant yeast species in the end of fermentation process (Urso et al., 2008).

397 out of 469 isolated microorganisms were identified by molecular or biochemical methods. 72 isolates were not identified due to failure to grow on the agar and/or failure to obtain the ITS results. The numbers of identified non-*Saccharomyces* and *Saccharomyces* yeasts were 104 and 293, respectively (Figure 3.27 and Figure 3.28). 104 non-*Saccharomyces* and 77 out of 293 *Saccharomyces* yeasts were identified by DNA sequencing of ITS region and/or D1/D2 domain. 59 out of 77 *Saccharomyces* strains were isolated from lysine medium. The growth of *Saccharomyces* strains on the Lysine medium has also been previously observed and reported (Ženišová et al., 2014). 13 *Saccharomyces* strains were isolated from Ethanol Sulfate Agar (ESA), which is a specific agar for *Saccharomyces* (Kish et al., 1983; Heard and Fleet, 1985). The other *Saccharomyces* isolates (221) were also characterized according to biochemical tests and not sequenced due to their nonsuitability for phenotypic properties (low alcohol tolerance and high H_2S production). Finally, 29 *Saccharomyces* isolates were found with high technological properties used as a starter culture.

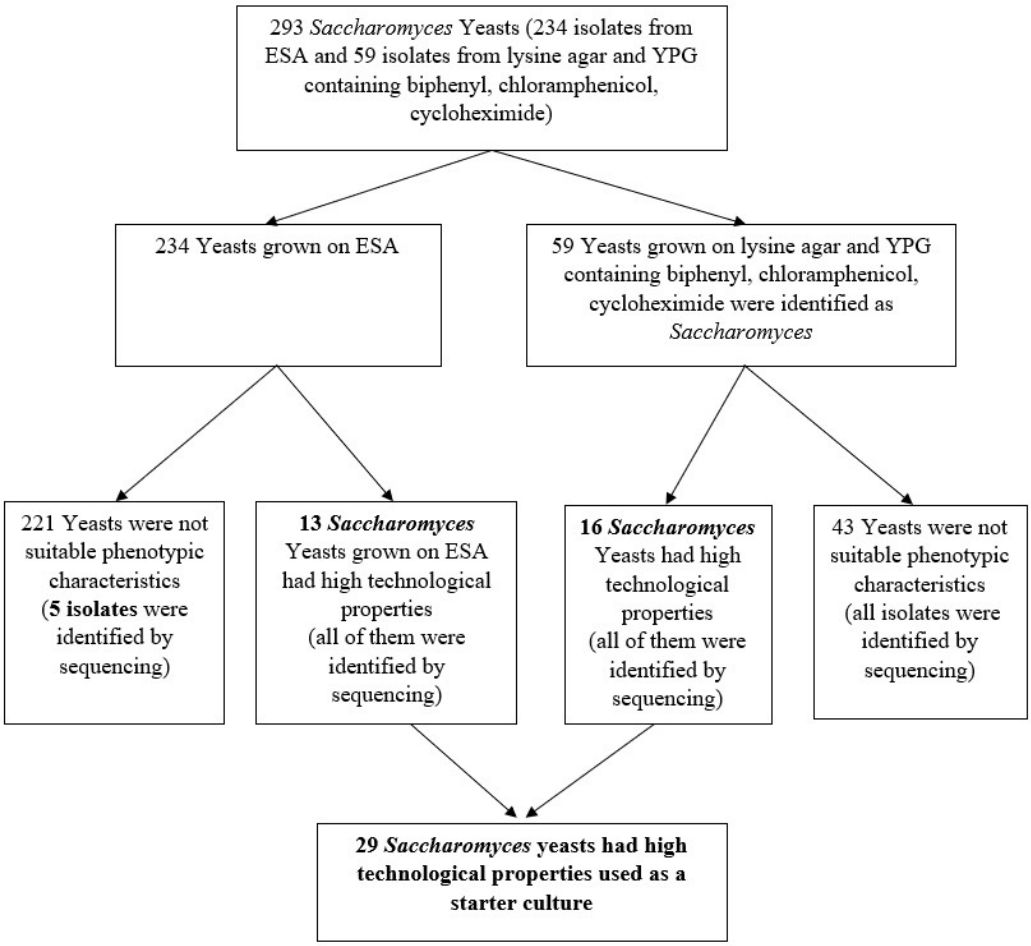


Figure 3.27. The Numbers of Isolated *Saccharomyces* Yeasts in The Culture Collection

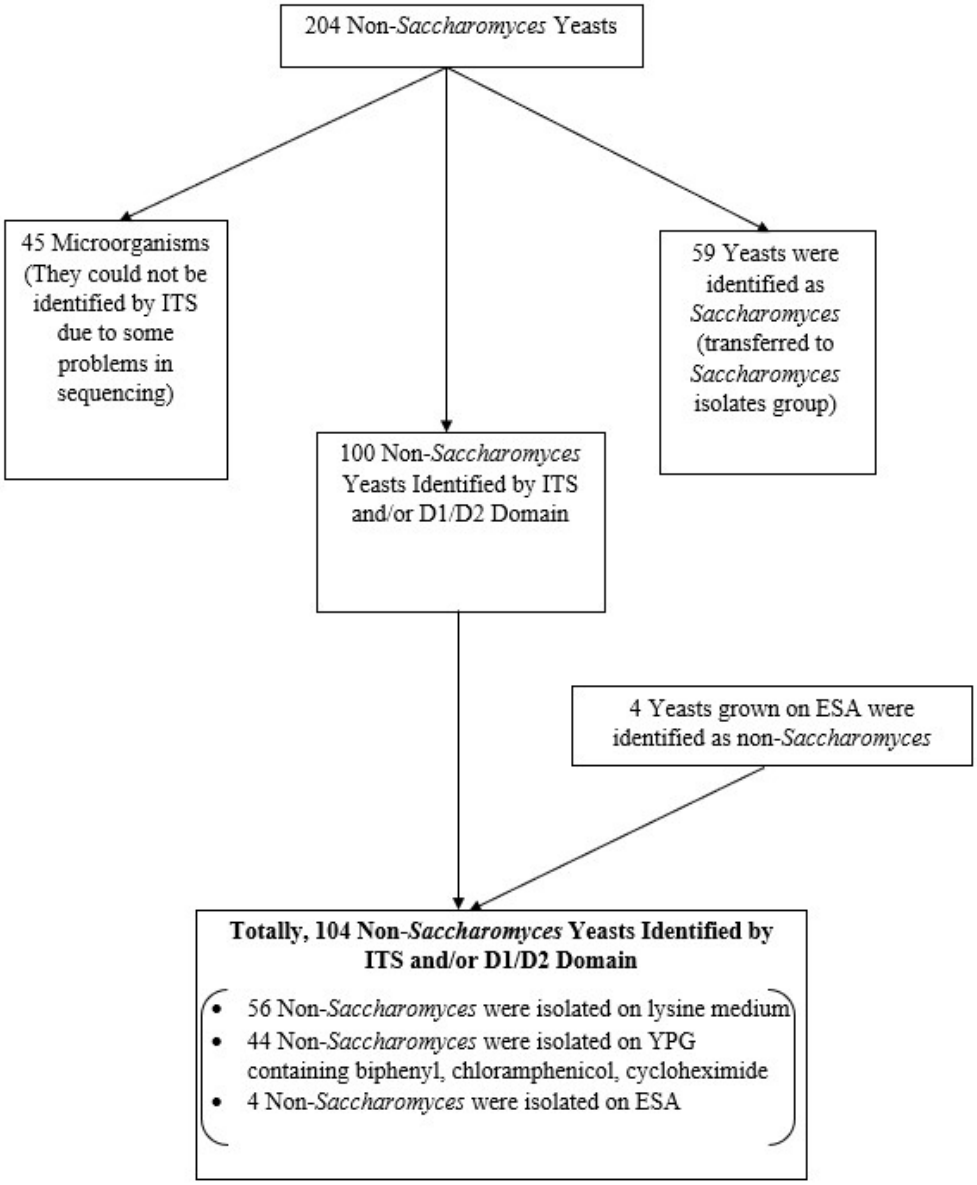


Figure 3.28. The Numbers of Isolated Non-*Saccharomyces* Yeasts in The Culture Collection

3.6. **Phylogenetic Tree**

After obtaining BLAST result, the sequences were aligned with ClustalW in MEGA X. After alignment, the phylogenetic trees were created with the Neighbor-Joining and UPGMA Method (unweighted pair group method with arithmetic mean). Distances of pairwise were calculated with the Tajima-Nei Model. The number of bootstrap replications was 100 iterations.

The evolutionary relationships of taxa using Neighbour-Joning Method were shown the following figures (Figure 3.29-3.36) while the phylogenetic trees which created with UPGMA Method were shown in Appendix B.

Phylogenetic trees of each grape varieties were firstly created. After these trees, different species were selected in these phylogenetic trees and then, the other phylogenetic tree with respect to different yeast species and different grape varieties was generated.

According to DNA sequencing results with ITS region, 4 different genera (*Rhodotorula*, *Wickerhamomyces, Hanseniaspora* and *Saccharomyces)* were identified in Kalecik Karası's must and wine. One of them was *Rhodotorula mucilaginosa*. 2 strains were defined as *Wickerhamomyces anomalus*. Moreover, 25 strains were found as *Hanseniaspora opuntiae*, while 7 strains were identified as *Hanseniaspora uvarum* and 9 strains were defined as *Hanseniaspora guilliermondii*. In addition, 8 of 53 microorganisms were belonged to *Saccharomyces cerevisiae.* The evolutionary relationship of these isolates was shown in the following phylogenetic tree (Figure 3.29).

It was interesting to observe that clusters of *Hanseniaspora* spp. were not closely related. However, *Wickerhamomyces anomalus* and *Saccharomyces cerevisiae* clusters were more closely related to one of those *Hanseniaspora* clusters than the other *Hanseniaspora* clusters.

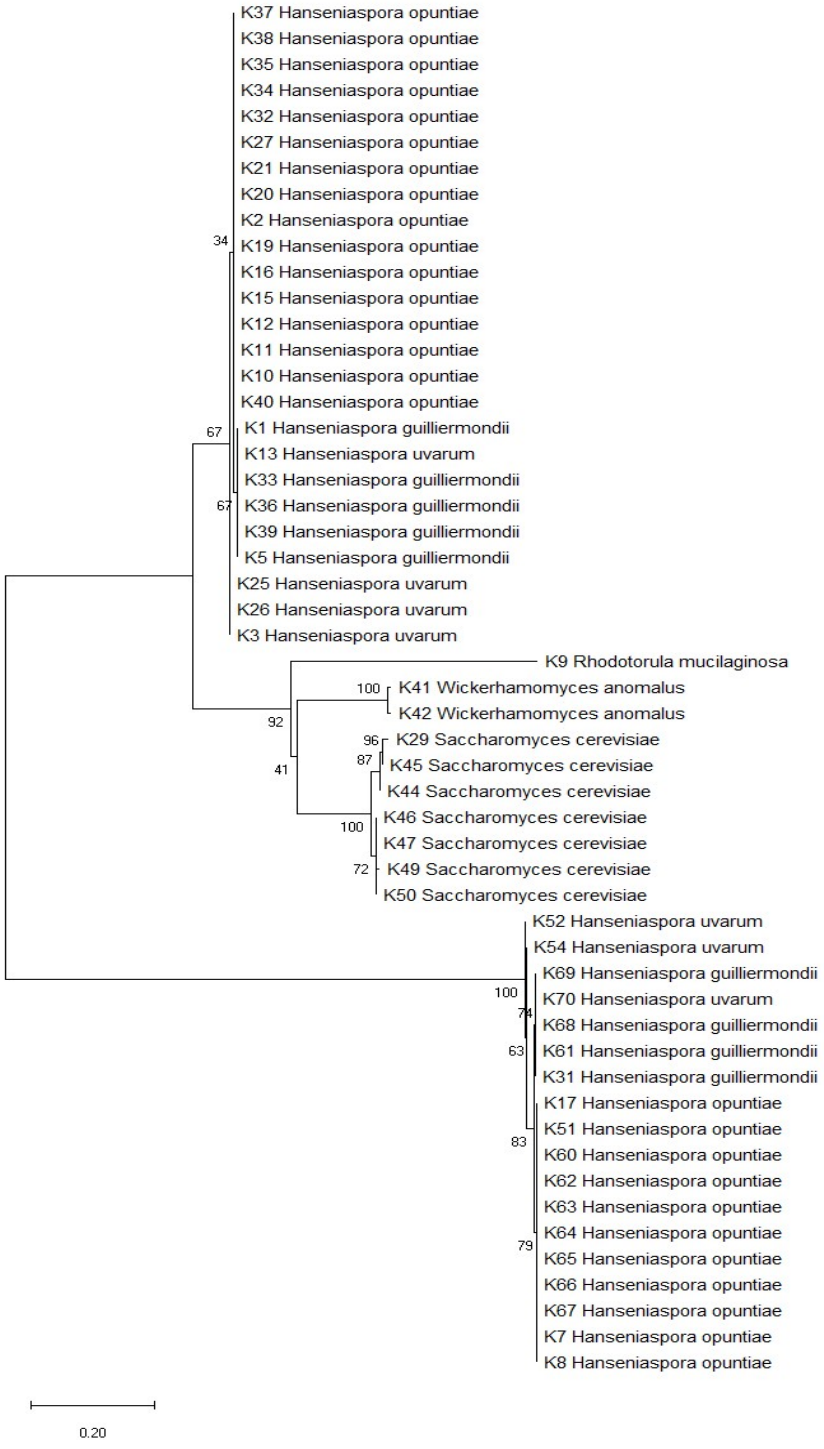


Figure 3.29. Phylogenetic Tree of Non-*Saccharomyces* and *Saccharomyces* Yeast in Kalecik Karası Must and Wine with respect to ITS Region. The scale bar indicates substitutions per base pair.

According to DNA sequencing results with ITS region, 3 different genera (*Lachancea*, *Hanseniaspora* and *Saccharomyces)* were identified in Öküzgözü's must and wine. 31 of 36 strains were defined as *Lachancea thermotolerans.* 2 strains were found as *Hanseniaspora opuntiae,* and 3 strains were identified as *Saccharomyces cerevisiae.*

The evolutionary relationship of these isolates was shown in the following phylogenetic tree (Figure 3.30).

It was interesting to observe that *Lachancea thermotolerance* clusters were not closely related to each other. However, *Hanseniaspora opuntia* and *Saccharomyces cerevisiae* clusters were more closely related to one of those *Lachancea* clusters than the other *Lachancea* clusters. According to the alignment of these two *Lachancea* clusters, it was found over 300 base pair differences. On the other hand, PCR products of these strains gave 675 bp in size. It was shown in Figure 3.15-3.16. It also referred to these strains were *Lachancea thermotolerance* (Table 3.10). In addition, *Kluyveromyces marxianus* and *Kluyveromyces lactis* gave 720 bp and 740 bp in size, respectively (Pham et al., 2011). *Lachancea* (*Kluyveromyces*) *thermotolerance* gave a more different base pair than *Kluyveromyces marxianus* and *Kluyveromyces lactis* with respect to the size of PCR product although they were the same genus.

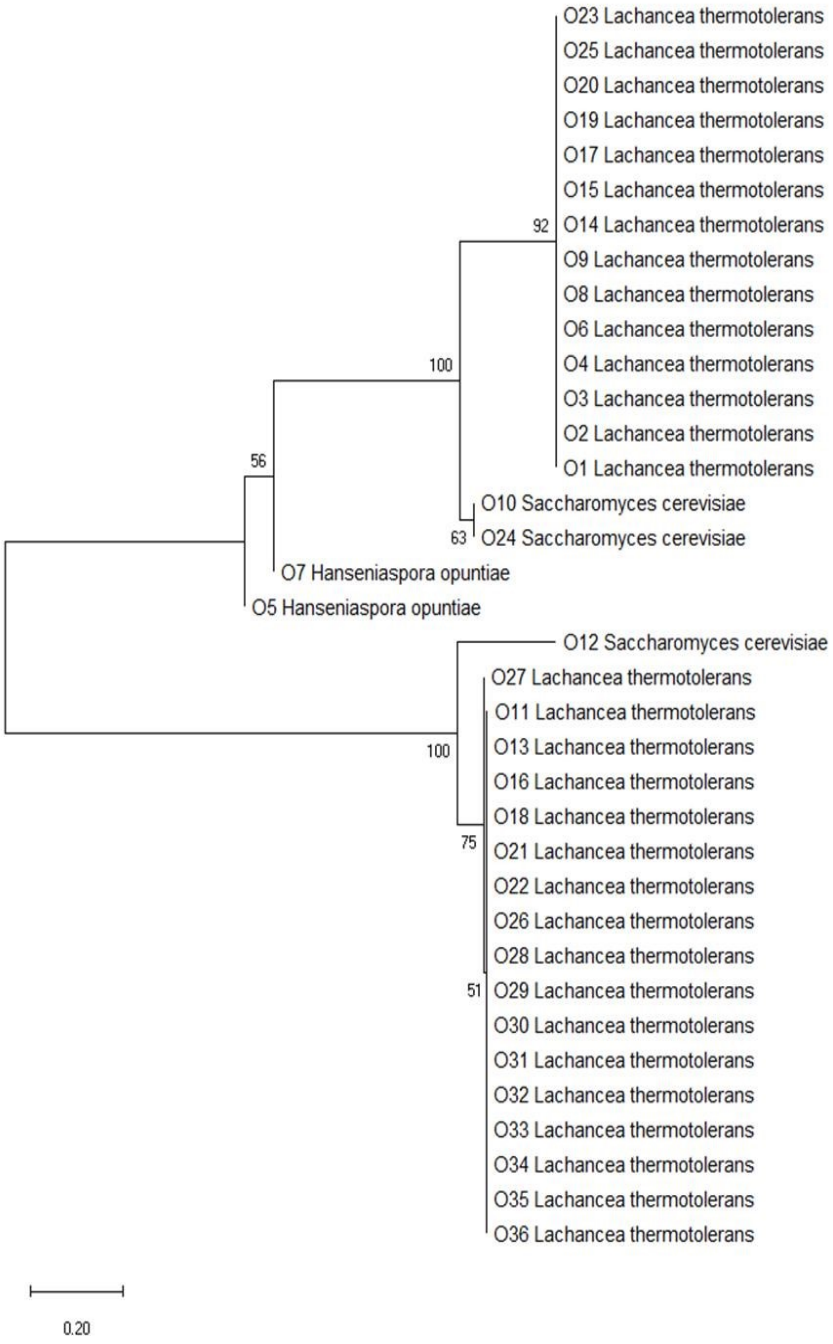


Figure 3.30. Phylogenetic Tree of Non-*Saccharomyces* and *Saccharomyce*s Yeast in Öküzgözü Must and Wine with respect to ITS Region. The scale bar indicates substitutions per base pair.

According to DNA sequencing results with ITS region, 3 different genera (*Metschnikowia*, *Solicoccozyma* and *Saccharomyces)* were identified in Boğazkere's must and wine. 5 of them were found as *Metschnikowia pulcherrima* while only one strain was defined as *Solicoccozyma aeria.* In addition, 23 of 28 microorganisms were belonged to *Saccharomyces cerevisiae.* The evolutionary relationship of these isolates was shown in the following phylogenetic tree (Figure 3.31).

Interestingly, one cluster of *Saccharomyces cerevisiae* was not closely related to other *Saccharomyces cerevisiae* clusters due to over 300 base pair differences.

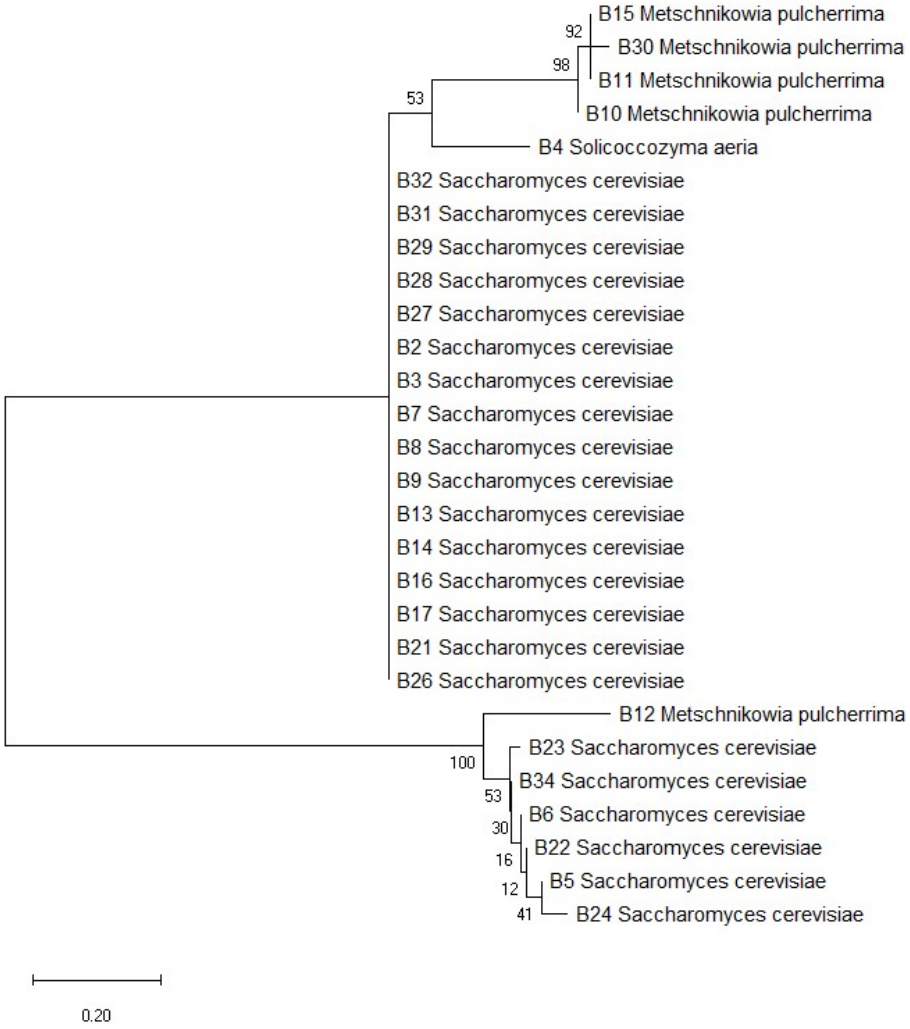


Figure 3.31. Phylogenetic Tree of Non-*Saccharomyces* and *Saccharomyces* Yeast in Boğazkere Must and Wine with respect to ITS Region. The scale bar indicates substitutions per base pair.

According to DNA sequencing results with ITS region, 2 different genera (*Metschnikowia* and *Starmerella)* were identified in Dimrit's must and wine. 5 of them were found as *Metschnikowia pulcherrima* while only one strain was defined as *Metschnikowia chrysoperlae.* In addition, one of them was defined as *Starmerella bacillaris*.

The evolutionary relationship of these isolates was shown in the following phylogenetic tree (Figure 3.32).

As it was expected, *Starmerella bacillaris* was not closely related to *Metschnikowia* spp. while *Metschnikowia pulcherrima* and *Metschnikowia chrysoperlae* had closely related each other.

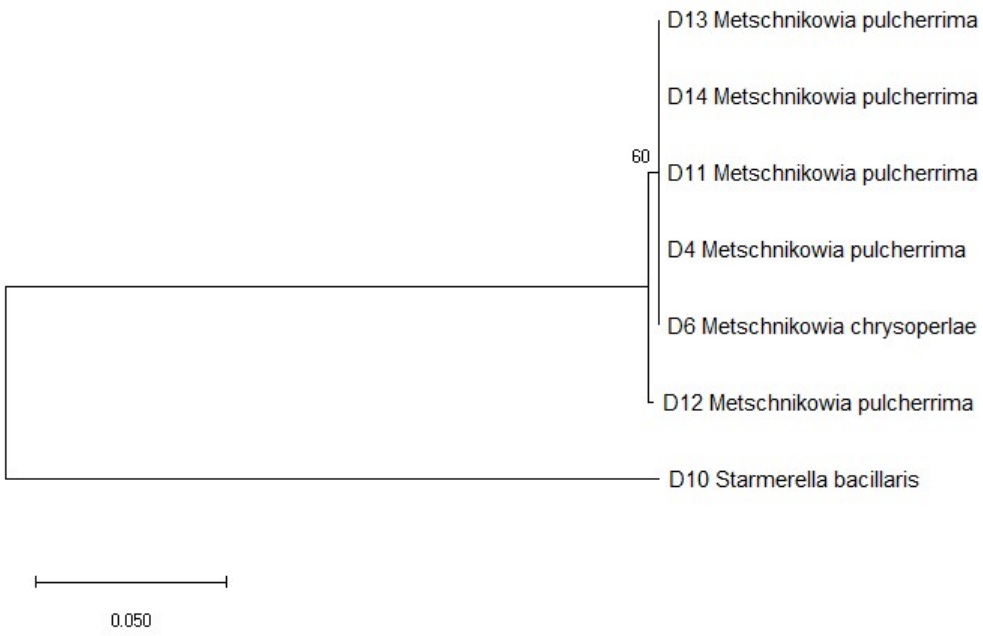


Figure 3.32. Phylogenetic Tree of Non-*Saccharomyces* and *Saccharomyces* Yeast in Dimrit Must and Wine with respect to ITS Region. The scale bar indicates substitutions per base pair.

According to DNA sequencing results with ITS region, 3 different genera (*Wickerhamomyces, Hanseniaspora* and *Saccharomyces)* were identified in Emir's must and wine. The one of them was *Wickerhamomyces anomalus*. Moreover, 4 strains were found as *Hanseniaspora uvarum*. In addition, rest of them belonged to *Saccharomyces cerevisiae*.

The evolutionary relationship of these isolates was shown in the following phylogenetic tree (Figure 3.33).

Similar unexpected results for members of some species were also noticed. *Saccharomyces cerevisiae* isolates formed two groups which were not closely related due to differences in their base pair alignments. On the other hand, *Saccharomyces* strains within the clusters showed very high similarity.

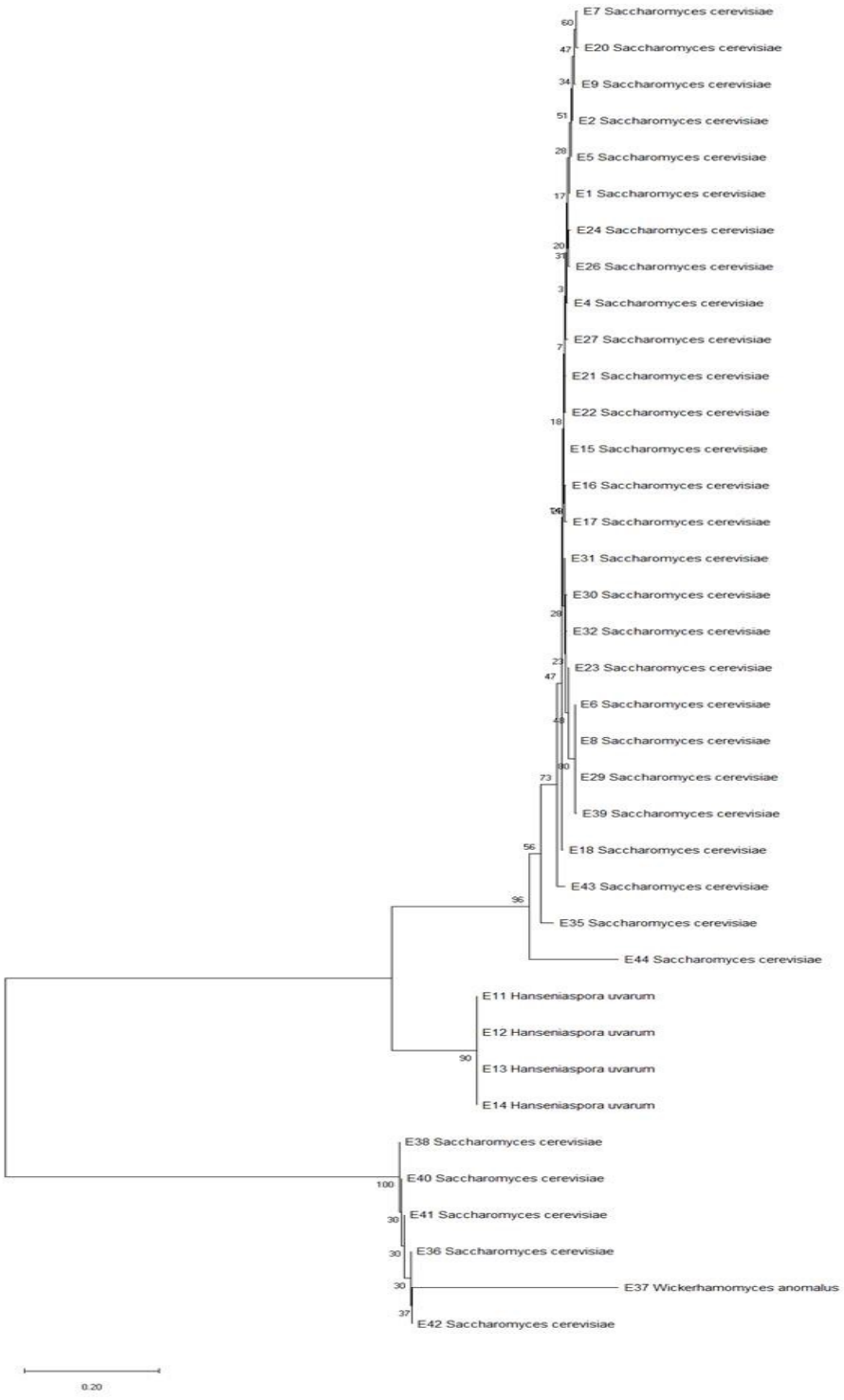


Figure 3.33. Phylogenetic Tree of Non-*Saccharomyces* and *Saccharomyces* Yeast in Emir Must and Wine with respect to ITS Region. The scale bar indicates substitutions per base pair.

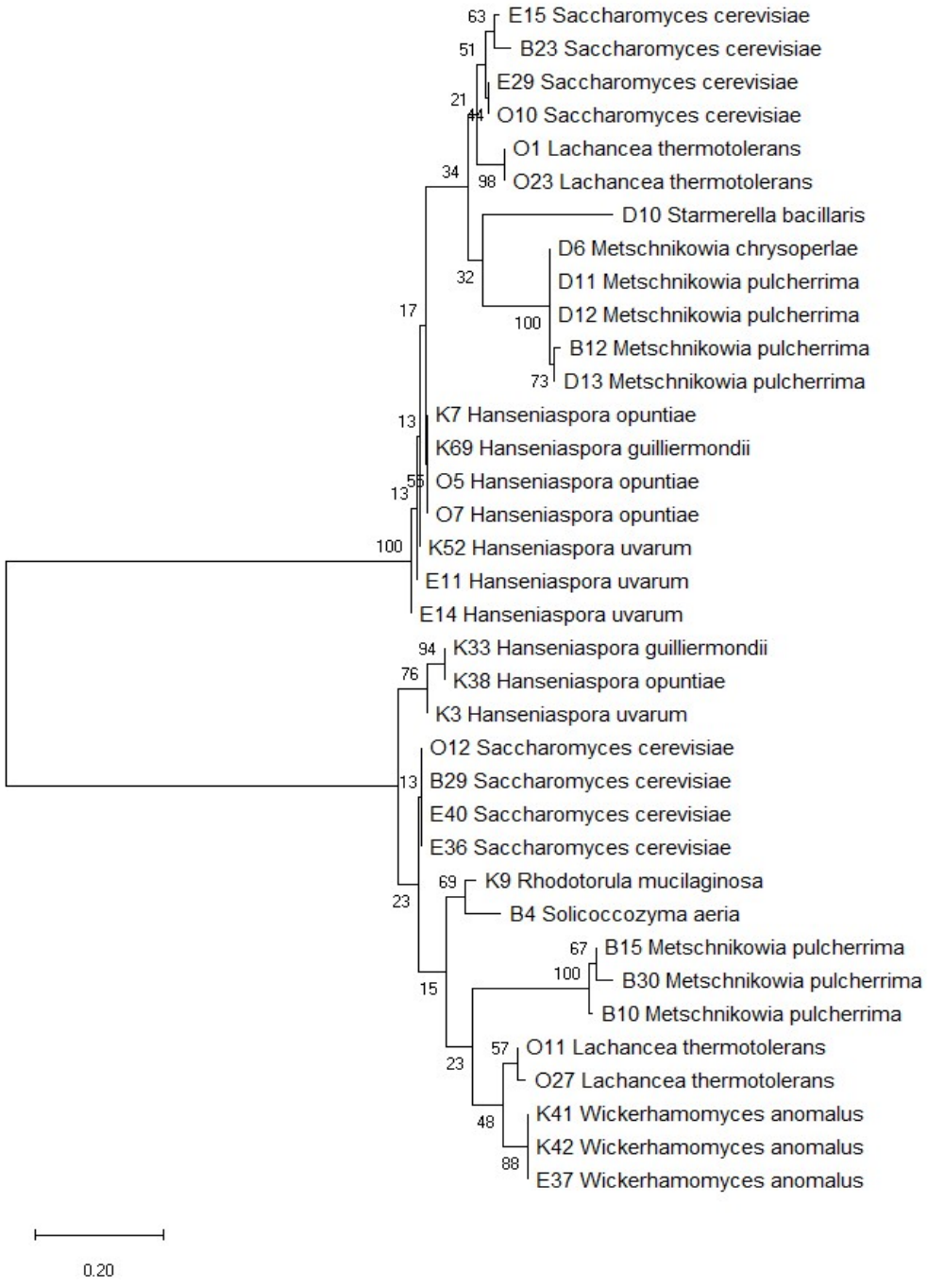


Figure 3.34. Phylogenetic Tree of Selected Non-*Saccharomyces* and *Saccharomyces* Yeast in Five Different Grapes' Musts and Wines with respect to ITS Region. The scale bar indicates substitutions per base pair.

The above phylogenetic tree was created with different selected species and different grape varieties. This showed the evolutionary relationship of each different microorganisms (Figure 3.34).

The similarities or differences of our isolates were determined according to phylogenetic tree. While the similarities of the same species were high, the species belonging to the same genus were clustered with high similarities as expected.

The numbers which were at nodes refer percentage of frequency. It indicated the stability of each branches in the tree.

It was concluded that the isolates of the same species from the same grape types were not related. These strains of the same species have been found in over 300 base pair differences. The difference between the same species concerning sequences of 26S rDNA regions was also found in studies about palm wine yeasts in recent years (Nwaiwu, 2019).

The following phylogenetic trees were created with respect to ITS region and D1/D2 domain of rDNA sequencing, respectively. This showed the evolutionary relationship of each different microorganisms according to ITS region and D1/D2 domain of ribosomal DNA. (Figure 3.35 and Figure 3.36).

According to the phylogenetic trees, *Hanseniaspora* species were found similar with respect to D1/D2 domains of rDNA sequences. Hesham et al. (2014) also revealed that D1/D2 domains of rDNA sequencing was more accurate method than 5.8S rDNA sequencing for identification of the microorganisms.

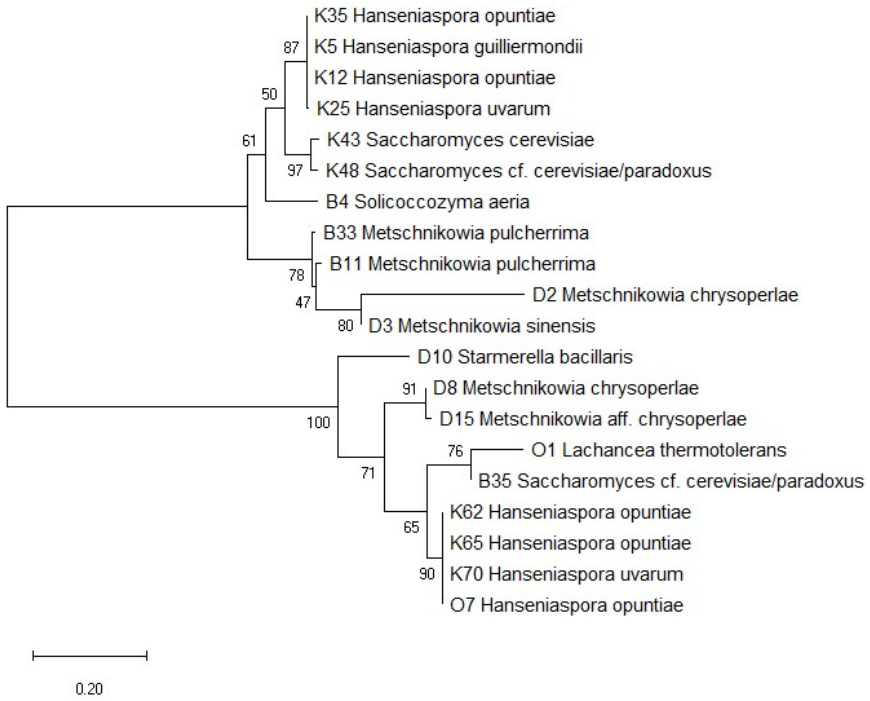


Figure 3.35. Phylogenetic Tree of Some Yeasts with respect to ITS Region. The scale bar indicates substitutions per base pair.

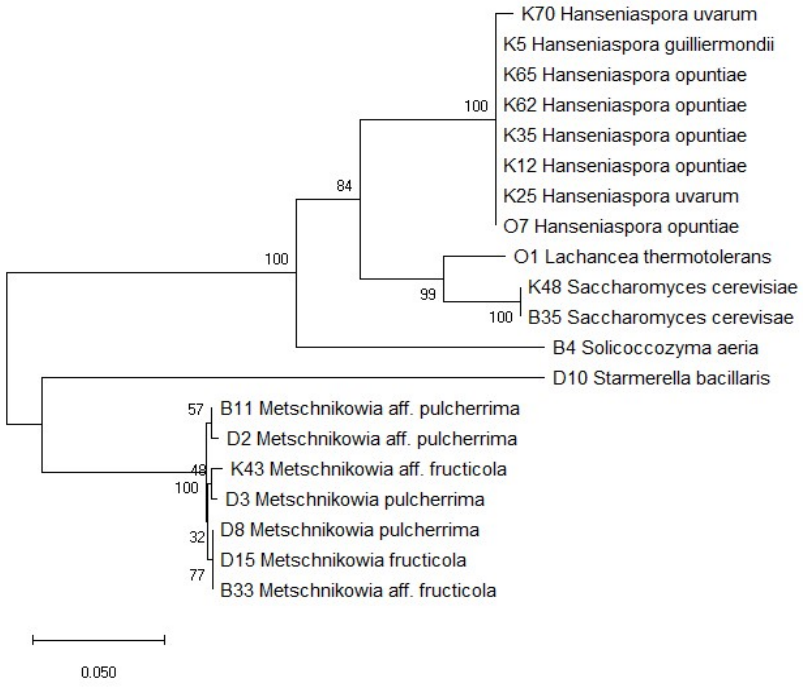


Figure 3.36. Phylogenetic Tree of Some Yeasts with respect to D1/D2 Domain. The scale bar indicates substitutions per base pair.

3.7. **Phenotypic Characterization of Non-*Saccharomyces* Yeasts**

The alcohol tolerances of non-*Saccharomyces* strains were generally found very low level. This is an expected result (Table 3.13). These strains, which are active during cold and normal maceration, leave the wine production to alcohol tolerant *Saccharomyces* strains (Urso et al., 2008). Non-*Saccharomyces* yeasts having low alcohol tolerance were used as a starter culture for production of wine containing low alcohol content (Jolly, Augustyn, & Pretorius, 2006). Therefore, these isolated non-*Saccharomyces* yeasts can be used as a starter culture for making the wine having low alcohol content. On the other hand, some isolated strains were found high alcohol tolerance. These isolates were *Wickerhamomyces anomalus* (KB 0.CM S5 and OA 4.CM S3), *Hanseniaspora opuntiae* (OA 4.CM NS4) and *Metschnikowia aff. pulcherrima* (DA 0.CM NS2) strains. These non-*Saccharomyces* yeasts can also be used as a starter culture with pure or mixed inoculation of the musts.

Moreover, these non-*Saccharomyces* yeasts highly produced H_2S. This situation was very similar to the literature. Çelik et al. (2017) were found high level H_2S producing non-*Saccharomyces* yeasts.

SO_2 addition was used to inhibit undesirable microorganisms' growth and control oxidation. SO_2 is a highly toxic compound for non-*Saccharomyces* yeasts. Therefore, SO_2 tolerance is a very desirable property for non-*Saccharomyces* yeasts for using as a starter culture of wine (González-Arenzana et al., 2017). Isolated non-*Saccharomyces* yeasts had high SO_2 tolerance in Table 3.13. Only one *Metschnikowia aff. fructicola* strain (KA 4.CM S1) had low SO_2 tolerance in this table. These isolates having high SO_2 tolerance can be used as a starter culture for winemaking.

In addition, phenotypic properties of all non-*Saccharomyces* yeasts were given Appendix D.

Table 3.13. Technological Properties of Non-*Saccharomyces* Strains

Non-Saccharomyces	*Name*	*Alcohol Tolerance (%)*				*SO_2 Tolerance (mg/L)*			*H_2S Production*	*Identification*	
		10	*13*	*15*	*50*	*100*	*150*	*200*		*ITS*	*D1/D2*
Hanseniaspora guilliermondii	KA 0.CM NS1	-	-	-	+	+	+	+	3	+	nd
	KA 0.CM NS5	-	-	-	+	+	+	+	4	+	+
Hanseniaspora opuntiae	KA 0.CM NS2	-	-	-	+	+	+	+	3	+	nd
	KB 0.CM NS5	vw	vw	vw	+	+	+	+	3	+	nd
	KA 2.NM NS1	+	-	-	+	+	+	-	2	+	nd
	KA 4.NM NS5	-	-	-	+	+	+	+	2	+	nd
Rhodotorula mucilaginosa	KB 0.CM NS4	-	-	-	+	+	+	+	3	+	nd
Hanseniaspora uvarum	KA 4.CM NS3	+	vw	-	+	+	+	+	3	+	nd
	KA 2.NM NS4	-	-	-	+	+	+	+	3	+	nd
Wickerhamomyces anomalus	KA 0.CM S1	-	-	-	+	+	+	+	3	+	nd
	KB 0.CM S5	+	+	+	+	+	+	+	ng	+	nd
Metschnikowia aff. fructicola	KA 4.CM S1	-	-	-	-	-	-	-	ng	+	+
Hanseniaspora uvarum	EA 1.W NS1	-	-	-	+	+	+	+	3	+	nd
	EA 1.W NS4	vw	vw	vw	+	+	+	+	3	+	nd
Wickerhamomyces anomalus	EA 0.NM NS8	-	-	-	+	+	+	+	3	+	nd
Lachancea thermotolerans	OA 0.CM NS1	-	-	-	+	+	+	+	3	+	+
	OB 4.CM NS4	-	-	-	+	+	+	+	3	+	nd
Wickerhamomyces anomalus	OA 4CM S3	+	+	w	+	+	+	+	3	nd	+
Hanseniaspora opuntiae	OA 4.CM NS2	vw	vw	vw	+	+	+	+	3	+	nd
	OA 4.CM NS4	+	+	+	+	+	+	+	4	+	+
Metschnikowia pulcherrima	BB 0.CM NS2	w	w	-	+	+	+	+	4	+	nd
Metschnikowia aff. fructicola	BB 4.CM NS8	-	-	-	+	+	+	+	3	+	+
Metschnikowia aff. pulcherrima	BB 0.CM NS3	-	-	-	+	+	+	+	5	+	+
Solicoccozyma aeria	BA 0.CM NS4	-	-	-	+	w	w	w	5	+	+
Metschnikowia aff. pulcherrima	DA 0.CM NS2	+	+	+	+	+	+	+	ng	+	+
Metschnikowia sinensis (ITS)	DA 0.CM NS3	-	-	-	+	+	+	+	3	+	
Metschnikowia pulcherrima (D1/D2)											+
Starmeralla bacillaris	DA 4.CM NS2	w	w	-	+	+	+	+	4	+	+
Metschnikowia pulcherrima	DA 4.CM NS3	-	-	-	+	+	+	+	2	+	nd
	DA 4.CM NS4	-	-	-	+	+	+	+	3	+	nd
Metschnikowia chrysoperlae	DB 0.CM NS2	-	-	-	+	+	+	+	4	+	nd
Metschnikowia fructicola	DB 4.CM NS3	-	-	-	+	+	+	+	4	+	+

KA: A Parallel of Wine Made from Kalecik Karası Grape , KB: B Parallel of Wine Made from Kalecik Karası Grape, OA: A Parallel of Wine Made from Öküzgözü Grape, OB: B Parallel of Wine Made from Öküzgözü Grape, BA: A Parallel of Wine Made from Boğazkere Grape, BB: B Parallel of Wine Made from Boğazkere Grape, DA: A Parallel of Wine Made from Dimrit Grape, DB: B Parallel of Wine Made from Dimrit Grape, EA: A Parallel of Wine Made from Emir Grape, EB: B Parallel of Wine Made from Emir Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 2NM: 2. Day of Normal Maceration, 4NM: 4. Day of Normal Maceration, 1W: 1. Week; NS: Non-*Saccharomyces* ; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; nd: Not determined.

3.8. **The Results of Wine Analysis Produced with Our Starter Cultures**

Ethanol, total acidity, pH, volatile acidity, free SO_2, total SO_2, reducing sugar, malic acid and citric acid contents of our wines which were produced by adding our starter cultures were given in the Table 3.14.

Table 3.14. The Results of Wine Analysis

Samples	*Ethanol (% v/v)*	*Total Acidity (g/L sulphuric acid)*	*pH*	*Volatile Acid (g/L sulphuric acid)*	*Total SO_2 (mg/L)*	*Reducing Sugar (g/L)*	*Malic Acid (g/L)*	*Citric Acid (g/L)*
E-LT-SC	12,6	2,2	3,8	0,16	221	0	1,42	0,38
E-WA-SC	12,7	2,2	3,8	0,2	119	0	1,42	0,22
E-SC	11,7	2,2	3,6	0,11	255	0	1,48	0,37
O-LT-SC	12,4	5,5	3,2	0,78	15	5,8	0,35	0,13
O-HO-SC	14,1	4,5	3,4	0,85	25	5,3	0,64	0,13
O-HG-SC	12,1	4,3	3,4	0,91	7	9,6	0,57	0,15
O-SC	13	5	3,1	0,39	27	1,2	1,51	0,28

E-LT-SC: Wine made by sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains in Emir grapes, E-WA-SC: Wine made by sequential inoculation of our *Wickerhamomyces anomalus* and *Saccharomyces cerevisiae* strains in Emir grapes, E-SC: Wine made by inoculation of our *Saccharomyces cerevisiae* strain in Emir grapes, O-LT-SC: Wine made by sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes, O-HO-SC: Wine made by sequential inoculation of our *Hanseniaspora opuntiae* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes, O-HG-SC: Wine made by sequential inoculation of our *Hanseniaspora guilliermondii* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes, O-SC: Wine made by inoculation of our *Saccharomyces cerevisiae* strain in Öküzgözü grapes.

Alcohol contents of all wines were within the limits according to the Turkish food codex as shown in Table 3.15. Although the total acidities of emir wines were slightly lower than expected, this value was suitable for Öküzgözü wines. It was higher than 2,29 g/L sulphuric acid. Moreover, the wine should be between pH 3 to 3,5. Although pH of Emir wines was slightly above this range, pH of Öküzgözü wines was within this value. Even though the amount of volatile acid was slightly higher in O-HG-SC, these values were still within the limits for all wines.

According to the reducing sugar quantity, wines made from emir grapes fall into the dry wine category, while wines made from Öküzgözü grape fall into the semi-dry category except O-SC. O-SC also fall into the dry wine category.

Although the total amount of SO_2 is slightly higher than the limits for Emir wines, this value decreases with time.

These values were found above and below the expected limits. These values were probably obtained because there is no curative treatment. This topic will be taken into consideration in our next wine trials.

Table 3.15. Limits of Wine Contents (Turkish Food Codex, 2008)

Compounds	*Limits*
Alcohol	9< and <15 (%v/v)
Total Acidity	>2,29 g/L sulphuric acid
pH	3<and <3,5
Volatile Acid	<0,886 g/L sulphuric acid for white and rose wines
	<0,985 g/L sulphuric acid for red wines
Total SO_2	<250 mg/L for white and rose wines (for sugar content more than 5 g/L)
	<200 mg/L for white and rose wines (for sugar content less than 5 g/L)
	<200 mg/L for red wines (for sugar content more than 5 g/L)
	<150 mg/L for red wines (for sugar content less than 5 g/L)
Reducing Sugar (g/L)	<4 g/L for dry wines
	4≤ and <12 g/L for semi-dry wine

3.9. **The Results of Volatile Compounds and Sensory Analysis of Produced Wines**

3.9.1. The Results of Volatile Compound Analysis

Before giving the results of volatile compound for each wine, odour threshold values and odour description of tested each aroma compounds were shown in the following table (Table 3.16) This table was created with respect to literature values.

Table 3.16. Volatile Compounds' Odour Threshold Values and Odour Descriptions

Compound	*Odour Threshold (µg/L)*	*Odour Description*
Alcohols		
1-Propanol	306000 [3]	Ripe fruit, alcohol [3]
Isobutyl Alcohol	40000 [1]	Alcohol, winelike, nail polish [1]
1-Butanol	150000 [1]	Medicinal, alcohol[1]
Isoamyl Alcohol	60000 [1]	Whiskey, nail polish [1]
3-Methyl-1-pentanol	50000 [1]	Herbaceous, cocoa [1]
3-Ethoxy-1-propanol	100 [4]	Fruity [4]
Methionol	500 [4]	Cooked vegetable[4]
Benzyl Alcohol	100000 [1]	Almond [1]
Phenylethyl Alcohol	10000 [1]	Rose, pollen, perfume [1]
3-Methyl-3-butene-1-ol	600 [4]	Sweet fruity [4]
1-Pentanol	64000 [4]	Almond, synthetic, balsamic [4]
4-Methyl-1-pentanol	5000 [1]	Almond, toasted [1]
2,3-Butanediol	150000 [4]	Fruity [4]
1-Heptanol	1000 [1]	Green, sweet [1]
(Z)-3-Hexene-1-ol	400 [1]	Green, cypress [1]
(E)-3-Hexene-1-ol	400 [5]	Green grass, herb [2]
2-(Methylthio)ethanol	250 [6]	French bean, cauliflower [6]
2-Hexanol	not found	Herbaceous, medicine [12]
3-Hexanol	400 [9]	Flowery, soap [12]
1-Hexanol	8000 [1]	Green, grass [1]
Acetates		
Isoamyl acetate	30 [1]	Banana, fruity, sweet [1]
Isopropyl acetate	not found	Fruity [9]
Phenethyl acetate	250 [1]	Pleasant, floral [1]
Esters		
Ethyl lactate	154636 [1]	Lactic, raspberry[1]
Ethyl octanoate	5 [1]	Fruity, pineapple, pear, floral [1]
Ethyl-3-hydroxybutyrate	20000 [3]	Green grape, marshmallow [3]
Ethyl 9-decenoate	100 [1]	Fruity [1]
Diethyl succinate	6000 [1]	Light fruity, wine [1]
Ethyl butyrate	20 [1]	Strawberry, apple, banana [1]
Ethyl decanoate	200 [1]	Waxy, fruity, rose [1]
Ethyl hexanoate	5 [1]	Flowery, fruity [1]

Table 3.16 *(continued)*

Compound	*Odour Threshold (µg/L)*	*Odour Description*
Aldehydes		
Nonanal	2,8 [4]	Citrusy, floral [4]
Acids		
Butanoic acid	10000 [4]	Rancid, cheese [4]
Hexanoic acid	3000 [1]	Cheese, fatty [1]
Octanoic acid	1000[1]	Cheese, fatty acid, rancid, harsh [1]
Decanoic acid	10000 [1]	Fatty, unpleasant [1]
Propanoic acid	8100 [1]	Cheese [1]
Nonanoic acid	3000 [4]	Fatty [4]
Tetradecanoic acid	10000 [4]	Not found [4]
Dodecanoic acid	1000 [1]	Dry, metallic, laurel oil flavour [1]
Pentanoic acid	3000 [4]	Cheese [4]
Isobutyric acid	2300 [1]	Cheese, butter, rancid [1]
Heptanoic acid	not found [4]	Sweaty, cheese [4]
Acetic acid	1200000[13]	Unpleasant [13]
Isovaleric acid	30 [11]	Rancid, cheese, feet, floral [11]
Lactones		
γ-butyrolactone	20000 [11]	Faint, sweet, caramel [11]
Pantolactone	2000[11]	Spicy, caramel [11]
Phenols		
2-Methoxy-4-vinylphenol	40 [4]	Spices, curry [4]
4-vinyl-phenol	180 [9]	Pharmaceutical [10]
Hydrocarbons		
Phenol	7100 [7]	Sickeningly sweet, irritating [8]
Other Compounds		
Guaiacol	10 [4]	Smoke, sweet, medicine [4]
Acetoin	150000 [9]	Flowery, wet [2]
Geraniol	20 [3]	Roses, geranium [3]
Syringol	570 [7]	Not found

(1) Wang, X., et. al., 2017
(2) Liu, N., et. al., 2015
(3) Arcari, S., et. al., 2017
(4) Welke, J., et. al., 2014
(5) Tao, Y., et. al., 2010
(6) Moreira, N., et al., 2010
(7) Parker, M., et. al., 2012
(8) Vries, C., et. al., 2016
(9) Escudero, A., et. al, 2007
(10) Swiegers, J., et. al., 2005
(11) Celik, Z., et. al., 2018
(12) Darıcı, M., et. al., 2013
(13) Macías, M., et. al., 2012.

3.9.1.1. The Result of Volatile Compound Analysis of White Wine

White wines were made from Emir grapes which were taken from Cappadocia at 2018. One of the white wines was prepared with sequential inoculation with strain OB 4.CM NS4 (*Lachancea thermotolerans*) and strain OB 4.CM S1 (*Saccharomyces cerevisiae*) (E-LT-SC). The other was made with strain OB 4.CM S1 (*Saccharomyces cerevisiae*) (E-SC). The following two diagrams were shown the peaks of volatile compounds in GC-MS chromatogram for E-LT-SC and E-SC, respectively (Figure 3.37 and 3.38).

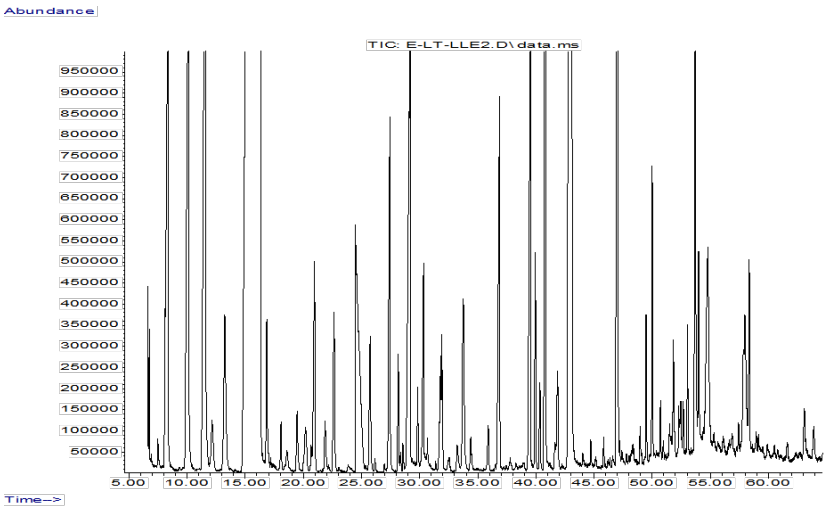


Figure 3.37. GC-MS Chromatogram of E-LT-SC Sample

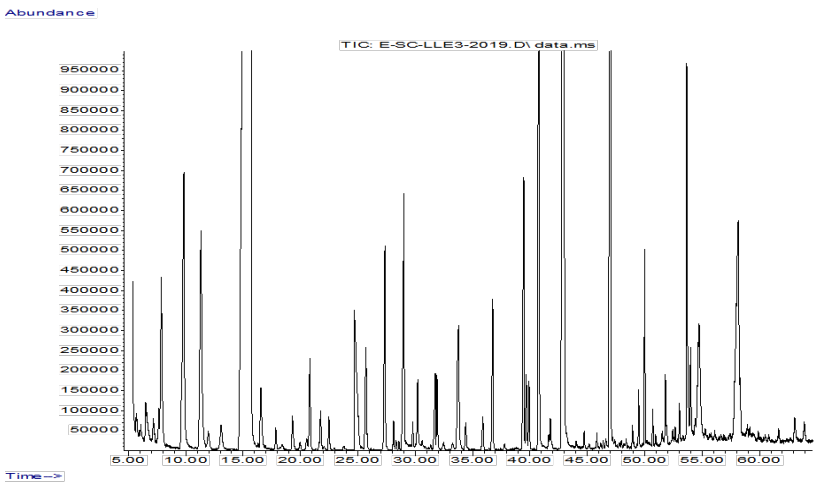


Figure 3.38. GC-MS Chromatogram of E-SC Sample

Moreover, traditional wine (E-A) and commercial wine with using the Laffort starter culture (E-Laff) were made in 2017. These Emir grapes also were taken in Cappadocia.

Table 3.17 was shown volatile compounds of four wine samples (E-A, E-Laff, E-LT-SC, and E-SC). According to GS-MS results, 42 aroma compounds were identified for E-LT-SC and E-SC while 59 volatile compounds were found in E-A and E-Laff. These compounds included alcohols, acetates, esters, aldehydes, acids, lactones, phenols, and other compounds such as tyrosol and acetoin. 46 of them were significantly different among these samples. The total concentrations of aroma compounds were found 150.4 mg/L in E-A, 144.4 mg/L in E-Laff, 131.7 mg/L in E-LT-SC and 113.2 mg/L in E-SC.

The highest amount of volatile compounds was found alcohols, then acids and esters were followed this alignment. Higher alcohols, acids and esters have important roles in giving flavor of wines with respect to amounts and concentration of these compounds (Valero, Moyano, Millan, Medina, & Ortega, 2002).

When concentrations of alcohols were under 300 mg/L, they gave desirable flavor of wine. In contrast, if these values were over 400 mg/L, they attributed negative impacts (Pastor, Huerta, Mateo, & Jime, 2001). The amounts of alcohols were found 140.8 mg/L, 130.9 mg/L, 112.6 mg/L and 95.4 mg/L for E-A, E-Laff, E-LT-SC and E-SC, respectively. In these alcohols, isoamyl alcohol and phenethyl alcohol were found very high level in all of the wine samples while 3-Ethoxy-1-propanol were only identified highly in E-LT-SC and E-SC. Isoamyl alcohol and phenethyl alcohol had suprathreshold OAVs (OAV>1) and gave whiskey and rose aroma in these wines, respectively (Table 3.18). Moreover, fruity aroma (3-Ethoxy-1-propanol) was found higher in E-LT-SC wine. Cabaroglu et al. (1997) mentioned that alcohols were an important part of aroma substances in neutral aromatic grape varieties such as Emir.

Table 3.17. Aroma Compounds (µg/L) of Emir and Kalecik Karası Wines with GS-MS Results

Compound	*RI*	*E-A*	*E-Laff*	*E-LT-SC*	*E-SC*	*K-13*	*K-HU*	*K-SC*	*K-A*
Alcohols									
1-Propanol*	1031	585.94±30.66^{E}	535.50±32.59^{E}	6096.35±252.05^{A}	3168.24±188.72^{B}	1315.1±64.92^{D}	1485.67±146.46^{D}	1709.22±136.9^{D}	2765.34±103.52^{C}
Isobutyl Alcohol*	1098	7094.13±545.87^{CD}	5791.22±456.99^{DE}	5249.09±135.80^{E}	4709.24±48.74^{E}	8164.57±613.75^{C}	8473.2±328.31^{C}	15508.45±966.7^{A}	12600.61±474.10^{B}
1-Butanol*	1151	Nd	Nd	505.50±31.02^{A}	298.61±17.98^{B}	331.86±17.25^{B}	138.2±12.79^{D}	191.70±13.17^{C}	479.13±7.32^{A}
Isoamyl Alcohol*	1236	107983.46±10207.44^{ABC}	100487.00±9980.9^{BCD}	83097.76±115.89^{DE}	71677.76±1129.77^{E}	93417.79±6180.34^{CD}	85286.88±295.02^{DE}	123340.20±10766.2^{A}	113586.80±3887.80^{AB}
3-Methyl-1-pentanol*	1341	74.19±7.82^{B}	100.39±9.51^{A}	Nd	Nd	91.38±6.91^{A}	58.94±1.80^{BC}	45.93±2.47^{C}	61.43±4.53^{BC}
3-Ethoxy-1-propanol*	1389	38.09±3.77^{E}	41.06±3.75^{E}	510.90±20.70^{A}	185.95±3.26^{C}	92.19±6.22^{D}	229.08±1.01^{B}	52.90±4.90^{E}	227.37±9.25^{B}
3-(Ethylthio)-1-propanol*	1802	33.15±3.13^{A}	23.21±0.39^{B}	Nd	Nd	Nd	Nd	Nd	Nd
Methionol*	1721	417.14±18.52^{C}	418.77±29.46^{C}	94.32±8.25^{D}	127.47±4.84^{D}	405.97±32.63^{C}	731.69±15.33^{A}	542.25±45.98^{B}	712.09±26.68^{A}
Benzyl Alcohol*	1853	42.60±3.86^{F}	57.01±4.44^{EF}	73.10±2.07^{E}	54.69±0.64^{EF}	200.40±19.08^{B}	165.95±3.27^{C}	139.55±13.20^{D}	255.13±8.93^{A}
2-Methyl-2-buten-1-ol*	1332	37.53±3.51^{B}	34.16±2.46^{BC}	Nd	102.43±2.58^{A}	37.03±1.88^{B}	28.09±1.48^{C}	Nd	Nd
Phenylethyl Alcohol*	1916	21882.72±759.51^{C}	20826.49±1767.25^{C}	12913.18±514.45^{D}	12587.35±295.67^{D}	21740.58±510.83^{C}	26839.23±527.02^{B}	19789.79±836.44^{C}	30431.02±637.41^{A}
3-Methyl-3-butene-1-ol*	1250	88.64±5.39^{C}	111.31±7.95^{B}	Nd	Nd	90.62±8.94^{C}	74.34±5.25^{CD}	71.75±4.45^{D}	134.04±1.18^{A}
1-Pentanol*	1262	73.91±6.93^{BC}	104.35±5.62^{A}	Nd	Nd	79.88±6.15^{B}	63.56±3.11^{C}	71.68±2.87^{BC}	82.61±6.48^{B}
4-Methyl-1-pentanol*	1328	35.19±2.90^{AB}	34.33±2.64^{AB}	Nd	Nd	40.77±3.38^{A}	30.25±1.32^{B}	Nd	Nd
2.3-Butanediol*	1517	1840.09±141.79^{E}	1592.14±34.41^{E}	2554.09±130.33^{D}	1727.77±51.04^{E}	4379.08±409.24^{B}	3347.99±227.38^{C}	3621.41±120.30^{C}	5195.34±209.66^{A}
1-Heptanol*	1421	108.91±7.31^{A}	45.07±4.01^{C}	58.23±5.21^{C}	Nd	88.44±3.80^{B}	48.14±3.30^{C}	57.75±4.35^{C}	51.87±4.81^{C}
(Z)-3-Hexene-1-ol*	1394	53.36±4.27^{B}	91.12±8.92^{A}	Nd	Nd	32.99±1.98^{CD}	22.21±1.59^{D}	32.64±2.79^{D}	45.11±2.68^{BC}
(E)-3-Hexene-1-ol*	1384	34.83±3.27^{A}	34.93±3.11^{A}	Nd	Nd	37.91±2.79^{A}	25.41±0.65^{B}	40.23±2.42^{A}	39.99±3.17^{A}

Table 3.17 (continued)

Alcohols	***RI***	***E-A***	***E-Laff***	***E-LT-SC***	***E-SC***	***K-13***	***K-HU***	***K-SC***	***K-A***
2-(Methylthio)ethanol*	1497	40.93±4.26^{D}	39.80±2.30^{D}	63.78±3.58^{BC}	46.87±2.66^{D}	75.72±2.38^{B}	94.76±7.13^{A}	66.58±6.37^{BC}	62.38±2.90^{C}
1.2-Propanediol*	1583	46.65±2.40^{C}	53.21±3.61^{C}	Nd	Nd	77.44±6.87^{B}	54.70±3.13^{C}	85.12±6.36^{B}	103.07±5.38^{A}
3-Penten-2-ol*	1160	130.82±12.47^{C}	298.33±28.66^{B}	938.13±37.06^{A}	311.43±6.10^{B}	78.97±3.12^{CD}	52.14±3.89^{D}	120.10±8.77^{C}	266.97±7.10^{B}
2-Hexanol*	1313	108.76±6.05^{B}	100.90±3.36^{B}	228.55±8.52^{A}	244.79±13.11^{A}	60.06±5.92^{C}	32.84±2.79^{D}	55.44±4.47^{C}	33.77±2.93^{D}
3-Hexanol*	1207	22.14±1.05^{B}	51.91±0.92^{A}	Nd	Nd	Nd	Nd	Nd	Nd
1-Hexanol	1347	Nd	Nd	191.67±3.30^{A}	161.11±13.93^{A}	Nd	Nd	Nd	Nd
2-Phenoxyethanol*	2142	34.42±1.38^{A}	22.43±1.51^{B}	Nd	Nd	Nd	Nd	Nd	Nd
Total		*140773.18*	*130894.64*	*112574.65*	*95403.71*	*130838.75*	*127283.27*	*165542.69*	*167134.07*
Acetates									
Isoamyl acetate*	1132	460.66±20.99^{F}	1410.11±25.91^{D}	2749.99±87.16^{A}	1768.53±42.58^{C}	1743.33±80.64^{C}	1452.16±9.78^{D}	2242.31±186.81^{B}	807.86±59.84^{E}
Isopropyl acetate	913	70.87±2.37^{A}	69.56±6.43^{A}	Nd	Nd	Nd	Nd	Nd	Nd
Phenethyl acetate*	1827	82.99±7.38^{E}	151.87±14.80^{D}	290.88±11.20^{B}	146.32±4.04^{D}	273.17±2.35^{B}	330.34±7.50^{A}	227.86±22.65^{C}	226.46±14.20^{C}
Propyl acetate*	953	53.62±5.53^{A}	41.9±3.60^{B}	Nd	Nd	Nd	Nd	Nd	Nd
Isobutyl acetate	1029	Nd	Nd	189.28±12.10	Nd	Nd	Nd	Nd	Nd
Total		668.14	1673.44	3230.1500	1914.85	2016.5	1782.5	2470.17	1034.32
Esters									
Ethyl lactate*	1363	218.76±21.50^{E}	202.77±19.88^{E}	565.15±18.23^{BCD}	485.53±24.10^{CD}	611.23±19.31^{BC}	693.95±14.65^{B}	436.28±41.28^{D}	2059.53±125.75^{A}
Ethyl octanoate*	1412	178.13±13.64^{D}	256.34±12.37^{C}	338.60±7.76^{B}	409.85±1.13^{A}	133.46±6.95^{E}	81.48±12.95^{F}	230.00±12.24^{C}	150.67±6.73^{DE}

Table 3.17 (continued)

Esters	***RI***	***E-A***	***E-Laff***	***E-LT-SC***	***E-SC***	***K-13***	***K-HU***	***K-SC***	***K-A***
Ethyl-3-hydroxybutyrate*	1472	90.16±7.27^{D}	86.90±5.75^{D}	182.24±15.36^{C}	96.76±8.53^{D}	206.56±18.12^{BC}	249.23±8.90^{A}	218.01±18.89^{ABC}	245.64±24.47^{AB}
Ethyl 9-decenoate	1712	24.44±0.70^{A}	27.47±2.04^{A}	Nd	Nd	Nd	Nd	Nd	Nd
Diethyl succinate*	1701	44.04±2.40^{F}	64.27±4.58^{EF}	74.64±2.48^{EF}	76.24±4.24^{E}	228.97±7.68^{B}	142.09±12.56^{D}	198.97±6.40^{C}	259.38±19.83^{A}
Ethyl 4-hydroxybutanoate*	1819	1264.82±69.81^{DE}	1480.22±106.25^{D}	1314.64±37.43^{DE}	1124.60±52.76^{E}	2922.64±103.64^{B}	2344.84±66.16^{C}	2058.77±202.55^{C}	3684.69±129.87^{A}
Monoethyl succinate*	2350	659.10±41.33^{E}	Nd	1046.13±42.87^{DE}	722.32±30.37^{DE}	2610.71±248.74^{A}	1157.67±84.94^{D}	1700.59±97.33^{C}	2107.06±177.58^{B}
Ethyl hydrogen succinate	1687	Nd	541.61±39.90	Nd	Nd	Nd	Nd	Nd	Nd
Ethyl butyrate	1044	259.37±3.43^{A}	279.63±23.63^{A}	Nd	Nd	Nd	Nd	Nd	Nd
Ethyl-3-hydroxypropionate*	1587	26.60±1.39^{C}	26.39±1.79^{C}	Nd	Nd	88.55±1.18^{A}	65.98±5.53^{B}	73.37±5.41^{B}	65.18±5.02^{B}
Ethyl decanoate*	1610	40.52±3.11^{B}	55.39±0.81^{B}	463.98±29.26^{A}	496.05±14.03^{A}	Nd	Nd	Nd	Nd
Ethyl 2-hydroxy-3-phenylpropanoate*	2223	Nd	Nd	Nd	Nd	92.33±5.08^{B}	Nd	73.46±6.62^{B}	135.75±11.14^{A}
Methyl 4-hydroxybutanoate*	1802	Nd	Nd	Nd	Nd	20.68±1.03^{C}	28.92±1.65^{B}	16.07±1.34^{D}	56.39±1.68^{A}
Ethyl hexanoate*	1241	469.11±38.99^{B}	449.26±32.27^{B}	444.94±30.92^{B}	579.79±38.80^{A}	248.64±17.46^{C}	209.52±18.45^{C}	396.67±33.92^{B}	249.93±23.04^{C}
Total		*3275.05*	*3470.25*	*4430.32*	*3991.14*	*7163.77*	*4973.68*	*5402.19*	*9014.22*
Aldehydes									
Nonanal	1658	922.22±0.00	922.22±0.00	922.22±0.00	922.22±0.00	922.22±0.00	922.22±0.00	922.22±0.00	922.22±0.00

Table 3.17 (continued)

Acids	***RI***	***E-A***	***E-Laff***	***E-LT-SC***	***E-SC***	***K-13***	***K-HU***	***K-SC***	***K-A***
Butanoic acid*	1604	107.35±8.41^{C}	250.48±22.72^{B}	335.22±27.29^{A}	345.60±9.32^{A}	Nd	Nd	353.34±27.40^{A}	161.70±12.85^{C}
Hexanoic acid*	1832	696.70±38.14^{D}	1741.68±54.76^{C}	2428.84±147.12^{B}	3339.72±72.71^{A}	848.87±239.94^{D}	794.08±3.06^{D}	1528.31±136.78^{C}	556.21±50.67^{D}
Octanoic acid*	2106	1057.21±50.64^{E}	2251.81±58.47^{C}	3300.29±195.00^{B}	3973.74±113.58^{A}	527.04±3.10^{F}	548.38±22.41^{F}	1317.59±69.03^{D}	433.89±35.17^{F}
Decanoic acid*	2231	127.71±10.38^{A}	138.02±9.34^{A}	132.54±8.44^{A}	78.99±6.42^{B}	Nd	Nd	77.44±5.59^{B}	Nd
Propanoic acid*	1508	43.21±3.44^{D}	53.86±3.07^{D}	106.87±3.01^{B}	58.65±0.27^{D}	134.87±12.60^{A}	99.56±5.07^{BC}	89.04±6.67^{C}	124.89±5.71^{A}
Nonanoic acid*	2157	28.21±2.66^{D}	49.46±3.38^{C}	171.29±8.93^{A}	109.98±4.13^{B}	43.71±3.92^{C}	8.99±0.44^{E}	49.80±1.64^{C}	22.81±0.73^{D}
Tetradecanoic acid*	2717	39.64±3.69^{B}	69.45±3.13^{A}	Nd	Nd	Nd	Nd	Nd	Nd
Dodecanoic acid*	2479	56.71±3.53^{B}	108.84±9.01^{A}	Nd	Nd	Nd	Nd	Nd	Nd
Pentanoic acid*	1689	104.49±9.15^{E}	374.67±6.30^{D}	Nd	Nd	623.99±24.75^{B}	405.91±4.83^{CD}	804.82±58.30^{A}	463.38±43.73^{C}
Isobutyric acid*	1579	72.21±2.66^{E}	229.29±15.09^{D}	197.95±16.20^{D}	119.39±1.35^{DE}	491.97±44.85^{B}	360.52±10.55^{C}	885.63±75.51^{A}	389.59±29.94^{C}
Heptanoic acid*	1934	Nd	Nd	86.06±4.65^{A}	Nd	70.31±3.63^{BC}	62.65±4.21^{C}	30.37±0.93^{D}	74.43±1.94^{B}
Acetic acid*	1403	652.16±26.70^{D}	541.41±1.49^{D}	1662.24±58.48^{B}	1317.76±78.73^{C}	1522.34±103.41^{BC}	691.19±20.50^{D}	1379.79±130.75^{C}	3414.62±56.48^{A}
Diethyl dl-malate*	2053	Nd	Nd	Nd	Nd	35.80±2.19^{A}	29.20±2.13^{B}	27.01±1.67^{B}	36.58±2.27^{A}
Total		*2985.6*	*5808.97*	*8421.3*	*9343.83*	*4298.9*	*3000.48*	*6543.14*	*5678.1*
Lactones									
γ-butyrolactone*	1592	283.19±25.34^{E}	339.38±21.98^{E}	522.28±29.07^{CD}	578.69±4.20^{C}	1216.72±30.83^{A}	1074.37±20.60^{B}	495.74±41.53^{D}	1175.99±30.32^{A}
Pantolactone*	2034	62.26±6.14^{CDE}	50.40±0.91^{E}	72.87±5.18^{BC}	54.41±4.55^{DE}	65.24±6.42^{BCD}	64.53±3.69^{BCD}	86.67±2.77^{A}	77.34±3.87^{AB}
Total		*345.45*	*389.78*	*595.15*	*633.1*	*1281.96*	*1138.9*	*582.41*	*1253.33*

Table 3.17 (continued)

Phenols	***RI***	***E-A***	***E-Laff***	***E-LT-SC***	***E-SC***	***K-13***	***K-HU***	***K-SC***	***K-A***
2-Methoxy-4-vinylphenol*	2168	142.37±9.09^{C}	176.56±5.31^{B}	283.40±18.50^{A}	290.51±5.90^{A}	79.03±1.40^{D}	52.17±4.49^{E}	286.06±0.67^{A}	153.11±7.83^{BC}
4-vinyl-phenol*	2334	Nd	Nd	329.95±28.57^{A}	254.27±12.56^{B}	Nd	Nd	212.27±6.16^{B}	100.22±4.13^{C}
Total		*142.37*	*176.56*	*613.35*	*544.78*	*79.03*	*52.17*	*498.33*	*253.33*
Hydrocarbons									
Phenol*	1947	24.18±1.77^{A}	12.16±0.81^{B}	Nd	Nd	Nd	Nd	Nd	Nd
Other Compounds									
Tyrosol*	2965	1874.52±36.44^{B}	1723.01±51.70^{C}	1666.29±25.31^{C}	1208.80±9.31^{D}	722.41±66.06^{F}	906.56±18.25^{E}	1656.07±60.20^{C}	2217.50±33.10^{A}
Soleron*	2096	35.13±3.36^{C}	22.47±0.57^{C}	Nd	Nd	81.83±7.33^{B}	34.52±3.10^{C}	82.17±5.29^{B}	97.06±8.48^{A}
Guaiacol*	1840	63.04±4.82^{B}	57.14±1.00^{B}	Nd	Nd	61.30±1.36^{B}	37.13±3.36^{C}	57.41±5.72^{B}	94.69±4.78^{A}
Acetoin*	1291	190.28±10.74^{C}	175.87±15.96^{C}	168.09±0.18^{C}	178.74±7.77^{C}	200.67±19.09^{C}	270.36±26.70^{B}	190.79±14.51^{C}	1292.28±26.83^{A}
Geraniol*	1844	Nd	Nd	Nd	Nd	24.01±1.64^{B}	25.28±1.423^{B}	36.58±3.65^{A}	25.89±1.60^{B}
Syringol*	2854	Nd	Nd	Nd	Nd	61.30±5.04^{C}	37.53±1.21^{D}	163.60±11.08^{B}	190.71±0.51^{A}
Total		*2162.97*	*1978.49*	*1834.38*	*1387.54*	*1151.52*	*1311.38*	*2186.62*	*3918.13*
TOTAL		*150376.94*	*144404.29*	*131699.3*	*113218.95*	*146830.43*	*139542.38*	*183225.55*	*188285.5*

E-A: Emir traditional wine. E-Laff: Emir commercial wine. E-LT-SC: Emir wine sample inoculated with strain OB 4.CM NS4 (*Lachancea thermotolerans*) and strain OB 4.CM S1 (*Saccharomyces cerevisiae*). E-SC: Emir wine sample inoculated with strain OB 4CM S1 (*Saccharomyces cerevisiae).* K-13: Kalecik karası wine sample inoculated with strain 13 (*Saccharomyces cerevisiae*). K-HU: Kalecik karası wine sample inoculated with *Hanseniaspora uvarum* K-SC: Kalecik karası wine sample inoculated with commercial *Saccharomyces cerevisiae* (Chr. Hansen) K-A: Traditional wine made by Elnaz Seyid Monir. RI: retention indices. *: significantly differ($P<0.05$). $^{A.B.C.D.E.F}$: refer significantly different. Nd: not determined.

3.27 mg/L, 3.47 mg/L, 4.43 mg/L and 3.99 mg/L of esters were found in E-A, E-Laff, E-LT-SC and E-SC, respectively. Ethyl 4-hydroxybutanoate, monoethyl succinate, ethyl lactate, ethyl decanoate, ethyl hexanoate, and ethyl octanoate were found high amount in these wines. They had important roles for young wines and occurred in maceration time. In addition, these aromas played critical roles for giving fruity flavor in the wines (Selli, et. al, 2004; Herraiz, et. al., 1991) Ethyl octanoate, ethyl decanoate, and ethyl hexanoate had suprathreshold OAVs and gave fruity aroma. Especially, these aroma compounds were found at a higher level in E-LT-SC and E-SC than E-A and E-Laff. The amount of ethyl decanoate was found at 10 times high in E-LT-SC and E-SC in comparison with E-A and E-Laff. Erten & Tanguler (2010) also stated the similar result obtained in the Emir wine sample which produced in the mixed inoculation of *Williopsis saturnus* and *Saccharomyces cerevisiae* (OAV>1).

Table 3.18. Suprathreshold Compounds for E-A, E-Laff, E-LT-SC and E-SC of Emir Wines

Compound	*RI*	*Odour Threshold (µg/L)*	*Odour Activity Values (OAV)*	*Odour Description*
Alcohols				
Isoamyl Alcohol	1236	60000	>1	Whiskey, nail polish [(1)]
3-Ethoxy-1-propanol	1389	100	>1	Fruity [(2)]
Phenylethyl Alcohol	1916	10000	>1	Rose, pollen, perfume [(1)]
Acetates				
Isoamyl acetate	1132	30	>1	Banana, fruity, sweet [(1)]
Phenethyl acetate	1827	250	>1	Pleasant, floral [(1)]
Esters				
Ethyl octanoate	1412	5	>1	Fruity, pineapple, pear, floral [(1)]
Ethyl decanoate	1610	200	>1	Waxy, fruity, rose [(1)]
Ethyl hexanoate	1241	5	>1	Flowery, fruity [(1)]
Aldehydes				
Nonanal	1658	2.8	>1	Citrusy, floral [(4)]
Acids				
Hexanoic acid	1832	3000	>1	Cheese, fatty [(1)]
Octanoic acid	2106	1000	>1	Cheese, fatty acid, rancid, harsh [(1)]
Phenols				
2-Methoxy-4-vinylphenol	2168	40	>1	Spices, curry [(2)]
4-vinyl-phenol	2334	180	>1	Pharmaceutical [(3)]

E-LT-SC: Emir wine sample inoculated with strain OB 4.CM NS4 (*L. thermotolerans*) and strain OB 4.CM S1 (*S. cerevisiae*), E-SC: Emir wine sample inoculated with strain OB 4CM S1 (*S. cerevisiae),* RI: retention indices, OAV: Odour activity values calculated by dividing found concentration by threshold of the compound.
(1) Wang, X., *et. al*., 2017; (2) Welke, J., et. al., 2014; (3) Swiegers, J., et. al., 2005; (4) Celik, Z., et. al., 2018.

The amounts of acetates were found as 0.67 mg/L for E-A, 1.67 mg/L for E-Laff, 3.23 mg/L for E-LT-SC and 1.91 mg/L for E-SC. Although banana flavor was found in all wine samples, the amount of isoamyl acetate was higher in E-LT-SC than the others. Isoamyl acetate differ significantly among the samples of wines. In this study, these amounts of isoamyl acetate were 1.41, 2.75, and 1.77 mg/L for E-Laff, E-LT-SC, and E-SC, respectively. Zohre & Erten (2002) also mentioned that the amounts of isoamyl acetate in the mixed inoculation of *Saccharomyces cerevisiae/Candida pulcherrima* and *Saccharomyces cerevisiae/ Kloeckera apiculata/Candida pulcherrima* were found 1.29 and 1.16 mg/L in the Emir wine samples, respectively. In addition, phenethyl acetate was significantly different and gave pleasant aroma in E-LT-SC. However, this aroma did not have the suprathreshold OAV in E-SC, E-A and E-Laff (OAV<1).

The amount of fatty acids was higher in E-SC than E-LT-SC, E-A and E-Laff. Especially, the concentration of hexanoic and octanoic acids were quite higher than the other compounds and significantly different among the Emir wine samples. These acids gave cheese aroma in the wines. This cheese aroma was noticed remarkably in E-SC.

The concentration of phenols was more considerable in E-LT-SC than E-SC. While 2-methoxy-4-vinylphenol gave curry spice aroma, 4-vinyl-phenol contributed pharmaceutical in both the wines. On the hand, 4-vinyl-phenol were not detected in E-A and E-Laff while 2-methoxy-4-vinylphenol was found lower level in E-A and E-Laff.

The other compounds such as tyrosol, soleron, guaiacol and acetoin were also detected. The concentration level of acetoin was obtained very low for odour in all these wine samples and it was not significantly different among these samples. Guaiacol was found detectable level in E-A and E-Laff. This aroma gave smoke odour in the wines. On the other hand, the odour threshold value of tyrosol and soleron were not found in the literature.

3.9.1.2. The Result of Volatile Compound Analysis of Red Wine

Red wines were made from Kalecik Karası grapes which were taken from Ankara at 2017. One of the red wines was prepared with strain 1 (*Hanseniaspora uvarum*) (K-HU). The other was made with strain 13 (*Saccharomyces cerevisiae*) (K-13). In order to compare, the other wines were traditional wine (K-A) made by Elnaz Seyid Monir and commercial wine made with using commercial Chr. Hansen starter culture (*Saccharomyces cerevisiae*) (K-SC).

The following three diagrams were shown the peaks of volatile compounds in GC-MS chromatogram for K-13, K-HU and K-SC, respectively (Figure 3.39-3.41).

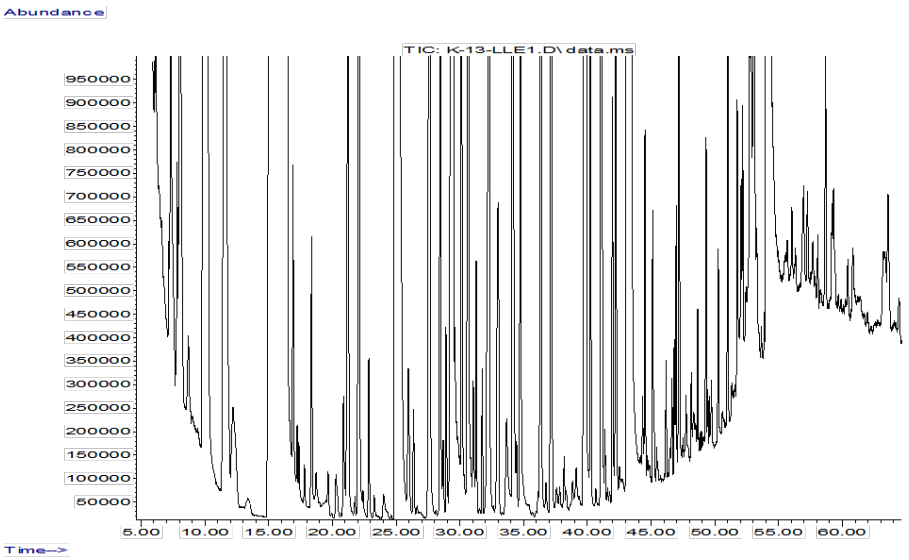


Figure 3.39. GC-MS Chromatogram of K-13 Sample

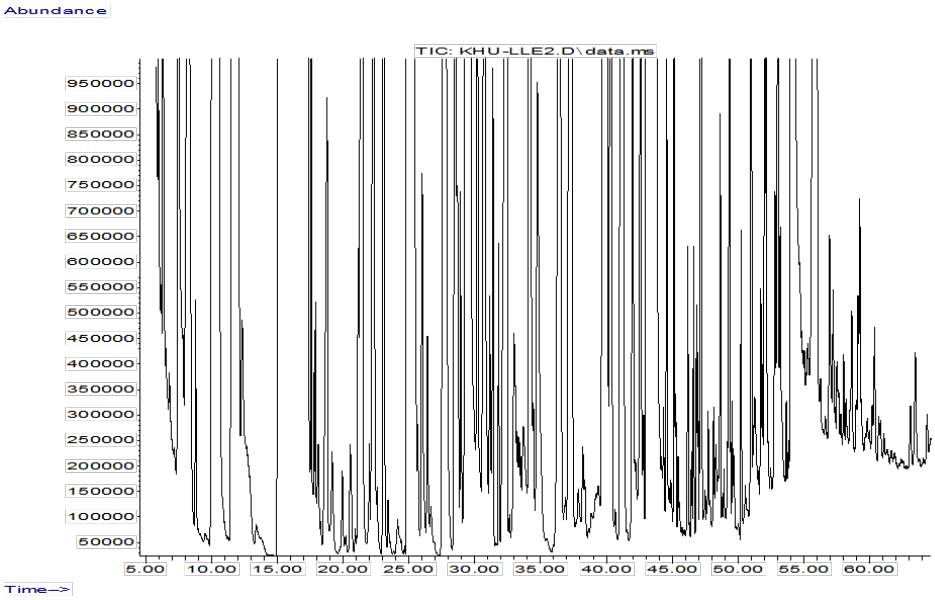


Figure 3.40. GC-MS Chromatogram of K-HU Sample

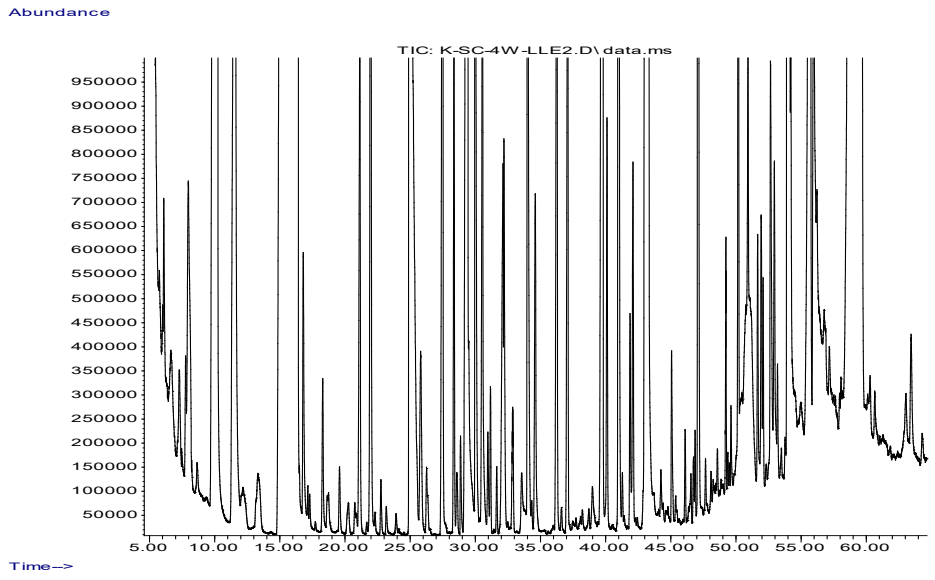


Figure 3.41. GC-MS Chromatogram of K-SC Sample

According to GS-MS results, 55 aroma compounds were identified for K-13, K-HU, K-SC and K-A (Table 3.17). These compounds included alcohols, acetates, esters, aldehydes, acids, lactones, phenols, and other compounds such as tyrosol, soleron, guaiacol, acetoin, geraniol and syringol. 52 of them were significantly different for these samples. The total concentrations of aroma compounds were found 146.83

mg/L in K-13, 139.54 mg/L in K-HU, 183.23 mg/L in K-SC and 188.28 mg/L in K-A. High alcohols and esters are the most abundant aroma in the wines. In previous studies, similar results have been reported in Dona Branca, Treixadura and Loureira wines (Falqué, Fernández, & Dubourdieu, 2002), Pinot Noir wines (Girard, Yuksel, Cliff, Delaquis, & Reynolds, 2001), Merlot and Cabernet Sauvignon wines (Kotseridis & Baumes, 2000).

The amounts of alcohols were found 130.84 mg/L, 127.28 mg/L, 165.54 mg/L and 167.13 mg/L for K-13, K-HU, K-SC and K-A respectively. In these alcohols, isobutyl alcohol, isoamyl alcohol, phenethyl alcohol and 2,3-butanediol were found very high level in these three wines. Isoamyl alcohol is an aroma compound that plays a role in the formation of the flavour of Kalecik karası wine (Sincar, 2010). Isoamyl alcohol and phenethyl alcohol had suprathreshold OAVs and gave whiskey and rose aroma, respectively in these wine samples (Table 3.19). In the previous studies, phenethyl alcohol, gave the rose aroma, was also reported to be important aroma compounds in Pinot Noir wine and Riesling wine. Moreover, fruity aroma (3-Ethoxy-1-propanol) was found higher in K-HU wine, and it was significantly different than K-13 and K-SC samples. In addition, odour of cooked vegetables was detected highly in K-HU, K-A and K-SC samples (OAV>1).

Esters contributes fruity and floral aroma in young wines (Rapp & Mandery, 1986). 7.16 mg/L, 4.97 mg/L, 5.40 mg/L 9.01 mg/L of esters were found in K-13, K-HU, K-SC and K-A, respectively. Ethyl 4-hydroxybutanoate and monoethyl succinate were found high amount and significantly differ among these wines. However, the odour threshold values of these aroma compounds were not found in the literature. According to OAV's, ethyl octanoate, and ethyl hexanoate affected aromas of these wines. They gave fruity aroma. Sincar (2010) also obtained a similar result in Kalecik karası wines with the application of cold maceration.

The amounts of acetates were found as 2.02 mg/L for K-13, 1.78 mg/L for K-HU, 2.47 mg/L for K-SC, 1.03 mg/L for K-A. Isoamyl acetate gave banana aroma in these wines. On the other hand, pleasant aroma (phenethyl acetate) enhanced remarkably in K-HU and K-13.

The concentrations of fatty acids were 4.30 mg/L, 3.00 mg/L, 6.54 mg/L and 5.68 in K-13, K-HU, K-SC, and K-A, respectively. Even though fatty acids may tend to have an adverse effect on wine flavor profile, they participate in the equilibrium reaction through the formation of this ester (Wang, Capone, Wilkinson, & Jeffery, 2016). Acetic acid, hexanoic acid, octanoic acid, isobutyric acid were found higher level in these wines with respect to total concentration.

The concentration of phenols was more considerable in K-SC than K-13, K-HU and K-A. 2-methoxy-4-vinylphenol gave curry spice aroma in these wines. Especially, 2-methoxy-4-vinyphenol enhanced remarkably in K-SC. Moreover, 4-vinyl-phenol was found as high odour value in K-SC (OAV>1). This gave pharmaceutical aroma in this wine.

The other compounds such as tyrosol, soleron, guaiacol, acetoin, geraniol, and syringol were also detected. Guaiacol and geraniol had suprathreshold OAVs (OAV>1). While guaiacol gave smoke flavors, geraniol contributes rose aroma for these wines. Geraniol was also a remarkable compound that was identified in orange wine and apricot wine (Kocabey, 2013).

Table 3.19. Suprathreshold Compounds for K-A, K-13, K-HU and K-SC in Wines of Kalecik Karası

Compound	*RI*	*Odour Threshold (µg/L)*	*Odour Activity Values*	*Odour Description*
Alcohols				
Isoamyl Alcohol	1236	60000	>1	Whiskey, nail polish (1)
3-Ethoxy-1-propanol	1389	100	>1	Fruity (3)
Methionol	1721	500	>1	Cooked vegetable (3)
Phenylethyl Alcohol	1916	10000	>1	Rose, pollen, perfume (1)
Acetates				
Isoamyl acetate	1132	30	>1	Banana, fruity, sweet (1)
Phenethyl acetate	1827	250	>1	Pleasant, floral (1)
Esters				
Ethyl octanoate	1412	5	>1	Fruity, pineapple, pear, floral (1)
Ethyl hexanoate	1241	5	>1	Flowery, fruity (1)
Aldehydes				
Nonanal	1658	2.8	>1	Citrusy, floral (3)
Phenols				
2-Methoxy-4-vinylphenol	2168	40	>1	Spices, curry (3)
Other Compounds				
Guaiacol	1840	10	>1	Smoke, sweet, medicine (3)
Geraniol	1844	20	>1	Roses, geranium (2)

K-13: Kalecik karası wine sample inoculated with strain 13 (*Saccharomyces cerevisiae*), K-HU: Kalecik karası wine sample inoculated with *Hanseniaspora uvarum* K-SC: Kalecik karası wine sample inoculated with commercial *Saccharomyces cerevisiae* (Chr. Hansen), K-A: Traditional wine made by Elnaz Seyid Monir RI: retention indices, OAV: Odour activity values calculated by dividing found concentration by threshold of the compound.
(1)Wang, X., et. al., 2017; (2) Arcari, S., et. al., 2017; (3) Welke, J., et. al., 2014; (4) Celik, Z., et. al., 2018

3.9.2. The Results of Sensory Analysis of Wine

Sensory analysis was made by the degustators. They evaluated the wines by giving the points. These points change between 1 (weak) to 5 (strong).

The sensory evaluation of Emir wines was based on colour, flavour, fullness, sweetness, acidness, bitterness, astringency, final astringency and general impression characteristics. Figure 3.42 showed that E-LT-SC, made by sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains in Emir grapes, was found more desirable than others with respect to flavour and general impression.

On the other hand, E-WA-SC, made by sequential inoculation of our *Wickerhamomyces anomalus* and *Saccharomyces cerevisiae* strains in Emir grapes, was liked with sweetness.

Gobbi et al. (2013) also reported that LT-SC sequential inoculation enhanced desirable aroma in white wines. Spicy notes and acidness were found significantly different in LT-SC wine.

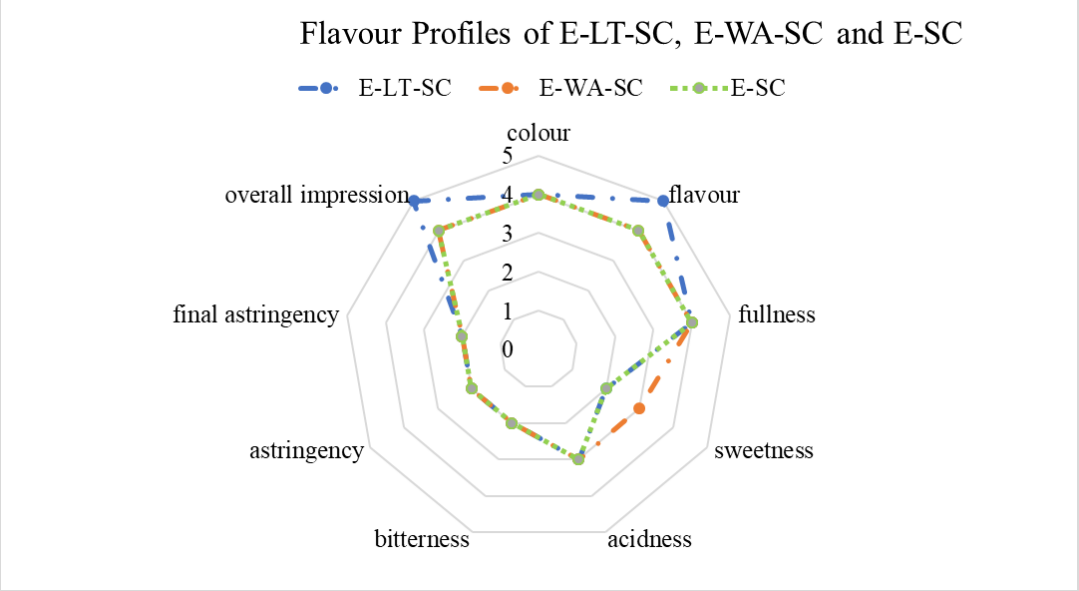


Figure 3.42. Flavour Profiles of E-LT-SC, E-WA-SC and E-SC

Figure 3.43 showed that traditional wines (E-A and E-B) were found more desirable than the commercial wine with respect to flavour and fullness, but they have not changed the overall impression score.

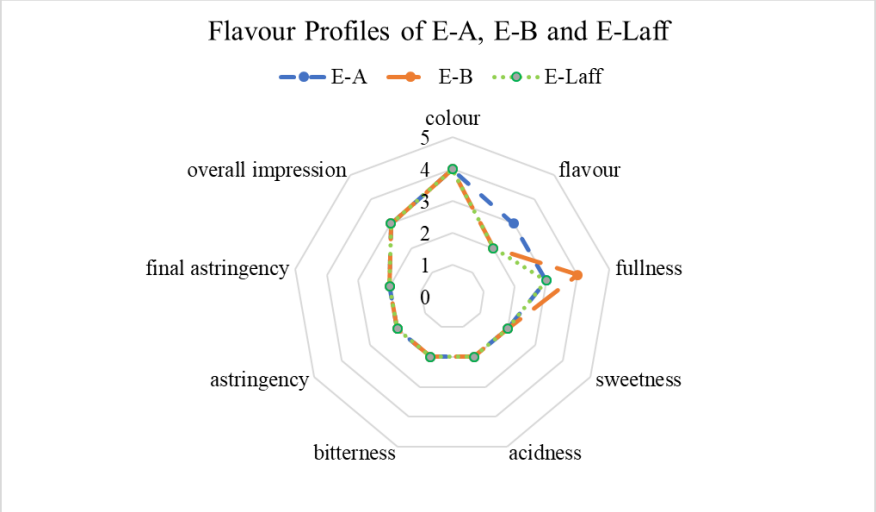


Figure 3.43. Flavour Profiles of E-A, E-B and E-Laff

Figure 3.44 showed that K-13, made by inoculation of our *Saccharomyces cerevisiae* strain in Kalecik Karası grapes, was found more desirable than others according to colour, flavour, fullness, and overall impression.

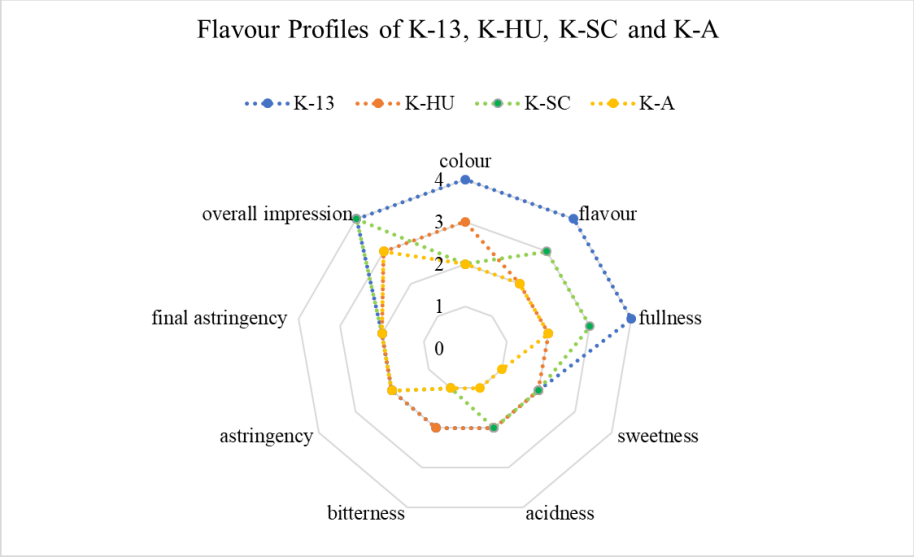


Figure 3.44. Flavour Profiles of K-13, K-HU, K-SC, and K-A

Figure 3.45 showed that O-LT-SC, made by sequential inoculation of our *Lachancea thermotolerans* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes, was found more desirable than others according to flavour, fullness, and overall impression. In

addition, acidity of O-HG-SC, made by sequential inoculation of our *Hanseniaspora guilliermondii* and *Saccharomyces cerevisiae* strains in Öküzgözü grapes was found higher than others.

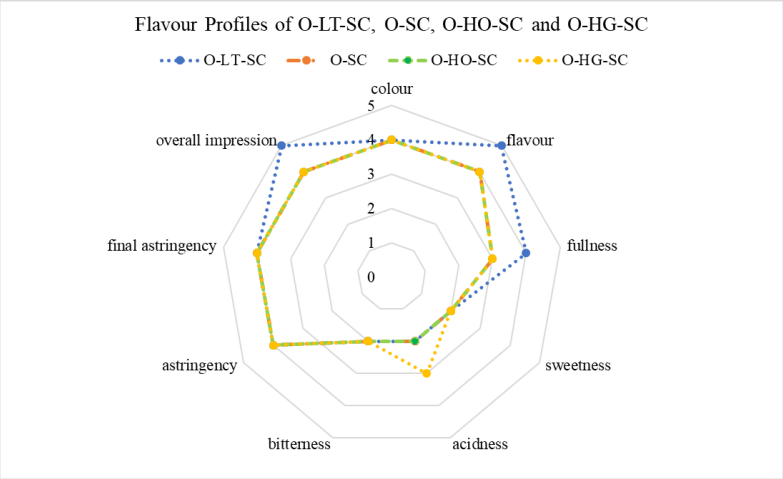


Figure 3.45. Flavour Profiles of O-LT-SC, O-SC, O-HO-SC, and O-HG-SC

Figure 3.46 showed that there was no significant difference between traditional and commercial wines of Öküzgözü grapes except flavour.

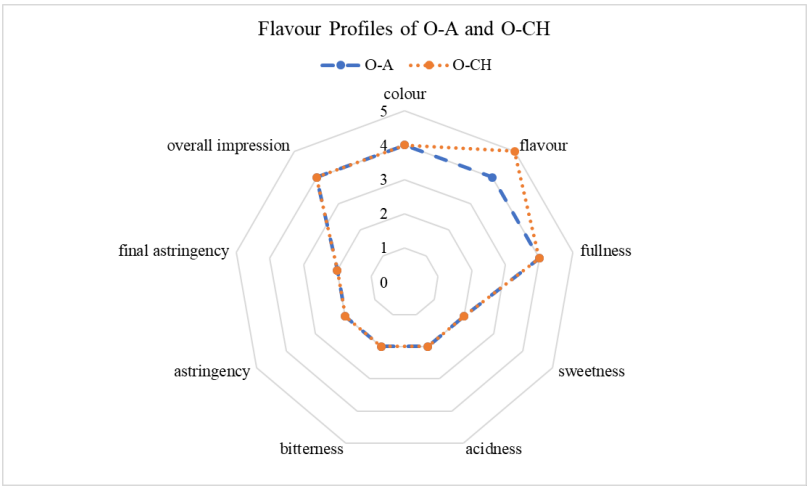


Figure 3.46. Flavour Profiles of O-A and O-CH

CHAPTER 4

CONCLUSION AND RECOMMENDATIONS

In this study, traditional wines were made from 5 type of grapes (Kalecik Karası, Öküzgözü, Boğazkere, Dimrit, and Emir) from 3 different states (Ankara, Elazığ, and Cappadocia) in Turkey. In these musts and wines, totally, 397 microorganisms were isolated. Strains which were selected according to phenotypic properties were identified by molecular (DNA sequencing for ITS region and/or D1/D2 domain) and biochemical methods (carbohydrate fermentation test). The numbers of isolated non-*Saccharomyces* and *Saccharomyces* yeasts in the culture collection were 104 and 293, respectively (Figure 4.1).

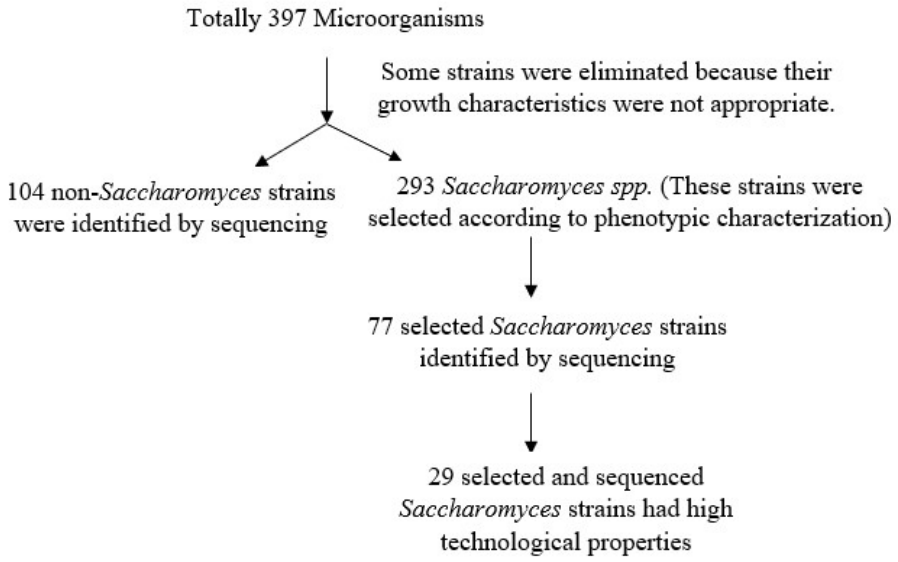


Figure 4.1. The Numbers of Isolated Non-*Saccharomyces* and *Saccharomyces* Yeasts in the Culture Collection

In this study, 16 different species were obtained as *Hanseniaspora guilliermondii*, *Hanseniaspora opuntiae*, *Hanseniaspora uvarum*, *Rhodotorula mucilaginosa*, *Wickerhamomyces anomalus*, *Metschnikowia aff. fructicola*, *Metschnikowia fructicola*, *Lachancea thermotolerans*, *Solicoccozyma aeria*, *Metschnikowia aff. pulcherrima*, *Metschnikowia pulcherrima*, *Metschnikowia sinensis, Metschnikowia chrysoperlae*, *Starmerella bacillaris*, *Saccharomyces cerevisiae* and *Saccharomyces cerevisiae/paradoxus.* However, *Metschnikowia sinensis* was identified as *Metschnikowia pulcherrima* and *Saccharomyces cerevisiae/paradoxus* as *Saccharomyces cerevisiae* by D1/D2 sequencing.

Phenotypic characterization was performed for isolated and identified strains. Firstly, alcohol tolerance and H_2S production of *Saccharomyces* yeasts were tested and having a high alcohol tolerance and low H_2S producing isolates were selected for each grape variety. SO_2, pH, temperature tolerance and carbohydrate fermentation abilities of selected isolates were also tested. According to these properties, the selection table was created (Table 3.17). General properties of these selected yeasts were 13% and above 13% alcohol tolerance, low H_2S production (1 or 2), resistance to pH (3, 4 and 6) (except DA 4. CM S3 strain), growth at 28˚C and 37˚C, fermentation of sucrose and maltose, dissimilation of maltose and lactose. These *Saccharomyces* isolates with high technological properties for wine production were selected as starter cultures.

In addition, non-*Saccharomyces* isolates were generally found low alcohol tolerance (below 10%), high SO_2 tolerance (200 mg/L), and intermediate and high H_2S production (3 and above 3). On the other hand, some of them were found high alcohol tolerance (15%) such as OA 4.CM S3 (*Wickerhamomyces anomalus*), OA 4.CM NS4 (*Hanseniaspora opuntiae*), KB 0.CM NS5 (*Wickerhamomyces anomalus*), DA 0.CM NS2 (*Metschnikowia aff. pulcherrima*). In addition, KA 2.NM NS1 (*Hanseniaspora opuntiae*), KA 4.NM NS5 (*Hanseniaspora opuntiae*) and DA 4.CM NS3 (*Metschnikowia pulcherrima*) produced low level of H_2S (2).

White and red wines were made using some isolates in our culture collection as a starter culture in order to analyze volatile compounds and flavour profiles. According to flavour profiles, Emir and Öküzgözü wines with *Lachancea thermotolerans* strain were found successful by degustators. Our *Lachancea thermotolerans* strain was randomly chosen from Öküzgözü grapes and inoculated sequentially with our *Saccharomyces cerevisiae* as starter cultures to produce wine. The total aroma concentrations were found higher in E-LT-SC (131.7 mg/L) than E-SC (113.2 mg/L) with respect to GS-MS results. 3-Ethoxy-1-propanol (fruity), isoamyl acetate (banana) and phenylethyl acetate (pleasant aroma) were higher in E-LT-SC wine while ethyl octanoate (pineapple), ethyl hexanoate (flowery), and hexanoic acid (cheese odour) were found highly in E-SC.

K-13 was found more successful than others by the degustators while the total concentrations of aroma compounds were 146.83 mg/L in K-13, 139.54 mg/L in K-HU and 183.23 mg/L in K-SC. 3-Ethoxy-1-propanol (fruity), methionol (cooked vegetable) and phenethyl acetate (pleasant) were found higher in K-HU, while guaiacol (smoke) was high level in K-13. On the other hand, isoamyl alcohol (whiskey aroma), phenylethyl alcohol (rose), isoamyl acetate (banana), ethyl octanoate (pineapple), ethyl hexanoate (flowery), 2-methoxy-4-vinylphenol (curry spice), and geraniol (rose) were found in all wine's samples (OAV>1).

This study revealed native non-*Saccharomyces* and *Saccharomyces* yeast populations in Turkey. Selected strains of starter cultures for authentic wine productions can be used to improve aroma and quality of native wines.

REFERENCES

Andorrà, I., Berradre, M., Rozès, N., Mas, A., Guillamón, J. M., & Esteve-Zarzoso, B. (2010). Effect of pure and mixed cultures of the main wine yeast species on grape must fermentations. *European Food Research and Technology*, *231*(2), 215–224. https://doi.org/10.1007/s00217-010-1272-0

Arbefeville, S., Harris, A., & Ferrieri, P. (2017). Comparison of sequencing the D2 region of the large subunit ribosomal RNA gene (MicroSEQ ®) versus the internal transcribed spacer (ITS) regions using two public databases for identification of common and uncommon clinically relevant fungal species. *Journal of Microbiological Methods*, 140, 40–46. https://doi.org/10.1016/j.mimet.2017.06.015

Arcari, S. G., Caliari, V., Sganzerla, M., & Godoy, H. T. (2017). Volatile composition of Merlot red wine and its contribution to the aroma: Optimization and validation of analytical method. Talanta, 174, 752-766. doi:10.1016/j.talanta.2017.06.074

Assis, M. O., Pereira, A., Santos, C., Rosa, C. A., Eugênia, M., & Mamede, D. O. (2014). Impact of a Non- *Saccharomyces* Yeast Isolated in the Equatorial Region in the Acceptance of Wine Aroma. *Food and Nutrition Sciences*, (April), 759–769. https://doi.org/10.4236/fns.2014.59086

Azzolini, M., Tosi, E., Lorenzini, M., Finato, F., & Zapparoli, G. (2015). Contribution to the aroma of white wines by controlled *Torulaspora delbrueckii* cultures in association with *Saccharomyces cerevisiae*. *World Journal of Microbiology and Biotechnology*, *31*(2), 277–293. https://doi.org/10.1007/s11274-014-1774-1

Bağder, S. (2008). Türkiye'de Değişik Şarap Bölgelerinden İzole Edilmiş Şarap Mayalarının Teknolojik Özellikleri. *(Master Thesis) Ankara University Ankara, Turkey.* https://doi.org/10.1017/CBO9781107415324.004

Baker, J. & Clarke, J. R. (2012). Wine flavour. *Wine Flavour Chemistry, Second Edition*. https://doi.org/10.1002/9780470995594

Balkan Pazar (n.d.). Retrieved from http://www.balkanpazar.org/tr_sarap.asp

Baleiras-Couto, M. M., & Eiras-Dias, J. E. (2006). Detection and identification of grape varieties in must and wine using nuclear and chloroplast microsatellite markers. *Analytica Chimica Acta*, *563*(1-2 SPEC. ISS.), 283–291. https://doi.org/10.1016/j.aca.2005.09.076

Barnett J.A., Payne R.W. and Yarrow D. (2000) *Yeasts: Characteristics and Identification*, 3rd edn. Cambridge University Press Cambridge, UK

Beckner, M. E., Carlin, S., Jacobson, D., Weighill, D., Divol, B., Conterno, L., Vrhovsek, U. (2015). Early fermentation volatile metabolite profile of non-*Saccharomyces* yeasts in red and white grape must : A targeted approach. *LWT - Food Science and Technology*, *64*(1), 412–422. https://doi.org/10.1016/j.lwt.2015.05.018

Boekhout, T., & Robert, V. (2014). *Yeasts in food: Beneficial and detrimental aspects*. London: Elsevier.

Belloch, C., Barrio, E., Garcia, M. D., & Querol, A. (1998). Phylogenetic reconstruction of the yeast genus *Kluyveromyces* : Restriction map analysis of the 5.8S rRNA gene and the two ribosomal internal transcribed spacers. *Systematic Nd Applied Microbiology*, (21), 266–273. https://doi.org/10.1016/S0723-2020(98)80032-5

Bouchilloux, P., Darriet, P., & Henry, R. (1998). Identification of volatile and powerful odorous thiols in bordeaux red wine varieties. *Journal of Agricultural and Food Chemistry*, *8561*(97), 3095–3099. https://doi.org/10.1021/jf971027d

Bowers, J., Boursiquot, J.M., This, P., Chu, K., Johansson, H., & Meredith, C. (1999). Historical genetics: the parentage of Chardonnay, Gamay, and other wine grapes of Northeastern France, *Ed. Science*, 285, 1562-1565. Retrieved from http://prodinra.inra.fr/record/56459

Cabaroglu, T., Canbas, A., Baumes, R., Bayonove, C., Lepoutre, J. P., & Günata, Z. (1997). Aroma composition of a white wine of *Vitis vinifera* L. cv. Emir as affected by skin contact. *Journal of Food Science*, *62*(4), 680–683. https://doi.org/10.1111/j.1365-2621.1997.tb15434.x

Cañas, P. M. I., García, A. T. P., & Romero, E. G. (2011). Enhancement of flavour properties in wines using sequential inoculations of non-*Saccharomyces* (*Hansenula* and *Torulaspora*) and *Saccharomyces* yeast. *VITIS - Journal of Grapevine Research*, *50*(4), 177–182. Retrieved from http://pub.jki.bund.de/index.php/VITIS/article/view/4088

Capece, A., Romaniello, R., Siesto, G., Pietrafesa, R., Massari, C., Poeta, C., & Romano, P. (2010). Selection of indigenous *Saccharomyces cerevisiae* strains for Nero d'Avola wine and evaluation of selected starter implantation in pilot fermentation. *International Journal of Food Microbiology*, *144*(1), 187–192. https://doi.org/10.1016/j.ijfoodmicro.2010.09.009

Cappello, M. S., Bleve, G., Grieco, F., Dellaglio, F., & Zacheo, G. (2004). Characterization of *Saccharomyces cerevisiae* strains isolated from must of grape grown in experimental vineyard. *Journal of Applied Microbiology*, *97*(6), 1274–1280. https://doi.org/10.1111/j.1365-2672.2004.02412.x

Carrau, F. M., Medina, K., Boido, E., Farina, L., Gaggero, C., Dellacassa, E., Henschke, P. A. (2005). De novo synthesis of monoterpenes by *Saccharomyces cerevisiae* wine yeasts. *FEMS Microbiology Letters*, *243*, 107–115. https://doi.org/10.1016/j.femsle.2004.11.050

Chavan, P., Mane, S., Kulkarni, G., Shaikh, S., Ghormade, V., Nerkar, D. P., Deshpande, M. V. (2009). Natural yeast flora of different varieties of grapes used for wine making in India. *Food Microbiology*, *26*(8), 801–808. https://doi.org/10.1016/j.fm.2009.05.005

Christoph, M. E., & Thomas, H.-K. (2001). Identification of *Brettanomyces/Dekkera* species based on polymorphism in the rRna internal transcribed spacer region. *American Journal of Enology and Viticulture*, *52*(3), 241–246.

Ciani, M. and Fatichenti, F. (1999). Selective sugar consumption by apiculate yeasts. *Lett. Appl. Microbiol*. 28: 203–206.

Ciani, M., & Ferraro, L. (1998). Combined use of immobilized *Candida stellata* cells and *Saccharomyces cerevisiae* to improve the quality of wines. *Journal of Applied Microbiology*, *85*(2), 247–254. https://doi.org/10.1046/j.1365-2672.1998.00485.x

Ciani, Maurizio, Beco, L., & Comitini, F. (2006). Fermentation behaviour and metabolic interactions of multistarter wine yeast fermentations. *International Journal of Food Microbiology*, *108*(2), 239–245. https://doi.org/10.1016/j.ijfoodmicro.2005.11.012

Clemente-Jimenez, J. M., Mingorance-Cazorla, L., Martínez-Rodríguez, S., Las Heras-Vázquez, F. J., & Rodríguez-Vico, F. (2005). Influence of sequential yeast mixtures on wine fermentation. *International Journal of Food Microbiology*, *98*(3), 301–308. https://doi.org/10.1016/j.ijfoodmicro.2004.06.007

Clemente-Jimenez, Josefa María, Mingorance-Cazorla, L., Martínez-Rodríguez, S., Las Heras-Vázquez, F. J., & Rodríguez-Vico, F. (2004). Molecular characterization and oenological properties of wine yeasts isolated during spontaneous fermentation of six varieties of grape must. *Food Microbiology*, *21*(2), 149–155. https://doi.org/10.1016/S0740-0020(03)00063-7

Cocolin, L., Pepe, V., Comitini, F., Comi, G., & Ciani, M. (2004). Enological and genetic traits of *Saccharomyces cerevisiae* isolated from former and modern wineries. *FEMS Yeast Research*, *5*(3), 237–245. https://doi.org/10.1016/j.femsyr.2004.08.005

Comitini, F., Gobbi, M., Domizio, P., Romani, C., Lencioni, L., Mannazzu, I., & Ciani, M. (2011). Selected non-*Saccharomyces* wine yeasts in controlled multistarter fermentations with *Saccharomyces cerevisiae*. *Food Microbiology*, *28*(5), 873–882. https://doi.org/10.1016/j.fm.2010.12.001

Cordero-bueso, G., Mangieri, N., Maghradze, D., Foschino, R., Valdetara, F., Cantoral, J. M., & Vigentini, I. (2017). Wild grape-associated yeasts as promising biocontrol agents against vitis vinifera fungal pathogens, *8*(November). https://doi.org/10.3389/fmicb.2017.02025

Çelik, Z. D., Erten, H., Darici, M., & Cabaroğlu, T. (2017). Molecular characterization and technological properties of wine yeasts isolated during spontaneous fermentation of *Vitis vinifera L.cv*. Narince grape must grown in ancient wine making area Tokat, Anatolia. *BIO Web of Conferences*, 9, 02017. https://doi.org/10.1051/bioconf/20170902017

D'Agata, I. (2014) Native wine grapes of Italy. Ed. *University of California Press*.

Dias, L., Dias, S., Sancho T., Stender, Querol H., A., Malfeito-Ferreira M., and Loureiro, V. (2003). Identification of yeasts isolated from wine-related environments and capable of producing 4-ethylphenol. Food Microbiol. 20: 567–574.

Don, B. (2006). *Handbook of Enology Volume 1 The Microbiology of Wine and Vinifications* 2 nd Edition (Vol. 1).

Ebeler, S. E., & Thorngate, J. H. (2009). *Wine chemistry and flavor* : *Looking into the Crystal Glas*s, 8098–8108. https://doi.org/10.1021/jf9000555

Englezos, V., Rantsiou, K., Torchio, F., Rolle, L., Gerbi, V., & Cocolin, L. (2015). Exploitation of the non-*Saccharomyces* yeast *Starmerella bacillaris* (synonym *Candida zemplinina*) in wine fermentation : Physiological and molecular characterizations. *International Journal of Food Microbiology*, *199*, 33–40. https://doi.org/10.1016/j.ijfoodmicro.2015.01.009

Erten, H. (2002). Relations between elevated temperatures and fermentation behaviour of *Kloeckera apiculata* and *Saccharomyces cerevisiae* associated with winemaking in mixed cultures. *World Journal of Microbiology and Biotechnology*, *18*(4), 377–382. https://doi.org/10.1023/a:1015221406411

Erten, H., & Tanguler, H. (2010). Influence of *Williopsis saturnus* yeasts in combination with *Saccharomyces cerevisiae* on wine fermentation. *Letters in Applied Microbiology*, *50*(5), 474–479. https://doi.org/10.1111/j.1472-765X.2010.02822.x

Escudero, A., Campo, E., Fariña, L., Cacho, J., & Ferreira, V. (2007). Analytical characterization of the aroma of five premium red wines. Insights into the role of odor families and the concept of fruitiness of wines. *Journal of Agricultural and Food Chemistry*, 55(11), 4501-4510. doi:10.1021/jf0636418

Esteve-Zarzoso, B., Belloch, C., Uruburu, F., & Querol, A. (2009). Identification of yeasts by RFLP analysis of the 5.8S rRNA gene and the two ribosomal internal transcribed spacers. *International Journal of Systematic Bacteriology*, *49*(1), 329–337. https://doi.org/10.1099/00207713-49-1-329

Esteve-Zarzoso, B., Peris-Toran, M. J., Garcia-Maiquez, E., Uruburu, F., & Querol, A. (2001). Yeast population dynamics during the fermentation and biological aging of sherry wines, *67*(5), 2056–2061. https://doi.org/10.1128/AEM.67.5.2056

Fang, Y., & Qian, M. C. (2016). Development of C_{13}-norisoprenoids , carotenoids and other volatile compounds in *Vitis vinifera L . Cv* . Pinot noir grapes. *Food Chemistry*, *192*, 633–641. https://doi.org/10.1016/j.foodchem.2015.07.050

FAO (2012). Retrieved from http://www.fao.org/home/en/

Fazzalari, F. A. (Ed.). (1978). Compilation of odor and taste threshold values data. doi: 10.1520/ds48a-eb

Fernandez-Espinar, M. T, Esteve-Zarzoso, B., Querol, A., & Barrio, E. (2000). RFLP analysis of the ribosomal internal transcribed spacers and the 5.8S rRNA gene region of the genus Saccharomyces: a fast method for species identification and the differentiation of flor yeasts. *Kl*, *78*, 87–97. https://doi.org/10.1023/B

Fernandez-Espinar, M. T., Llopis, S., Querol, A., & Barrio, E. (2011). Molecular Identification and Characterization of Wine Yeasts. https://doi.org/10.1016/B978-0-12-375021-1.10005-0

Fleet, G. H. (2003). Yeast interactions and wine flavour. *International Journal of Food Microbiology*, *86*(1–2), 11–22. https://doi.org/10.1016/S0168-1605(03)00245-9

Fugelsang, K. C., & Edwards, C. G. (2007). *Wine microbiology: Practical applications and procedures*. https://doi.org/10.1007/978-0-387-33349-6

Gaillardin C. and Heslot H. (1987) *Lalevure.* LaRecherche, 188 (18) 586–596.

Galet, P. (2015) Dictionnaire encyclopédique des cépages et de leurs synonymes. *Ed. Libre&Solidaire.*

Galet, P. (1990) Cépages et vignobles de France. *Ed. Ministère de la Recherche et de la Technologie*, Vol II.

Garavaglia, J., Schneider, R. de C. de S., Camargo Mendes, S. D., Welke, J. E., Zini, C. A., Caramão, E. B., & Valente, P. (2015). Evaluation of *Zygosaccharomyces bailii* BCV 08 as a co-starter in wine fermentation for the improvement of ethyl esters production. *Microbiological Research*, *173*, 59–65. https://doi.org/10.1016/j.micres.2015.02.002

García, M., Esteve-zarzoso, B., Crespo, J., Cabellos, J. M., & Arroyo, T. (2017). Yeast monitoring of wine mixed or sequential fermentations made by native strains from D.O."Vinos de Madrid " using real-time quantitative PCR, *8*(December), 1–15. https://doi.org/10.3389/fmicb.2017.02520

Ghosh, S. (2017). Metagenomic screening of cell wall hydrolases , their anti-fungal activities and potential role in wine fermentation. (March 2015). https://doi.org/10.13140/RG.2.2.28479.71846

Girard, B., Yuksel, D., Cliff, M. A., Delaquis, P., & Reynolds, A. G. (2001). Vinification effects on the sensory, colour and GC profiles of Pinot noir wines from British Columbia. *Food Research International*, *34*(6), 483–499. https://doi.org/10.1016/S0963-9969(00)00177-0

Gobbi, M., Comitini, F., Domizio, P., Romani, C., Lencioni, L., Mannazzu, I., & Ciani, M. (2013). *Lachancea thermotolerans* and *Saccharomyces cerevisiae* in simultaneous and sequential co-fermentation: A strategy to enhance acidity and improve the overall quality of wine. *Food Microbiology*, *33*(2), 271–281. https://doi.org/10.1016/j.fm.2012.10.004

Goldhawke, B., Kahlon, M., Lotto, J., & Deeg, C. M. (2016). Yeasts from greenhouse grapes show less phenotypic and genetic diversity than yeasts from vineyard grapes when isolated from grape crush cultured in liquid media, *2*(June), 8–15.

González-Arenzana, L., Garijo, P., Berlanas, C., López-Alfaro, I., López, R., Santamaría, P., & Gutiérrez, A. R. (2017). Genetic and phenotypic intraspecific variability of non-*Saccharomyces* yeasts populations from La Rioja winegrowing region (Spain). *Journal of Applied Microbiology*, *122*(2), 378–388. https://doi.org/10.1111/jam.13341

Guillamön, J. M., Sabaté, J., Barrio, E., Cano, J., & Querol, A. (1998). Rapid identification of wine yeast species based on RFLP analysis of the ribosomal internal transcribed spacer (ITS) region. *Archives of Microbiology*, *169*(5), 387–392. https://doi.org/10.1007/s002030050587

Guimaraes, T. M., Moriel, D. G., Machado, I. P., Fadel Picheth, C. M. T., Bonfim, T. (2006). Isolation and characterization of *Saccharomyces cerevisiae* strains of winery interest. *Revista Brasileira de Ciencias Farmaceuticas*, *42*(1), 119–126. https://doi.org/10.1590/S1516-93322006000100013

Henick-Kling, T., Edinger, W., Daniel, P., & Monk, P. (1998). Selective effects of sulfur dioxide and yeast starter culture addition on indigenous yeast populations and sensory characteristics of wine. *Journal of Applied Microbiology*, *84*, 865–876. https://doi.org/10.1046/j.1365-2672.1998.00423.x

Herraiz, T., Reglero, G., Martin-Alvarez, P. J., Herraiz, M., & Cabezudo, M. D. (1991). Identification of aroma components of Spanish 'Verdejo' wine. *Journal of the Science of Food and Agriculture*, 55(1), 103-116. doi:10.1002/jsfa.2740550111

Hesham, A. E., & Hashem, M. M. (2011). Molecular genetic identification of yeast strains isolated from egyptian soils for solubilization of inorganic phosphates and growth promotion of corn plants. *J. Microbial. Biotechnol.*, *21*(November 2010), 55–61. https://doi.org/10.4014/jmb.1006.06045

Hesham, A. E. L., Wambui, V., Ogola J.O., H., & Maina, J. M. (2014). Phylogenetic analysis of isolated biofuel yeasts based on 5.8S-ITS rDNA and D1/D2 26S rDNA sequences. *Journal of Genetic Engineering and Biotechnology*, *12*(1), 37–43. https://doi.org/10.1016/j.jgeb.2014.01.001

Hidalgo, L. (2002) Tratado de Viticultura General. *Ed. Mundi-Prensa*.

Hierro, N., González, Á., Mas, A., & Guillamón, J. M. (2006). Diversity and evolution of non-*Saccharomyces* yeast populations during wine fermentation: Effect of grape ripeness and cold maceration. *FEMS Yeast Research*, *6*(1), 102–111. https://doi.org/10.1111/j.1567-1364.2005.00014.x

Hu, K., Zhu, X. L., Mu, H., Ma, Y., Ullah, N., & Tao, Y. S. (2016). A novel extracellular glycosidase activity from *Rhodotorula mucilaginosa*: ITS application potential in wine aroma enhancement. *Letters in Applied Microbiology*, *62*(2), 169–176. https://doi.org/10.1111/lam.12527

Hyma, K. E., Saerens, S. M., Verstrepen, K. J., & Fay, J. C. (2011). Divergence in wine characteristics produced by wild and domesticated strains of *Saccharomyces cerevisiae*. *FEMS Yeast Research, 11*(7), 540-551. doi:10.1111/j.1567-1364.2011.00746.x

International Organisation of Vine and Wine. (2017). Retrieved from http://www.oiv.int/

Jolly, N. P., Augustyn, O. P. H., & Pretorius, I. S. (2006). The role and use of non-*Saccharomyces* yeasts in wine production. *South African Journal of Enology & Viticulture*, *27*(1). https://doi.org/10.21548/27-1-1475

Karabat, S. (2014). *Dünya ve Türkiye Bağcılığı*. Retrieved from http://apelasyon.com/Yazi/33-dunya-ve-turkiye-bagciligi

Kim, D. H., Hong, Y. A., & Park, H. D. (2008). Co-fermentation of grape must by *Issatchenkia orientalis* and *Saccharomyces cerevisiae* reduces the malic acid content in wine. *Biotechnology Letters*, *30*(9), 1633–1638. https://doi.org/10.1007/s10529-008-9726-1

King, A., & Dickinson, J. R. (2000). Biotransformation of monoterpene alcohols by *Saccharomyces cerevisiae*, *Torulaspora delbrueckii* and *Kluyveromyces lactis*. *Yeast*, (16), 499–506.

Kish, S., Sharf, R., & Margalith, P. (1983). A note on a selective medium for wine yeasts. *Journal of Applied Microbiology*, 55(1), 177-179.

Kocabey, N. (2013). Arapgir'de Yetiştirilen Karaoğlan ve Aşık Beyazı Üzümlerinin ve Bu Üzümlerden Elde Edilen Şarapların Fenol Bileşiklerinin ve Aroma Maddelerinin Belirlenmesi. *(Master Thesis)* Inonu University, Malatya, Turkey

Kotseridis, Y., & Baumes, R. (2000). Identification of impact odorants in Bordeaux red grape juice, in the commercial yeast used for its fermentation, and in the produced wine. *Journal of Agricultural and Food Chemistry*, *48*(2), 400–406. https://doi.org/10.1021/jf990565i

Kurtzman, C. P. (2011). Discussion of teleomorphic and anamorphic ascomycetous yeasts and yeast-like taxa. *The Yeasts* (Vol. 2). Elsevier B.V. https://doi.org/10.1016/B978-0-444-52149-1.00013-6

Kurtzman, C. P., Fell, J. W., Boekhout, T., & Robert, V. (n.d.). Methods for Isolation, Phenotypic Characterization and Maintenance of Yeasts. *The Yeasts, A Taxonomic Study*. Elsevier B.V. https://doi.org/10.1016/B978-0-444-52149-1.00007-0

Kurtzman, C. P., & Robnett, C. J. (1998). Identification and phylogeny of ascomycetous yeasts from analysis of nuclear large subunit (26S) ribosomal DNA partial sequences. *Antonie van Leeuwenhoek, International Journal of General and Molecular Microbiology*, *73*(4), 331–371. https://doi.org/10.1023/A:1001761008817

Lacombe, T., (2012) Contribution à l'étude de l'histoire évolutive de la vigne cultivée (Vitis vinifera L.) par l'analyse de la diversité génétique neutre et de gènes d'intérêt, Montpellier, France.

Lambrechts, M., & Pretorius, I. S. (2000). Yeast and its importance to wine aroma-a review. *South African Journal of Enology & Viticulture*, (21), 97–129.

Li, S. S., Cheng, C., Li, Z., Chen, J. Y., Yan, B., Han, B. Z., & Reeves, M. (2010). Yeast species associated with wine grapes in China. *International Journal of Food Microbiology*, *138*(1–2), 85–90. https://doi.org/10.1016/j.ijfoodmicro.2010.01.009

Liu, N., Song, Y., Dang, G., Ye, D., Gong, X., & Liu, Y. (2015). Effect of wine closures on the aroma properties of chardonnay wines after four years of storage. South African Journal of Enology and Viticulture, 36(3). doi:10.21548/36-3-963 Maul, E., & Topfer, R., Vitis International Variety Catalogue (VIVC): A cultivar database referenced by genetic profiles and morphology, BIO Web of conferences Vol. 5, Article No. 01009, 2015

Macías, M., Manso, A., Orellana, C., Velasco, H., Caballero, R., & Chamizo, J. (2012). Acetic acid detection threshold in synthetic wine samples of a portable electronic nose sensors, 13(1), 208-220. doi:10.3390/s130100208

Mateo, J. J., & Jimenez, M. (2000). Monoterpenes in grape juice and wines. *J. Chromatogr. A*, *881*, 557–567

Medina, K., Boido, E., Fariña, L., Gioia, O., Gomez, M. E., Barquet, M., Carrau, F. (2013). Increased flavour diversity of Chardonnay wines by spontaneous fermentation and co-fermentation with *Hanseniaspora vineae*. *Food Chemistry*, *141*(3), 2513–2521. https://doi.org/10.1016/j.foodchem.2013.04.056

Meredith, C., & Boursiquot, J.M. (2008) Origins and importance of Syrah around the world, in: Proceedings of the International Syrah Symposium, 17-20. Presented at the International Syrah Symposium, Lyon (France). Retrieved from http://prodinra.inra.fr/record/184458

Mendoza, L. M., De Nadra, M. C. M., & Farias, M. E. (2007). Kinetics and metabolic behavior of a composite culture of *Kloeckera apiculata* and *Saccharomyces cerevisiae* wine related strains. *Biotechnology Letters*, (29), 1057–1063. https://doi.org/10.1007/s10529-007-9355-0

Meyer, S.A., Payne, R.W. and Yarrow, D. (1998) *Candida* Berkhout. In: The Yeasts. C.P. Kurtzman and J.W. Fell (Eds.), 4th edition, Chapter 64, pp. 454–573. Elsevier, New York, NY.

Moreira, N., Mendes, F., Guedes de Pinho, P., Hogg, T., & Vasconcelos, I. (2008). Heavy sulphur compounds, higher alcohols and esters production profile of *Hanseniaspora uvarum* and *Hanseniaspora guilliermondii* grown as pure and mixed cultures in grape must. *International Journal of Food Microbiology*, *124*(3), 231–238. https://doi.org/10.1016/j.ijfoodmicro.2008.03.025

Moreira, Nathalie, Mendes, F., Hogg, T., & Vasconcelos, I. (2005). Alcohols, esters and heavy sulphur compounds production by pure and mixed cultures of apiculate wine yeasts. *International Journal of Food Microbiology*, *103*(3), 285–294. https://doi.org/10.1016/j.ijfoodmicro.2004.12.029

Moreira, N., Pinho, P. G., Santos, C., & Vasconcelos, I. (2010). Volatile sulphur compounds composition of monovarietal white wines. Food Chemistry, 123(4), 1198-1203. doi:10.1016/j.foodchem.2010.05.086

Morinaga, K., (2001) Grape production in Japan, in: Papademetriou, M.K. & Dent, F.J., Grape production in the Asia-Pacific region, *Ed. FAO*, pp. 38-52.

Nwaiwu, O. (2019). Phylogeny of three palmwine yeasts genera. recent advances in phylogenetics. doi:10.5772/intechopen.79958

Nelsen M.P. (2018) Primer maps. http://sites.google.com/site/mpnelsen/primer-maps.

Nikolaou, E., Soufleros, E. H., Bouloumpasi, E., & Tzanetakis, N. (2006). Selection of indigenous *Saccharomyces cerevisiae* strains according to their oenological characteristics and vinification results. *Food Microbiology*, *23*(2), 205–211. https://doi.org/10.1016/j.fm.2005.03.004

Nurgel, C., Erten, H., Canbas, A., Cabaroglu, T., & Selli, S. (2005). Yeast flora during the fermentation of wines made from *Vitis vinifera L. cv*. Emir and Kalecik Karasi grown in Anatolia. *World Journal of Microbiology and Biotechnology*, *21*(6–7), 1187–1194. https://doi.org/10.1007/s11274-005-1106-6

Padilla, B., Gil, J. V., & Manzanares, P. (2016). Past and future of non-*Saccharomyces* yeasts: From spoilage microorganisms to biotechnological tools for improving wine aroma complexity. Frontiers in Microbiology, 7(MAR), 1–20. https://doi.org/10.3389/fmicb.2016.00411

Pallmann, C. L., Brown, J. A., Olineka, T. L., Cocolin, L., Mills, D. A., & Bisson, L. F. (2001). Use of WL medium to profile native flora fermentations. Am. J. Enol. Vitic., 52(3), 198-203

Parker, M., Osidacz, P., Baldock, G. A., Hayasaka, Y., Black, C. A., Pardon, K. H., . . . Francis, I. L. (2012). Contribution of Several Volatile Phenols and Their Glycoconjugates to Smoke-Related Sensory Properties of Red Wine. Journal of Agricultural and Food Chemistry, 60(10), 2629-2637. doi:10.1021/jf2040548

Pastor, A., Huerta, T., Mateo, J. J., & Jime, M. (2001). Yeast starter cultures affecting wine fermentation and volatiles, *34*.

Pham, T., Wimalasena, T., Box, W., G., Koivuranta, K., Storgards, E., Smart, K. A., & Gibson, B. R. (2011). Evaluation of ITS PCR and RFLP for differentiation and identification of brewing yeast and brewery “wild” yeast contaminants. *Journal of the Institute of Brewing*, *117*(4), 556–568. https://doi.org/10.1002/j.2050-0416.2011.tb00504.x

Pina, C., Santos, C., Couto, J. A., & Hogg, T. (2004). Ethanol tolerance of five non-*Saccharomyces* wine yeasts in comparison with a strain of *Saccharomyces cerevisiae* - Influence of different culture conditions. *Food Microbiology*, *21*(4), 439–447. https://doi.org/10.1016/j.fm.2003.10.009

Pretorius, I. S. (n.d.). The tailoring of grapevine cultivars and wine yeast strains for a market-directed and quality-focused wine industry : Novel approaches to the ancient art of winemaking. *Yeast*.

Rantsiou, K., Dolci, P., Giacosa, S., Torchio, F., Tofalo, R., Torriani, S., Cocolin, L. (2012). *Candida zemplinina* can reduce acetic acid produced by *Saccharomyces cerevisiae* in sweet wine fermentations. *Applied and Environmental Microbiology*, *78*(6), 1987–1994. https://doi.org/10.1128/aem.06768-11

Rapp, A., & Mandery, H. (1986). Wine aroma. *Experientia*, *42*(8), 873–884.

Rapp, A., & Versini, G. (1995). Influence of nitrogen compounds in grapes on aroma compounds of wines, 1659–1694.

Rodriguez, M. E., Lopes, C. A., Van Broock, M., Valles, S., Ramon, D., & Caballero, A. C. (2004). Screening and typing of Patagonian wine yeasts for glycosidase activities, 84–95. https://doi.org/10.1046/j.1365-2672.2003.02032.x

Rojas, V., Gil, J. V., Piñaga, F., & Manzanares, P. (2003). Acetate ester formation in wine by mixed cultures in laboratory fermentations. *International Journal of Food Microbiology*, *86*(1–2), 181–188. https://doi.org/10.1016/S0168-1605(03)00255-1

Romancino, D. P., Maio, S. Di, Muriella, R., & Oliva, D. (2008). Analysis of non-*Saccharomyces* yeast populations isolated from grape musts from Sicily (Italy), *105*, 2248–2254. https://doi.org/10.1111/j.1365-2672.2008.03894.x

Romanelli, A. M., Fu, J., Herrera, M. L., & Wickes, B. L. (2014). A universal DNA extraction and PCR amplification method for fungal rDNA sequence-based identification. *Mycoses*, *57*(10), 612–622. https://doi.org/10.1111/myc.12208

Romano, P., Fiore, C., Paraggio, M., Caruso, M., & Capece, A. (2003). Function of yeast species and strains in wine flavour. *International Journal of Food Microbiology*, *86*, 169–180. https://doi.org/10.1016/S0168-1605(03)00290-3

Romano, P., Suzzi, G., Comi, G., Zironi, R., & Maifreni, M. (1997). Glycerol and other fermentation products of apiculate wine yeasts. *Journal of Applied Microbiology*, *82*(5), 615–618. https://doi.org/10.1111/j.1365-2672.1997.tb02870.x

Ru, M., Bernal-grande, M. C., Cordero-bueso, G., & Hughes-herrera, D. (2017). A microtiter plate assay as a reliable method to assure the identification and classification of the veil-forming yeasts during sherry wines ageing. https://doi.org/10.3390/fermentation3040058

Selli, S., Cabaroglu, T., Canbas, A., Erten, H., Nurgel, C., Lepoutre, J., & Gunata, Z. (2004). Volatile composition of red wine from *cv.* Kalecik Karası grown in central Anatolia. Food Chemistry, 85(2), 207-213. doi:10.1016/j.foodchem.2003.06.008

Sidhu, D., Lund, J., Kotseridis, Y., Saucier, C., Sidhu, D., Lund, J., & Kotseridis, Y. (2015). Methoxypyrazine analysis and influence of viticultural and enological procedures on their levels in grapes , musts , and wines *Crit. Rev. Food Sci. Nutr.*, 485–502. https://doi.org/10.1080/10408398.2012.658587

Sincar, Ö. (2010). Kalecik karası üzümlerinden kırmızı şarap üretiminde soğuk maserasyon uygulamasının aroma ve antosiyanin bileşikleri üzerine etkileri. *(Master Thesis)* Cukurova University, Adana, Turkey

Smith, M.Th. 1998b. Brettanomyces Kufferath and van Laer. In: The Yeasts. C.P. Kurtzman and J.W. Fell (Eds.), 4th edition, Chapter 63, pp. 450–453. Elsevier, New York, NY

Snow, P.G. and Gallander, J.F. (1979) Deacidification of white table wines through partial fermentation with *Schizosaccharomyces pombe*. *Am. J. Enol. Vitic*. 30, 45-48.

Swiegers, J. H., & Pretorius, I. S. (2005). Yeast modulation of wine flavor. *Advances in Applied Microbiology*, *57*(SUPPL. A), 131–175. https://doi.org/10.1016/S0065-2164(05)57005-9

Tao, Y., & Zhang, L. (2010). Intensity prediction of typical aroma characters of cabernet sauvignon wine in Changli County (China). LWT - Food Science and Technology, 43(10), 1550-1556. doi:10.1016/j.lwt.2010.06.003

Thomas, D.S. & Davenport R.R. (1985). *Zygosaccharomyces bailii* a profile of characteristics and spoilage activities. Food Microbiol. 2: 157–169.

Tofalo, R., Chaves-López, C., Di Fabio, F., Schirone, M., Felis, G. E., Torriani, S. (2009). Molecular identification and osmotolerant profile of wine yeasts that ferment a high sugar grape must. *International Journal of Food Microbiology*, 130(3), 179-187.

Toro, M. E., & Vazquez, F. (2002). Fermentation behaviour of controlled mixed and sequential cultures of *Candida cantarellii* and *Saccharomyces cerevisiae* wine yeasts. *World Journal of Microbiology & Biotechnology*, *18*, 347–354. https://doi.org/10.1023/A:1015242818473

Tristezza, M., Tufariello, M., Capozzi, V., Spano, G., Mita, G., & Grieco, F. (2016). The oenological potential of *Hanseniaspora uvarum* in simultaneous and sequential co-fermentation with *Saccharomyces cerevisiae* for industrial wine production. *Frontiers in Microbiology*, *7*(MAY), 1–14. https://doi.org/10.3389/fmicb.2016.00670

Türk Gıda Kodeksi Şarap Tebliği (NO: 2008/67). Retrieved from http://www.gidamo.org.tr/mevzuat/mevzuat_detay.php?kod=76

Urso, R., Rantsiou, K., Dolci, P., Rolle, L., Comi, G., & Cocolin, L. (2008). Yeast biodiversity and dynamics during sweet wine production as determined by molecular methods. https://doi.org/10.1111/j.1567-1364.2008.00364.x

Ükelgi, N. (2011). Isolation, identification and characterization of wine yeast species from grapes of three different vineyards in Turkey. *(Master Thesis)* Sabancı University, Istanbul, Turkey.

Valero, E., Moyano, L., Millan, M. C., Medina, M., & Ortega, J. M. (2002). Higher alcohols and esters production by *Saccharomyces cerevisiae*. Influence of the initial oxygenation of the grape must. *Food Chemistry*, *78*(1), 57–61. https://doi.org/10.1016/S0308-8146(01)00361-2

Van der Aa Kühle, A., & Jespersen, L. (1998). Detection and identification of wild yeasts in lager breweries. International Journal of Food Microbiology, 43(3), 205-213.

Van der Walt, J.P. and Van Kerken, A. E. (1961). The wine yeasts of the Cape. Part V. Studies on the occurrence of *Brettanomyces intermedius* and *Brettanomyces schanderlii*. Antonie van Leeuwenhoek 27: 81–90.

Van Dijken, J.P., and Harder, W.(1974) Optimal conditions for the enrichment and isolation of methanol-assimilating yeasts. *J .Gen. Microbiol*. 84, 409-411

Vaughan-Martini, A. and Martini, A. (1998) Determination of ethanol production, In: The Yeasts, A Taxonomic Study. Kurtzman, C.P. and Fell, J.W. (eds), Elsevier, pp. 107, Amsterdam.

Viana, F., Gil, J. V., Genovés, S., Vallés, S., & Manzanares, P. (2008). Rational selection of non-*Saccharomyces* wine yeasts for mixed starters based on ester formation and enological traits. *Food Microbiology*, *25*(6), 778–785. https://doi.org/10.1016/j.fm.2008.04.015

Villa-Carvajal, M., Querol, A., & Belloch, C. (2006). Identification of species in the genus *Pichia* by restriction of the internal transcribed spacers (ITS1 and ITS2) and the 5.8S ribosomal DNA gene. *Antonie van Leeuwenhoek, International Journal of General and Molecular Microbiology*, *90*(2), 171–181. https://doi.org/10.1007/s10482-006-9071-0

Vries, C. D., Buica, A., Brand, J., & Mckay, M. (2016). The impact of smoke from vegetation fires on sensory characteristics of cabernet sauvignon wines made from affected grapes. South African Journal of Enology and Viticulture, 37(1). doi:10.21548/37-1-755

Wang, J., Capone, D. L., Wilkinson, K. L., & Jeffery, D. W. (2016). Chemical and sensory profiles of rosé wines from Australia. *Food Chemistry*, *196*, 682–693. https://doi.org/10.1016/j.foodchem.2015.09.111

Wang, X. C., Li, A. H., Dizy, M., Ullah, N., Sun, W. X., & Tao, Y. S. (2017). Evaluation of aroma enhancement for "Ecolly" dry white wines by mixed inoculation of selected *Rhodotorula mucilaginosa* and *Saccharomyces cerevisiae*. *Food Chemistry*, *228*, 550–559. https://doi.org/10.1016/j.foodchem.2017.01.113

Welke, J. E., Zanus, M., Lazzarotto, M., & Zini, C. A. (2014). Quantitative analysis of headspace volatile compounds using comprehensive two-dimensional gas chromatography and their contribution to the aroma of Chardonnay wine. Food Research International, 59, 85-99. doi:10.1016/j.foodres.2014.02.002

Wines of Turkey. (2019). Retrieved from http://www.winesofturkey.org/

Ye, M., Yue, T., & Yuan, Y. (2014). Effects of sequential mixed cultures of *Wickerhamomyces anomalus* and *Saccharomyces cerevisiae* on apple cider fermentation. *FEMS Yeast Research*, *14*(6), 873–882. https://doi.org/10.1111/1567-1364.12175

Zalacain, A., Marin, J., Alonso, G. L., & Salinas, M. R. (2007). Analysis of wine primary aroma compounds by stir bar sorptive extraction. *Talanta*, *71*, 1610–1615. https://doi.org/10.1016/j.talanta.2006.07.051

Zanol, G. C., Baleiras-Couto, M. M., & Duarte, F. L. (2010). Restriction profiles of 26S rDNA as a molecular approach for wine yeasts identification. *Ciencia e Tecnica Vitivinicola*, *25*(2), 75–85.

Ženišová, K., Chovanová, K., Chebeňová-Turcovská, V., Godálová, Z., Kraková, L., Kuchta, T., Brežná, B. (2014). Mapping of wine yeast and fungal diversity in the Small Carpathian wine-producing region (Slovakia): evaluation of phenotypic, genotypic and culture-independent approaches. *Annals of Microbiology*, *64*(4), 1819–1828. https://doi.org/10.1007/s13213-014-0827-x

Zohre, D. E., & Erten, H. (2002). The influence of *Kloeckera apiculata* and *Candida pulcherrima* yeasts on wine fermentation. *Process Biochemistry*, *38*(3), 319–324. https://doi.org/10.1016/S0032-9592(02)00086-9

Zott, K., Miot-Sertier, C., Claisse, O., Lonvaud-Funel, A., & Masneuf-Pomarede, I. (2008). Dynamics and diversity of non-*Saccharomyces* yeasts during the early stages in winemaking. *International Journal of Food Microbiology*, *125*(2), 197–203. https://doi.org/10.1016/j.ijfoodmicro.2008.04.001

APPENDICES

A. DNA Sequencing of Isolated Yeasts

Table A.1. DNA Sequencing of Isolated Yeasts

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KA 0.CM NS1 (K1)	*Hanseniaspora guilliermondii*	100%	ITS	GGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTAGTTTTAG ATCTTTTACAATAATGTGTATCTTTATTGAAGATGTGCGCTTAATTGCGC TGCTTTTTTAAAGTGTCGCAGTAGAAGTAATCTTGCTTGAATCTCAGTCA ACGTTTACACACATTGGAGTTTTTTTACTTTAATTTAATTCTTTCTGCTTT GAATCGAAAGGTTCAAGGCAAAAAACAAACACAAACAATTTTATTTTAT TATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTTAAAATAA TTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC GTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGTGAATCATT GAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGGGCATGCCT GTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTGTG GGCGATACTCAGGGTTAGCTTGAAATTGAAGATTGTTTCAATCTTTTTTA ATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATTTA TGAATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGTACCTTAGGCA AAGGGTTGCTTTTAATATTCATCAAGTTGACCTCAA
KA 0.CM NS2 (K2)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAG
KA 0.CM NS3 (K3)	*Hanseniaspora uvarum*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAGGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTATTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAACGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTTGACCTC
KA 0.CM NS5 (K5)	*Hanseniaspora guilliermondii*	100%	D1/D2 Domain	CGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTTTCAGT GCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATG TTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGG ATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAATG CAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGA GACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGA AAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTG ATCAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCT CTCAAAAATTTCACTGGGCCAACATCAGTTCTGGCAGCAGGATAAATCA TTAAGAATGTAGCTACCTCGGTAGTGTTATAGCTTATTGGAATACTGCT AGCTGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGCATAATGGTTA AATGCCGCCCG
		100%	ITS	CGGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTAGTTTTA GATCTTTTACAATAATGTGTATCTTTATTGAAGATGTGCGCTTAATTGCG CTGCTTTTTTAAAGTGTCGCAGTAGAAGTAATCTTGCTTGAATCTCAGTC AACGTTTACACACATTGGAGTTTTTTTACTTTAATTTAATTCTTTCTGCTT TGAATCGAAAGGTTCAAGGCAAAAAACAAACACAAACAATTTTATTTT ATTATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTTAAAAT AATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA ACGTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGTGAATCA TTGAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGGGCATGC CTGTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTG TGGGCGATACTCAGGGTTAGCTTGAAATTGAAGATTGTTTCAATCTTTTT TAATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATT TATGAATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGTACCTTAGG CAAAGGGTTGCTTTTAATATTCATCAAGTTGACCTC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 0.CM NS2 (K7)	*Hanseniaspora opuntiae*	100%	ITS	GTCAACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACC ATTTCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGA GAACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAA CAGTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAAT AAAAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTT GAGAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACG AGTATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGA TGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAAT TTCCGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAAT TGTTTGTGTTTGTTTTT
KB 0.CM NS3 (K8)	*Hanseniaspora opuntiae*	100%	ITS	GTCAACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACC ATTTCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGA GAACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAA CAGTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAAT AAAAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTT GAGAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACG AGTATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGA TGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAAT TTCCGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAAT TGTTTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAA TTAAATTAAAGTAAAA
KB 0.CM NS4 (K9)	*Rhodotorula mucilaginosa*	100%	ITS	TCCGTAGGGTGAACCTGCGGAAGGATCATTAGTGAATATAGGACGTCC AACTTAACTTGGAGTCCGAACTCTCACTTTCTAACCCTGTGCATTTGTTT GGGATAGTAACTCTCGCAAGAGGGCGAACTCCTATTCACTTATAAACAC AAAGTCTATGAATGTATTAAATTTTATAACAAAATAAAACTTTCAACAA CGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAA GTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACC TTGCGCTCCATGGTATTCCGTGGAGCATGCCTGTTTGAGTGTCATGAAT ACTTCAACCCTCCTCTTTCTTAATGATTGAAGAGGTGTTTGGTTTCTGAG CGCTGCTGGCCTTTAGGGTCTAGCTCGTTCGTAATGCATTAGCATCCGC AATCGAACTTCGGATTGACTTGGCGTAATAGACTATTCGCTGAGGAATT CTAGTCTTCGGACTAGAGCCGGGTTGGGTTAAAGGAAGCTTCTAATCAG AATGTCTACATTTTAAGATTAGATCTCAA
KB 0.CM NS5 (K10)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTTGACCTCAA
KA 4.CM NS1 (K11)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KA 4.CM NS2 (K12)	*Hanseniaspora opuntiae*	100%	D1/D2 Domain	CTTAGTACGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTAC TTTCAGTGCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTT GTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTG GCGAGGATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTG GGAATGCAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTG GCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGA ACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGG GCATTTGATCAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCT TGGGCCTCTCAAAAATTTCACTGGGCCAACATCAATTCTGGCAGTAGGA TAAATCATTAAGAATGTAGCTACCTCGGTAGTGTTATAGCTTATTGGAA TACTGCTAGCTGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGCATA ATGGTTAAATGCCGCCCGTCTTGAAACACGGACC
	Hanseniaspora opuntiae	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTTGACCTCAAATC
KA 4.CM NS3 (K13)	*Hanseniaspora uvarum*	100%	ITS	ACCTGCGGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTA GTTTTAGATCTTTTACAATAATGTGTATCTTTATTGAAGATGTGCGCTTA ATTGCGCTGCTTTTTTAAAGTGTCGCAGTAGAAGTAATCTTGCTTGAATC TCAGTCAACGTTTACACACATTGGAGTTTTTTTACTTTAATTTAATTCTTT CTGCTTTGAATCGAAAGGTTCAAGGCAAAAAACAAACACAAACAATTT TATTTTATTATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTT AAAATAATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGAT GAAGAACGTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGT GAATCATTGAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGG GCATGCCTGTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTT TTGGTTGTGGGCGATACTCAGGGTTAGCTTGAAATTGAAGATTGTTTCA ATCTTTTTTAATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGT GATGTATTTATGAATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGT ACCTTAGGCAAAGGGTTGCTTTTAATATTCATCAAGTTGACCTCAAA
KA 4.CM NS5 (K15)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGG CAAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAA ACCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAAC GGATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAG TAATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACAT TGCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTT CTCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAG CTTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCT TTGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTAC TTTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATA TTCATCAAGTTGACCTCAAATC
KB 4.CM NS1 (K16)	*Hanseniaspora opuntiae*	100%	ITS	GGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTTGTTTAGA TCTTTTACAATAATGTGTATCTTTATTGGAGATGTGCGCTTAATTGCGCT GCTTCATTAGAGTGTCGCAGTAGAAGTAGTCTTGCTTGAATCTCAGTCA ACGTTTACACACATTGGAGTTTTTTACTTTAATTTAATTCTTTCTGCTTTG AATCGAAAGGTTCAAGGCAAAAAACAAACACAAACAATTTTATTTTATT ATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTTAAAATAAT TTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACG TAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGTGAATCATTG AATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGGGCATGCCTG TTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTGTGG GCGATACTCAGGGTTAGCTTGAAATTGGAGACTGTTTCAGTCTTTTTTAA TTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATTTAT GGATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGTACCTTAGGCA AAGGGTTGCTTTTAATATTCATCAAGTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 4.CM NS2 (K17)	*Hanseniaspora opuntiae*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAA
KB 4.CM NS4 (K19)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTTGACCTCAA
KB 4.CM NS5 (K20)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTTGACCTCAAAT
KA 2.NM NS1 (K21)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGT
KA 2.NM NS9 (K25)	*Hanseniaspora uvarum*	100%	D1/D2 Domain	AGCGGTAAAAGCTCAAATTTGAAATCTGGTACTTTCAGTGCCCGAGTTG TAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATGTTCCTTGGAA CAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGGATACCTTTTCT CTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAG TGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGC GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTG AAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATG GTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCTCTCAAAAATT TCACTGGGCCAACATCAATTCTGGCAGCAGGATAAATCATTAAGAATGT AGCTACT
	Hanseniaspora uvarum	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAGGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTATTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAACGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 2.NM NS2 (K26)	*Hanseniaspora uvarum*	99%	ITS	TGCGGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTTGTTT AGATCTTTTACAATAATGTGTATCTTTATTGAAGATGTGCGCTTAATTGC GCTGCTTCTTTAGAGTGTCGCAGTGAAAGTAGTCTTGCTTGAATCTCAGT CAACGCTACACACATTGGAGTTTTTTTACTTTAATTTAATTCTTTCTGCTT TGAATCGAAAGGTTCAAGGCAAAAAAACAAACACAAACAATTTTATTTT ATTATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTTAAAAT AATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA ACGTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGTGAATCA TTGAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAGGGGCATGC CTGTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTATTATTTTTTGGTT GTGGGCGATACTCAGGGTTAGCTTGAAATTGGAGACTGTTTCAGTCTTT TTTAATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTA TTTATGGATTTATTCGTTTTACTTTACAAAGGGAAATGGTAACGTACNCT TAGGCAAAGGGTTGCTTTTAATATTCATC
KB 2.NM NS4 (K27)	*Hanseniaspora opuntiae*	100%	ITS	GCGGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTTGTTTA GATCTTTTACAATAATGTGTATCTTTATTGGAGATGTGCGCTTAATTGCG CTGCTTCATTAGAGTGTCGCAGTAGAAGTAGTCTTGCTTGAATCTCAGT CAACGTTTACACACATTGGAGTTTTTTACTTTAATTTAATTCTTTCTGCTT TGAATCGAAAGGTTCAAGGCAAAAAAACAAACACAAACAATTTTATTTT ATTATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTTAAAAT AATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA ACGTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGTGAATCA TTGAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGGGCATGC CTGTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTG TGGGCGATACTCAGGGTTAGCTTGAAATTGGAGACTGTTTCAGTCTTTTT TAATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATT TATGGATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGTACCTTAGG CAAAGGGTTGCTTTTAATATTCATCAAGTT
KB 2.NM NS8 (K29)	*Saccharomyces cerevisiae*	98%	ITS	GGATCATTAAAGAAATTTAATAATTTTGAAAATGGATTTTTTTGTTTTGG CAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGT CCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTT CTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGA CAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGC AACTTTTTCTTTGGGCATTCGAGCAATCGGGGGCCCAGAGGTAACNAACA CAAACAATTTTATTTATTCATTAAATTTTTGTCAAAAACAAGAATTTTTG TAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGATTTTTTGG TTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATT GCAGAATTCCGTGAATCATCGAATCTTTGAACGCCCCTTGCGCCCCTTG GTATTCCCGGGGGCATGCCTGTTTGAGCGTCATTTCCTTTTCAAACCTTT TGTTTGGTAGTGAGTGATACTTTTTGGAGTTAACTTGAAATTGCTGGCCT TTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTTTGCGTGCTTGAGG TATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTT TTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAG GCGAACAATGTTCTTAAAG
KA 4.NM NS2 (K31)	*Hanseniaspora guilliermondii*	100%	ITS	GGTCAACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTAC CATTTCCCTTGTAAAGTAAAACGAATAAATTCATAAATACATCACAGCG AGAACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGATTGAA ACAATCTTCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAA TAAAAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCT TGAGAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACG AGTATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGA TGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAAT TTCCGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAAT TGTTTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAA TTAAATTAAAGTAAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATT CAAGCAAGATTACTTCTACTGCGACACTTTAAAAAAGCAGCGCAATTAA GCGCACATCTTCAATAAAGATACACATTATTGTAAAAGATCTAAAACTA GAACTCGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGTC
KA 4.NM NS4 (K32)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KA 4.NM NS6 (K33)	*Hanseniaspora guilliermondii*	100%	ITS	GCGGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTAGTTTT AGATCTTTTACAATAATGTGTATCTTTATTGAAGATGTGCGCTTAATTGC GCTGCTTTTTTAAAGTGTCGCAGTAGAAGTAATCTTGCTTGAATCTCAGT CAACGTTTACACACATTGGAGTTTTTTTACTTTAATTTAATTCTTTCTGCT TTGAATCGAAAGGTTCAAGGCAAAAAACAAACACAAACAATTTTATTTT ATTATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTTAAAAT AATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA ACGTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGTGAATCA TTGAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGGGCATGC CTGTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTG TGGGCGATACTCAGGGTTAGCTTGAAATTGAAGATTGTTTCAATCTTTTT TAATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATT TATGAATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGTACCTTAGG CAAAGGGTTGCTTTTAATATTCATCAAGTTGACCTCAAA
KA 4.NM NS8 (K34)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGTTGACCTCAA
KA 4.NM NS10 (K35)	*Hanseniaspora opuntiae*	100%	D1/D2 Domain	ACGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTTTCAG TGCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTAT GTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAG GATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAAT GCAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAG AGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTG AAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTT GATCAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCC TCTCAAAAATTTCACTGGGCCAACATCAATTCTGGCAGTAGGATAAATC ATTAAGAATGTAGCTACCTCGGTAGTGTTATAGCTTATTGGAATACTGC TAGCTGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGCATAATGGTT AAATGCCGCCCGTCTTGAA
	Hanseniaspora opuntiae	99%	ITS	CATTGGAGTTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGG TTCAAGGCAAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTT AAACTAAACCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTT CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTG CGATAAGTAATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAA CGCACATTGCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTC ATTTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTC AGGGTTAGCTTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACT TAGCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATT CGTTTTACTTTACAAAGGGAAAATGGTAATGTACTCTTAGGCAAAGGGT TGCTTTTAAATATTCATC
KB 4.NM NS1 (K36)	*Hanseniaspora guilliermondii*	100%	ITS	ACCTGCGGAAGGATCATTAGATTGAATTATCATTGTTGCTCGAGTTCTA GTTTTAGATCTTTTACAATAATGTGTATCTTTATTGAAGATGTGCGCTTA ATTGCGCTGCTTTTTTAAAGTGTCGCAGTAGAAGTAATCTTGCTTGAATC TCAGTCAACGTTTACACACATTGGAGTTTTTTTACTTTAATTTAATTCTTT CTGCTTTGAATCGAAAGGTTCAAGGCAAAAAACAAACACAAACAATTT TATTTTATTATAATTTTTTAAACTAAACCAAAATTCCTAACGGAAATTTT AAAATAATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGAT GAAGAACGTAGCGAATTGCGATAAGTAATGTGAATTGCAGATACTCGT GAATCATTGAATTTTTGAACGCACATTGCGCCCTTGAGCATTCTCAAGG GCATGCCTGTTTGAGCGTCATTTCCTTCTCAAAAGATAATTTTTTATTTT TTGGTTGTGGGCGATACTCAGGGTTAGCTTGAAATTGAAGATTGTTTCA ATCTTTTTTAATTCAACACTTAGCTTCTTTGGAGACGCTGTTCTCGCTGT GATGTATTTATGAATTTATTCGTTTTACTTTACAAGGGAAATGGTAATGT ACCTTAGGCAAAGGGTTGCTTTTAATATTCATCAAGTTGACCTCAAATC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 4.NM NS3 (K37)	*Hanseniaspora opuntiae*	99%	ITS	TTGGAGTTTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTT CAAGGCAAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAA ACTAAACCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCA ACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCG ATAAGTAATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACG CACATTGCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCAT TTCCTTCTCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAG GGTTAGCTTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTA GCTTCTTTGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCG TTTTACTTTACTAAGGGAAATGGTAATGTACCCTTAGGCAAAGGGTTGC TTTTAATATTCA
KB 4.NM NS5 (K38)	*Hanseniaspora opuntiae*	100%	ITS	GGAGTTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCA AGGCAAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAAC TAAACCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAAC AACGGATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGAT AAGTAATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCA CATTGCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTC CTTCTCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGT TAGCTTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCT TCTTTGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTT TACTTTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTA ATATTCATC
KB 4.NM NS7 (K39)	*Hanseniaspora guilliermondii*	100%	ITS	TCCGTAGGTGAACCTGCGGAAGGATCATTAGATTGAATTATCATTGTTG CTCGAGTTCTAGTTTTAGATCTTTTACAATAATGTGTATCTTTATTGAAG ATGTGCGCTTAATTGCGCTGCTTTTTTAAAGTGTCGCAGTAGAAGTAAT CTTGCTTGAATCTCAGTCAACGTTTACACACATTGGAGTTTTTTTACTTT AATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGCAAAAAACAAA CACAAACAATTTTATTTTATTATAATTTTTTAAACTAAACCAAAATTCCT AACGGAAATTTTAAAATAATTTAAAACTTTCAACAACGGATCTCTTGGT TCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGTAATGTGAATTG CAGATACTCGTGAATCATTGAATTTTTGAACGCACATTGCGCCCTTGAG CATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAAAGATA ATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGCTTGAAATTGA AGATTGTTTCAATCTTTTTTAATTCAACACTTAGCTTCTTTGGAGACGCT GTTCTCGCTGTGATGTATTTATGAATTTATTCGTTTTACTTTACAAGGGA AATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATATTCATCAAGT
KB 4.NM NS9 (K40)	*Hanseniaspora opuntiae*	100%	ITS	TTTTTTACTTTAATTTAATTCTTTCTGCTTTGAATCGAAAGGTTCAAGGC AAAAAACAAACACAAACAATTTTATTTTATTATAATTTTTTAAACTAAA CCAAAATTCCTAACGGAAATTTTAAAATAATTTAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCGAATTGCGATAAGT AATGTGAATTGCAGATACTCGTGAATCATTGAATTTTTGAACGCACATT GCGCCCTTGAGCATTCTCAAGGGCATGCCTGTTTGAGCGTCATTTCCTTC TCAAAAGATAATTTTTTATTTTTTGGTTGTGGGCGATACTCAGGGTTAGC TTGAAATTGGAGACTGTTTCAGTCTTTTTTAATTCAACACTTAGCTTCTT TGGAGACGCTGTTCTCGCTGTGATGTATTTATGGATTTATTCGTTTTACT TTACAAGGGAAATGGTAATGTACCTTAGGCAAAGGGTTGCTTTTAATAT TCATCAAGT
KA 0.CM S1 (K41)	*Wickerhamomyces anomalus*	100%	ITS	GCGGAAGGATCATTATAGTATTCTATTGCCAGCGCTTAATTGCGCGGCG ATAAACCTTACACACATTGTCTAGTTTTTTTGAACTTTGCTTTGGGTGGT GAGCCTGGCTTACTGCCCAAAGGTCTAAACACATTTTTTTTAATGTTAA AACCTTTAACCAATAGTCATGAAAATTTTTAACAAAAATTAAAATCTTC AAAACTTTCAACAACGGATCTCTTGGTTCTCGCAACGATGAAGAACGCA GCGAAATGCGATACGTATTGTGAATTGCAGATTTTCGTGAATCATCGAA TCTTTGAACGCACATTGCACCCTCTGGTATTCCAGAGGGTATGCCTGTTT GAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCT GTCAAGGGTTAACTTGAAATATTGACTTAGCAAGAGTGTACTAATAAGC AGTCTTTCTGAAATAATGTATTAGGTTCTTCCAACTCGTTATATCAGCTA GGCAGGTTTAGAAGTATTTTAGGCTCGGCTTAACAACAATAAACTAAAA GTTGACCTC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 0.CM S5 (K42)	*Wickerhamomyces anomalus*	100%	ITS	CGGAAGGATCATTATAGTATTCTATTGCCAGCGCTTAATTGCGCGGCGA TAAACCTTACACACATTGTCTAGTTTTTTTGAACTTTGCTTTGGGTGCAT CAGCCTAGCTGCGTGCCCAAAGGTCTAAACACATTTTTTAATGTTAAAA CCTTTAACCAATAGTCATGAAAATTTTTAACAAAAATTAAAATCTTCAA AACTTTCAACAACGGATCTCTTGGTTCTCGCAACGATGAAGAACGCAGC GAAATGCGATACGTATTGTGAATTGCAGATTTTCGTGAATCATCGAATC TTTGAACGCACATTGCACCCTCTGGTATTCCAGAGGGTATGCCTGTTTG AGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTG TCAAGGGTTAACTTGAAATATTGACTTAGCAAGAGTGTACTAATAAGCA GTCTTTCTGAAATAATGTATTAGGTTCTTCCAACTCGTTATATCAGCTAG GCAGGTTTAGAAGTATTTTAGGCTCGGCTTAACAACAATAAA
KA 4.CM S1 (K43)	*Metschnikowia aff. fructicola*	99%	D1/D2 Domain	ACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAATT GTAATTTGAAGAGATTTGGGTCCGGCCGGCGGGGGTTAAGTCCACTGGA AAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCTTCAAAGCCCT CATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTG GGTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCG AACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGA AAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTT AACTGGGCCAGCATCGGGGCGGCGGGAAACAAAACCACCGGGGAATGT ACCTTTCGAGGATTATAACCCCGGTCTCAATTTCCTTGTTGCCCCGAGGC CTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAA CCACGGA
	Not identified		ITS	CAATCGGGGCCCAGAGGTAACAAACACAAACAATTTTATTTATTCATTA AATTTTTGTCAAAAACAAGAATTTTTGTAACTGGAAATTTTAAAATATT AAAAACTTTCAACAACGGATTTTTTGGTTCTCGCATCGATGAAGAACGC AGCGAAATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGA ATCTTTGAACGCACATTGCGCCCCTTGGTATTCCCGGGGGCATGCCTGTT TGAGCGTCATTTCCTTTTCAAACCTTTTGTTTGGTAGTGAGTGATACTCT TTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCA AAGAGAGGTTTCTTTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTT TAGGTTTTACCAACTGCGGCTAATCTTTTTTTTATACTGAGCGTATTGGAA CGTTATCGATAAGAAGAGAGCGTCTAGGCGAACAATGTT
KB 4.CM S5 (K44)	*Saccharomyces cerevisiae*	99%	ITS	TTAAAGAAATTTAATAATTTTGAAAATGGATTTTTTTGTTTTGGCAAGAG CATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCC GGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTT GCTATTCCAAACGGTGAGAGATTTTTGTGCTTTTGTTATAGGACAATTA AAACCGTTTCAATACAACACACTGTGGAGTTTTCATATTTTTGCAACTTT TTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAAC AATTTTATTTATTCATTAAATTTTTGTCAAAAACAAGAATTTTTGTAACT GGAAATTTTAAAATATTAAAAACTTTCAACAACGGATTTTTTGGTTCTC GCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG AATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATT CCCGGGGGCATGCCTGTTTGAGCGTCATTTCCTTTTCAAACCTTTTGTTT GGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCA TTGGATGTTTTTTTTCCAAAGAGAGGTTTCTTTGCGTGCTTGAGGTATAA TGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTA TACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGA ACAATGTTCTTAAAGT
KA 2.NM S6 (K45)	*Saccharomyces cerevisiae*	99%	ITS	GGATCATTAAAGAAATTTAATAATTTTGAAAATGGATTTTTTTGTTTTGG CAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGT CCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTT CTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGA CAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGC AACTTTTTCTTTGGGCATTNGAGCAATCGGGGCCCAGAGGTAACAAACA CAAACAATTTTATTTATTCATTAAATTTTTGTCAAAAACAAGAATTTTTG TAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGATTTTTTGG TTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATT GCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTG GTATTCCCGGGGGCATGCCTGTTTGAGCGTCATTTCCTTTTCAAACCTTT TGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCT TTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTTTGCGTGCTTGAGG TATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTT TTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAG GCGAACAATGTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 2.NM S4 (K46)	*Saccharomyces cerevisiae*	100%	ITS	CCTGCGGAAGGATCATTAAAGAAATTTAATAATTTTGAAAATGGATTTT TTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAG ATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCT TGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTT GTTATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTC ATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAG GTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAAC AAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAAC GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACG TAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACAT TGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTT CTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAA ATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTG CGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTG CGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAA GAGAGCGTCTAGGCGAACAATGTTCTTAAA
KA 4.NM S4 (K47)	*Saccharomyces cerevisiae*	100%	ITS	AAATTTAATAATTTTGAAAATGGATTTTTTTGTTTTGGCAAGAGCATGA GAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGGCC TGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCTAT TCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAAAACC GTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTTTTCTT TGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAACAATTT TATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACTGGAA ATTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATC GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTC CGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCAG GGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGTA GTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGG ATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCA AGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTATACT GAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGAACAA TGTTCTTAAAG
KA 4.NM S8 (K48)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CGGCAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAA TTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAAC AGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCT TTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG TGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGC GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTG AAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATG GTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACT GGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTT GCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAG GACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG TCTTGA
	Saccharomyces cf. cerevisiae/paradoxus	100%	ITS	GGACTGCGGAAGGATCATTAAAGAAATTTAATAATTTTGAAAATGGATT TTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAG AGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGG CTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTT TTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTT TCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGA GGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAA CAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAA CGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAC GTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACA TTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCT TCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGA AATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCT GCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACT GCGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGA AGAGAGCGTCTAGGCGAACAATGTTCTTAAAGTTGACCTCAAAT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 4.NM S2 (K49)	*Saccharomyces cerevisiae*	99%	ITS	GGAAGGATCATTAAAGAAATTTAATAATTTTGAAAATGGATTTTTTTGT TTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGG AGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTA AGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTA TAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATAT CTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAA CAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGA ATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGAT TCCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAAT GTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCG CCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCA AACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTG CTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTG CTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGC TAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGA GCGTCTAGGCGAACAATGTTCTTAAAGTT
KB 4.NM S10 (K50)	*Saccharomyces cerevisiae*	100%	ITS	TTAAAGAAATTTAATAATTTTGAAAATGGATTTTTTTGTTTTGGCAAGAG CATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCC GGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTT GCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTA AAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTT TTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAAC AATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACT GGAAATTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTC GCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG AATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATT CCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTT GGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCA TTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAA TGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTA TACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGA ACAATGTTCTTAAA
KA 2.NM NS2 (K51)	*Hanseniaspora opuntiae*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAC
KA 2.NM NS4 (K52)	*Hanseniaspora uvarum*	100%	ITS	CCTTTGCCTAAGGTACGTTACCATTTCCCTTGTAAAGTAAAACGAATAA ATCCATAAATACATCACAGCGAGAACAGCGTCTCCAAAGAAGCTAAGT GTTGAATTAAAAAAGACTGAAACAGTCTCCAATTTCAAGCTAACCCTGA GTATCGCCCACAACCAAAAAATAATAAATTATCTTTTGAGAAGGAAATG ACGCTCAAACAGGCATGCCCCTGAGAATGCTCAAGGGCGCAATGTGCG TTCAAAAATTCAATGATTCACGAGTATCTGCAATTCACATTACTTATCGC AATTCGCTACGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGA AAGTTTTAAATTATTTTAAAATTTCCGTTAGGAATTTTGGTTTAGTTTAA AAAATTATAATAAAATAAAATTGTTTGTGTTTGTTTTTTGCCTTGAACCT TTCGATTCAAAGCAGAAAGAATTAAATTAAAGTAAAAAAC
KA 2.NM NS8 (K54)	*Hanseniaspora uvarum*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACGTTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA TAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 2.NM NS9 (K60)	*Hanseniaspora opuntiae*	100%	ITS	ACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATTT CCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGAA CAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACAG TCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAAA AAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGAG AATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGTA TCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGCG AGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTCC GTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGTT TGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTAA ATTAAAGTAAAAAAC
KA 4.NM NS1 (K61)	*Hanseniaspora guilliermondii*	100%	ITS	GTCAACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACC ATTTCCCTTGTAAAGTAAAACGAATAAATTCATAAATACATCACAGCGA GAACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGATTGAAA CAATCTTCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAAT AAAAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTT GAGAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACG AGTATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGA TGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAAT TTCCGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAAT TGTTTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAA TTAAATTAAAGTAAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATT CAAGCAAGATTACTTCTACTGCGACACTTTAAAAAAGCAGCGCAATTAA GCGCACATCTTCAATAAAGATACACATTATTGTAAAAGATCTAAAACTA GAACTCGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGT
KA 4.NM NS3 (K62)	*Hanseniaspora opuntiae*	100%	D1/D2 Domain	CGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTTTCAGT GCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATG TTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGG ATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAATG CAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGA GACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGA AAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTG ATCAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCT CTCAAAAATTTCACTGGGCCAACATCAATTCTGGCAGTAGGATAAATCA TTAAGAATGTAGCTACCTCGGTAGTGTTATAGCTTATTGGAATACTGCT AGCTGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGCATAATGGTTA AATGCCGCCCGTCTTGAA
	Hanseniaspora opuntiae	100%	ITS	TTGAGGTCAACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACA TTACCATTTCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCAC AGCGAGAACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGAC TGAAACAGTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAA AAAATAAAAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCAT GCCCTTGAGAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGAT TCACGAGTATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTC ATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTT AAAATTTCCGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAAT AAAATTGTTTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGA AAGAATTAAATTAAAGTAAAAAA
KA 4.NM NS5 (K63)	*Hanseniaspora opuntiae*	99%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATTCAA GCAAGACTACTTCTACTGCGACACTCTAATAAAGCAGCGCAATTAACCG CACATCTTCATTAAAGATACACATTATTGTAAAAGATCTAAACAAGAAC TCGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KA 4.NM NS7 (K64)	*Hanseniaspora opuntiae*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAA
KA 4.NM NS9 (K65)	*Hanseniaspora opuntiae*	99%	D1/D2 Domain	ACGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTTTCAG TGCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTAT GTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAG GATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAAT GCAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAG AGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTG AAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTT GATCAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCC TCTCAAAAATTTCACTGGGCCAACATCAATTCTGGCAGTAGGATAAATC ATTAAGAATGTAGCTACCTCGGTAGTGTTATAGCTTATTGGAATACTGC TAGCTGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGCATAATGGTT AAATGCCGCCCGTCTTGAACCACGGAC
	Hanseniaspora opuntiae	99%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATTCAAG CAAGACTACTTCTACTGCGACACTCTAATGAAGCAGCGCAATTAAGCGC ACATCTCCAATAAAGATACACATTATTGTAAAAGATCTAAACAAGAACT CGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGTTCCCT
KB 4.NM NS2 (K66)	*Hanseniaspora opuntiae*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAA
KB 4.NM NS4 (K67)	*Hanseniaspora opuntiae*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KB 4.NM NS6 (K68)	*Hanseniaspora guilliermondii*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATTCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGATTGAAACA ATCTTCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATTCAA GCAAGATTACTTCTACTGCGACACTTTAAAAAAGCAGCGCAATTAAGCG CACATCTTCAATAAAGATACACATTATTGTAAAAGATCTAAAACTAGAA CTCGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGTTC
KB 4.NM NS8 (K69)	*Hanseniaspora guilliermondii*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATTCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGATTGAAACA ATCTTCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATTCAA GCAAGATTACTTCTACTGCGACACTTTAAAAAAGCAGCGCAATTAAGCG CACATCTTCAATAAAGATACACATTATTGTAAAAGATCTAAAACTAGAA CTCGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGTTCC
KB 4.NM NS10 (K70)	*Hanseniaspora uvarum*	98%	D1/D2 Domain	TACGGCGAGTGAGCGGTAAAGCTCAAATTTGAAATCTGGTACTTTCAGT GCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATG TTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGG ATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAATG CAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGA GACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGA AAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTG ATCAAACTGGTGTTTTTGGATGCACTCCCCTCTCGGGGGCTTGGGCCTCT CAAAATTT
	Hanseniaspora uvarum	98%	ITS	GAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATTTCCCTTGT AAAGTAAAACGAATAAATTCATAAATACATCACAGCGAGAACAGCGTC TCCAAAGAAGCTAAGTGTTGAATTAAAAAAGATTGAAACAATCTTCAAT TTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAAAAAATTATC TTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGAGAATGCTCA AGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGTATCTGCAAT TCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGCGAGAACCA AGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTCCGTTAGGA ATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGTTTGTGTTTG TTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTAAATTAAAG TAAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATTCAAGCAAGATT ACTTCTACTGCGACACTTTAAAGAAGCAGCGCAATTAAGCGCACATCTT CAATAAAGATACACATTATTGTAAAAGATCTAAAACTAGAACTCGAGC AACAATGATAATTCAATCTAATGATCCTTCCGCAGGTTCAC
KA 32.NM S2 (K71)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGT GCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTA TGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGA GGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGA ATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTT TGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCAT TTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAAT CTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCAT AGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCC AGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGG TTATATGCCGCCCGTCTTG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
KA 4.NM S2 (K72)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	GGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAA TTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAAC AGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCT TTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG TGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGC GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTG AAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATG GTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACT GGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTT GCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAG GACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG TCTTG
EA 0.W NS1 (E1)	*Saccharomyces cerevisiae*	96%	ITS	AACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGC TCAGTATAAAAAAAAGATTACCCGCAGTTGGTAAAACCTAAAACGACCG TACTTGCATTATACCTCAACCACGCAAAAAAAACCTCTCTTTGGAAAAAA AACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCCAAAAAGTATC ACTCACTACCAAACAAAATGTTTGAAAAGGAAATGACGCTCAAACAGG CATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAAATTCGAT GATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC TTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATT TTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAAAATTTAATGAA TAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTGCTCGAATG CCCAAAAAAAAAAGTTGCAAAAATATGAAAACTCCACAGTGTGTTGTATT GAAACGGTTTTAATTGTCCTATAACAAAACCACAAAAATCTCTCACCGT TTGGAATACCAAAAAAAAAACTTACAACCCTACCAAAACCGCCCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTTTTCTTGCCCAGTAAA ACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATTA AATTTCTTTAATGATCCTTCCGCAGGT
EA 0.W NS2 (E2)	*Saccharomyces cerevisiae*	96%	ITS	ACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGCT CAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTAAAACGACCGT ACTTGCATTATACCTCAACCACGCAAAAAAACCTCTCTTTGGAAAAAAA ACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCCAAAAAGTATCA CTCACTACCAAACAAAATGTTTGAAAAGGAAATGACCCTCAAACAGGC ATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAAATTCGATG ATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTCT TCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATTT TAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAAAATTTAATGAAT AAATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTGCTCGAATGC CCAAAAAAAAAGTTGCAAAAATATGAAAACTCCACAGTGTGTTGTATT GAAACGGTTTTAATTGTCCTATAACAAAACCACAAAAATCTCTCACCGT TTGGAATACCAAAAAAAAAACTTACAACCCTACCAAAACCGCCCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCAGTAA AACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATT AAATTTCTTTAATGATCCTTCCGCAGT
EA 0.W NS4 (E4)	*Saccharomyces cerevisiae*	97%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTT TGGAAAAAAAACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCC AAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAA AAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAACCACAAA AATCTCTCACCGTTTGGAATACCAAAAAAAAAACTTACAACCCTACCAC AACCGCCCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTTTTC TTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTT TCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EA 0.W NS5 (E5)	*Saccharomyces cerevisiae*	96%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAACCACGCAAAAAAACCTCTCTT TGGAAAAAAAACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCC AAAAAGTATCACTCACTACCAAACAAAATGTTTGAAAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAA AAATTTAATGAATAAATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAACCACAAA AATCTCTCACCGTTTGAAATACCAAAAAAAAAACTTACAACCCTACCAC AACCGCCCACTTAACCCCAGGCCCGGCTGGACTCTCCATCTCTTGTTTTC TTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTT TCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT
EB 0.W NS1 (E6)	*Saccharomyces cerevisiae*	99%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAAGATTAGCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAGAGAAACCTCTCTT TGGAAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCC AAAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAA AAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGA AATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAACA AGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCT TCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCAT TTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT
EB 0.W NS2 (E7)	*Saccharomyces cerevisiae*	95%	ITS	ACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTC CAATACGCTCAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTAA AACGACCGTACTTGCATTATACCTCAACCACCCAAAAAAACCTCTCTTT GGAAAAAAAACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCCA AAAAGTATCACTCACTACCAAACAAAATGTTTGAAAAGGAAATGACCC TCAAACAGGCATGCCCCCTGGAATACCAAGGGGCCCAATGTGCGTTCA AAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATT TCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAG TTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAA AATTTAATGAATAAATAAAATTGTTGGGGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAACCACAAA AATCTCTCACCGTTTGAAATACCAAAAAAAAAACTTACAACCCTACCAC AACCGCCCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTTTTC TTGCCCAGTAAAACCTCTCATGCTCTTGCCAAACAAAAAAATCCATTTT CAAAATTATTAAATTCCTTTAATGATCCTTCCGCAGTTACTAC
EB 0.W NS3 (E8)	*Saccharomyces cerevisiae*	99%	ITS	AAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACG CTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTAAAACGACC GTACTTGCATTATACCTCAAGCACGCAGAGAAACCTCTCTTTGGAAAAA AAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAAGAGTA TCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGACGCTCAAACA GGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAGATTC GATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGC GTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAA TATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAA TGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTGCTCG AATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCACAGTGTGTT GTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAAATCTCTC ACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAACAAGACCGCG CACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCA GTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAAT TATTAAATTTCTTTAATGATCCTTCCGCAGGTTCACCTACGGGAAGGATC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EB 0.W NS4 (E9)	*Saccharomyces cerevisiae*	96%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAACCACGCAAAAAAACCTCTCTT TGGAAAAAAAACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCC AAAAAGTATCACTCACTACCAAACAAAATGTTTGAAAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCCCAATGTGCGTTCA AAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATT TCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAG TTTTTAATATTTTAAAATTTCCAGTTACAAAAATTTTTGTTTTTGACAAA AATTTAATGAATAAATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCCG ATTGCTCAAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAACCCCAAA AATCTCTCACCGTTTGGAATACCAAAAAAAAAACTTACAACCCTACCAA AACCGCCCACTTAACCCCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTC TTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTT TCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT
EA 1.W NS1 (E11)	*Hanseniaspora uvarum*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACGTTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA TAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAACTCCAATGTGTGTAGCGTTGACTGAGATTCAAG CAAGACTACTTTCACTGCGACACTCTAAAGAAGCAGCGCAATTAAGCGC ACATCTTCAATAAAGATACACATTATTGTAAAAGATCTAAACAAGAACT CGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGTTC
EA 1.W NS2 (E12)	*Hanseniaspora uvarum*	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACGTTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA TAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAAACTCCAATGTGTGTAGCGTTGACTGAGATTCAAG CAAGACTACTTTCACTGCGACACTCTAAAGAAGCAGCGCAATTAAGCGC ACATCTTCAATAAAGATACACATTATTGTAAAAGATCTAAACAAGAACT CGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGT
EA 1.W NS3 (E13)	*Hanseniaspora uvarum*	100%	ITS	ACGCCTTTGCCTAAGGTACGTTACCATTTCCCTTGTAAAGTAAAACGAA TAAATCCATAAATACATCACAGCGAGAACAGCGTCTCCAAAGAAGCTA AGTGTTGAATTAAAAAAGACTGAAACAGTCTCCAATTTCAAGCTAACCC TGAGTATCGCCCACAACCAAAAAATAATAAATTATCTTTTGAGAAGGAA ATGACGCTCAAACAGGCATGCCCCTGAGAATGCTCAAGGGCGCAATGT GCGTTCAAAAATTCAATGATTCACGAGTATCTGCAATTCACATTACTTA TCGCAATTCGCTACGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTG TTGAAAGTTTTAAATTATTTTAAAATTTCCGTTAGGAATTTTGGTTTAGT TTAAAAAATTATAATAAAATAAAATTGTTTGTGTTTGTTTTTTGCCTTGA ACCTTTCGATTCAAAGCAGAAAGAATTAAATTAAAGTAAAAAAACTCC AATGTGTGTAGCGTTGACTGAGATTCAAGCAAGACTACTTTCACTGCGA CACTCTAAAGAAGCAGCGCAATTAAGCGCACATCTTCAATAAAGATAC ACATTATTGTAAAAGATCTAAACAAGAACTCGAGCAACAATGATAATTC AATCTAATGATCCTTCCGCAGGTTCACC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EA 1.W NS4 (E14)	*Hanseniaspora uvarum*	100%	ITS	CCTTTGCCTAAGGTACGTTACCATTTCCCTTGTAAAGTAAAACGAATAA ATCCATAAATACATCACAGCGAGAACAGCGTCTCCAAAGAAGCTAAGT GTTGAATTAAAAAAGACTGAAACAGTCTCCAATTTCAAGCTAACCCTGA GTATCGCCCACAACCAAAAAATAATAAATTATCTTTTGAGAAGGAAATG ACGCTCAAACAGGCATGCCCCTGAGAATGCTCAAGGGCGCAATGTGCG TTCAAAAATTCAATGATTCACGAGTATCTGCAATTCACATTACTTATCGC AATTCGCTACGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGA AAGTTTTAAATTATTTTAAAATTTCCGTTAGGAATTTTGGTTTAGTTTAA AAAATTATAATAAAATAAAATTGTTTGTGTTTGTTTTTTGCCTTGAACCT TTCGATTCAAAGCAGAAAGAATTAAATTAAAGTAAAAAAACTCCAATG TGTGTAGCGTTGACTGAGATTCAAGCAAGACTACTTTCACTGCGACACT CTAAAGAAGCAGCGCAATTAAGCGCACATCTTCAATAAAGATACACAT TATTGTAAAAGATCTAAACAAGAACTCGAGCAACAATGATAATTCAATC TAATGATCCTTCCGCAGGTT
EA 1.W NS5 (E15)	*Saccharomyces cerevisiae*	97%	ITS	GAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGAT AACGTTCCAATACGCTCAGTATAAAAAAAGATTACCCGCAGTTGGTAAA ACCTAAAACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAACCT CTCTTTGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTA ACTCCAAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGAAA TGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTG CGTTCAAAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGTAT CGCATTTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTTGT TGAAAGTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTT GACAAAAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGG GCCCCGATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAA CTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAG CACAAAAATCTCTCACCGTTTGGAATACCAAAAAAAAAAACTTACAACCC TACCAAGACCGCCCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCT TGTTTTCTTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAA TCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGT
EA 1.W NS6 (E16)	*Saccharomyces cerevisiae*	98%	ITS	CATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGCTC AGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTAAAACGACCGTA CTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTTTGGAAAAAAAA CATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAAAAGTATCAC TCACTACCAAACAGAATGTTTGAAAAGGAAATGACGCTCAAACAGGCA TGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAAATTCGATGA TTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTCTT CATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATTTT AAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAAT AGATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCCGATTGCTCGAATG CCCAAAAAAAAAAGTTGCAAAGATATGAAAACTCCACAGTGTGTTGTATT GAAACGGTTTTAATTGTCCTATAACAAAAGCACAAAAATCTCTCACCGT TTGGAATAGCAAAAAAAAAACTTACAACCCCACCAAGACCGCGCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCAGTAA AAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATT AAATTTCTTTAATGATCCTTCCGCAGGTT
EA 1.W NS7 (E17)	*Saccharomyces cerevisiae*	98%	ITS	AACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGC TCAGTATAAAAAAAGATTACCCGCAGTTGGTAAAACCTAAAACGACCG TACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTTTGGAAAAAAA AACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAAAAGTAT CACTCACTACCAAACAAAATGTTTGAAAAGGAAATGACGCTCAAACAG GCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAAATTCG ATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGT TCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATA TTTTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAAAATTTAATG AATAGATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCCGATTGCTCGA ATGCCCAAAAAAAAAAGTTGCAAAAATATGAAAACTCCACAGGGTGTTG TATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAAAAATCTCTCA CCGTTTGGAATACCAAGAAAGAAACTTACAAGCCTAGCAAGACCGCCC ACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCAG TAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATT ATTAAATTTCTTTAATGATCCTTCCGCAGGTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EA 1.W NS8 (E18)	*Saccharomyces cerevisiae*	98%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTT TGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCC AAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAA AAATTTAATGAATAAATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAGATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAAA AATCTCTCACCGTTTGGAATACCAAGAAAAAAACTTACAAGCCTAGCAA GACCGCGCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTT CTTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATT TTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT
EA 1.W NS10 (E20)	*Saccharomyces cerevisiae*	95%	ITS	ACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGCT CAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTAAAACGACCGT ACTTGCATTATACCTCAACCACCCAAAAAAACCTCTCTTTGGAAAAAAA ACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCCAAAAAGTATCA CTCACTACCAAACAAAATGTTTGAAAAGGAAATGACCCTCAAACAGGC ATGCCCCCTGGAATACCAAGGGGCCCAATGTGCGTTCAAAAATTCAATG ATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTCT TCATCGATGCAAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATTT TAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAAAATTTAATGAAT AAATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCCGATGGCTCGAATG CCCAAAAAAAAAAGTTGCAAAAATATGAAAACTCCACAGGGTGTTGTAT TGAAACGGTTTTAATTGTCCTATAACAAAACCACAAAAATCTCTCACCG TTTGAAATACCAAAAAAAAAACTTACAACCCTACCAAAACCGCCCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTTTTCTTGCCCAGTAAA ACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATTA AATTTCTTTAATGATCCTTCCGCAGGTTACT
EB 1.W NS1 (E21)	*Saccharomyces cerevisiae*	97%	ITS	TTGAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCG ATAACGTTCCAATACGCTCAGTATAAAAAAAGATTACCCGCAGTTGGTA AAACCTAAAACGACCGTACTTGCATTATACCTCAACCACGCAAAAAAA CCTCTCTTTGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGT TAACTCCAAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGA AATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATG TGCGTTCAAAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGT ATCGCATTTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTT GTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTT TTGACAAAAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTG GGCCCCGATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAA ACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAA GCACAAAAATCTCTCACCGTTTGGAATACCAAAAAAAAAACTTACAAC CCTACCAAAACCGCCCACTTAACCGCAGGCCCGGCTGGACTCTCCATCT CTTGTTTTCTTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAA AATCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT
EB 1.W NS2 (E22)	*Saccharomyces cerevisiae*	97%	ITS	TTGAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCG ATAACGTTCCAATACGCTCAGTATAAAAAAAGATTACCCGCAGTTGGTA AAACCTAAAACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAA CCTCTCTTTGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGT TAACTCCAAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGA AATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATG TGCGTTCAAAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGT ATCGCATTTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTT GTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTT TTGACAAAAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTG GGCCCCGATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAA ACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAA CCACAAAAATCTCTCACCGTTTGGAATACCAAGAAAGAAACTTACAACC CTACCAAGACCGCGCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTC TTGTTTTCTTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAA ATCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EB 1.W NS3 (E23)	*Saccharomyces cerevisiae*	98%	ITS	ACTTTAAGAACATTGTTCGCCTNACGCTCTCTTCTTATCGATAACGTTCC AATACGCTCAGTATAAAAAAAGATTACCCGCAGTTGGTAAAACCTAAA ACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTTTG GAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAA AGAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACGCT CAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAA AGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTC GCTGCGTTCTTCATCGATGCGAGAACCAAAAGATCCGTTGTTGAAAGTT TTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAAAA TTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATT GCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCACAGT GTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAAAT CTCTCACCGTTTGGAATACCAAGAAAAAAACTTACAAGCCTAGCAAGA CCGCGCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTT GCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTC AAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGT
EB 1.W NS4 (E24)	*Saccharomyces cerevisiae*	97%	ITS	AACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGC TCAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTAAAACGACCG TACTTGCATTATACCTCAACCACGCAAAAAAACCTCTCTTTGGAAAAAA AACATCCAATGAAAAGGCCACCAATTTCAAGTTAACTCCAAAAAGTATC ACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACGCTCAAACAGG CATGCCCCCTGGAATACCAAGGGGCCCAATGTGCGTTCAAAAATTCGAT GATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC TTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATT TTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAAAATTTAATGAA TAGATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCCGATTGCTCGAATG CCCAAAAAAAAAAGTTGCAAAAATATGAAAACTCCACAGTGTGTTGTATT GAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAAATCTCTCACCGT TTGGAATACCAAAAAAAAAAACTTACAACCCTACCAAGACCGCGCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTTTTCTTGCCCAGTAAA ACCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATTA AATTTCTTTAATGATCCTTCCGCAGGTT
EB 1.W NS6 (E26)	*Saccharomyces cerevisiae*	96%	ITS	TTGAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCG ATAACGTTCCAATACGCTCAGTATAAAAAAAAATTACCCGCAGTTGGTA AAACCTAAAACGACCGTACTTGCATTATACCTCAACCACGCAAAAAAA CCTCTCTTTGGAAAAAAAACATCCAATGAAAAGGCCACCAATTTCAAGT TAACTCCAAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGA AATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATG TGCGTTCAAAAATTCGATGATTCACGGAATTCTGCAATTCACATTACGT ATCGCATTTCGCTGCGTTCTTCATCGATGCGAAAACCAAAAAATCCGTT GTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTT TTGACAAAAATTTAATGAATAGATAAAATTGTTTGGGTTTGTTACCTCT GGGCCCCGATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAA AACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAA ACCACAAAAATCTCTCACCGTTTGGAATACCAAAAAAAAAACTTACAA CCCTACCAAAACCGCCCACTTAACCGCAGGCCCGGCTGGACTCTCCATC TCTTGTTTTCTTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAA AATCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT
EB 1.W NS7 (E27)	*Saccharomyces cerevisiae*	97%	ITS	CATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGCTC AGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTAAAACGACCGTA CTTGCATTATACCTCAACCACGCAAAAAAACCTCTCTTTGGAAAAAAAA CATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAAAAGTATCAC TCACTACCAAACAGAATGTTTGAAAAGGAAATGACGCTCAAACAGGCA TGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAAATTCGATGA TTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTCTT CATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATTTT AAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAAT AAATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTGCTCGAATGC CCAAAAAAAAAGTTGCAAAAATATGAAAACTCCACAGTGTGTTGTATT GAAACGGTTTTAATTGTCCTATAACAAAAGCACAAAAATCTCTCACCGT TTGGAATAGCAAAAAAAAAACTTACACGCCTAGCAAGACCGCGCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCAGTAA AAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATT AAATTTCTTTAATGATCCTTCCGCAGGTTCACCTACGGGAAGGATC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EB 1.W NS9 (E29)	*Saccharomyces cerevisiae*	99%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAGAGAAACCTCTCTT TGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCC AAAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAA AAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGA AATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAACA AGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCT TCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCAT TTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGG
EB 1.W NS10 (E30)	*Saccharomyces cerevisiae*	98%	ITS	ACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGCT CAGTATAAAAAAAAATTACCCGCAGTTGGTAAAACCTAAAACGACCGT ACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTTTGGAAAAAAA ACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAAAAGTATC ACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACGCTCAAACAGG CATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAGATTCGAT GATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC TTCATCGATGCGAGAACCAAAAAATCCGTTGTTGAAAGTTTTTAATATT TTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAA TAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTGCTCGAATG CCCAAAAAAAAAAGTTGCAAAGATATGAAAACTCCACAGTGTGTTGTATT GAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAAATCTCTCACCGT TTGGAATACCAAGAAAAAAAACTTACAACCCTACCAAGACCGCGCACTT AACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCAGTAA AAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTATT AAATTTCTTTAATGATCCTTCCGCAGGTTACCTA
EA 2.W NS1 (E31)	*Saccharomyces cerevisiae*	98%	ITS	AACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCAATACGC TCAGTATAAAAAAAGATTACCCGCAGTTGGTAAAACCTAAAACGACCG TACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTTTGGAAAAAA AACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAAAAGTAT CACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACGCTCAAACAG GCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAAGATTCG ATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGT TCTTCATCGATGCGAAAACCAAAAAATCCGTTGTTGAAAGTTTTTAATA TTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATG AATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTGCTCGAA TGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCACAGTGTGTTGT ATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAAATCTCTCAC CGTTTGGAATACCAAGAAAGAAACTTACAACCCTACCAAGACCGCGCA CTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTGCCCAGT AAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCAAAATTA TTAAATTTCTTTAATGATCCTTCCGCAGGTTACTA
EA 2.W NS2 (E32)	*Saccharomyces cerevisiae*	98%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAGATTACCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTT TGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCC AAAAAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAGAACCAAAAAATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAA AAATTTAATGAATAGATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCC GATTGCTCGAATGCCCAAAAAAAAAGTTGCAAAGATATGAAAACTCCA CAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAG AAATCTCTCACCGTTTGGAATACCAAGAAAGAAACTTACAACCCTACCA AGACCGCGCACTTAACCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCT TCTTGCCCAGTAAAACCTCTCATGCTCTTGCCAAAACAAAAAAATCCAT TTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EA 0.W NS6 (E35)	*Saccharomyces cerevisiae*	91%	ITS	TTGAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCG ATAACGTTCCAATACGCTCAGTATAAAAAAAAATTACCCGCATTTGGTA AAACCTAAAACAACCGTACTTGCATTATACCTCAGGCACGCAAAAAAA CCTCTCTTTGGAAAAAAAACATCCAAGGAAAAGGCCAGCAATTTCAAG TTAACTCCAAAAAGTATCACTCACTACCAAACAAAAGGTTTGAAAAGG AAAGGACGCTCAAACAGGCAGGCCCCCGGGAATACCAAGGGGCGCATG GTGCGTTCAAAAATTCAATGATTCACGGAATTCTGCAATTCACATTACG TATCGCATTTCCCTGCGTTTCTTCATCAATGCGAAAAACCAAAAAATCC GTTGTTGAAAGTTTTTAATATTTTAAAATTTCCATTTACAAAAATTCTGG TTTTTGACAAAAATTTAAGGAATAAATAAAATTGTTGGGGTTGGTTACC TCTGGGCCCCAATTGCTCAAAGGCCCAAAAAAAAATTTGCAAAAATAT GAAAACTCCACATTGGGTTGAATTGAAACGGTTTTAATTGTCCAATAAC AAAACCACAAAATTCTCTCACCGTTGGAAATACCAGAAAAAAAACTTA CAACCCAACCAGAACCGCCCACTTAACCCCAGGCCCGGCTGGACTCCCC ATCCCTGGCCTTCTTGCCCATTAAAAACCTCTTCAGGCCTCTTGCCAAAA CCAAAAAAAATCCC
EA 0.W NS7 (E36)	*Saccharomyces cerevisiae*	99%	ITS	TGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGG GCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGC TATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAAA ACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTTTT CTTTGGGCATTCGAGCAATCGGGGGCCCAGAGGTAACAAACACAAACAA TTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACTGG AAATTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTCGC ATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAA TTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCC AGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGG TAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATT GGATGTTTTTATTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAAT GCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTAT ACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGAA CAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAAC TTAAGCATATCAAT
EA 0.W NS8 (E37)	*Wickerhamomyces anomalus*	100%	ITS	CGCTTATTGCGCGGCGATAAACCTTACACACATTGTCTAGTTTTTTTGAA CTTTGCTTTGGGTGGTGAGCCTGGCTTACTGCCCAAAGGTCTAAACACA TTTTTTTTAATGTTAAAACCTTTAACCAATAGTCATGAAAATTTTTAACA AAAATTAAAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCA ACGATGAAGAACGCAGCGAAATGCGATACGTATTGTGAATTGCAGATT TTCGTGAATCATCGAATCTTTGAACGCACATTGCACCCTCTGGTATTCCA GAGGGTATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGG TATTGAGTGATACTCTGTCAAGGGTTAACTTGAAATATTGACTTAGCAA GAGTGTACTAATAAGCAGTCTTTCTGAAATAATGTATTAGGTTCTTCCA ACTCGTTATATCAGCTAGGCAGGTTTAGAAGTATTTTAGGCTCGGCTTA ACAACAATAAACTAAAAGTTTGACCTCAAATCAGGTAGGACTACCCGCT GAACTTAAGCATATCAATA
EA 0.W NS9 (E38)	*Saccharomyces cerevisiae*	99%	ITS	ATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGA AGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTC TTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTT CTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTG TGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGG GGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTT GTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACT TTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAA TGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTG AACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCG TCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAG TTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGA GGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTT TACCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGAAACGTTATC GATAAAAAAAAAGCGTCTAGGCAAACAATGTTCTTAAAGTTTGACCTCA AATCAGGTAGGAGTACCCGCTGAACTTAACCATATCATAAA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EA 0.W NS10 (E39)	*Saccharomyces cerevisiae*	99%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAGAGAAACCTCTCTT TGGAATAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCC AAAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTC AAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAA AAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCG ATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCAC AGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGA AATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAGCA AGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCT TCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCAT TTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGC
EB 0.W NS6 (E40)	*Saccharomyces cerevisiae*	99%	ITS	ATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGA AGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTC TTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTT CTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTG TGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGG GGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTT GTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACT TTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAA TGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTG AACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCG TCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAG TTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGA GGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTT TACCAACTGCGGCTAATCTTTTTTTTATACTGAGCGTATTGAAACGTTATC GATAAAAAAAAAAGCGTCTAGGCAAACAATGTTCTTAAAGTTTGACCTCA AATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAAAAGGCGAAGG A
EB 0.W NS7 (E41)	*Saccharomyces cerevisiae*	99%	ITS	ATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGA AGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTC TTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTT CTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTG TGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGG GGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTT GTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACT TTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAA TGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTG AACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCG TCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAG TTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGA GGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTT TACCAACTGCGGCTAATCTTTTTTTTATACTGAGCGTATTGAAACGTTATC GATAAAAAAAAAGCGTCTAGGCGAACAATGTTCTTAAAGTTTGACCTCA AATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAATAA
EB 0.W NS8 (E42)	*Saccharomyces cerevisiae*	99%	ITS	ATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGA AGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTC TTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTT CTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTG TGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGG GGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTT GTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACT TTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAA TGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTG AACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCG TCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAG TTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGA GGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTT TACCAACTGCGGCTAATCTTTTTTTTATACTGAGCGTATTGGAACGTTTA TCGATAAA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
EB 0.W NS9 (E43)	*Saccharomyces cerevisiae*	98%	ITS	ACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTC CAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTAA AACGACCGTACTTGCATTATACCTCAAGCACGCAAAGAAACCTCTCTTT GGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCA AAGAGTATCACTCACTACCAAACAAAAGGTTTGAAAAGGAAATGACGC TCAAACAGGCATGCCCCCGGGAATACCAAGGGGCGCAAGGGGCGTTCA AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATT TCCCTGCGTTCTTCATCGATGCGAGAACCAAAAAATCCGTTGTTGAAAG TTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAA AATTTAATGAATAAATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGA TTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAACTCCACA GTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAAAA ATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAGCAA GACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTT CTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATT TTCAAAATTATTAAATTTCTTTAATGATCCTTCC
EB 0.W NS10 (E44)	*Saccharomyces cerevisiae*	99%	ITS	GCTCTCTTCTTATCGATAACGTTCNAATACGCTCAGTATAAAAAAAAAT TACCCGAAGTGGGTAAAACCTAAAACGACCGTCCTGGCTTTATCCCTAA GGCCCCCAAAAAACCCTTTTTTTGGAAAAAAAACATCCAAGGAAAAGG CCAGCATTTTAAAGTTAACTCCAAAAAGTTTAACTNNTTCCCAACCAAA AGGTTGGAAAAGGAAAGGACGTTAAACCAGGCTTGCCCCCGGGAATCC CAAGGGGCGCATGGGGCGTTCAAGGATTCNAGGATTAACGGAATTTTG CATTNNACATTCCGTATNGAATTTCNTTGNGTTTTTAATNGAGGCAAAA CCCAAAAAATCCGTGGTGGAAAGTTTTTAATATTTTAAAATTTCCAGTT CCAAAAATTTTGGTTTTGGCCAAAAATTAAAGGAATAAATAAAATGGTT GGGGTTGGTTACCTNTGGGCCCCNATGGTTCNAAGGCCCAAAAAAAAA GTGGCAAANATNTGAAACCTCNACAGGGGGTGGNTTGGAACCGGTTTT AATGGNCNNNTNNNANAAGCNCAAAAATTTTTAACCGTTGGGATTA
EB 3.W S5 (E45)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CGGCAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAA TTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAAC AGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCT TTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG TGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGC GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTG AAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATG GTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACT GGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTT GCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAG GACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG TCTTGAAA
OA 0.CM NS1 (O1)	*Lachancea thermotolerans*	99%	D1/D2 Domain	CGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGG TGTCCGAGTTGTAATTTGAAGAAGCTACTTTGGGGCTAGTCCTTGTCTAT GTTCCTTGGAACAGGACGTCATGGAGGGTGAGAATCCCGTATGGCGAG GAGTCTAGTCCTATGTAAAGTGCTTTCGACGAGTCGAGTTGTTTGGGAA TGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGA GAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTT GAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATT TGATCAGACATGGTGTTTTGCGACCCTCGCTCCTTGTGGGTGGGGATCT CGCAGCTCACTGGGCCAACATCAGTTTTGGCGGTAGGATAAATCTTTGG GAATGTGGCTTGTCTTCGGAAAAGCGTTATAGCCCAGGGGAATACTACC AGCCGGGACTGAGGACTGCGACTTTTGTCAAGGATGTTGGCATAATGGT TAAATGCCGCCCGTCTTG
		99%	ITS	GTCAACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCGTAAAAGC CTTTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGC AGAGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATG GCCAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACC CGAGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAA TACCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATC TGCAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGA AAAATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACC CTTGGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCC ACAGTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCC GCGCAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAAT TCTTTAATGATCCTTCCGCAGGTTCAC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OB 0.CM NS2 (O2)	*Lachancea thermotolerans*	99%	ITS	ACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAAAAGCCTT TAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAG AGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGC CAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCG AGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATA CCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTG CAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAA CCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAA AATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTT GGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACA GTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCG CAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCT TTAATGATCCTTCCGCAGGTTCCC
OB 0.CM NS3 (O3)	*Lachancea thermotolerans*	99%	ITS	AACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAAAAGCCT TTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAG AGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGC CAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCG AGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATA CCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTG CAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAA CCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAA AATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTT GGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACA GTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCG CAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCT TTAATGATCCTTCCGCAGGTTCCCT
OB 0.CM NS5 (O4)	*Lachancea thermotolerans*	99%	ITS	AACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAAAAGCCT TTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAG AGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGC CAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCG AGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATA CCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTG CAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAA CCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAA AATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTT GGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACA GTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCG CAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCT TTAATGATCCTTCCGCAGGTTC
OA 4.CM NS2 (O5)	*Hanseniaspora opuntiae*	100%	ITS	CCCTTTGCCTAAGGTACATTACCATTTCCCTTGTAAAGTAAAACGAATA AATCCATAAATACATCACAGCGAGAACAGCGTCTCCAAAGAAGCTAAG TGTTGAATTAAAAAAGACTGAAACAGTCTCCAATTTCAAGCTAACCCTG AGTATCGCCCACAACCAAAAAATAAAAAATTATCTTTTGAGAAGGAAA TGACGCTCAAACAGGCATGCCCTTGAGAATGCTCAAGGGCGCAATGTG CGTTCAAAAATTCAATGATTCACGAGTATCTGCAATTCACATTACTTATC GCAATTCGCTACGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTT GAAAGTTTTAAATTATTTTAAAATTTCCGTTAGGAATTTTGGTTTAGTTT AAAAAATTATAATAAAATAAAATTGTTTGTGTTTGTTTTTTGCCTTGAAC CTTTCGATTCAAAGCAGAAAGAATTAAATTAAAGTAAAAAAACTCCAA TGTGTGTAAACGTTGACTGAGATTCAAGCAAGACTACTTCTACTGCGAC ACTCTAATGAAGCAGCGCAATTAAGCGCACATCTTCAATAAAGATACAC ATTATTGTAAAAGATCTAAACAAGAACTCGAGCAACAATGATAATTCA ATCTAATGATCCTTCCGCAGGTTC
OA 4.CM NS3 (O6)	*Lachancea thermotolerans*	99%	ITS	CTTTATGAATACTGTTTGCCGACTGTCTGTACTTTCAGTAAAAGCCTTTA AAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAGAG TATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGCCA GCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCGAG GGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACC AGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTGCA ATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAACC AAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAAA ATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTTG GGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACAG TGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCGC AATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCTT TAATGATCCTTCCGCAGGTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OA 4.CM NS4 (O7)	*Hanseniaspora opuntiae*	100%	D1/D2 Domain	CGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTTTCAGT GCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATG TTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGG ATACCTTTTCTCTGTAAGACTTTTTCGAAGAGTCGAGTTGTTTGGGAATG CAGCTCAAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGA GACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGA AAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTG ATCAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCT CTCAAAAATTTCACTGGGCCAACATCAATTCTGGCAGTAGGATAAATCA TTAAGAATGTAGCTACCTCGGTAGTGTTATAGCTTATTGGAATACTGCT AGCTGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGCATAATGGTTA AATGCCGCCCGTCTTGAA
	Hanseniaspora opuntiae	100%	ITS	AACTTGATGAATATTAAAAGCAACCCTTTGCCTAAGGTACATTACCATT TCCCTTGTAAAGTAAAACGAATAAATCCATAAATACATCACAGCGAGA ACAGCGTCTCCAAAGAAGCTAAGTGTTGAATTAAAAAAGACTGAAACA GTCTCCAATTTCAAGCTAACCCTGAGTATCGCCCACAACCAAAAAATAA AAAATTATCTTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCTTGA GAATGCTCAAGGGCGCAATGTGCGTTCAAAAATTCAATGATTCACGAGT ATCTGCAATTCACATTACTTATCGCAATTCGCTACGTTCTTCATCGATGC GAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTATTTTAAAATTTC CGTTAGGAATTTTGGTTTAGTTTAAAAAATTATAATAAAATAAAATTGT TTGTGTTTGTTTTTTGCCTTGAACCTTTCGATTCAAAGCAGAAAGAATTA AATTAAAGTAAAAAACTCCAATGTGTGTAAACGTTGACTGAGATTCAAG CAAGACTACTTCTACTGCGACACTCTAATGAAGCAGCGCAATTAAGCGC ACATCTCCAATAAAGATACACATTATTGTAAAAGATCTAAACAAGAACT CGAGCAACAATGATAATTCAATCTAATGATCCTTCCGCAGGT
OB 4.CM NS3 (O8)	*Lachancea thermotolerans*	99%	ITS	AACTTTATGAATACTGTTTGCCGACTGTCTGTACTTTCGTAAAAGCCTTT AAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAGA GTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGCC AGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCGA GGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATAC CAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTGC AATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAAC CAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAA AATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTT GGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACA GTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCG CAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCT TTAATGATGCTTCCGCAGGTTC
OB 4.CM NS4 (O9)	*Lachancea thermotolerans*	99%	ITS	CTTTATGAATACTGTTTGCCGACTGTCTGTACTTTCAGTAAAAGCCTTTA AAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAGAG TATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGCCA GCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCGAG GGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACC AGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTGCA ATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAACC AAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAAA ATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTTG GGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACAG TGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCGC AATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCTT TAATGATCCTTCCGCAGGTTCCT
OB 4.CM NS5 (O10)	*Saccharomyces cerevisiae*	99%	ITS	TTGAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCG ATAACGTTCCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTA AAACCTAAAACGACCGTACTTGCATTATACCTCAAGCACGCAGAGAAA CCTCTCTTTGGAATAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGT TAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGA AATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATG TGCGTTCAAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGT ATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTT GTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTT TTGACAAAAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTG GGCCCCGATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAA ACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAA GCACAGAAATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAG CCTAGCAAGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCT CTTGTCTTCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAA AATCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OA 0.CM NS2 (O11)	*Lachancea thermotolerans*	99%	ITS	GGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTTCTGT TAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTACAAC GCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAATTA TTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAATATTT AAAACTTTCAACAACGGATCTCTTGATTCTCGCATCGATGAAGAACGCA GCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATCGAA TCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCTGTTT GAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTACTCT TTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTGAGG TTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTCGTA GTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAG
OA 0.CM NS3 (O12)	*Saccharomyces cerevisiae*	100%	ITS	TTTTGAAAATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTG GGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTG CGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGA GAGATTTCTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAA CACACTGTGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAG CAATCGGGGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTA AATTTTTGTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATT AAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGC AGCGAAATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGA ATCTTTGAACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGT TTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTC TTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCC AAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTT TTAGGTTTTACCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGGA ACGTTATCGATAAGAAGAGAGCGTCTAGGCGAACAATGTTCTTAAAGTT TGACCTCAAATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAA
OA 0.CM NS4 (O13)	*Lachancea thermotolerans*	99%	ITS	GCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTT CTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTAC AACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAA TTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAATA TTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC GCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATC GAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCT GTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTA CTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTG AGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTC GTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACA GTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTA CCCGCTGAACTTAAGCATATCAATAA
OA 0.CM NS5 (O14)	*Lachancea thermotolerans*	99%	ITS	GAGGTCAACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAA AAGCCTTTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAAT ACGCAGAGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCA GATGGCCAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCA AACCCGAGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCT GGAATACCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGA ATATCTGCAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGAT GCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTA AAATGAAAAATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTT GTAACCCTTGGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAAT TACTCCACAGTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCAT CGGCCGCGCAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAAC AAAATTCTTTAATGATCCTTCCGCAGGT
OA 0.CM NS6 (O15)	*Lachancea thermotolerans*	99%	ITS	ATTTGAGGTCAACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCA GTAAAAGCCTTTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACC TAATACGCAGAGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACA GCCAGATGGCCAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACT ACCAAACCCGAGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCC CCCTGGAATACCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCA CGAATATCTGCAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATC GATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTT CTAAAATGAAAAATAATTGACAATGTTTAAAATACAATAATTGTTTGTG TTTGTAACCCTTGGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATA AATTACTCCACAGTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCAT CATCGGCCGCGCAATCAAGCGCAGGCTTCTGAACTTTCCCGGCAGCTCT AACAAAATTCATTAATGATCCTTCCGGG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OA 0.CM NS7 (O16)	*Lachancea thermotolerans*	99%	ITS	GCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTT CTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTAC AACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAA TTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAATA TTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC GCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATC GAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCT GTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTA CTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTG AGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTC GTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACA GTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTA CCCGCTGAACTTAAGCATATCAATAA
OA 0.CM NS8 (O17)	*Lachancea thermotolerans*	99%	ITS	AACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAAAAGCCT TTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAG AGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGC CAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCG AGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATA CCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTG CAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAA CCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAA AATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTT GGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACA GTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCG CAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCT TTAATGATCCTTCCGCA
OA 0.CM NS9 (O18)	*Lachancea thermotolerans*	99%	ITS	AGCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTT TCTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTA CAACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACA ATTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAAT ATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA CGCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCAT CGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCC TGTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGT ACTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACT GAGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACT CGTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGAC AGTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATT ACCCGCTGAACTTAAGCATATC
OA 0.CM NS10 (O19)	*Lachancea thermotolerans*	99%	ITS	ATTTGAGGTCAACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCA GTAAAAGCCTTTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACC TAATACGCAGAGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACA GCCAGATGGCCAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACT ACCAAACCCGAGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCC CCCTGGAATACCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCA CGAATATCTGCAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATC GATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTT CTAAAATGAAAAATAATTGACAATGTTTAAAATACAATAATTGTTTGTG TTTGTAACCCTTGGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATA AATTACTCCACAGTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCAT CATCGGCCGCGCAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCT AACAAAATTCTTTAATGATCCTTCC
OB 0.CM NS1 (O20)	*Lachancea thermotolerans*	99%	ITS	GATTTGAGGTCAACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTC AGTAAAAGCCTTTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAAC CTAATACGCAGAGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAAC AGCCAGATGGCCAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCAC TACCAAACCCGAGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGC CCCCTGGAATACCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTC ACGAATATCTGCAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCAT CGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTT TCTAAAATGAAAAATAATTGACAATGTTTAAAATACAATAATTGTTTGT GTTTGTAACCCTTGGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAAT AAATTACTCCACAGTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGC ATCATCGGCCGCGCAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCT CTAACAAAATTCTTTAATGATCCTTCCGCAGGTTCACCTACGGAAGGTT GGAACACCCGGGAAGTTTGAAAGACCGCCCGGAAAGTTCGGACGCCGA ACTTGTTTGTGCGGACGAGGATGCTTTCTGATAACGAC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OB 0.CM NS4 (O21)	*Lachancea thermotolerans*)	100%	ITS	AGCAGCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGAT GCTTTCTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTAT TTTACAACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACA AACAATTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAA AAATATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGA AGAACGCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGA ATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGC ATGCCTGTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGA GTGGTACTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGC TGACTGAGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTAC CAACTCGTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTA CAGACAGTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTA GGATTACCCGCTGAACTTAAGCATATCAATAAA
OB 0.CM NS6 (O22)	*Lachancea thermotolerans*	99%	ITS	TCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTTCTGTTAACGA CTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTACAACGCTTCTT CTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAATTATTGTATT TTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAAATATTTAAAACTT TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAAT GCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATCGAATCTTTGA ACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCTGTTTGAGCGT CATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTACTCTTTCTGG GTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTGAGGTTTTAG TCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTCGTAGTGGCG TTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACAGTCTGGCAA ACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAA CTTA
OA 4.CM NS1 (O23)	*Lachancea thermotolerans*	99%	ITS	ACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAAAAGCCTT TAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAATACGCAG AGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCAGATGGC CAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCAAACCCG AGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATA CCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGAATATCTG CAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAA CCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTAAAATGAAA AATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTTGTAACCCTT GGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAATTACTCCACA GTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCATCGGCCGCG CAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAACAAAATTCT TTAATGATCCTTCCGCAGGC
OA 4.CM NS5 (O24)	*Saccharomyces cerevisiae*	100%	ITS	ATTTGAGGTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTAT CGATAACGTTCCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGG TAAAACCTAAAACGACCGTACTTGCATTATACCTCAAGCACGCAGAGA AACCTCTCTTTGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCA AGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAG GAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAA TGTGCGTTCAAAGATTCGATGATTCACGGAATTCTGCAATTCACATTAC GTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCG TTGTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGT TTTTGACAAAAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTC TGGGCCCCGATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGA AAACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAA AAGCACAGAAATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACA AGCCTAGCAAGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCAT CTCTTGTCTTCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAA AAATCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGGTT CACCTACGGAAGAAAAAGG
OA 4.CM NS6 (O25)	*Lachancea thermotolerans*	99%	ITS	GAGGTCAACTTTATGAATACTGTTTGCCAGACTGTCTGTACTTTCAGTAA AAGCCTTTAAAACGCCTACTAACGCCACTACGAGTTGGTAAAACCTAAT ACGCAGAGTATCAGCGGACTGGACTAAAACCTCAGTCAGCAACAGCCA GATGGCCAGCATTTTCAAGTTAACCCAGAAAGAGTACCACTCACTACCA AACCCGAGGGTTTGAGAAGGAAATGACGCTCAAACAGGCATGCCCCCT GGAATACCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACGA ATATCTGCAATTCACAATACTTATCGCATTTCGCTGCGTTCTTCATCGAT GCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATATTTTTTTTCTA AAATGAAAAATAATTGACAATGTTTAAAATACAATAATTGTTTGTGTTT GTAACCCTTGGGCCGTAAAGCCCAAAGAAGAAGCGTTGTAAAATAAAT TACTCCACAGTGTGTGTGTAGAGAGACAGTCGTTAACAGAAAGCATCAT CGGCCGCGCAATCAAGCGCAGGCTTCTGAACTTTCCCGGCTGCTCTAAC AAAATTCTTTAATGATCCTT

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OA 4.CM NS7 (O26)	*Lachancea thermotolerans*	99%	ITS	AAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTTCTGTTAACGACTGT CTCTCTACACACACACTGTGGAGTAATTTATTTTACAACGCTTCTTCTTT GGGCTTTACGGCCCAAGGGTTACAAACACAAACAATTATTGTATTTTAA ACATTGTCAATTATTTTTCATTTTAGAAAAAAAAATATTTAAAACTTTCAA CAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGA TAAGTATTGTGAATTGCAGATATTCGTGAATCATCGAATCTTTGAACGC ACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTT CCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTACTCTTTCTGGGTTAA CTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTGAGGTTTTAGTCCAG TCCGCTGATACTCTGCGTATTAGGTTTTACCAACTCGTAGTGGCGTTAGT AGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACAGTCTGGCAAACAGT ATTCATAAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAACTTAA
OA 4.CM NS8 (O27)	*Lachancea thermotolerans*	99%	ITS	GCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTT CTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTAC AACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAA TTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAAATA TTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC GCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATC GAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCT GTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTA CTCTTTCTGGGTTTACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTG AGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTC GTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACA GTCTGGCAAACAGTATTCATAAAGTTT
OA 4.CM NS9 (O28)	*Lachancea thermotolerans*	99%	ITS	CAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTTCTGTTAACGAC TGTCTCTCTACACACACACTGTGGAGTAATTTATTTTACAACGCTTCTTC TTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAATTATTGTATTT TAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAAATATTTAAAACTTT CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATG CGATAAGTATTGTGAATTGCAGATATTCGTGAATCATCGAATCTTTGAA CGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTC ATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTACTCTTTCTGGG TTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTGAGGTTTTAGTC CAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTCGTAGTGGCGTT AGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACAGTCTGGCAAAC AGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAACT TAA
OA 4.CM NS10 (O29)	*Lachancea thermotolerans*	99%	ITS	AGCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTT TCTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTA CAACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACA ATTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAAT ATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA CGCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCAT CGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCC TGTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGT ACTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACT GAGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACT CGTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGAC AGTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATT ACCCGCTGAACTTAAGCATATC
OB 4.CM NS1 (O30)	*Lachancea thermotolerans*	99%	ITS	GCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTT CTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTAC AACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAA TTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAAATA TTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC GCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATC GAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCT GTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTA CTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTG AGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTC GTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACA GTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTA CCCGCTGAACTTAAGCATATCAATA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OB 4.CM NS2 (O31)	*Lachancea thermotolerans*	99%	ITS	AGCAGCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGAT GCTTTCTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTAT TTTACAACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACA AACAATTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAA AAATATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGA AGAACGCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGA ATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGC ATGCCTGTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGA GTGGTACTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGC TGACTGAGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTAC CAACTCGTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTA CAGACAGTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTA GGATTACCCGCTGAACTTAAGCATAT
OB 4.CM NS6 (O32)	*Lachancea thermotolerans*	99%	ITS	GAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTTCTGTTAACGACTG TCTCTCTACACACACACTGTGGAGTAATTTATTTTACAACGCTTCTTCTT TGGGCTTTACGGCCCAAGGGTTACAAACACAAACAATTATTGTATTTTA AACATTGTCAATTATTTTTCATTTTAGAAAAAAAATATTTAAAACTTTCA ACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCG ATAAGTATTGTGAATTGCAGATATTCGTGAATCATCGAATCTTTGAACG CACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCAT TTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTACTCTTTCTGGGTT AACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTGAGGTTTTAGTCC AGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTCGTAGTGGCGTTA GTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACAGTCTGGCAAACA GTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAACTT AAGCATATCA
OB 4.CM NS7 (O33)	*Lachancea thermotolerans*	99%	ITS	TGATTGCGCGGCCGATGATGCTTTCTGTTAACGACTGTCTCTCTACACAC ACACTGTGGAGTAATTTATTTTACAACGCTTCTTCTTTGGGCTTTACGGC CCAAGGGTTACAAACACAAACAATTATTGTATTTTAAACATTGTCAATT ATTTTTCATTTTAGAAAAAAAAATATTTAAAACTTTCAACAACGGATCTCT TGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTATTGTGA ATTGCAGATATTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCT CTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACC CTCGGGTTTGGTAGTGAGTGGTACTCTTTCTGGGTTAACTTGAAAATGCT GGCCATCTGGCTGTTGCTGACTGAGGTTTTAGTCCAGTCCGCTGATACTC TGCGTATTAGGTTTTACCAACTCGTAGTGGCGTTAGTAGGCGTTTTAAA GGCTTTTACTGAAAGTACAGACAGTCTGGCAAACAGTATTCATAAAGTT TGACCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAAAA
OB 4.CM NS8 (O34)	*Lachancea thermotolerans*	99%	ITS	AGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCTTTCTGTTAA CGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTTACAACGCTT CTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAACAATTATTGT ATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAATATTTAAAA CTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGA AATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCATCGAATCTT TGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGCCTGTTTGAG CGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGGTACTCTTTC TGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGACTGAGGTTT TAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAACTCGTAGTG GCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGACAGTCTGG CAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGATTACCCGCT GAACTTAAGCATATCAATA
OB 4.CM NS9 (O35)	*Lachancea thermotolerans*	99%	ITS	CAGCCGGGAAGTTCAGAAGCCTGCGCTTGATTGCGCGGCCGATGATGCT TTCTGTTAACGACTGTCTCTCTACACACACACTGTGGAGTAATTTATTTT ACAACGCTTCTTCTTTGGGCTTTACGGCCCAAGGGTTACAAACACAAAC AATTATTGTATTTTAAACATTGTCAATTATTTTTCATTTTAGAAAAAAAA TATTTAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA ACGCAGCGAAATGCGATAAGTATTGTGAATTGCAGATATTCGTGAATCA TCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCATGC CTGTTTGAGCGTCATTTCCTTCTCAAACCCTCGGGTTTGGTAGTGAGTGG TACTCTTTCTGGGTTAACTTGAAAATGCTGGCCATCTGGCTGTTGCTGAC TGAGGTTTTAGTCCAGTCCGCTGATACTCTGCGTATTAGGTTTTACCAAC TCGTAGTGGCGTTAGTAGGCGTTTTAAAGGCTTTTACTGAAAGTACAGA CAGTCTGGCAAACAGTATTCATAAAGTTTGACCTCAAATCAGGTAGGAT TACCCGCTGAACTTAAGCATATC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
OB 4.CM NS10 (O36)	*Lachancea thermotolerans*	99%	ITS	GCGCGGCCGATGATGCTTTCTGTTAACGACTGTCTCTCTACACACACAC TGTGGAGTAATTTATTTTACAACGCTTCTTCTTTGGGCTTTACGGCCCAA GGGTTACAAACACAAACAATTATTGTATTTTAAACATTGTCAATTATTTT TCATTTTAGAAAAAAAATATTTAAAACTTTCAACAACGGATCTCTTGGT TCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTATTGTGAATTG CAGATATTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGG TATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACCCTCG GGTTTGGTAGTGAGTGGTACTCTTTCTGGGTTAACTTGAAAATGCTGGC CATCTGGCTGTTGCTGACTGAGGTTTTAGTCCAGTCCGCTGATACTCTGC GTATTAGGTTTTACCAACTCGTAGTGGCGTTAGTAGGCGTTTTAAAGGC TTTTACTGAAAGTACAGACAGTCTGGCAAACAGTATTCATAAAGTTTGA CCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATAT
OA 4.CM S3 (O37)	*Wickerhamomyces anomalus*	100%	D1/D2 Domain	CGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTAGCACCTTCGGTGTT CGAGTTGTAATTTGAAGATGGTAACCTTGGGTTTGGCTCTTGTCTATGTT CCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTCTGATGAGATG CCCATTCCTATGTAAGGTGCTATCGAAGAGTCGAGTTGTTTGGGAATGC AGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAG ACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAA AAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTAGA TCAGACTTGGTGTTTTACGATTATCTTCTCTTCTTGAGTTGTGCACTCGT ATTTCACTGGGCCAGCATCGATTCGGATGGCAAGATAATGGCAGTTGAA TGTGGCTTCACTTCGGTGGAGTGTTATAGCTTCTGCTGATATTGCCTGTC TGGATCGAGGGCTGCGTCTTTTGACTAGGATGCTGGCGTAATGATCTAA TGCCGCCCGTCTTG
OB 0.CM S6 (O38)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CCTTAGTACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGT ACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTT CCTTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCG TGTGGCGAGGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTT GTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAA TATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAA AAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGG AAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGT AGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGAT AAATCCATAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGA ATACTGCCAGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGG CATAATGGTTATATGCCGCCCGTC
OB 4.CM S2 (O40)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	GGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAA TTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAAC AGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCT TTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG TGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGC GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTG AAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATG GTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACT GGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTT GCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAG GACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG TCT
OB 4.CM S1 (O39)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGT GCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTA TGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGA GGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGA ATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTT TGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCAT TTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAAT CTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCAT AGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCC AGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGG TTATATGCCGCCCG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BA 0.CM NS2 (B2)	*Saccharomyces cerevisiae*	100%	ITS	GTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGAT GGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTG TAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGT TATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCAT ATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGT AACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAA GAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGG ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTA ATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTG CGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCT CAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAA TTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGC GTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGC GGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAG AGAGCGT
BA 0.CM NS3 (B3)	*Saccharomyces cerevisiae*	99%	ITS	ATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGA AGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTC TTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTT CTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTG TGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGG GGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTT GTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACT TTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAA TGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTG AACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCG TCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAG TTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGA GGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTT TACCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGAAACGTTATC
BA 0.CM NS4 (B4)	*Solicoccozyma aeria*	99%	D1/D2 Domain	ATTTGAAATCTGGCAGCCTCAGGTTGTCCGAGTTGTAATCTATAGAAAC GTTTTCCGCGCTGGCCCATGTACAAGTCCCTTGGAATAGGGCGTCATAG AGGGTGAGAATCCCGTCCTTGACACGGACCACCAGTGCTTTGTGATACG TTTTCAACGAGTCGAGTTGTTTGGGAATGCAGCTCAAAATGGGTGGTAA ATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTA CCGTGAGGGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAACAGTAT GTGAAATTGTTGAAAGGGAAACGATTGAAGTCAGTCGTGTCTATGGGA CTCAGCCGGTTCTGCCGGTGTACTTCCTTTAGATGGGGTCAACATCAGTT TTGATCGCTGGAAAAGGGCGGGAGGAATGTAGCACTCTCGGGTGAACT TATAGCCTTCCGTCGTATACGGTGGTTGGGACTGAGGAACGCAGCATGC CTTTATGGCCGGGGTTCGCCCACGTACATGCTTAGGATGTTGACATAAT GGCTTTAAACAACCCGTCT
		100%	ITS	GCAAGGCCCTTGCTTAACTCACATCCCAACACCTGTGAACTGTAAGGCG CATGACTAGGTTCGCCCAAGTCATCGTCTGCCCTTTTTAACAAACAATT AATGTAACAAACGTAGTCTTATTATAACCTAATAAAACTTTCAACAACG GATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGT AATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTT GCGCTCTTTGGTATTCCGAAGAGCATGCCTGTTTGAGTGTCATGAAAAT ATCAACCTTGACTTGGGTTTTGTGCTCTAGTCTCGGCTTGGAATTGGGTG CTTGCCGCTTTTACGAGCGGCTCACCTTAAATGTATTAGCTGGATCTGTC TTTGAGACTTGGTTTGACTTGGCGTAATAAGTATTTCGCTAAGGACATTC TTCGGAGTGGCCTCGTTTCTAGGACGCTTGTCCGCTTTCCAATACAAGTT CCACCTCGTGGACATGACTTTTTATTATCTGGCCTCAAATCAGGTAGGA CTACCCGCT
BA 0.CM NS5 (B5)	*Saccharomyces cerevisiae*	99%	ITS	TTATCGATAACGTTCCAATACGCTCAGTATAAAAAAAGATTAGCCGCAG TTGGTAAAACCTAAAACGACCGTACTTGCATTATACCTCAAGCACGCAG AGAAACCTCTCTTTGGAAAAAAAAACATCCAATGAAAAGGCCAGCAATT TCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAG AAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCG CAATGGGCGTTCAAAGATTCGATGATTCACGGAATTCTGCAATTCACAT TACGTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGAT CCGTTGTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCT TGTTTTTGACAAAAATTTAATGAATAGATAAAATTGTTTGGGTTTGTTAC CTCTGGGCCCCGATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATAT GAAAACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAAC AAAAGCACAGAAATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTA CAAGCCTAGCAAGACCGCGCACTTAAGCGCAGG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BA 0.CM NS6 (B6)	*Saccharomyces cerevisiae*	99%	ITS	ACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTC CAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTAA AACGACCGTACTTGCATTATACCTCAAGCACGCAAAGAAACCTCTCTTT GGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCA AAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGACGC TCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATT TCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAG TTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAA AATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGA TTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCACA GTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAA ATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAGCAA GACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTT CTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATT TTCAAAATTATTAAATTTCTTTAATGATCCTTCCGC
BA 0.CM NS7 (B7)	*Saccharomyces cerevisiae*	100%	ITS	AAAATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCA AGAAGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCG GTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGA TTTCTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACAC TGTGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATC GGGGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTT TTGTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAA CTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGA AATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTT TGAACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAG CGTCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGG AGTTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGA GAGGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGG TTTTACCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTT ATCGATAAGAAGAGAGCGTCTAGGCGAACAATGTTCTTAAAGTTTGACC TCAAATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAATAA
BA 0.CM NS8 (B8)	*Saccharomyces cerevisiae*	99%	ITS	TTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAG ATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCT TGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTT GTTATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTC ATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGGCCCAGAG GTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAAC AAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAAC GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACG TAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACAT TGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTT CTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAA ATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTG CGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTG CGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAAAA AAAAGCGTCTAGGCAAACAATGTTCTTAAAGTTTGACCTCAAATCAGGT AGGAGTACCC
BB 0.CM NS1 (B9)	*Saccharomyces cerevisiae*	100%	ITS	GAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGG CCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCT ATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAAAA CCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTTTTC TTTGGGCATTCGAGCAATCGGGGGCCCAGAGGTAACAAACACAAACAAT TTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACTGGA AATTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCAT CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATT CCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCA GGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGT AGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTG GATGTTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGC AAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTATAC TGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGAACA ATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAACTT AAGCATATCA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BB 0.CM NS2 (B10)	*Metschnikowia pulcherrima*	99%	ITS	TAACCCTCAATAACTTTATTAAAAAACTTTCAACAACGGATCTCTTGGTT CTCGCATCGATGAAGAACGCAGCGAATTGCGATACGTAATATGACTTGC AGACGTGAATCATTGAATCTTTGAACGCACATTGCGCCCCGGGGTATTC CCCAGGGCATGCGTGGGTGAGCGATATTTACTCTCAAACCTCCGGTTTG GTCCTGCTTCGGCCTAATATCAACGGCGCTAGAATAAGTTTTAGCCCCA TTCTTTTTCCTCACCCTCGTAAGACTACCCGCTGAACTTAAGCATATCAA TAAG
BB 0.CM NS3 (B11)	*Metschnikowia aff. pulcherrima*	99%	D1/D2 Domain	CGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTG TAATTTGAAGAGATTTGGGTCCGGCCGGCAGGGGTTAAGTCCACTGGAA AGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCCTCAACGCCCTC ATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGG GTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGA ACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAA AAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTA ACTGGGCCAGCATCGGGGCGGCGGGAAGCAAAACCACCGGGGAATGTA CCTTTCGAGGATTATAACCCCGGCCCTTACTCCCATACCACCCCGAGGC CTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAA
	Metschnikowia pulcherrima	98%	ITS	CTTTATTAAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGA AAAACGCACCGAATTGCGATACGTAATATGACTTGCAAACGTGAATCAT TGAATCTTTGAACGCACATTGCGCCCCGGGGTATTCCCCAGGGCATGCG TGGGTGAGCGATATTTACTCTCAAACCTCCGGTTTGGTCCTGCTTCGGCC TAATATCAACGGCGCTAGAATAAGTTTTACCCCCATTCTTTTTCCTCACC CTCGTAAAACTACCCGCTGAACTTAACCATATCA
BB 0.CM NS4 (B12)	*Metschnikowia pulcherrima*	99%	ITS	TGGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGAC CAAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTAATAAAGTTATTGAGGGTT AAAATTTAAAGTTTGTGCCTAAAAGGG
BB 0.CM NS5 (B13)	*Saccharomyces cerevisiae*	99%	ITS	TTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGG AGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTA AGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTA TAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATAT CTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAA CAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGA ATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGAT CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAAT GTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCG CCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCA AACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTG CTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTG CTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGC TAATCTTTTTTTATACTGACCGTATTGGAACGTTATCGATAAGAAGAGA GCGTCTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGA GT
BB 0.CM NS6 (B14)	*Saccharomyces cerevisiae*	100%	ITS	CCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTC TTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATT AAAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTT TTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAAC AATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACT GGAAATTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTC GCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG AATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATT CCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTT GGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCA TTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAA TGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTA TACTGAGCGTATTGGAACGTTATCGATAA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BB 0.CM NS7 (B15)	*Metschnikowia pulcherrima*	97%	ITS	AACTCTAATCTTAACCCTCAATAACTTTATTAAAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAAAACGCACCGAATTGCGATACGT AATATGACTTGCAAACGTGAATCATTGAATCTTTGAACGCACATTGCGC CCCGGGGTATTCCCCAGGGCATGCGTGGGTGAGCGATATTTACTCTCAA ACCTCCGGTTTGGTCCTGCTTCGGCCTAATATCAACGGCGCTAGAATAA GTTTTACCCCCATTCTTTTTCCTCACCCTCGTAAAACTACCCGCTGAACT TAACCATATCA
BB 0.CM NS8 (B16)	*Saccharomyces cerevisiae*	99%	ITS	GGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGA GTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGT TTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAG GACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTT TGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAA ACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTT TCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGATCTCT TGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTG AATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCC CTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAAC ATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTG GCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTT GAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAA TCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCG TCTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAATCANGTAGGAGTA CCCGCTGA
BA 4.CM NS1 (B17)	*Saccharomyces cerevisiae*	100%	ITS	AGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGGCCT GCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCTATT CCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAAAACCG TTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTTTTCTTT GGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAACAATTTT ATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACTGGAAA TTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCG ATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCC GTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCAGG GGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGTAG TGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGGA TGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCAA GTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTATACTG AGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGAACAAT GTTCTTAAAGTTTGACCTCAAATCA
BA 4.CM NS5 (B21)	*Saccharomyces cerevisiae*	99%	ITS	AGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGGCCT GCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCTATT CCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAAAACCG TTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTTTTCTTT GGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAACAATTTT ATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACTGGAAA TTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCG ATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCC GTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCAGG GGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGTAG TGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGGA TGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCAA GTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTATACTG AGCGTATTGGAACGTTATCGATAAGAANAGAGCGTCTAGGCGAACAAT GTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BA 4.CM NS6 (B22)	*Saccharomyces cerevisiae*	99%	ITS	TTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTCCA ATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTAAAA CGACCGTACTTGCATTATACCTCAAGCACGCAAAGAAACCTCTCTTTGG AAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCAAA GAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGACGCTC AAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCAAA GATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCG CTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTT TTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGACAAAAAT TTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGATTG CTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCACAGTG TGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAGAAATC TCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAGCAAGAC CGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTTCTTG CCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATTTTCA AAATTATTAAATTTCTTTAATGATCCTTCCGCAGT	
BA 4.CM NS7 (B23)	*Saccharomyces cerevisiae*	98%	ITS	ACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTTC CAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTAA AACGACCGTACTTGCATTATACCTCAAGCACGCAAAAAAACCTCTCTTT GGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCCA AAAAGTATCACTCACTACCAAACAAAATGTTTGAAAAGGAAATGACCC TCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAAGGTGCGTTCA AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATT TCCCTGCGTTCTTCATCGATGCGAGAACCAAAAAATCCGTTGTTGAAAG TTTTTAATATTTTAAAATTTCCAGTTACAAAAATTCTTGTTTTTGACAAA AATTTAATGAATAAATAAAATTGTTTGTGTTTGTTACCTCTGGGCCCCGA TTGCTCGAATGCCCAAAAAAAAAGTTGCAAAAATATGAAAACTCCACA GTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAAAA ATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAGCAA GACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTGTCTT CTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATCCATT TTCAAAATTATTAAATTTCTTT	
BA 4.CM NS8 (B24)	*Saccharomyces cerevisiae*	98%	ITS	AACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAACGTT CCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACCTA AAACGACCGTACTTGCATTATACCTCAAGCACGCAAAGAAACCTCTTTT TGGAAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACTCC AAAGAGTATCACTCACTACCAAACAGAATGTTTGAAAAGGAAATGACG CTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAAGGGGCGTTC AAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCAT TTCGCTGCGTTCTTCATCGATGCGAGAACCAAAAAATCCGTTGTTGAAA GTTTTTAATATTTTAAAATTTCCAGTTCCAAAAATTCTTGTTTTTGACAA AAATTTAATGAATAGATAAAATTGTTTGGGTTTGTTACCTCTGGGCCCC GATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTCCA CAGGGGGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCACAG AAATCTTTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTAGCA AGACCG	
BB 4.CM NS1 (B26)	*Saccharomyces cerevisiae*	100%	ITS	GGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAG ACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTT GCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCT GTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTGTG GAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGG CCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGT CAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTT CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATG CGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAA CGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTC ATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTT AACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGG TTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTA CCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGA TAAGAAGAGAGCGTCTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAA TCAGGTAGGAGTACCCGCTGAACTTAAGCATATC	

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BB 4.CM NS2 (B27)	*Saccharomyces cerevisiae*	99%	ITS	TGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGA TGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTT GTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTG TTATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCA TATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGT AACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAA GAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGG ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTA ATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTG CGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCT CAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAA TTGCTGGCCTTTTCATTGGATGTTTTTATTCCAAAGAGAGGTTTCTCTGC GTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGC GGCTAATCTTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAG AGAGCGTCTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTA GGAGTACCCGCTGAACTTAAGCATATCATAA
BB 4.CM NS3 (B28)	*Saccharomyces cerevisiae*	100%	ITS	TGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAA GACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCT TGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTC TGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTGT GGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGG GCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTG TCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTT TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAAT GCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGA ACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGT CATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGT TAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAG GTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTT ACCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCG ATAAGAAGAGAGCGTCTAGGCGAACAATGTTCTTAAAGTTTGACCTCAA ATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCATA
BB 4.CM NS4 (B29)	*Saccharomyces cerevisiae*	99%	ITS	ATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGAC AAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCT AGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTG CTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAG TTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCC AGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAA AAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAA CAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGA TACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGC ACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTT CCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACT TGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTC TCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCA ACTGCGGCTAATCTTTTTTTATACTGACCGTATTGGAACGTTATCGATAA AAAAAAAGCGTCTAGGCAAACAATGTTCTTAAAGTTTGACCTCAAATCA GGTAGGAGTACCCGCTGAACTTAAGCATAT
BB 4.CM NS5 (B30)	*Metschnikowia pulcherrima*	96%	ITS	TAACTTTATTAAAAAACTTTCAACAACGGATCTCTGGGTTCTCGCATCG ATGAAAAACCCACCGAATTGCGATACTTAATATGACTTGCAAACTTGAA TCATTGAATCTTTGAACGCACATTGCGCCCCGGGGTATTCCCCAGGGCA TGCGTGGGTGAGCGATATTTACTCTCAAACCTCCGGTTTGGTCCTGCTTC GGCCTAATATCAACGGCCCTAGAATAATTTTTACCCCCATTCTTTTTCCT CACCCTCGTAAAACTACCCGCTGAACTTAACCATATCA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BB 4.CM NS6 (B31)	*Saccharomyces cerevisiae*	99%	ITS	ATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGA AGACAAGAGATGGAGAGTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTC TTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTT CTGTGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTG TGGAGTTTTCATATCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGG GGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTT GTCAAAAACAAGAATTTTCGTAACTGGAAATTTTAAAATATTAAAAACT TTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAA TGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTG AACGCACATTGCGCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCG TCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAG TTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGA GGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTANGTTT TACCAACTGCGGGCTAATCTTTTTTTTATACTGAGCGT
BB 4.CM NS7 (B32)	*Saccharomyces cerevisiae*	99%	ITS	GGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGA GTCCAGCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGT TTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAG GACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTT TGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAA ACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTT TCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGATCTCT TGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTG AATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCC CTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAAC ATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTG GCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTT GAGGTATAATGCAAGTACGGTCGTTTTANGTTTTACCAACTGCGGCTAA TCTTTTTTTATACTGACCGTATTGGAACGTTATCGATAANAAAA
BB 4.CM NS8 (B33)	*Metschnikowia aff. fructicola*	100%	D1/D2 Domain	GGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTGTAATTTGAAGAGAT TTGGGTCCGGCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAG AGGGTGACAGCCCCGTGAACCCCTTCAACGCCCTCATCCCAGATCTCCA AGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCAT CTAAAGCTAAATACCGGCGAGAGACCGATAGCGAACAAGTACAGTGAT GGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAAT TGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATC GGGGCGGCGGGAAACAAAACCACCGGGGAATGTACCTTTCGAGGATTA TAACCCCGGTCTCAATTTCCTTGTTGCCCCGAGGCCTGCAATCTAAGGA TGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAAACA
	Metschnikowia pulcherrima	99%	ITS	ACTCTAAATCTTAACCCTCAATAACTTTATTAAAAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAATTGCGATACGT AATATGACTTGCAGACGTGAATCATTGAATCTTTGAACGCACATTGCGC CCCGGGGTATTCCCCAGGGCATGCGTGGGTGAGCGATATTTACTCTCAA ACCTCCGGTTTGGTCCTGCTTCGGCCTAATATCAACGGCGCTAGAATAA GTTTTAGCCCCATTCTTTTTCCTCACCCTCGTAAGACTACCCGCTGAACT TAAGCATATCAATAA
BA 6.NM NS1 (B34)	*Saccharomyces cerevisiae*	99%	ITS	CTTATCGATAACGTTCCAATACGCTCAGTATAAAAAAAGATTAGCCGCA GTTGGTAAAACCTAAAACGACCGTACTTGCATTATACCTCAAGCACGCA AAGAAACCTCTCTTTGGAAAAAAAAACATCCAATGAAAAGGCCAGCAAT TTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGA AAAGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGC GCAATGTGCGTTCAAAGATTCGATGATTCACGGAATTCTGCAATTCACA TTACGTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAACCAAAAAA TCCGTTGTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACAAAAATTC TTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTTTGTTA CCTCTGGGCCCCGATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGAT ATGAAAACTCCACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATA ACAAAAGCACAAAAATCTCTCACCGTTTGGAATAGCAAGAAAGAAACT TACAAGCCTAGCAAGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTC TCCATCTCTTGTCTTCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAA CAAAAAAATCCATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCC

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
BA 6.NM NS2 (B35)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	GGCGAGTGAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGC CCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATG TTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAAT GCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAG AGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTG AAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTT GATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATC TCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATA GGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCA GCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGT TATATGCCGCCCGTCTTGA
	Saccharomyces cf. cerevisiae/paradoxus	100%	ITS	GTCAACTTTAAGAACATTGTTCGCCTAGACGCTCTCTTCTTATCGATAAC GTTCCAATACGCTCAGTATAAAAAAAGATTAGCCGCAGTTGGTAAAACC TAAAACGACCGTACTTGCATTATACCTCAAGCACGCAGAGAAACCTCTC TTTGGAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAACT CCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGAAGGAAATGA CGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGT TCAAAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGC ATTTCGCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGA AAGTTTTTAATATTTTAAAATTTCCAGTTACGAAAATTCTTGTTTTTGAC AAAAATTTAATGAATAGATAAAATTGTTTGTGTTTGTTACCTCTGGGCC CCGATTGCTCGAATGCCCAAAGAAAAAGTTGCAAAGATATGAAAACTC CACAGTGTGTTGTATTGAAACGGTTTTAATTGTCCTATAACAAAAGCAC AGAAATCTCTCACCGTTTGGAATAGCAAGAAAGAAACTTACAAGCCTA GCAAGACCGCGCACTTAAGCGCAGGCCCGGCTGGACTCTCCATCTCTTG TCTTCTTGCCCAGTAAAAGCTCTCATGCTCTTGCCAAAACAAAAAAATC CATTTTCAAAATTATTAAATTTCTTTAATGATCCTTCCGCAGG
BB 4.CM S10 (B36)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	GTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGA GTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCT TGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGC GGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGC TCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACC GATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAG AGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCA GACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCAT TTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATAGGAATG TAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGG ACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGC CGCCCGTCTTGAAA
DA 0.CM NS2 (D2)	*Metschnikowia aff. pulcherrima*	99%	D1/D2 Domain	CGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTG TAATTTGAAGAGATTTGGGTCCGGCCGGCAGGGGTTAAGTCCACTGGAA AGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCCTCAACGCCCTC ATCCCAAATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGG GTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGA ACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAA AAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTA ACTGGGCCAGCATCGGGGCGGCGGGAAGCAAAACCACCGGGGAATGTA CCTTTCGAGGATTATAACCCCGGCCCTTACTCCCATACCACCCCGAGGC CTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAA ACACGG
	Metschnikowia chrysoperlae	100%	ITS	TAAACACTTACCNTTGAATTTTTAAAACACANATTAAAAAATTTTAAAA CCGGGTATCTTTGGTTTCTCATATNNGAAAAAAACACAGAAATGCGATA CCCNATATGACTTTGGCACACGAAANATTTNAAATTTTNACACACATTT TGCCCCCGGGGGTTTCCCCCGGGGTGCGCGGGGGAGCGATATTTACTCT CAAAACCCCCGGTTGGGNCCGTGTTNGGCTAAAATCAACNGGGCTCTA AAAAANTTTANCCCCCCTCTTTTTTCTCTCCCCCTTAAAACACCCCCCTG TACTTTAACATATAAAAAAACGGGGGG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
DA 0.CM NS3 (D3)	*Metschnikowia pulcherrima*	99%	D1/D2 Domain	GGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTGTAATTTGAAGAGAT TTGGGTCCGGCCGGCGGGGGTTAAGTCCACTGGAAAGTGGCGCCACAG AGGGTGACAGCCCCGTGAACCCCTTCAACGCCCTCATCCCAAATCTCCA AGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCAT CTAAAGCTAAATACCGGCGAGAGACCGATAGCGAACAAGTACAGTGAT GGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAAT TGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATC GGGGCGGCGGGAAGCAAAACCACCGGGGAATGTACCTTTCGAGGATTA TAACCCCGGTCCTTACTCCCATGCCGCCCCGAGGCCTGCAATCTAAGGA TGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGA
	Metschnikowia sinensis	94%	ITS	CTTTTAGGAAAAAAACCGAACCTTTTTTTTAATAACACAATTAAAAAAC TTTTAACAACGGATCTCTTGGGTCTCGCATCGATGAAAAACGCACCGAA TTGCGATACGTAATATGACTTGCAGACGCGAATCATTGAATCTTTGAAC GCACATTGCGCCCCGGGGTATTTCCCAGGGGATGCGTGGGGGAGCGAT ATTTACTCTCAAACCTCCGGGTTGGGCCTGCTTTGGCCTAATATCAACG GGGCTNTAATAAGTTTTAGCCCCATTCTTTTTTCTCACCCTCGTAAGACT ACCCGCTGAACTTAAACATATCAATAAACG
DA 0.CM NS4 (D4)	*Metschnikowia pulcherrima*	99%	ITS	GGTGAGGAAAAAGGAATGGGGCTAAAACTTATTCTAGCGCCGTTGATA TTAGGCCGAAGCAGGACCAAACCAGGAGGTTTGAGAGTAAATATCGCT CACCCACGCATGCCCTGGGGAATACCCCGGGGCGCAATGTGCGTTCAA AGATTCAATGATTCACGTCTGCAAGTCATATTACGTATCGCAATTCGCT GCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTT T
DB 0.CM NS2 (D6)	*Metschnikowia chrysoperlae*)	100%	ITS	GGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGACC AAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTAATTGTGTATTTGA
DB 0.CM NS4 (D8)	*Metschnikowia pulcherrima*	99%	D1/D2 Domain	CTCAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCC GGGAATTGTAATTTGAAGAGATTTGGGTCCGGCCGGCAGGGGTTAAGTC CACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCTTCA ACGCCCTCATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCT CTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACC GATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAG AGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCA GACACTTAACTGGGCCAGCATCGGGGCGGCGGGAAACAAAACCACCGG GGAATGTACCTTTCGAGGATTATAACCCCGGTCCTTATTCCCTTGCTGCC CCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCG TCTTGAAACACGGAC
	Metschnikowia chrysoperlae	95%	ITS	GGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGACC AAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTAATTGTGTTATTGAAGAAT AAAATGATAAGTGTTTATGCCTAAAAGTGTGTAAGTGATATTTTAGAGA TCCCTCCGCAGGCTCACATAGAGAAAAGGAGAATTAGTAAAAAATTTTT CGCCTTTTGGGGGAAAACTGAATTTTTTATTATTCCTCAAACAATCAATT AACATAACCAACCGATAGGTTGTTTCTGCATCAATAAACAAGCAACGA AGTGAGATACTTAGTATGACTTACAGACGTGAATCATTCAATCTTTGAA GCGATTGCGCCCTATGTATTCCCCGGCATGCGTGAGTGAGCGATATTTA CTCTCAACGTCTGGTTCGGTCTGCTCCGCCTAATATCACCTCGCTGAAAT ATTATCTAGCCCTTTCTCTTCCTCCCTAGTATAACTATCACTTAACTCA

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
DA 4.CM NS2 (D10)	*Starmerella bacillaris*	100%	D1/D2 Domain	GGCGAGTGAACAGGCAAGAGCTCAGATTTGAAAGGCACTTTTGTGCCG TTGTATTCTGAAGTTAGGGTCCTGAGAAACGATGCTTAAGTCTTCTGGA AAGGAGCGCCATGGAGGGTGATAGCCCCGTCTAGCATTGACCTCATATA GGATCTTAACATGGAGTCGAGTTGTTTGGGAATGCAGCTCAAATGGGTG GTATGCTCCATCTAAAGCTAAATATCTGCGAGAGACCGATAGTAAACAA GTACTGTGAGGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAA GTACGTGAAATTGTTGAAATGGAAGGGTAGGCCGCTAACCATGTAGAG CCGTGTTTGGGGGGAAGATAAATGCTGTAGAATGTAGCTCCTCGGAGTA TTATAGATGCAGTTCATATTCCCACCCGAGCGCGAGGATCTCAGGTTCT ACTAAATGGTGGTCTACCACCCGTCTTGA
		100%	ITS	GAGTTAATTAACGTGTGCACTTCCATGATTTTAACTCCTAAAAGGAGCA AGACCTCATACCAAAAATGGTTGAGAGGAAGATTATCACTCCAACAAG CATGCTATTAGACAAACTAATAGCGCAATATGCGTTCAAAAATTCAATG ACTCACGTCTGCAATTCGCATTACCTATCGCGCTTTGCTGCGTTCTTCAT CGATACGAGAACCAAGAGATCCGTTGTTGAAAGTTTTAAATTTTCATTG TTTCAGAACAAATATAAAAGTTTTAAAGATTGGGCGCCTTTCGACACCC AAGCAATTGCAAAGACCGAAGTCTAAGCTGTTCACAGTGGTTTTGGCAA AAAGCCTTCAGAAATGATCCTTCCGCAGGT
DA 4.CM NS3 (D11)	*Metschnikowia pulcherrima*	99%	ITS	TGGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGAC CAAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTAATTGTGTTATTGACGGTTA AGATTTAGAGTTTGTGCCTAAAAGGGTGTAAAAACAATTTTAATGATCC TTCCGCAGGTTC
DA 4.CM NS4 (D12)	*Metschnikowia pulcherrima*	96%	ITS	TGGGGCTAAAACTTATTCTAGCGCCGTTGATATTATGCCGAAGCAGGAC CAAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTAATTGTGTTATTGAAGAAT AAGATTTAAAGTTTTTGCCCAAAAATGTGTAAAAATGTTTTTTAAGAGC CCTTCCCACGTTCC
DB 4.CM NS1 (D13)	*Metschnikowia pulcherrima*	99%	ITS	TGGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGAC CAAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTAATAGTGTTATTGAGGGTT AAGATTTAGAGTTTGTGCCTAAAAGGGTGTAATTACAATATTAATGATC CTTCCGCAGGTCAACCTACGGAA
DB 4.CM NS2 (D14)	*Metschnikowia pulcherrima*	99%	ITS	GGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGACC AAACCGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGG GAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGTCT GCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGAG AACCAAGAGATCCGTTGTTGAAAGTTTTTTTATAGTGTTATTGAGGGTT AAGATTTAGAGTTTGTGCCTAAAAGGGTGTAAAAACAATATTAATGATC CTTCCGCAGGTTCACCTACGGAA
DB 4.CM NS3 (D15)	*Metschnikowia fructicola*	99%	D1/D2 Domain	GTACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAA TTGTAATTTGAAGAGATTTGGGTCCGGCCGGCAGGGGTTAAGTCCACTG GAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCTTCAACGCC CTCATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG TGGGTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAG CGAACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGT GAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACAC TTAACTGGGCCAGCATCGGGGCGGCGGGAAACAAAACCACCGGGGAAT GTACCTTTCGAGGATTATAACCCCGGTCTCAATTTCCTTGTTGCCCCGAG GCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTG AACAACGGAC
	Metschnikowia aff. chrysoperlae	97%	ITS	ATGGGGCTAAAACTTATTCTAGCGCCGTTGATATTAGGCCGAAGCAGGA CCAAACCAGGAGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTG GGGAATACCCCGGGGCGCAATGTGCGTTCAAAGATTCAATGATTCACGT CTGCAAGTCATATTACGTATCGCAATTCGCTGCGTTCTTCATCGATGCGA GAACCAAGAGATCCGTTGTTGAAAGTTTTTTAATTGGGTTATTGAAAAA TAAAATGATAAGTGTTTTTCCCTAAAAGTG

Table A.1. *(continued)*

Name	*BLAST Result*	*Similarity*	*Region*	*Sequence*
DA 4.NM S1 (D16)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGT GCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTA TGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGA GGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGA ATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTT TGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCAT TTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAAT CTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCAT AGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCC AGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGG TTATATGCCGCCCG
DA 4.CM S3 (D17)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	GGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGT GCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTA TGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGA GGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGA ATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTT TGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCAT TTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAAT CTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCAT AGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCC AGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGG TTATATGCCGCCCG
DA 4.CM S1 (D18)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CGGCAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAA TTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAAC AGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCT TTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG TGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGC GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTG AAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATG GTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACT GGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTT GCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAG GACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG TCTTGAACC
DA 4.CM S8 (D19)	*Saccharomyces cerevisiae*	100%	D1/D2 Domain	CTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGA GGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAACAGGACGTC ATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCTTTGTAAAGT GCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTA AATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGT ACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGT ACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTG TGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACTGGGCCAG CATCAGTTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTTGCCTCGG TAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAGGACTGCG ACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCGTCTTG
Commercial *Saccharomyces cerevisiae*		100%	D1/D2 Domain	GGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTCGGT GCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTA TGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGA GGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGA ATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTT TGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCAT TTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAAT CTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCAT AGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCC AGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGG TTATATGCCGCCCGTC
Metschnikowia pulcherrima (DSM:70336)		100%	D1/D2 Domain	GGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTGT AATTTGAAGAGATTTGGGTCCGGCCGGCGGGGGTTAAGTCCACTGGAA AGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCTTCAACGCCCTC ATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGG GTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGA ACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAA AAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTA ACTGGGCCAGCATCGGGGCGGCGGGGAGCAAAACCACCGGGGAATGTA CCTTTCGAGGATTATAACCCCGGTCCTTACTCCCATACCACCCCGAGGC CTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAA C

B. Phylogenetic Trees According to UPGMA Method

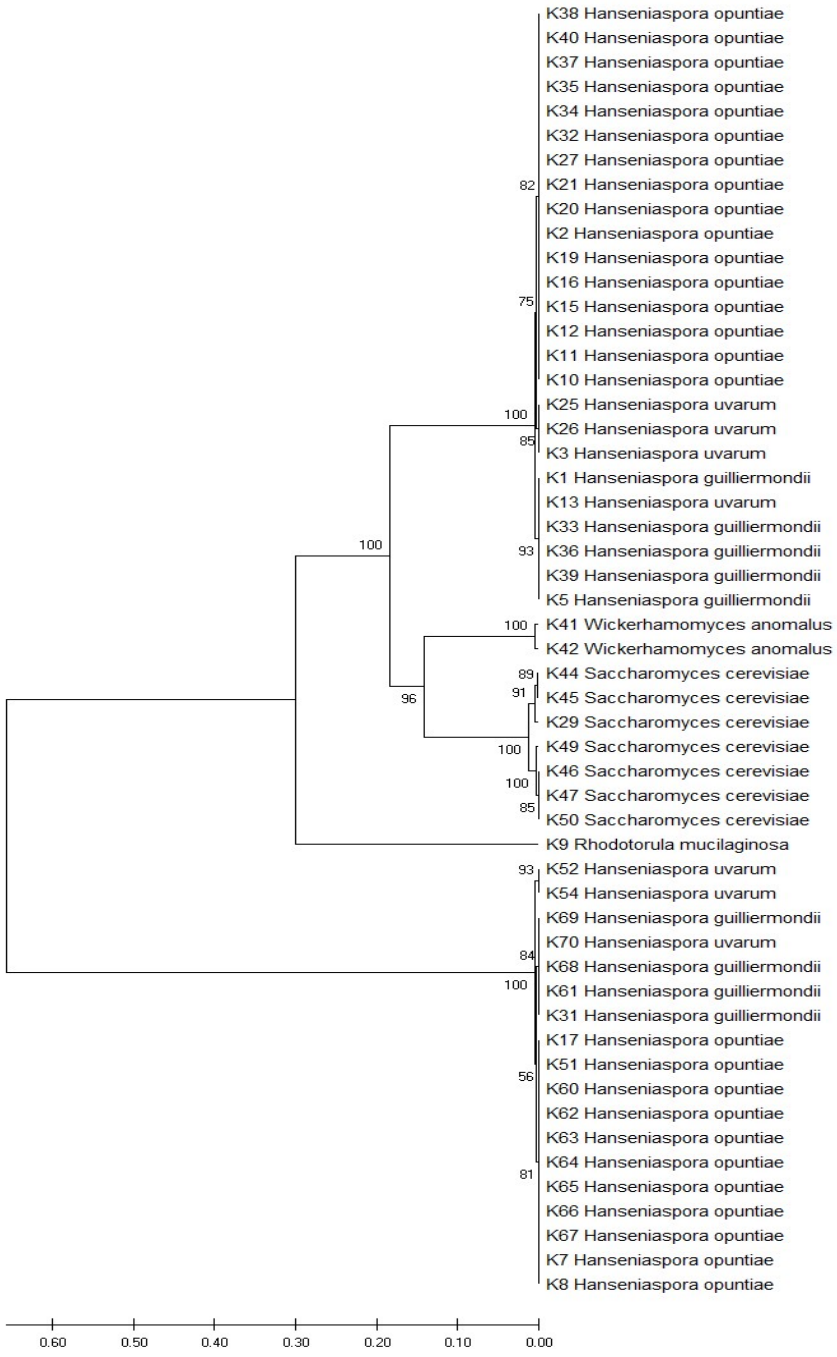


Figure B.1. Phylogenetic Tree with UPGMA Method of Non-*Saccharomyces* and *Saccharomyces* in Kalecik Karası Must and Wine with respect to ITS Region

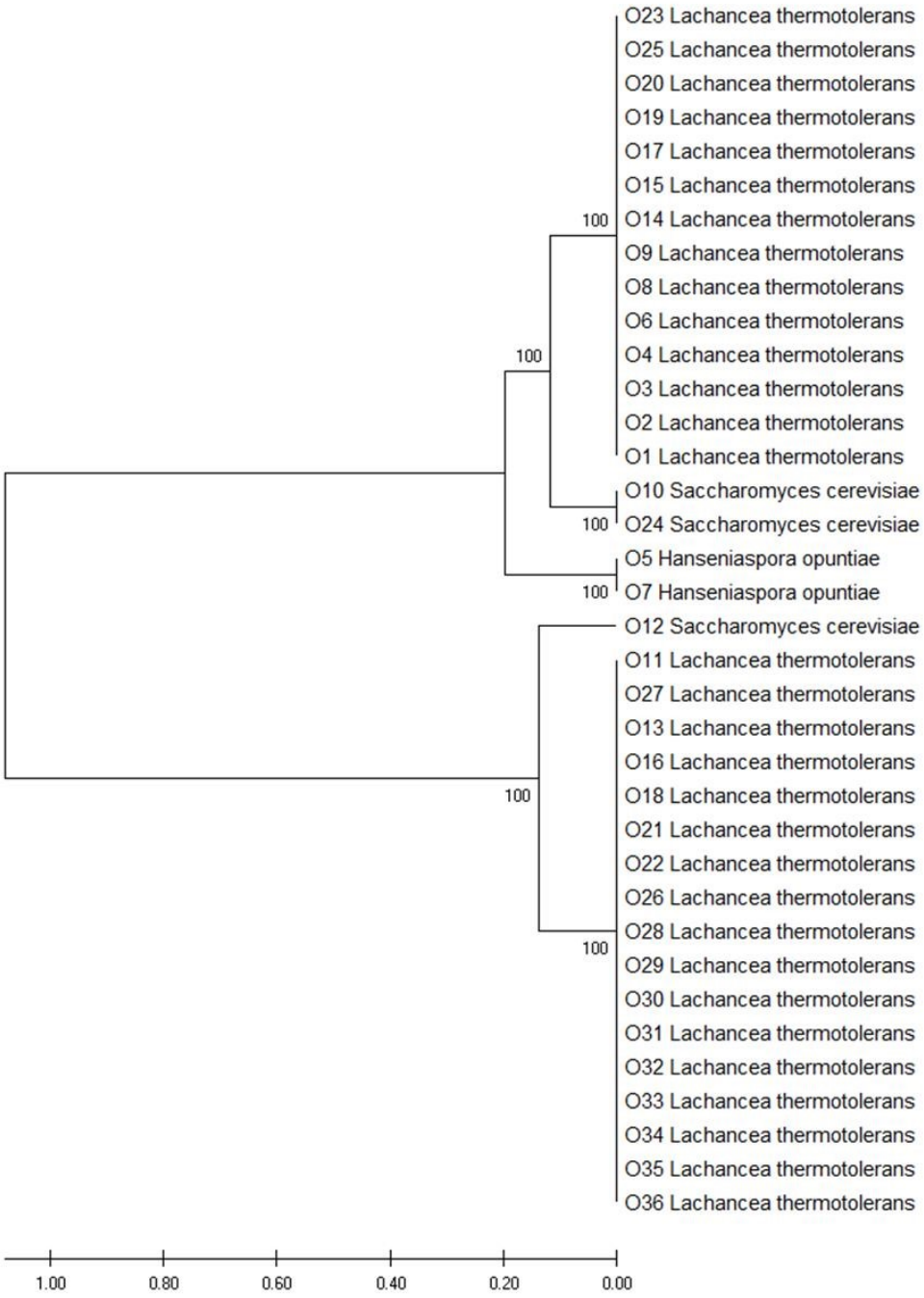


Figure B.2. Phylogenetic Tree with UPGMA Method of Non-*Saccharomyces* and *Saccharomyces* in Öküzgözü Must and Wine with respect to ITS Region

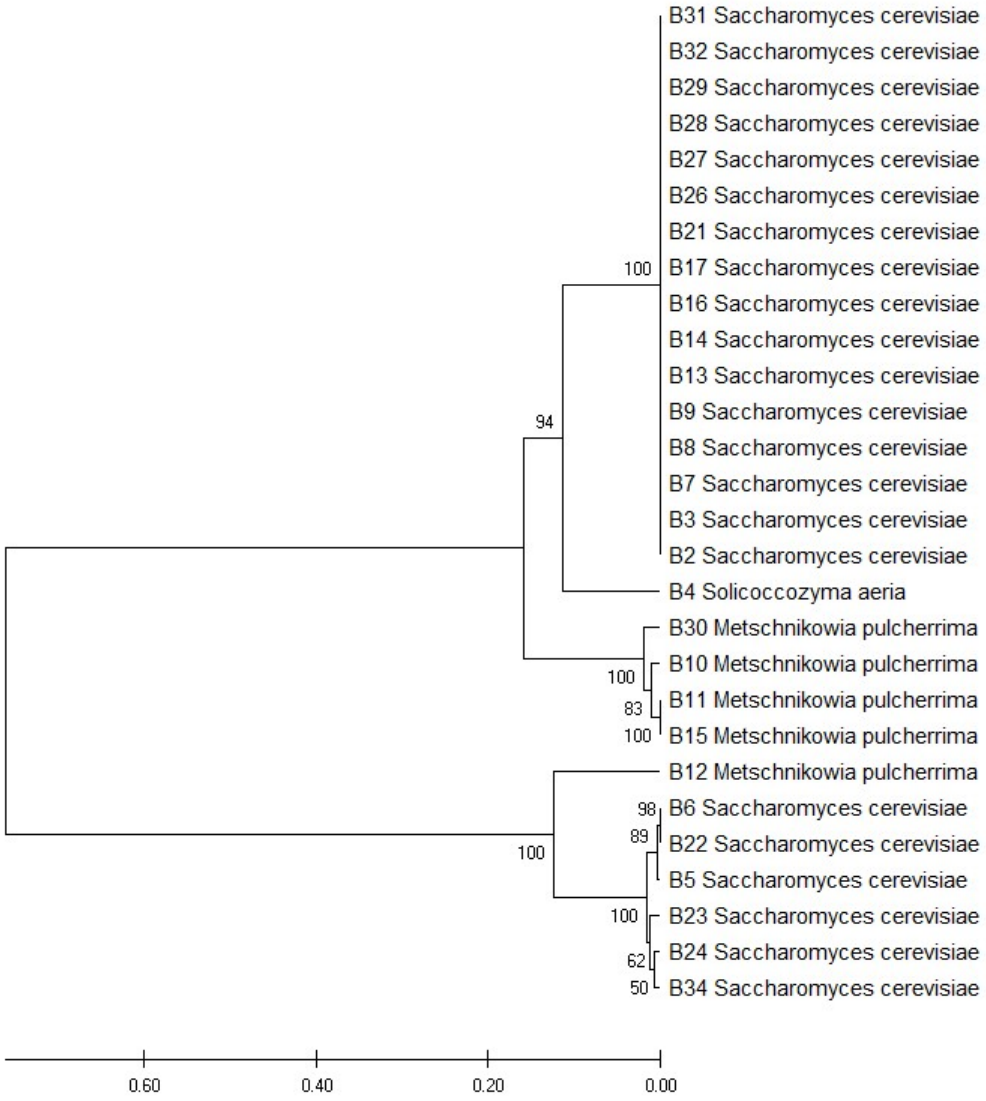


Figure B.3. Phylogenetic Tree with UPGMA Method of Non-*Saccharomyces* and *Saccharomyces* in Boğazkere Must and Wine with respect to ITS Region

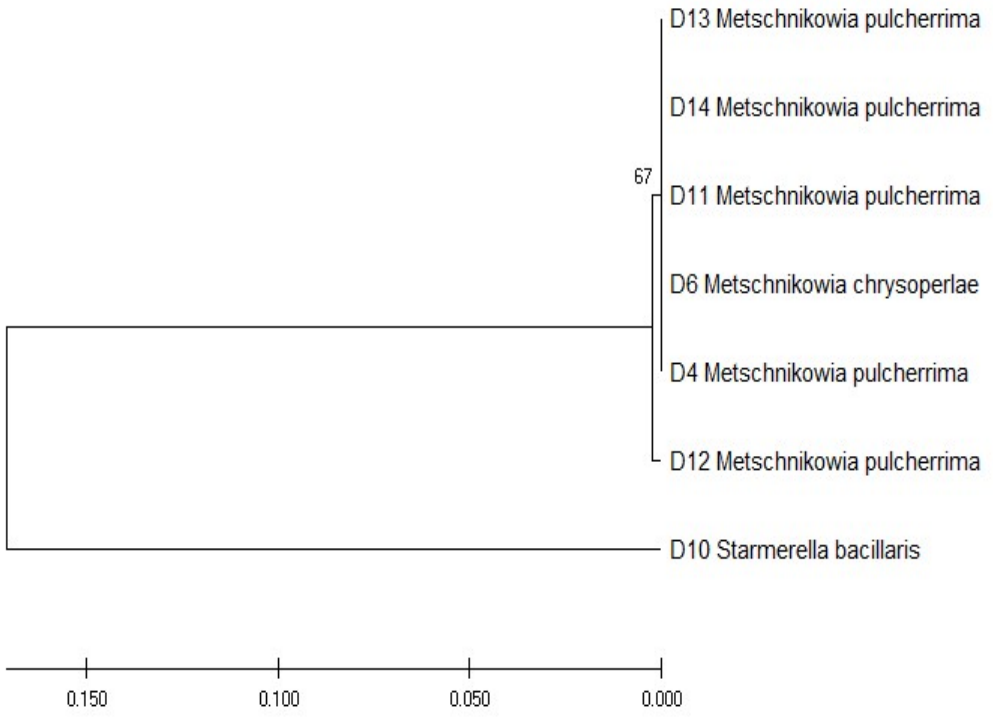


Figure B.4. Phylogenetic Tree with UPGMA Method of Non-*Saccharomyces* and *Saccharomyces* in Dimrit Must and Wine with respect to ITS Region

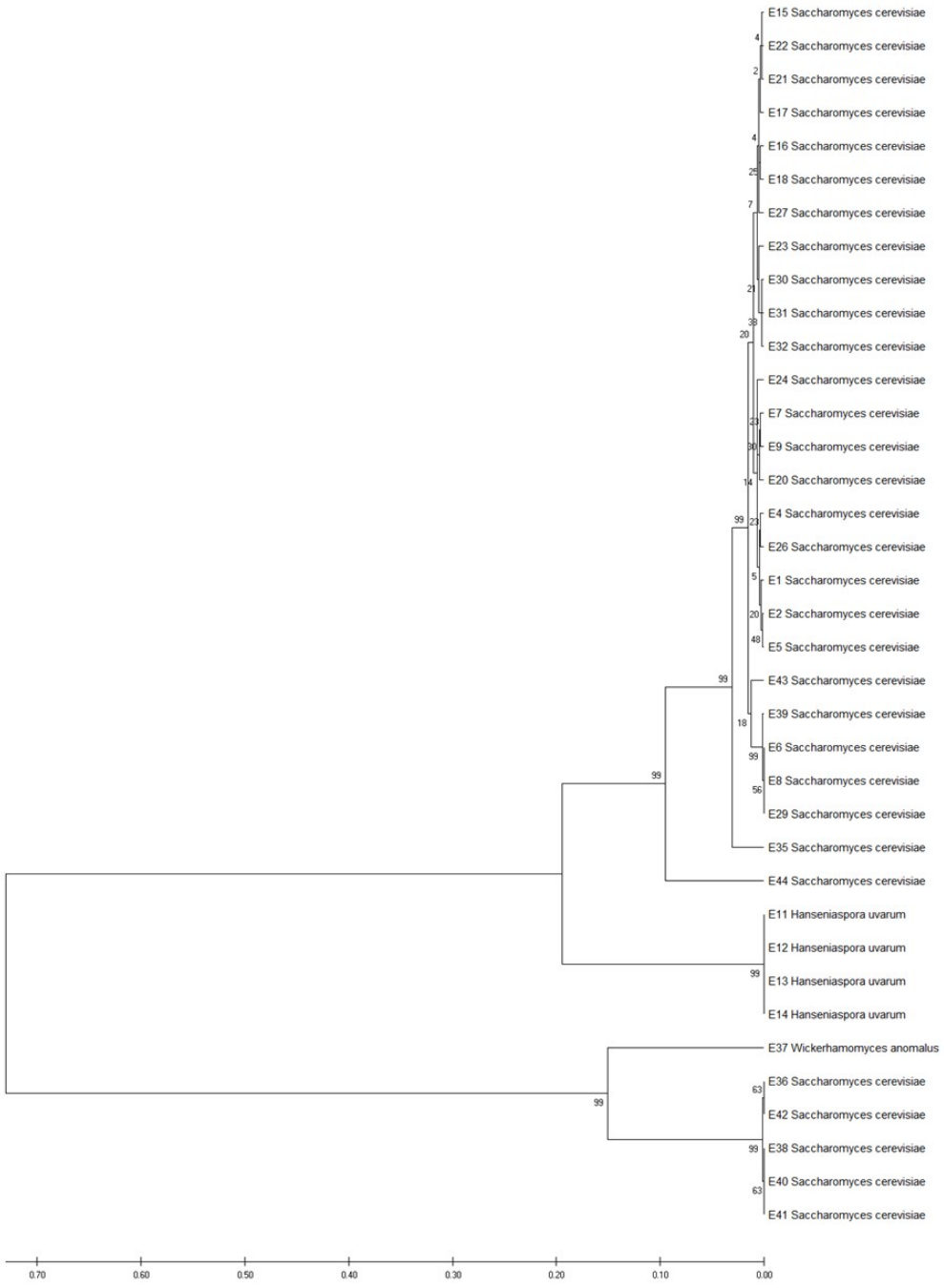


Figure B.5. Phylogenetic Tree with UPGMA Method of Non-*Saccharomyces* and *Saccharomyces* in Emir Must and Wine with respect to ITS Region

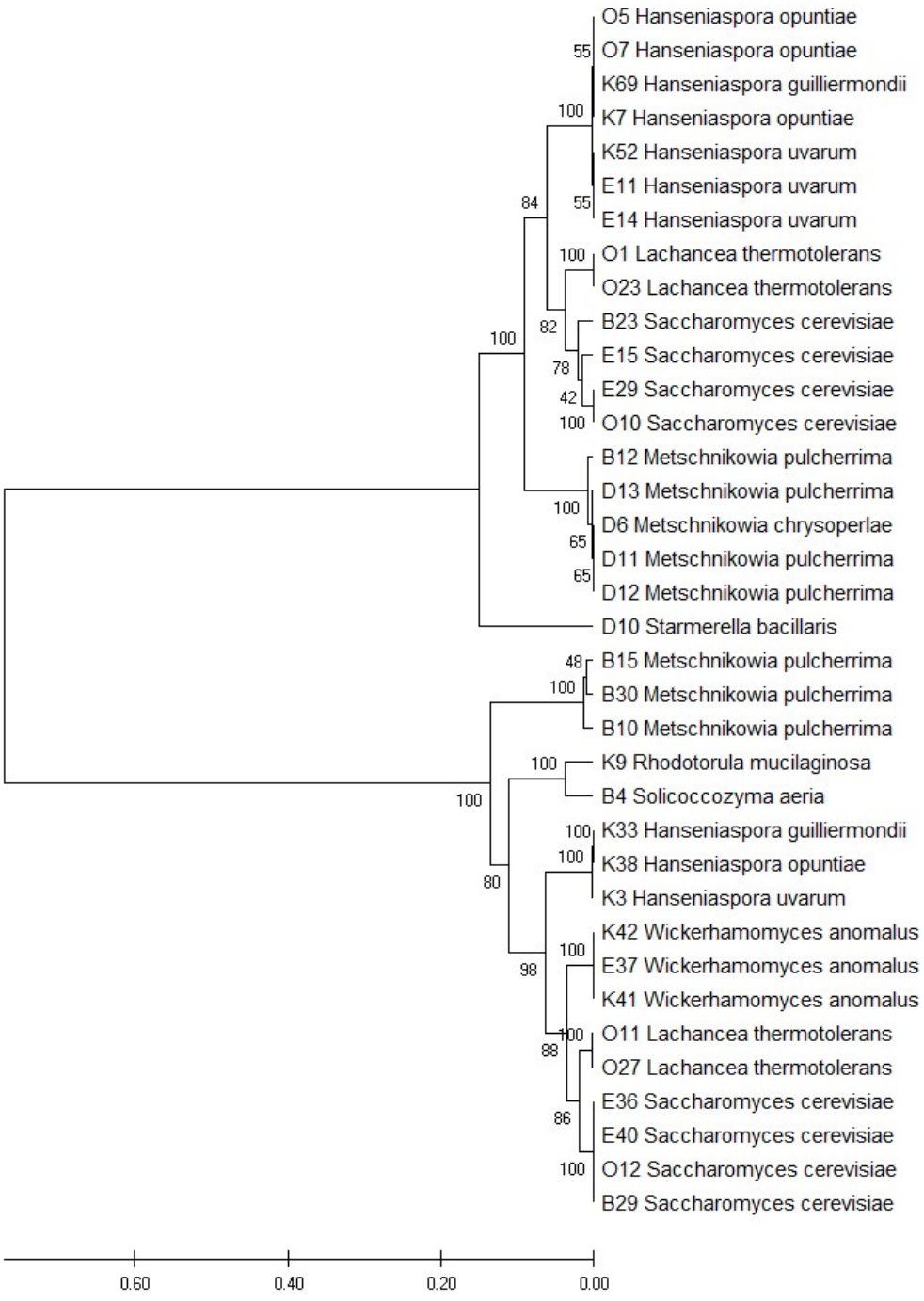


Figure B.6. Phylogenetic Tree with UPGMA Method of Selected Non-*Saccharomyces* and *Saccharomyces* in Five Different Grapes' Musts and Wines with respect to ITS Region

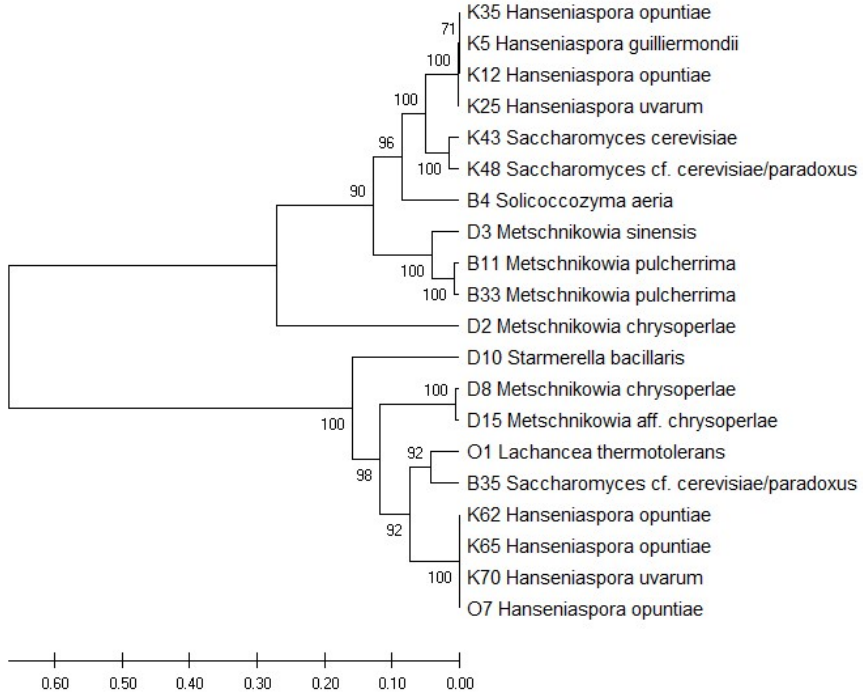


Figure B.7. Phylogenetic Tree with UPGMA Method Some Yeasts with Respect to ITS Region

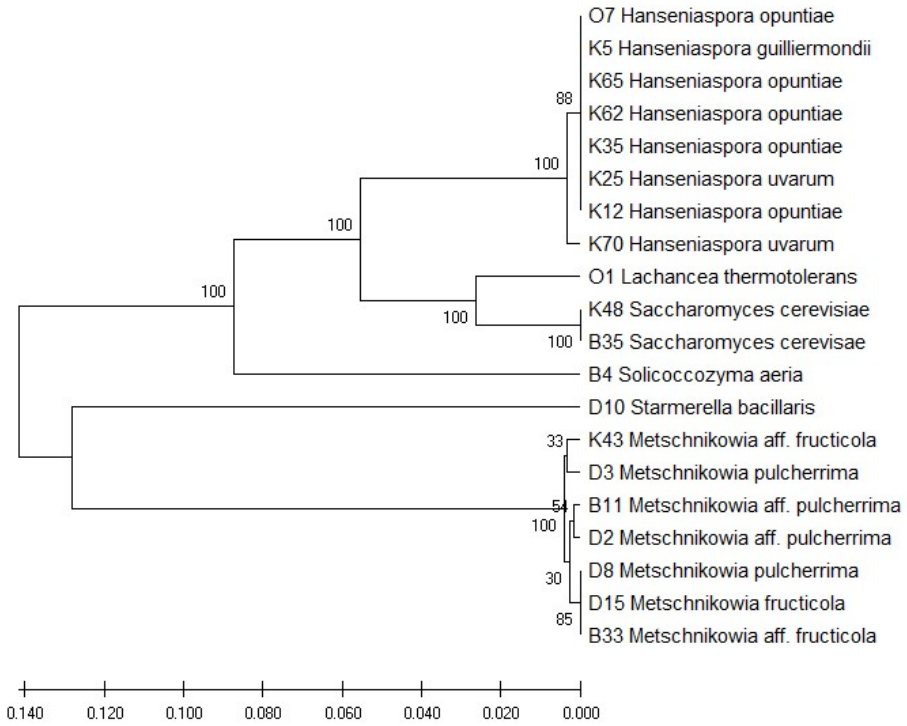


Figure B.8. Phylogenetic Tree with UPGMA Method Some Yeasts with Respect to D1/D2 Domain

C. Phenotypic Properties of All Isolated *Saccharomyces* Yeasts

Table C.1. The Results of Carbohydrate Fermentation Test and Phenotypic Properties of *Saccharomyces* Strains from Isolated in Must and Wine of Kalecik Karası

Name	Alcohol Tolerance (%)			SO_2 Tolerance (mg/L)				Temperature Tolerance (°C)			pH Tolerance			Carbohydrate Fermentation Test				H_2S Product	Identification	
	10	13	15	50	100	150	200	28	37	45	6	4	3	Sucrose	Maltose	Mannitol	Lactose		ITS	D1/D2
KA 0CM S2	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	ng	nd	nd
KA 0CM S4	+	-	-	+	+	+	+	+	+	-	w	w	-	w	w	w	w	5	nd	nd
KA 4CM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
KA 4CM S3	+	w	w	+	+	+	+	+	+	-	-	-	-	w	-	w	-	ng	nd	nd
KA 2NM S1	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+	w	-	4	nd	nd
KA 2NM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4	nd	nd
KA 2NM S3	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	-	w	3	nd	nd
KA 2NM S4	w	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4	nd	nd
KA 2NM S5	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
KA 2NM S6	+	+	+															4	+	nd
KA 2NM S7	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	-	-	4	nd	nd
KA 2NM S8	+	W	w	+	+	+	+	+	+	-	-	+	+	+	+	-	-	4	nd	nd
KA 2NM S9	+	w	w	+	+	+	+	+	w	-	-	-	-	+	+	-	-	3	nd	nd
KA 2NM S10	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	-	-	4	nd	nd
KA 4NM S1	+	-	-	+	+	+	+											2	nd	nd
KA 4NM S2	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	+
KA 4NM S3	+	-	-	+	+	+	+											1	nd	nd
KA 4NM S4	+	-	-	+	+	+	+											1	+	nd
KA 4NM S5	+	-	-	+	+	+	+											3	nd	nd
KA 4NM S6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3	nd	nd
KA 4NM S7	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
KA 4NM S8	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
KA 4NM S9	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3	nd	nd
KA 4NMS10	+	+	+	+	+	+	+	+	+	-	+	w	+	+	+	-	-	4	nd	nd
KA 18NM S1	-	-	-	w	w	-	-	w	+	-	+	-	-	-	+	-	-	3	nd	nd
KA 18NM S2	-	-	-	+	+	+	+	-	+	-	-	-	-	+	+	-	-	2	nd	nd
KA 18NM S3	-	-	-	+	+	+	+	-	+	-	-	-	-	+	+	-	-	4	nd	nd
KA 18NM S4	-	-	-	+	+	+	+	+	+	-	w	w	w	-	+	-	-	3	nd	nd
KA 18NM S5	w	w	w	+	+	+	+	+	+	-	-	w	-	+	w	-	-	3	nd	nd
KA 32NM S1	w	w	w	+	+	+	+	+	+	-	+	+	+	-	+	-	-	4	nd	nd
KA 32NM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	1	nd	+
KA 32NM S3	+	+	w	+	+	+	+	+	+	-	+	+	+	-	+	-	-	4	nd	nd
KA 32NM S4	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4	nd	nd
KA 32NM S5	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
KB 4CM S5	+	+	+															3	+	nd
KB 2NM S1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4	nd	nd
KB 2NM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
KB 2NM S3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4	nd	nd

Table C.1 *(continued)*

Name	*Alcohol Tolerance (%)*			*SO_2 Tolerance (mg/L)*				*Temperature Tolerance (°C)*			*pH Tolerance*				*Carbohydrate Fermentation Test*				*H_2S Product*	*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*			*ITS*	*D1/D2*
KB 2NM S4	+	-	-	+	+	+	+	+	+	w	+	+	+	+	+	-	-	1		+	nd
KB 2NM S5	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4		nd	nd
KB 2NM S6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4		nd	nd
KB 2NM S7	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4		nd	nd
KB 2NM S8	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4		nd	nd
KB 2NM S9	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4		nd	nd
KB 2NM S10	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3		nd	nd
KB 2NM NS8	-	-	-	-	-	-	-	+	+	w	-	-	-	+	+	-	-	1		+	nd
KB 4NM S1	+	-	-	+	+	+	+											3		nd	nd
KB 4NM S2	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1		+	nd
KB 4NM S3	+	+	-	+	+	+	+											3		nd	nd
KB 4NM S4	+	-	-	+	+	+	+											2		nd	nd
KB 4NM S5	+	-	-	+	+	+	+											3		nd	nd
KB 4NM S6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3		nd	nd
KB 4NM S7	+	+	+	+	+	+	+	+	+	w	w	+	+	+	+	w	-	3		nd	nd
KB 4NM S8	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	+	3		nd	nd
KB 4NM S9	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4		nd	nd
KB 4NM S10	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2		+	nd
KB 18NM S2																		3		nd	nd
KB 18NM S1	-	-	-	w	w	w	+	-	+	-	-	-	-	-	+	-	-	2		nd	nd
KB 18NM S3	+	+	+	+	+	+	+	+	+	-	w	w	-	-	+	-	-	2		nd	nd
KB 18NM S4	-	-	-	+	w	+	+	+	+	-	w	-	-	-	+	-	-	2		nd	nd
KB 18NM S5	+	w	w	+	+	+	+	+	+	-	w	+	w	-	w	-	-	3		nd	nd
KB 32NM S1	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	w	-	4		nd	nd
KB 32NM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	w	-	3		nd	nd
KB 32NM S3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3		nd	nd
KB 32NM S4	+	+	+	+	+	+	+	+	+	-	+	+	w	+	+	-	-	4		nd	nd
KB 32NM S5	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4		nd	nd
K13 (Ç)*	+	+	-	+	+	+	+	+	+	-				+	+	-	-	4		+	nd
K15(Ç)*	+	+	+	+	+	+	+	+	+	-				+	+	-	-	4		+	nd
K16(Ç)*	+	+	-	+	+	+	+	+	+	-				-	+	-	-	4		+	nd

KA: A Parallel of Wine Made from Kalecik Karası Grape , KB: B Parallel of Wine Made from Kalecik Karası Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 2NM: 2. Day of Normal Maceration, 4NM: 4. Day of Normal Maceration, 18NM: 18. Day of Normal Maceration (Middle of the fermentation), 32NM: 32. Day of Normal Maceration (End of the fermentation); S: *Saccharomyces*; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; Ç*: Isolated by Çağrı Çavdaroğlu; nd: Not determined.

Table C.2. The Results of Carbohydrate Fermentation Test and Phenotypic Properties of *Saccharomyces* Strains from Isolated in Must and Wine of Öküzgözü

Name	*Alcohol Tolerance (%)*			*SO_2 Tolerance (mg/L)*			*Temperature Tolerance (°C)*				*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*	*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
OA 0CM S1	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4	nd	nd
OA 0CM S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OA 0CM S3																		4	nd	nd
OA 0CM S4	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OA 0CM S5	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	5	nd	nd
OA 0CM S7	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	5	nd	nd
OA 0CM S8	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OA 0CM S9	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4	nd	nd
OA 0CM S10	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
OA 0CM NS3	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
OA 4CM S1	+	w	w	+	+	+	+											4	nd	nd
OA 4CM S2	+	w	-	+	+	+	+											4	nd	nd
OA 4CM S4	w	-	-	+	+	+	+											4	nd	nd
OA 4CM S5	+	-	-	+	+	+	+											4	nd	nd
OA 4CM S6																		4	nd	nd
OA 4CM S7																		4	nd	nd
OA 4CM S8	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OA 4CM S9																		4	nd	nd
OA 4CM NS5	+	+	+															3	+	nd
OB 0CM S1	w	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	+	4	nd	nd
OB 0CM S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OB 0CM S3	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OB 0CM S5	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
OB 0CM S6	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	w	w	3	nd	+
OB 0CM S7																		4	nd	nd
OB 0CM S8	+	+	+	+	+	+	+	+	+	w	+	+	+	-	-	-	-	4	nd	nd
OB 0CM S9	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OB 0CM S10	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
OB 4CM S1*	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	+
OB 4CM S2	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	+
OB 4CM S3	-	-	-	+	+	+	+											3	nd	nd
OB 4CM S4	+	-	-	+	+	+	+											4	nd	nd
OB 4CM S5	+	w	w	+	+	+	+											4	nd	nd
OB 4CM S6																		4	nd	nd
OB 4CM S7																		4	nd	nd
OB 4CM S9																		4	nd	nd
OB 4CM S10																		4	nd	nd
OB 4CM NS5	+	+	+															4	+	nd

OA: A Parallel of Wine Made from Öküzgözü Grape , OB: B Parallel of Wine Made from Öküzgözü Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration; S*: Saccharomyces*; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black,; nd: not determined; *: the strain using for wine-making.

Table C.3. The Results of Carbohydrate Fermentation Test and Phenotypic Properties of *Saccharomyces* Strains from Isolated in Must and Wine of Boğazkere

Name	Alcohol Tolerance (%)			SO_2 Tolerance (mg/L)				Temperature Toleransı (°C)			pH Tolerance			Carbohydrate Fermentation Test				H_2S Product	Identification	
	10	13	15	50	100	150	200	28	37	45	6	4	3	Sucrose	Maltose	Mannitol	Lactose		ITS	D1/D2
BA 0CM S3	-	-	-	+	+	+	+	+	+	-	+	+	+	w	w	-	w	ng	nd	nd
BA 0CM S4	+	+	+	+	+	+	+	+	+	-	+	+	+	+	w	-	-	4	nd	nd
BA 0CM S5	+	+	w	+	+	+	+	+	+	-	+	+	-	+	+	-	-	3	nd	nd
BA 0CM S7	+	w	-	+	+	+	+	+	+	-	+	+	+	+	w	-	-	3	nd	nd
BA 0CM S8	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	4	nd	nd
BA 0CM S9																		3	nd	nd
BA 0CM S10	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
BA 0CM NS2	+	+	+															4	+	nd
BA 0CM NS3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	nd
BA 0CM NS5	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	nd
BA 0CM NS6	+	+	+															4	+	nd
BA 0CM NS7	+	+	+															4	+	nd
BA 0CM NS8	+	+	+															4	+	nd
BA 4CM S2	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
BA 4CM S5	+	+	w	+	+	+	+	+	+	-	+	+	+	+	w	-	-	3	nd	nd
BA 4CM S6	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	+	w	4	nd	nd
BA 4CM S7	+	w	w	+	+	+	+	+	+	-	+	+	+	+	-	-	-	4	nd	nd
BA 4CM S8																		3	nd	nd
BA 4CM S9	+	w	w	+	+	+	+	+	+	-	+	+	+	+	w	-	-	4	nd	nd
BA 4CM S10	+	w	-	+	+	+	+	+	+	-	+	+	+	w	w	-	-	3	nd	nd
BA 4CM NS1	+	+	+															4	+	nd
BA 4CM NS5	+	+	+															4	+	nd
BA 4CM NS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
BA 4CM NS7	+	-	+															4	+	nd
BA 4CM NS8	+	+	+															4	+	nd
BA 6NM S1	-	-	-	+	+	+	+											ng	nd	nd
BA 6NM S2	-	-	-	+	+	+	+											3	nd	nd
BA 6NM S3	+	-	-	+	+	+	+											3	nd	nd
BA 6NM S4	-	-	-	+	+	+	+											ng	nd	nd
BA 6NM S5	-	-	-	+	+	+	+											3	nd	nd
BA 6NM S6	+	w	w	+	+	+	+											3	nd	nd
BA 6NM S7	-	-	-	+	+	+	+											ng	nd	nd
BA 6NM S8	+	w	w	+	+	+	+											3	nd	nd
BA 6NM NS1	+	+	+															3	+	nd
BA 6NM NS2	+	-	-															3	+	+
BB 0CM S1	+	+	w	+	+	+	+	-	w	-	-	-	-	+	-	-	-	4	nd	nd
BB 0CM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
BB 0CM S3																		4	nd	nd
BB 0CM S4	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
BB 0CM S8	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
BB 0CM S9	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	4	nd	nd
BB 0CM S10																		5	nd	nd
BB 0CM NS1	+	+	+															4	+	nd
BB 0CM NS5	+	+	+															4	+	nd

Table C.3 *(continued)*

Name	*Alcohol Tolerance (%)*			*SO_2 Tolerance (mg/L)*				*Temperature Toleransı (ºC)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*	*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
BB 0CM NS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
BB 0CM NS8	+	+	+															4	+	nd
BB 4CM S1	+	-	-	+	+	+	+	+	+	-	+	+	+	+	w	-	-	ng	nd	nd
BB 4CM S2	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
BB 4CM S4	+	+	w	+	+	+	+	+	+	w	+	+	+	+	w	-	-	3	nd	nd
BB 4CM S6	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
BB 4CM S9	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
BB 4CM S10	+	+	w	+	+	+	+	+	+	-	+	+	+	+	w	-	-	2	nd	+
BB 4CM NS1	+	+	+															3	+	nd
BB 4CM NS2	+	+	+															4	+	nd
BB 4CM NS3	+	-	-															4	+	nd
BB 4CM NS4	+	+	+															4	+	nd
BB 4CM NS6	+	-	-															4	+	nd
BB 4CM NS7																		3	+	nd
BB 6NM S1	+	w	w	+	+	+	+											3	nd	nd
BB 6NM S2	+	w	w	+	+	+	+											3	nd	nd

BA: A Parallel of Wine Made from Boğazkere Grape , BB: B Parallel of Wine Made from Boğazkere Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 6NM: 6. Day of Normal Maceration; S: *Saccharomyces*; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; nd: not determined.

Table C.4. The Results of Carbohydrate Fermentation Test and Phenotypic Properties of *Saccharomyces* Strains from Isolated in Must and Wine of Dimrit

Name	*Alcohol Tolerance (%)*		*SO_2 Tolerance (mg/L)*					*Temperature Tolerance (°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*	*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
DA 0CM S1																		3	nd	nd
DA 0CM S2	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3	nd	nd
DA 0CM S3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
DA 0CM S4	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	2	nd	nd
DA 0CM S5	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd
DA 4CM S1	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2	nd	+
DA 4CM S2	+	+	w	+	+	+	+	+	w	-	w	w	-	-	+	w	-	2	nd	nd
DA 4CM S3	+	w	w	+	+	+	+	+	+	-	w	w	-	+	+	w	w	2	nd	+
DA 4CM S4	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	w	w	2	nd	nd
DA 4CM S5	+	w	w	+	+	+	+	+	+	-	+	+	+	-	-	w	w	3	nd	nd
DA 4CM S6	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	2	nd	nd
DA 4CM S7	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2	nd	nd
DA 4CM S8	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	+
DA 4CM S9	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd
DA 4CMS10	w	-	-	+	+	+	w	+	+	-	+	+	+	+	+	-	-	ng	nd	nd
DA 4NM S1	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	nd	+
DA 4NM S2	+	+	w	+	+	+	+											3	nd	nd
DA 4NM S3	+	-	-	+	+	+	+											3	nd	nd
DA 4NM S4	+	w	-	+	+	+	+											3	nd	nd
DB 0CM S1	w	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
DB 0CM S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
DB 0CM S3	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	+	4	nd	nd
DB 0CM S4	+	+	+	+	+	+	+	+	+	w	+	+	+	-	+	-	-	2	nd	nd
DB 0CM S5	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
DB 4CM S1	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
DB 4CM S2	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
DB 4CM S3	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd
DB 4CM S4	+	w	w	+	+	+	+	+	+	w	+	+	+	+	+	w	w	3	nd	nd
DB 4CM S5	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4	nd	nd
DB 4CM S6	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
DB 4CM S7	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2	nd	nd
DB 4CM S8	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	w	w	4	nd	nd
DB 4CM S9	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
DB 4CMS10	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
DB 4NM S1	+	w	w	+	+	+	+											3	nd	nd
DB 4NM S2	+	w	w	+	+	+	+											3	nd	nd
DB 4NM S3	+	w	w	+	+	+	+											4	nd	nd
DB 4NM S4	-	-	-	+	w	w	w											ng	nd	nd
DB 4NM S5	+	+	w	+	+	+	+											3	nd	nd
DB 4NMS6	+	w	w	+	+	+	+											4	nd	nd

DA: A Parallel of Wine Made from Dimrit Grape , DB: B Parallel of Wine Made from Dimrit Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 4NM: 4. Day of Normal Maceration; S*: Saccharomyces* ; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black,; ng: not grown, nd: not determined.

Table C.5. The Results of Carbohydrate Fermentation Test and Phenotypic Properties of *Saccharomyces* Strains from Isolated in Must and Wine of Emir

Name	*Alcohol Tolerance (%)*			*SO_2 Tolerance (mg/L)*				*Temperature Tolerance(°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*				*H_2S Product*	*Identification*	
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
EA 0W S2	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EA 0W S5	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EA 0W S9	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	ng	nd	nd
EA 0W NS1	+	+	+															3	+	nd
EA 0W NS2	+	+	-															4	+	nd
EA 0W NS4	+	+	-															3	+	nd
EA 0W NS5	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
EA 0W NS6	+	+	+															3	+	nd
EA 0W NS7	+	-	+															3	+	nd
EA 0W NS9	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
EA 0W NS10	+	+	-															3	+	nd
EA 1W S1	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	+	4	nd	nd
EA 1W S2	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EA 1W S3	w	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EA 1W S4	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EA 1W S5	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	+	3	nd	nd
EA 1W S6	+	-	-	+	+	+	+											4	nd	nd
EA 1W S7	+	-	-	+	+	+	+											4	nd	nd
EA 1W S8	+	-	-	+	+	+	+											4	nd	nd
EA 1W S9	+	-	-	+	+	+	+											4	nd	nd
EA 1W S10	+	w	-	+	+	+	+											4	nd	nd
EA 1W NS5	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	nd
EA 1WNS6	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	nd
EA 1W NS7	+	+	+															4	+	nd
EA 1W NS8	+	+	+															3	+	nd
EA 1W S10	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	-	-	2	+	nd
EA 2W S1	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EA 2W S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	4	nd	nd
EA 2W S3	w	w	-	+	+	+	+	+	+	-	+	+	+	-	w	w	w	3	nd	nd
EA 2W S4	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4	nd	nd
EA 2W S5	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EA 2W NS1	+	+	+															3	+	nd
EA 2W NS2	+	+	-															3	+	nd
EA 3W S1	w	w	w	+	+	+	+	+	+	-	+	+	+	-	+	-	-	3	nd	nd
EA 3W S2	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	2	nd	nd
EA 3W S3	+	-	-	+	+	+	+	+	+	-	+	+	+	+	-	-	-	2	nd	nd
EA 3W S4	+	-	-	+	+	+	+	+	+	-	+	+	+	-	-	w	w	1	nd	nd
EA 3W S5	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd
EA 4W S1	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	w	w	3	nd	nd
EA 4W S2	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3	nd	nd
EA 4W S3	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EA 4W S4	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EA 4W S5	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	nd	nd
EB 0W S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd

Table C.5 *(continued)*

Name	*Alcohol Tolerance(%)*			*SO_2 Tolerance (mg/L)*				*Temperature Tolerance (°C)*			*pH Tolerance*			*Carbohydrate Fermentation Test*					*H_2S Product*	*Identification*
	10	*13*	*15*	*50*	*100*	*150*	*200*	*28*	*37*	*45*	*6*	*4*	*3*	*Sucrose*	*Maltose*	*Mannitol*	*Lactose*		*ITS*	*D1/D2*
EB 0W S3	+	w	w	+	+	+	+	+	+	-	+	+	+	-	+	-	-	3	nd	nd
EB 0W S5	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	4	nd	nd
EB 0W S7	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EB 0W NS1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
EB 0W NS2	+	+	+															3	+	nd
EB 0W NS3	+	+	-															3	+	nd
EB 0W NS4	+	+	+															3	+	nd
EB 0W NS6	+	+	+															3	+	nd
EB 0W NS7	+	+	+															3	+	nd
EB 0W NS8	+	+	-															3	+	nd
EB 0W NS9	+	+	+															3	+	nd
EB 0W NS10	+	+	+															4	+	nd
EB 1W S1	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EB 1W S2	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EB 1W S3	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd
EB 1W S4	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EB 1W S5	+	+	+	+	+	+	+	+	+	-	+	+	+	-	-	-	-	2	nd	nd
EB 1W S6	+	w	-	+	+	+	+											4	nd	nd
EB 1W S7	+	w	-	+	+	+	+											4	nd	nd
EB 1W S8	+	w	-	+	+	+	+											4	nd	nd
EB 1W S9	-	-	-	+	+	+	+											ng	nd	nd
EB 1W S10	+	+	-	+	+	+	+											4	nd	nd
EB 1W NS1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	nd
EB 1W NS2	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
EB 1W NS3	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
EB 1W NS4	+	+	+															3	+	nd
EB 1W NS6	+	+	+															3	+	nd
EB 1W NS7	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	1	+	nd
EB 1W NS9	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	+	nd
EB 1W NS10	+	+	+															3	+	nd
EB 2W S1	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EB 2W S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	4	nd	nd
EB 2W S3	+	w	-	+	+	+	+	+	+	-	+	+	+	-	-	w	w	3	nd	nd
EB 2W S4	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EB 2W S5	+	+	w	+	+	+	+	+	+	-	+	+	+	-	-	w	w	2	nd	nd
EB 3W S1	+	-	-	+	+	+	+	+	+	-	+	+	+	-	+	-	-	2	nd	nd
EB 3W S2	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	3	nd	nd
EB 3W S3	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EB 3W S4	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd
EB 3W S5	+	+	w	+	+	+	+	+	+	-	w	+	w	+	+	-	-	1	nd	+
EB 4W S1	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	2	nd	nd
EB 4W S2	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EB 4W S3	+	w	W	+	+	+	+	+	+	-	+	+	+	+	+	-	-	3	nd	nd
EB 4W S4	+	w	-	+	+	+	+	+	+	-	+	+	+	+	+	-	+	3	nd	nd
EB 4W S5	+	w	w	+	+	+	+	+	+	-	+	+	+	+	+	-	w	3	nd	nd

EA: A Parallel of Wine Made from Emir Grape , EB: B Parallel of Wine Made from Emir Grape; 0W: 0.Week, 1W: 1.Week, 2W:2. Week, 3W: 3. Week, 4W: 4. Week;
S: *Saccharomyces* ; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black; nd: not determined.

D. Phenotypic Properties of All Isolated Non-*Saccharomyces* Yeasts

Table D.1. Phenotypic Properties of All Isolated Non-*Saccharomyces* Yeasts

Non-Saccharomyces	Name		Alcohol Tolerance (%)				SO_2 Tolerance (mg/L)			H_2S Production	Identification	
			10	13	15	50	100	150	200		ITS	D1/D2 Domain
Hanseniaspora guilliermondii	K1	KA 0.CM NS1	-	-	-	+	+	+	+	3	+	nd
	K5	KA 0.CM NS5	-	-	-	+	+	+	+	4	+	+
	K31	KA 4.NM NS2				+	+	+	-	4	+	nd
	K33	KA 4.NM NS6								4	+	nd
	K36	KB 4.NM NS1								4	+	nd
	K39	KB 4.NM NS7								4	+	nd
	K61	KA 4.NM NS1								4	+	nd
	K68	KB 4.NM NS6	w	-	-	+	+	+	+	4	+	nd
	K69	KB 4.NM NS8	-	-	-	+	+	+	+	5	+	nd
Hanseniaspora opuntiae	K2	KA 0.CM NS2	-	-	-	+	+	+	+	3	+	nd
	K7	KB 0.CM NS2								4	+	nd
	K8	KB 0.CM NS3	-	-	-	+	+	+	+	4	+	nd
	K10	KB 0.CM NS5	vw	vw	vw	+	+	+	+	3	+	nd
	K11	KA 4.CM NS1								4	+	nd
	K12	KA 4.CM NS2	-	-	-	+	+	+	+	3	+	+
	K15	KA 4.CM NS5	w	-	-	+	+	+	+	ng	+	nd
	K16	KB 4.CM NS1								ng	+	nd
	K17	KB 4.CM NS2	-	-	-	+	+	+	+	3	+	nd
	K19	KB 4.CM NS4	-	-	-	+	+	+	+	3	+	nd
	K20	KB 4.CM NS5	+	-	-	+	+	+	+	4	+	nd
	K21	KA 2.NM NS1	+	-	-	+	+	+	-	2	+	nd
	K27	KB 2.NM NS4								4	+	nd
	K32	KA 4.NM NS4	-	-	-	+	+	+	+	5	+	nd
	K34	KA 4.NM NS8	w			+	+	+	+	5	+	nd
	K35	KA 4.NM NS10								5	+	+
	K37	KB 4.NM NS3								4	+	nd
	K38	KB 4.NM NS5								4	+	nd
	K40	KB 4.NM NS9	+	-	-	+	+	+	+	4	+	nd
	K51	KA 2.NM NS2	-	-	-	+	+	+	+	4	+	nd
	K60	KB 2.NM NS9								4	+	nd
	K62	KA 4.NM NS3								4	+	+
	K63	KA 4.NM NS5	-	-	-	+	+	+	+	2	+	nd
	K64	KA 4.NM NS7	+	-	-	+	+	+	-	4	+	nd
	K65	KA 4.NM NS9								ng	+	+
	K66	KB 4.NM NS2	w			+	+	+	+	5	+	nd
	K67	KB 4.NM NS4	-	-	-	+	+	+	+	3	+	nd
Rhodotorula mucilaginosa	K9	KB 0.CM NS4	-	-	-	+	+	+	+	3	+	nd
Hanseniaspora uvarum	K13	KA 4.CM NS3	+	vw	-	+	+	+	+	3	+	nd
	K3	KA 0.CM NS3	-	-	-	+	+	+	+	5	+	nd
	K25	KA 2.NM NS9	w			+	+	+	+	6	+	+
	K26	KB 2.NM NS2	+	w	-	+	+	+	+	5	+	nd
	K52	KA 2.NM NS4	-	-	-	+	+	+	+	3	+	nd

Table D.1 *(continued)*

Non-Saccharomyces	Name		Alcohol Tolerance (%)			SO_2 Tolerance (mg/L)				H_2S Production	Identification	
			10	13	15	50	100	150	200		ITS	D1/D2 Domain
Hanseniaspora uvarum	K54	KA 2.NM NS8	w			+	+	+	+	5	+	nd
	K70	KB 4.NM NS10	+	-	-	+	+	+	-	ng	+	+
Wickerhamomyces anomalus	K41	KA 0.CM S1	-	-	-	+	+	+	+	3	+	nd
	K42	KB 0.CM S5	+	+	+	+	+	+	+	ng	+	nd
Metschnikowia aff. fructicola	K43	KA 4.CM S1	-	-	-	-	-	-	-	ng	+	+
Hanseniaspora uvarum	E11	EA 1.W NS1	-	-	-	+	+	+	+	3	+	nd
	E12	EA 1.W NS2								4	+	nd
	E13	EA 1.W NS3								ng	+	nd
	E14	EA 1.W NS4	vw	vw	vw	+	+	+	+	3	+	nd
Wickerhamomyces anomalus	E37	EA 0.NM NS8	-	-	-	+	+	+	+	3	+	nd
Lachancea thermotolerans	O1	OA 0.CM NS1	-	-	-	+	+	+	+	3	+	+
	O2	OB 0.CM NS2								4	+	nd
	O3	OB 0.CM NS3								4	+	nd
	O4	OB 0.CM NS5								ng	+	nd
	O6	OA 4.CM NS3								4	+	nd
	O8	OB 4.CM NS3								ng	+	nd
	O9	OB 4.CM NS4	-	-	-	+	+	+	+	3	+	nd
	O11	OA 0.CM NS2								ng	+	nd
	O13	OA 0.CM NS4								ng	+	nd
	O14	OA 0.CM NS5								5	+	nd
	O15	OA 0.CM NS6								5	+	nd
	O16	OA 0.CM NS7								5	+	nd
	O17	OA 0.CM NS8								5	+	nd
	O18	OA 0.CM NS9								5	+	nd
	O19	OA 0.CM NS10								5	+	nd
	O20	OB 0.CM NS1								5	+	nd
	O21	OB 0.CM NS4								5	+	nd
	O22	OB 0.CM NS6								5	+	nd
	O23	OA 4.CM NS1								ng	+	nd
	O25	OA 4.CM NS6								5	+	nd
	O26	OA 4.CM NS7								5	+	nd
	O27	OA 4.CM NS8								5	+	nd
	O28	OA 4.CM NS9								5	+	nd
	O29	OA 4.CM NS10								5	+	nd
	O30	OB 4.CM NS1								5	+	nd
	O31	OB 4.CM NS2								5	+	nd
	O32	OB 4.CM NS6								5	+	nd
	O33	OB 4.CM NS7								5	+	nd
	O34	OB 4.CM NS8								5	+	nd
	O35	OB 4.CM NS9								6	+	nd
	O36	OB 4.CM NS10								5	+	nd
Wickerhamomyces anomalus	O37	OA 4CM S3	+	+	w	+	+	+	+	3	nd	+
Hanseniaspora opuntiae	O5	OA 4.CM NS2	vw	vw	vw	+	+	+	+	3	+	nd
	O7	OA 4.CM NS4	+	+	+	+	+	+	+	4	+	+
Metschnikowia pulcherrima	B10	BB 0.CM NS2	w	w	-	+	+	+	+	4	+	nd
	B12	BB 0.CM NS4								5	+	nd

Table D.1 (continued)

Non-Saccharomyces	Name		Alcohol Tolerance (%)			SO_2 Tolerance (mg/L)				H_2S Production	Identification	
			10	13	15	50	100	150	200		ITS	D1/D2 Domain
Metschnikowia pulcherrima	B15	BB 0.CM NS7								5	+	nd
	B30	BB 4.CM NS5								5	+	nd
Metschnikowia aff. fructicola	B33	BB 4.CM NS8	-	-	-	+	+	+	+	3	+	+
Metschnikowia aff. pulcherrima	B11	BB 0.CM NS3								5	+	+
Solicoccozyma aeria	B4	BA 0.CM NS4	-	-	-	+	w	w	W	5	+	+
Metschnikowia aff. pulcherrima	D2	DA 0.CM NS2	+	+	+	+	+	+	+	ng	+	+
Metschnikowia sinensis (ITS)	D3	DA 0.CM NS3	-	-	-	+	+	+	+	3	+	
Metschnikowia pulcherrima (D1/D2)												+
Starmeralla bacillaris	D10	DA 4.CM NS2	w	w	-	+	+	+	+	4	+	+
Metschnikowia pulcherrima	D11	DA 4.CM NS3	-	-	-	+	+	+	+	2	+	nd
	D12	DA 4.CM NS4	-	-	-	+	+	+	+	3	+	nd
	D13	DB 4.CM NS1								5	+	nd
	D14	DB 4.CM NS2								4	+	nd
	D4	DA 0.CM NS4								4	+	nd
	D8	DB 0.CM NS4								4	+	+
Metschnikowia chrysoperlae	D6	DB 0.CM NS2								4	+	nd
Metschnikowia fructicola	D15	DB 4.CM NS3	-	-	-	+	+	+	+	4	+	+
Metschnikowia chrysoperlae	14 (Ç)		-	-	-	+	+	+	+	ng	+	nd
Metschnikowia aff. fructicola	M1 (Ç)		+	+	+	+	+	+	+	ng	nd	+

KA: A Parallel of Wine Made from Kalecik Karası Grape , KB: B Parallel of Wine Made from Kalecik Karası Grape, OA: A Parallel of Wine Made from Öküzgözü Grape, OB: B Parallel of Wine Made from Öküzgözü Grape, BA: A Parallel of Wine Made from Boğazkere Grape, BB: B Parallel of Wine Made from Boğazkere Grape, DA: A Parallel of Wine Made from Dimrit Grape, DB: B Parallel of Wine Made from Dimrit Grape, EA: A Parallel of Wine Made from Emir Grape, EB: B Parallel of Wine Made from Emir Grape; 0CM: 0. Day of Cold Maceration, 4CM: 4. Day of Cold Maceration, 2NM: 2. Day of Normal Maceration, 4NM: 4. Day of Normal Maceration, 6NM: 6. Day of Normal Maceration, 1W: 1. Week, 2W: 2. Week, 3W: 3. Week, 4W:4. Week; NS: Non-*Saccharomyces* ; + positive growth, w weak growth, - negative growth; 1: white, 2: cream, 3: light brown, 4: brown, 5: dark brown, 6: black. Ç*: Isolated by Çağrı Çavdaroğlu nd: Not determined

E. Statistical Analysis of Aroma Compounds for the Emir and Kalecik Karası Wines

One-way ANOVA: 1-Propanol versus Group

```
Source  DF        SS        MS       F      P
Group    7  70044176  10006311  512,25  0,000
Error   16    312545     19534
Total   23  70356721

S = 139,8   R-Sq = 99,56%   R-Sq(adj) = 99,36%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --------+---------+---------+---------+-
E-A      3   585,9   30,7   (*)
E-Laff   3   535,5   32,6  (-*)
E-LT-SC  3  6096,3  252,0                                       (*)
E-SC     3  3168,2  188,7                    (*)
K-13     3  1315,1   64,9        (*)
K-A      3  2765,3  103,5                 (*-)
K-HU     3  1485,7  146,5         (*)
K-SC     3  1709,2  136,9          (*-)
                          --------+---------+---------+---------+-
                               1500      3000      4500      6000

Pooled StDev = 139,8


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  6096,3  A
E-SC     3  3168,2     B
K-A      3  2765,3       C
K-SC     3  1709,2         D
K-HU     3  1485,7         D
K-13     3  1315,1         D
E-A      3   585,9           E
E-Laff   3   535,5           E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper      +---------+---------+---------+-------
--
E-Laff   -445,8   -50,4   345,0                          (*)
E-LT-SC  5115,0  5510,4  5905,8                                        (*-)
E-SC     2186,9  2582,3  2977,7                                  (-*)
```

```
K-13      333,8   729,2  1124,6                          (*-)
K-A      1784,0  2179,4  2574,8                               (*-)
K-HU      504,3   899,7  1295,1                           (*)
K-SC      727,9  1123,3  1518,7                           (-*)
                                  +---------+---------+---------+-------
--
                                -6000     -3000         0      3000


Group = E-Laff subtracted from:

Group     Lower  Center   Upper      +---------+---------+---------+-------
--
E-LT-SC  5165,5  5560,8  5956,2
(-*)
E-SC     2237,3  2632,7  3028,1                                   (-*)
K-13      384,2   779,6  1175,0                           (-*)
K-A      1834,4  2229,8  2625,2                               (*-)
K-HU      554,8   950,2  1345,6                           (*)
K-SC      778,3  1173,7  1569,1                            (*)
                                  +---------+---------+---------+-------
--
                                -6000     -3000         0      3000


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper      +---------+---------+---------+------
---
E-SC   -3323,5  -2928,1  -2532,7               (*-)
K-13   -5176,6  -4781,2  -4385,8         (*)
K-A    -3726,4  -3331,0  -2935,6              (*)
K-HU   -5006,1  -4610,7  -4215,3         (-*)
K-SC   -4782,5  -4387,1  -3991,7          (*-)
                                  +---------+---------+---------+------
---
                                -6000     -3000         0      3000


Group = E-SC subtracted from:

Group    Lower   Center    Upper      +---------+---------+---------+------
---
K-13   -2248,5  -1853,1  -1457,7                  (*)
K-A      -798,3   -402,9     -7,5                     (-*)
K-HU   -2078,0  -1682,6  -1287,2                  (*-)
K-SC   -1854,4  -1459,0  -1063,6                   (*)
                                  +---------+---------+---------+------
---
                                -6000     -3000         0      3000


Group = K-13 subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
K-A    1054,8  1450,2  1845,6                           (*)
K-HU   -224,8   170,6   566,0                      (-*)
K-SC     -1,3   394,1   789,5                       (*-)
                              +---------+---------+---------+---------
                            -6000     -3000         0      3000
```

```
Group = K-A subtracted from:

Group    Lower   Center   Upper      +---------+---------+---------+-------
--
K-HU   -1675,1  -1279,7  -884,3                   (-*)
K-SC   -1451,5  -1056,1  -660,7                    (*-)
                                    +---------+---------+---------+-------
--
                                 -6000     -3000         0      3000


Group = K-HU subtracted from:

Group   Lower  Center  Upper      +---------+---------+---------+---------
K-SC   -171,8   223,5  618,9                       (-*)
                           +---------+---------+---------+---------
                        -6000     -3000         0      3000
```

One-way ANOVA: Isobutyl Alcohol versus Group

```
Source  DF         SS        MS       F      P
Group    7  300833685  42976241  158,33  0,000
Error   16    4342980    271436
Total   23  305176665

S = 521,0   R-Sq = 98,58%   R-Sq(adj) = 97,95%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level    N   Mean  StDev  --------+---------+---------+---------+-
E-A      3   7094    546        (-*-)
E-Laff   3   5791    457     (-*)
E-LT-SC  3   5249    136   (-*-)
E-SC     3   4709     49  (*-)
K-13     3   8165    614            (*-)
K-A      3  12601    474                      (-*-)
K-HU     3   8473    328            (-*-)
K-SC     3  15508    967                               (-*-)
                         --------+---------+---------+---------+-
                              7000     10500     14000     17500

Pooled StDev = 521


Grouping Information Using Tukey Method

Group    N   Mean  Grouping
K-SC     3  15508  A
K-A      3  12601    B
K-HU     3   8473      C
K-13     3   8165      C
E-A      3   7094      C D
E-Laff   3   5791        D E
E-LT-SC  3   5249          E
E-SC     3   4709          E
```

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%

Group = E-A subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
E-Laff	-2777	-1303	171	(-*-)
E-LT-SC	-3319	-1845	-371	(-*-)
E-SC	-3859	-2385	-911	(--*-)
K-13	-403	1070	2544	(--*-)
K-A	4033	5506	6980	(-*-)
K-HU	-95	1379	2853	(-*-)
K-SC	6940	8414	9888	(-*-)
				--------+---------+---------+---------+-
				-7000 0 7000 14000

Group = E-Laff subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
E-LT-SC	-2016	-542	932	(-*-)
E-SC	-2556	-1082	392	(-*--)
K-13	899	2373	3847	(-*-)
K-A	5335	6809	8283	(-*-)
K-HU	1208	2682	4156	(-*-)
K-SC	8243	9717	11191	(-*-)
				--------+---------+---------+---------+-
				-7000 0 7000 14000

Group = E-LT-SC subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
E-SC	-2014	-540	934	(-*-)
K-13	1442	2915	4389	(-*-)
K-A	5878	7352	8825	(--*-)
K-HU	1750	3224	4698	(-*-)
K-SC	8785	10259	11733	(-*-)
				--------+---------+---------+---------+-
				-7000 0 7000 14000

Group = E-SC subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
K-13	1981	3455	4929	(-*-)
K-A	6417	7891	9365	(-*-)
K-HU	2290	3764	5238	(-*-)
K-SC	9325	10799	12273	(-*--)
				--------+---------+---------+---------+-
				-7000 0 7000 14000

```
Group = K-13 subtracted from:

Group  Lower  Center  Upper  --------+---------+---------+---------+-
K-A     2962    4436   5910                       (-*-)
K-HU   -1165     309   1783                 (-*--)
K-SC    5870    7344   8818                          (-*--)
                           --------+---------+---------+---------+-
                               -7000         0      7000     14000


Group = K-A subtracted from:

Group  Lower  Center  Upper  --------+---------+---------+---------+-
K-HU   -5601   -4127  -2654           (-*-)
K-SC    1434    2908   4382                    (-*-)
                           --------+---------+---------+---------+-
                               -7000         0      7000     14000


Group = K-HU subtracted from:

Group  Lower  Center  Upper  --------+---------+---------+---------+-
K-SC    5561    7035   8509                          (-*-)
                           --------+---------+---------+---------+-
                               -7000         0      7000     14000
```

One-way ANOVA: 1-Butanol versus Group

```
Source  DF      SS     MS       F      P
Group    5  329215  65843  200,11  0,000
Error   12    3948    329
Total   17  333164

S = 18,14   R-Sq = 98,81%   R-Sq(adj) = 98,32%


                          Individual 95% CIs For Mean Based on Pooled
StDev
Level    N    Mean  StDev    +---------+---------+---------+---------
E-LT-SC  3  505,50  31,02                                  (-*-)
E-SC     3  298,61  17,98                 (-*-)
K-13     3  331,86  17,26                    (-*-)
K-A      3  479,13   7,32                              (-*-)
K-HU     3  138,20  12,79    (-*)
K-SC     3  191,70  13,18        (-*-)
                             +---------+---------+---------+---------
                            120       240       360       480

Pooled StDev = 18,14


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  505,50  A
K-A      3  479,13  A
K-13     3  331,86    B
E-SC     3  298,61    B
```

```
K-SC     3  191,70      C
K-HU     3  138,20        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
E-SC   -256,64  -206,89  -157,15         (-*-)
K-13   -223,38  -173,63  -123,89          (-*-)
K-A     -76,11   -26,36    23,38                (-*-)
K-HU   -417,04  -367,30  -317,55  (-*-)
K-SC   -363,54  -313,80  -264,05    (-*-)
                                  -------+---------+---------+---------+--
                                      -250         0       250       500


Group = E-SC subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
K-13    -16,49    33,26    83,00                (-*-)
K-A     130,78   180,53   230,27                     (-*-)
K-HU   -210,15  -160,41  -110,66          (-*-)
K-SC   -156,65  -106,90   -57,16            (-*-)
                                  -------+---------+---------+---------+--
                                      -250         0       250       500


Group = K-13 subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
K-A      97,53   147,27   197,02                      (-*-)
K-HU   -243,41  -193,66  -143,92         (-*-)
K-SC   -189,91  -140,16   -90,42           (-*-)
                                  -------+---------+---------+---------+--
                                      -250         0       250       500


Group = K-A subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
K-HU   -390,68  -340,93  -291,19   (-*-)
K-SC   -337,18  -287,43  -237,69      (-*)
                                  -------+---------+---------+---------+--
                                      -250         0       250       500


Group = K-HU subtracted from:

Group  Lower  Center   Upper  -------+---------+---------+---------+--
K-SC    3,76   53,50  103,25                  (-*-)
                             -------+---------+---------+---------+--
                                 -250         0       250       500
```

One-way ANOVA: Isoamyl Alcohol versus Group

```
Source  DF          SS         MS      F      P
Group    7  6255623964  893660566  19,09  0,000
Error   16   748818100   46801131
Total   23  7004442064

S = 6841   R-Sq = 89,31%   R-Sq(adj) = 84,63%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --------+---------+---------+---------+-
E-A      3  107983  10207                    (---*---)
E-Laff   3  100487   9981                (---*---)
E-LT-SC  3   83098    116       (----*---)
E-SC     3   71678   1130  (---*---)
K-13     3   93418   6180             (---*---)
K-A      3  113587   3888                       (---*---)
K-HU     3   85287    295        (----*---)
K-SC     3  123340  10766                            (----*---)
                          --------+---------+---------+---------+-
                              80000    100000    120000    140000

Pooled StDev = 6841


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-SC     3  123340  A
K-A      3  113587  A B
E-A      3  107983  A B C
E-Laff   3  100487    B C D
K-13     3   93418      C D
K-HU     3   85287        D E
E-LT-SC  3   83098        D E
E-SC     3   71678          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper  --------+---------+---------+---------+-
E-Laff   -26850   -7496   11857             (----*----)
E-LT-SC  -44239  -24886   -5532         (----*----)
E-SC     -55659  -36306  -16952      (----*----)
K-13     -33919  -14566    4788            (---*----)
K-A      -13750    5603   24957                 (---*----)
K-HU     -42050  -22697   -3343         (----*----)
```

```
K-SC      -3997   15357   34710                    (----*----)
                                  --------+---------+---------+---------+-
                                     -40000         0     40000     80000
```

Group = E-Laff subtracted from:

```
Group     Lower  Center  Upper  --------+---------+---------+---------+-
E-LT-SC  -36743  -17389   1964           (----*---)
E-SC     -48163  -28809  -9456        (----*----)
K-13     -26423   -7069  12284             (----*----)
K-A       -6254   13100  32453                  (----*----)
K-HU     -34554  -15200   4154           (----*----)
K-SC       3500   22853  42207                    (----*----)
                                  --------+---------+---------+---------+-
                                     -40000         0     40000     80000
```

Group = E-LT-SC subtracted from:

```
Group   Lower  Center  Upper  --------+---------+---------+---------+-
E-SC   -30774  -11420   7934           (----*----)
K-13    -9034   10320  29674                (----*---)
K-A     11135   30489  49843                     (----*---)
K-HU   -17165    2189  21543                (----*---)
K-SC    20889   40242  59596                      (----*----)
                               --------+---------+---------+---------+-
                                  -40000         0     40000     80000
```

Group = E-SC subtracted from:

```
Group  Lower  Center  Upper  --------+---------+---------+---------+-
K-13    2386   21740  41094                  (---*----)
K-A    22555   41909  61263                       (---*----)
K-HU   -5745   13609  32963                 (---*----)
K-SC   32309   51662  71016                       (----*----)
                            --------+---------+---------+---------+-
                               -40000         0     40000     80000
```

Group = K-13 subtracted from:

```
Group   Lower  Center  Upper  --------+---------+---------+---------+-
K-A       815   20169  39523                  (----*----)
K-HU   -27485   -8131  11223           (----*----)
K-SC    10569   29922  49276                    (---*----)
                               --------+---------+---------+---------+-
                                  -40000         0     40000     80000
```

Group = K-A subtracted from:

```
Group   Lower  Center  Upper  --------+---------+---------+---------+-
K-HU   -47654  -28300  -8946       (----*----)
K-SC    -9600    9753  29107                (---*----)
                               --------+---------+---------+---------+-
                                  -40000         0     40000     80000
```

```
Group = K-HU subtracted from:

Group  Lower  Center  Upper  --------+---------+---------+---------+-
K-SC   18700   38053  57407                      (----*---)
                            --------+---------+---------+---------+-
                               -40000         0     40000     80000
```

One-way ANOVA: 3-Methyl-1-pentanol versus Group

```
Source  DF      SS      MS      F      P
Group    5  6445,2  1289,0  33,71  0,000
Error   12   458,8    38,2
Total   17  6904,0

S = 6,183   R-Sq = 93,35%   R-Sq(adj) = 90,59%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level   N    Mean  StDev  -+---------+---------+---------+--------
E-A     3   74,20   7,82               (---*---)
E-Laff  3  100,40   9,51                          (---*---)
K-13    3   91,39   6,91                       (---*---)
K-A     3   61,44   4,53          (---*---)
K-HU    3   58,95   1,81        (--*---)
K-SC    3   45,94   2,47  (---*---)
                         -+---------+---------+---------+--------
                         40        60        80       100

Pooled StDev = 6,18


Grouping Information Using Tukey Method

Group   N     Mean  Grouping
E-Laff  3  100,400  A
K-13    3   91,387  A
E-A     3   74,197    B
K-A     3   61,439    B C
K-HU    3   58,947    B C
K-SC    3   45,938      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:

Group     Lower   Center    Upper  --------+---------+---------+---------+-
E-Laff    9,246   26,203   43,161                     (----*---)
K-13      0,234   17,191   34,148                   (---*----)
K-A     -29,715  -12,757    4,200            (---*---)
K-HU    -32,207  -15,250    1,707           (---*---)
```

```
K-SC    -45,216  -28,259  -11,301         (---*---)
                                 --------+---------+---------+---------+-
                                        -40         0        40        80


Group = E-Laff subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-13   -25,970   -9,012    7,945             (---*---)
K-A    -55,918  -38,961  -22,003      (---*---)
K-HU   -58,410  -41,453  -24,496     (----*---)
K-SC   -71,419  -54,462  -37,505  (---*----)
                                 --------+---------+---------+---------+-
                                       -40         0        40        80


Group = K-13 subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-A    -46,906  -29,948  -12,991        (----*---)
K-HU   -49,398  -32,441  -15,483        (---*---)
K-SC   -62,407  -45,450  -28,492    (----*---)
                                 --------+---------+---------+---------+-
                                       -40         0        40        80


Group = K-A subtracted from:

Group    Lower   Center   Upper  --------+---------+---------+---------+-
K-HU   -19,450   -2,492  14,465              (---*----)
K-SC   -32,459  -15,501   1,456           (---*---)
                               --------+---------+---------+---------+-
                                     -40         0        40        80


Group = K-HU subtracted from:

Group    Lower   Center  Upper  --------+---------+---------+---------+-
K-SC   -29,966  -13,009  3,948            (---*---)
                             --------+---------+---------+---------+-
                                   -40         0        40        80
```

One-way ANOVA: 3-Ethoxy-1-propanol versus Group

```
Source  DF        SS       MS       F      P
Group    7  531008,1  75858,3  983,61  0,000
Error   16    1234,0     77,1
Total   23  532242,1

S = 8,782   R-Sq = 99,77%   R-Sq(adj) = 99,67%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --------+---------+---------+---------+-
E-A      3   38,10   3,78  (*)
E-Laff   3   41,06   3,75  (*)
E-LT-SC  3  510,90  20,70                                 (*)
```

```
E-SC     3  185,95   3,26            *)
K-13     3   92,19   6,23     (*)
K-A      3  227,38   9,25              (*)
K-HU     3  229,09   1,01               *)
K-SC     3   52,91   4,91   (*)
                          --------+---------+---------+---------+-
                                150       300       450       600

Pooled StDev = 8,78


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  510,90  A
K-HU     3  229,09    B
K-A      3  227,38    B
E-SC     3  185,95      C
K-13     3   92,19        D
K-SC     3   52,91          E
E-Laff   3   41,06          E
E-A      3   38,10          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper     +---------+---------+---------+--------
-
E-Laff   -21,88    2,97   27,81                        (*)
E-LT-SC  447,96  472,81  497,65
(*)
E-SC     123,01  147,85  172,70                             (*)
K-13      29,25   54,10   78,94                          (*)
K-A      164,43  189,28  214,12                               (*)
K-HU     166,15  190,99  215,84                               (*)
K-SC     -10,03   14,81   39,66                         (*)
                                  +---------+---------+---------+--------
-
                                -500      -250         0       250


Group = E-Laff subtracted from:

Group     Lower  Center   Upper     +---------+---------+---------+--------
-
E-LT-SC  445,00  469,84  494,69
(*)
E-SC     120,04  144,89  169,73                             (*)
K-13      26,29   51,13   75,97                          (*)
K-A      161,47  186,31  211,16                               (*)
K-HU     163,18  188,03  212,87                                (*)
K-SC     -13,00   11,85   36,69                         (*)
```

```
                                    +---------+---------+---------+--------
-
                                  -500      -250         0       250


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper     +---------+---------+---------+-------
--
E-SC   -349,80  -324,96  -300,11           (*)
K-13   -443,56  -418,71  -393,87       (*)
K-A    -308,37  -283,53  -258,69             (*)
K-HU   -306,66  -281,82  -256,97             (*)
K-SC   -482,84  -458,00  -433,15      (*)
                                    +---------+---------+---------+-------
--
                                  -500      -250         0       250


Group = E-SC subtracted from:

Group    Lower   Center    Upper     +---------+---------+---------+-------
--
K-13   -118,60   -93,76   -68,91                   (*)
K-A      16,58    41,43    66,27                        (*)
K-HU     18,30    43,14    67,98                        (*)
K-SC   -157,88  -133,04  -108,20                  (*)
                                    +---------+---------+---------+-------
--
                                  -500      -250         0       250


Group = K-13 subtracted from:

Group   Lower  Center   Upper     +---------+---------+---------+---------
K-A    110,34  135,18  160,03                          (*)
K-HU   112,05  136,90  161,74                          (*)
K-SC   -64,13  -39,28  -14,44                    (*)
                              +---------+---------+---------+---------
                            -500      -250         0       250


Group = K-A subtracted from:

Group    Lower   Center    Upper     +---------+---------+---------+-------
--
K-HU    -23,13     1,71    26,56                       (*)
K-SC   -199,31  -174,47  -149,62                (*)
                                    +---------+---------+---------+-------
--
                                  -500      -250         0       250


Group = K-HU subtracted from:

Group    Lower   Center    Upper     +---------+---------+---------+-------
--
K-SC   -201,02  -176,18  -151,34                (*)
                                    +---------+---------+---------+-------
--
```

```
                                -500      -250         0       250
```

One-way ANOVA: 3-(Ethylthio)-1-propanol versus Group

```
Source  DF      SS      MS      F      P
Group    1  148,35  148,35  29,77  0,005
Error    4   19,94    4,98
Total    5  168,29

S = 2,232   R-Sq = 88,15%   R-Sq(adj) = 85,19%


                          Individual 95% CIs For Mean Based on Pooled StDev
Level   N    Mean  StDev    -+---------+---------+---------+--------
E-A     3  33,156  3,132                      (------*------)
E-Laff  3  23,211  0,395    (------*-------)
                            -+---------+---------+---------+--------
                          20,0      25,0      30,0      35,0

Pooled StDev = 2,232


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-A     3  33,156  A
E-Laff  3  23,211    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group     Lower  Center   Upper  -----+---------+---------+---------+----
E-Laff  -15,006  -9,945  -4,884  (-------*--------)
                                 -----+---------+---------+---------+----
                                  -12,0      -6,0       0,0       6,0
```

One-way ANOVA: Methionol versus Group

```
Source  DF       SS      MS       F      P
Group    7  1164781  166397  245,18  0,000
Error   16    10859     679
Total   23  1175639

S = 26,05   R-Sq = 99,08%   R-Sq(adj) = 98,67%


                           Individual 95% CIs For Mean Based on
                           Pooled StDev
Level    N    Mean  StDev  -------+---------+---------+---------+--
```

```
E-A      3  417,14  18,53                  (-*)
E-Laff   3  418,77  29,47                  (-*-)
E-LT-SC  3   94,32   8,25  (-*)
E-SC     3  127,47   4,84    (*-)
K-13     3  405,97  32,63                  (*-)
K-A      3  712,09  26,69                              (-*)
K-HU     3  731,70  15,33                               (-*)
K-SC     3  542,26  45,98                        (*-)
                          -------+---------+---------+---------+--
                               200       400       600       800

Pooled StDev = 26,05


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-HU     3  731,70  A
K-A      3  712,09  A
K-SC     3  542,26    B
E-Laff   3  418,77      C
E-A      3  417,14      C
K-13     3  405,97      C
E-SC     3  127,47        D
E-LT-SC  3   94,32        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group      Lower   Center    Upper  --------+---------+---------+---------
+-
E-Laff    -72,07     1,63    75,33                  (-*-)
E-LT-SC  -396,52  -322,83  -249,13          (-*-)
E-SC     -363,37  -289,67  -215,97           (-*-)
K-13      -84,87   -11,17    62,53                  (-*-)
K-A       221,25   294,95   368,65                          (*-)
K-HU      240,86   314,55   388,25                          (-*-)
K-SC       51,42   125,12   198,82                     (-*-)
                                  --------+---------+---------+---------
+-
                                       -400         0       400       800


Group = E-Laff subtracted from:

Group      Lower   Center    Upper  --------+---------+---------+---------
+-
E-LT-SC  -398,16  -324,46  -250,76          (-*-)
E-SC     -365,00  -291,30  -217,60           (-*-)
K-13      -86,50   -12,80    60,90                  (-*-)
K-A       219,62   293,32   367,02                          (-*-)
K-HU      239,22   312,92   386,62                           (-*-)
```

```
K-SC       49,79   123,49   197,18                      (-*-)
                                    --------+---------+---------+---------
+-
                                         -400         0       400       800


Group = E-LT-SC subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
E-SC   -40,54   33,16  106,86                  (-*-)
K-13   237,96  311,66  385,36                         (-*-)
K-A    544,08  617,78  691,48                                 (*-)
K-HU   563,68  637,38  711,08                                 (-*-)
K-SC   374,24  447,94  521,64                            (-*-)
                                --------+---------+---------+---------+-
                                     -400         0       400       800


Group = E-SC subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-13   204,80  278,50  352,20                        (-*-)
K-A    510,92  584,62  658,32                                (-*)
K-HU   530,52  604,22  677,92                                (-*-)
K-SC   341,09  414,78  488,48                           (*-)
                                --------+---------+---------+---------+-
                                     -400         0       400       800


Group = K-13 subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-A    232,42  306,12  379,82                          (-*)
K-HU   252,02  325,72  399,42                          (-*-)
K-SC    62,59  136,28  209,98                     (*-)
                                --------+---------+---------+---------+-
                                     -400         0       400       800


Group = K-A subtracted from:

Group    Lower   Center   Upper  --------+---------+---------+---------+-
K-HU    -54,10    19,60   93,30                  (*-)
K-SC   -243,53  -169,83  -96,13            (-*-)
                               --------+---------+---------+---------+-
                                    -400         0       400       800


Group = K-HU subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-SC   -263,14  -189,44  -115,74            (-*-)
                              --------+---------+---------+---------+-
                                   -400         0       400       800
```

One-way ANOVA: Benzyl Alcohol versus Group

```
Source  DF        SS       MS       F      P
Group    7  130627,5  18661,1  223,31  0,000
Error   16    1337,0     83,6
Total   23  131964,6

S = 9,141   R-Sq = 98,99%   R-Sq(adj) = 98,54%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  -----+---------+---------+---------+----
E-A      3   42,60   3,87  (-*-)
E-Laff   3   57,01   4,44     (-*)
E-LT-SC  3   73,10   2,07       (-*-)
E-SC     3   54,69   0,64    (-*-)
K-13     3  200,40  19,08                              (*-)
K-A      3  255,14   8,93                                   (-*)
K-HU     3  165,96   3,28                         (-*-)
K-SC     3  139,55  13,21                   (-*-)
                          -----+---------+---------+---------+----
                              60       120       180       240

Pooled StDev = 9,14


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  255,14  A
K-13     3  200,40     B
K-HU     3  165,96       C
K-SC     3  139,55         D
E-LT-SC  3   73,10           E
E-Laff   3   57,01           E F
E-SC     3   54,69           E F
E-A      3   42,60             F

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff   -11,45   14,41   40,27                    (-*-)
E-LT-SC    4,63   30,49   56,35                     (--*-)
E-SC     -13,77   12,09   37,95                    (-*-)
K-13     131,94  157,80  183,66                              (-*-)
K-A      186,67  212,53  238,39                                   (-*-)
K-HU      97,49  123,35  149,21                            (-*-)
K-SC      71,08   96,95  122,81                          (-*-)
                          ---------+---------+---------+---------+
```

```
                                    -120         0       120       240
```

Group = E-Laff subtracted from:

```
Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-LT-SC   -9,78   16,08   41,94                  (-*-)
E-SC     -28,18   -2,32   23,54                 (-*-)
K-13     117,53  143,39  169,25                          (-*-)
K-A      172,26  198,12  223,99                              (--*-)
K-HU      83,08  108,94  134,80                        (-*-)
K-SC      56,68   82,54  108,40                      (-*-)
                          ---------+---------+---------+---------+
                                -120         0       120       240
```

Group = E-LT-SC subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
E-SC   -44,26  -18,40    7,46              (-*--)
K-13   101,45  127,31  153,17                        (--*-)
K-A    156,18  182,04  207,90                             (-*-)
K-HU    67,00   92,86  118,72                       (-*-)
K-SC    40,59   66,45   92,32                    (--*-)
                          ---------+---------+---------+---------+
                               -120         0       120       240
```

Group = E-SC subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-13   119,85  145,71  171,57                          (-*-)
K-A    174,58  200,44  226,31                               (-*-)
K-HU    85,40  111,26  137,12                         (-*-)
K-SC    59,00   84,86  110,72                      (-*-)
                          ---------+---------+---------+---------+
                               -120         0       120       240
```

Group = K-13 subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-A     28,87   54,73   80,59                    (--*-)
K-HU   -60,31  -34,45   -8,59             (-*-)
K-SC   -86,72  -60,85  -34,99           (-*-)
                          ---------+---------+---------+---------+
                               -120         0       120       240
```

Group = K-A subtracted from:

```
Group    Lower   Center   Upper  ---------+---------+---------+---------+
K-HU   -115,04   -89,18  -63,32         (--*-)
K-SC   -141,45  -115,59  -89,73       (-*--)
                          ---------+---------+---------+---------+
                               -120         0       120       240
```

```
Group = K-HU subtracted from:

Group   Lower  Center  Upper  ---------+---------+---------+---------+
K-SC   -52,27  -26,41  -0,55                (-*-)
                            ---------+---------+---------+---------+
                                  -120         0       120       240
```

One-way ANOVA: 2-Methyl-2-buten-1-ol versus Group

```
Source  DF        SS       MS       F      P
Group    4  11339,05  2834,76  458,77  0,000
Error   10     61,79     6,18
Total   14  11400,84

S = 2,486   R-Sq = 99,46%   R-Sq(adj) = 99,24%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level   N    Mean  StDev   +---------+---------+---------+---------
E-A     3   37,53   3,52       (*)
E-Laff  3   34,17   2,47     (-*)
E-SC    3  102,43   2,58                                  (*)
K-13    3   37,04   1,89       (*)
K-HU    3   28,10   1,48   (*-)
                          +---------+---------+---------+---------
                         25        50        75       100

Pooled StDev = 2,49


Grouping Information Using Tukey Method

Group   N     Mean  Grouping
E-SC    3  102,429  A
E-A     3   37,535    B
K-13    3   37,036    B
E-Laff  3   34,166    B C
K-HU    3   28,096      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,18%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ------+---------+---------+---------+---
E-Laff  -10,042  -3,368   3,305              (*-)
E-SC     58,221  64,894  71,568                                  (*)
K-13     -7,173  -0,499   6,174                (*)
K-HU    -16,113  -9,439  -2,766             (*)
                                 ------+---------+---------+---------+---
                                     -50         0        50       100
```

```
Group = E-Laff subtracted from:

Group    Lower  Center   Upper  ------+---------+---------+---------+---
E-SC    61,589  68,262  74,936                              (-*)
K-13    -3,804   2,869   9,543                 (-*)
K-HU   -12,744  -6,071   0,603              (-*)
                                  ------+---------+---------+---------+---
                                      -50         0        50       100


Group = E-SC subtracted from:

Group    Lower   Center    Upper  ------+---------+---------+---------+---
K-13   -72,067  -65,393  -58,720    (*)
K-HU   -81,007  -74,333  -67,660  (*)
                                  ------+---------+---------+---------+---
                                      -50         0        50       100


Group = K-13 subtracted from:

Group    Lower  Center   Upper  ------+---------+---------+---------+---
K-HU   -15,614  -8,940  -2,267              (*-)
                                  ------+---------+---------+---------+---
                                      -50         0        50       100
```

One-way ANOVA: Phenylethyl Alcohol versus Group

```
Source  DF         SS         MS       F      P
Group    7  785730191  112247170  157,63  0,000
Error   16   11393525     712095
Total   23  797123716

S = 843,9   R-Sq = 98,57%   R-Sq(adj) = 97,95%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level    N   Mean  StDev  -------+---------+---------+---------+--
E-A      3  21883    760                     (-*-)
E-Laff   3  20826   1767                   (-*-)
E-LT-SC  3  12913    514   (-*-)
E-SC     3  12587    296  (-*-)
K-13     3  21741    511                    (-*--)
K-A      3  30431    637                                    (-*-)
K-HU     3  26839    527                              (-*-)
K-SC     3  19790    836                (-*-)
                         -------+---------+---------+---------+--
                            15000     20000     25000     30000

Pooled StDev = 844


Grouping Information Using Tukey Method

Group    N   Mean  Grouping
K-A      3  30431  A
K-HU     3  26839    B
```

```
E-A      3  21883      C
K-13     3  21741      C
E-Laff   3  20826      C
K-SC     3  19790      C
E-LT-SC  3  12913        D
E-SC     3  12587        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center  Upper  -------+---------+---------+---------+--
E-Laff    -3444   -1056   1331               (-*-)
E-LT-SC  -11357   -8970  -6582         (-*-)
E-SC     -11683   -9295  -6908        (-*-)
K-13      -2529    -142   2245                (-*-)
K-A        6161    8548  10936                      (-*-)
K-HU       2569    4957   7344                   (-*-)
K-SC      -4480   -2093    294              (-*-)
                             -------+---------+---------+---------+--
                               -12000         0     12000     24000


Group = E-Laff subtracted from:

Group     Lower  Center  Upper  -------+---------+---------+---------+--
E-LT-SC  -10301   -7913  -5526         (-*-)
E-SC     -10626   -8239  -5852         (-*-)
K-13      -1473     914   3301                (-*-)
K-A        7217    9605  11992                      (-*-)
K-HU       3625    6013   8400                   (-*-)
K-SC      -3424   -1037   1351              (-*-)
                             -------+---------+---------+---------+--
                               -12000         0     12000     24000


Group = E-LT-SC subtracted from:

Group  Lower  Center  Upper  -------+---------+---------+---------+--
E-SC   -2713    -326   2061               (-*-)
K-13    6440    8827  11215                     (-*-)
K-A    15131   17518  19905                           (-*-)
K-HU   11539   13926  16313                        (-*-)
K-SC    4489    6877   9264                   (-*-)
                          -------+---------+---------+---------+--
                            -12000         0     12000     24000


Group = E-SC subtracted from:

Group  Lower  Center  Upper  -------+---------+---------+---------+--
K-13    6766    9153  11541                     (-*-)
K-A    15456   17844  20231                           (-*-)
```

```
K-HU   11865   14252  16639                              (-*-)
K-SC    4815    7202   9590                        (-*-)
                              -------+---------+---------+---------+--
                                -12000         0     12000     24000


Group = K-13 subtracted from:

Group  Lower  Center  Upper  -------+---------+---------+---------+--
K-A     6303    8690  11078                        (-*-)
K-HU    2711    5099   7486                     (-*-)
K-SC   -4338   -1951    436               (-*-)
                              -------+---------+---------+---------+--
                                -12000         0     12000     24000


Group = K-A subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-HU    -5979   -3592  -1205              (-*-)
K-SC   -13029  -10641  -8254        (-*-)
                               -------+---------+---------+---------+--
                                 -12000         0     12000     24000


Group = K-HU subtracted from:

Group  Lower  Center  Upper  -------+---------+---------+---------+--
K-SC   -9437   -7049  -4662           (-*-)
                              -------+---------+---------+---------+--
                                -12000         0     12000     24000
```

One-way ANOVA: 3-Methyl-3-butene-1-ol versus Group

```
Source  DF      SS      MS      F      P
Group    5  8451,5  1690,3  45,85  0,000
Error   12   442,4    36,9
Total   17  8893,9

S = 6,072   R-Sq = 95,03%   R-Sq(adj) = 92,95%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level   N    Mean  StDev  --------+---------+---------+---------+-
E-A     3   88,65   5,40           (--*---)
E-Laff  3  111,31   7,95                    (---*--)
K-13    3   90,62   8,94           (---*---)
K-A     3  134,05   1,19                                (---*---)
K-HU    3   74,35   5,26   (---*---)
K-SC    3   71,75   4,45  (---*---)
                         --------+---------+---------+---------+-
                                80       100       120       140

Pooled StDev = 6,07


Grouping Information Using Tukey Method
```

```
Group   N     Mean  Grouping
K-A     3  134,048  A
E-Laff  3  111,311    B
K-13    3   90,621      C
E-A     3   88,646      C
K-HU    3   74,350      C D
K-SC    3   71,752        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:

Group     Lower   Center   Upper    +---------+---------+---------+--------
-
E-Laff    6,013   22,664  39,316                          (---*---)
K-13    -14,677    1,975  18,626                   (---*----)
K-A      28,750   45,402  62,054                            (---*----)
K-HU    -30,948  -14,296   2,355               (---*----)
K-SC    -33,546  -16,894  -0,243               (---*---)
                           +---------+---------+---------+--------
-
                         -80       -40         0        40


Group = E-Laff subtracted from:

Group    Lower   Center    Upper    +---------+---------+---------+--------
-
K-13   -37,341  -20,690   -4,038              (---*---)
K-A      6,086   22,738   39,389                        (---*---)
K-HU   -53,612  -36,961  -20,309          (---*---)
K-SC   -56,210  -39,559  -22,907         (---*---)
                           +---------+---------+---------+--------
-
                         -80       -40         0        40


Group = K-13 subtracted from:

Group    Lower   Center   Upper    +---------+---------+---------+---------
K-A     26,776   43,427  60,079                             (---*---)
K-HU   -32,922  -16,271   0,381              (---*---)
K-SC   -35,520  -18,869  -2,217             (---*---)
                          +---------+---------+---------+---------
                        -80       -40         0        40


Group = K-A subtracted from:

Group    Lower   Center    Upper    +---------+---------+---------+--------
-
K-HU   -76,350  -59,698  -43,047     (---*---)
```

```
K-SC   -78,948  -62,296  -45,645    (---*----)
                                   +---------+---------+---------+--------
-
                                  -80       -40         0        40


Group = K-HU subtracted from:

Group    Lower  Center   Upper    +---------+---------+---------+---------
K-SC   -19,249  -2,598  14,054                  (---*----)
                                  +---------+---------+---------+---------
                                -80       -40         0        40
```

One-way ANOVA: 1-Pentanol versus Group

```
Source  DF      SS     MS      F      P
Group    5  2920,7  584,1  19,73  0,000
Error   12   355,3   29,6
Total   17  3276,1

S = 5,442   R-Sq = 89,15%   R-Sq(adj) = 84,63%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  --+---------+---------+---------+-------
E-A     3   73,92   6,93         (---*----)
E-Laff  3  104,36   5,62                              (----*---)
K-13    3   79,89   6,16              (---*----)
K-A     3   82,62   6,49                (---*----)
K-HU    3   63,57   3,11  (---*----)
K-SC    3   71,69   2,87       (----*---)
                          --+---------+---------+---------+-------
                           60        75        90       105

Pooled StDev = 5,44


Grouping Information Using Tukey Method

Group   N     Mean  Grouping
E-Laff  3  104,356  A
K-A     3   82,619    B
K-13    3   79,886    B
E-A     3   73,916    B C
K-SC    3   71,688    B C
K-HU    3   63,569      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:
```

```
Group     Lower   Center   Upper  ---------+---------+---------+---------+
E-Laff   15,517   30,440  45,364                          (----*----)
K-13     -8,953    5,970  20,893                 (----*----)
K-A      -6,220    8,703  23,627                  (----*----)
K-HU    -25,270  -10,347   4,576            (----*----)
K-SC    -17,151   -2,228  12,696              (----*----)
                                 ---------+---------+---------+---------+
                                        -30         0        30        60


Group = E-Laff subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-13   -39,394  -24,470   -9,547       (----*----)
K-A    -36,660  -21,737   -6,814        (----*----)
K-HU   -55,711  -40,787  -25,864  (----*----)
K-SC   -47,592  -32,668  -17,745     (----*----)
                                 ---------+---------+---------+---------+
                                        -30         0        30        60


Group = K-13 subtracted from:

Group    Lower   Center   Upper  ---------+---------+---------+---------+
K-A    -12,190    2,733  17,657               (----*----)
K-HU   -31,240  -16,317  -1,394          (----*----)
K-SC   -23,121   -8,198   6,726            (----*----)
                                 ---------+---------+---------+---------+
                                       -30         0        30        60


Group = K-A subtracted from:

Group    Lower   Center   Upper  ---------+---------+---------+---------+
K-HU   -33,974  -19,050  -4,127          (----*----)
K-SC   -25,855  -10,931   3,992            (----*----)
                                 ---------+---------+---------+---------+
                                       -30         0        30        60


Group = K-HU subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   -6,804   8,119  23,043                   (----*----)
                              ---------+---------+---------+---------+
                                     -30         0        30        60
```

One-way ANOVA: 4-Methyl-1-pentanol versus Group

```
Source  DF      SS     MS     F      P
Group    3  168,66  56,22  7,85  0,009
Error    8   57,26   7,16
Total   11  225,92

S = 2,675   R-Sq = 74,65%   R-Sq(adj) = 65,15%
```

```
                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  -------+---------+---------+---------+--
E-A     3  35,194  2,905           (------*-------)
E-Laff  3  34,332  2,647          (------*------)
K-13    3  40,770  3,382                       (-------*------)
K-HU    3  30,255  1,323  (-------*------)
                          -------+---------+---------+---------+--
                              30,0      35,0      40,0      45,0

Pooled StDev = 2,675


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
K-13    3  40,770  A
E-A     3  35,194  A B
E-Laff  3  34,332  A B
K-HU    3  30,255    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,74%


Group = E-A subtracted from:

Group     Lower  Center   Upper  --------+---------+---------+---------+-
E-Laff   -7,859  -0,862   6,135            (------*------)
K-13     -1,421   5,576  12,573                    (------*------)
K-HU    -11,937  -4,939   2,058         (------*------)
                                --------+---------+---------+---------+-
                                      -10         0        10        20


Group = E-Laff subtracted from:

Group    Lower  Center   Upper  --------+---------+---------+---------+-
K-13    -0,559   6,438  13,435                   (------*------)
K-HU   -11,075  -4,078   2,920          (------*------)
                               --------+---------+---------+---------+-
                                     -10         0        10        20


Group = K-13 subtracted from:

Group    Lower   Center   Upper  --------+---------+---------+---------+-
K-HU   -17,513  -10,515  -3,518  (------*------)
                                --------+---------+---------+---------+-
                                      -10         0        10        20
```

One-way ANOVA: 2,3-Butanediol versus Group

```
Source  DF        SS       MS       F      P
Group    7  35020872  5002982  113,44  0,000
Error   14    617411    44101
Total   21  35638284

S = 210,0   R-Sq = 98,27%   R-Sq(adj) = 97,40%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---------+---------+---------+---------+
E-A      3  1840,1  141,8    (-*--)
E-Laff   3  1592,1   34,4  (-*-)
E-LT-SC  2  2554,1  130,3          (-*--)
E-SC     2  1727,8   51,0   (-*--)
K-13     3  4379,1  409,2                        (-*--)
K-A      3  5195,3  209,7                               (-*-)
K-HU     3  3348,0  227,4                 (-*-)
K-SC     3  3621,4  120,3                   (-*-)
                          ---------+---------+---------+---------+
                                2400      3600      4800      6000

Pooled StDev = 210,0


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  5195,3  A
K-13     3  4379,1     B
K-SC     3  3621,4       C
K-HU     3  3348,0       C
E-LT-SC  2  2554,1         D
E-A      3  1840,1           E
E-SC     2  1727,8           E
E-Laff   3  1592,1           E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-Laff   -853,0  -247,9   357,1               (-*-)
E-LT-SC    37,6   714,0  1390,4                  (--*--)
E-SC     -788,7  -112,3   564,1               (--*-)
K-13     1934,0  2539,0  3144,0                         (-*--)
K-A      2750,2  3355,3  3960,3                            (-*--)
K-HU      902,9  1507,9  2112,9                      (-*-)
K-SC     1176,3  1781,3  2386,3                       (-*--)
                         -------+---------+---------+---------+--
```

```
                                  -2500         0      2500      5000
```

Group = E-Laff subtracted from:

```
Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-LT-SC   285,5   961,9  1638,4                   (--*--)
E-SC     -540,8   135,6   812,0                (--*-)
K-13     2181,9  2786,9  3391,9                          (-*--)
K-A      2998,2  3603,2  4208,2                             (-*--)
K-HU     1150,8  1755,8  2360,9                       (-*-)
K-SC     1424,3  2029,3  2634,3                        (-*--)
                               -------+---------+---------+---------+--
                                  -2500         0      2500      5000
```

Group = E-LT-SC subtracted from:

```
Group    Lower  Center   Upper  -------+---------+---------+---------+--
E-SC   -1567,3  -826,3   -85,3            (--*--)
K-13    1148,6  1825,0  2501,4                      (-*--)
K-A     1964,8  2641,3  3317,7                         (--*-)
K-HU     117,5   793,9  1470,3                  (--*--)
K-SC     390,9  1067,3  1743,8                    (-*--)
                              -------+---------+---------+---------+--
                                 -2500         0      2500      5000
```

Group = E-SC subtracted from:

```
Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-13   1974,9  2651,3  3327,7                          (--*-)
K-A    2791,2  3467,6  4144,0                             (--*--)
K-HU    943,8  1620,2  2296,6                       (-*--)
K-SC   1217,2  1893,6  2570,1                        (--*-)
                             -------+---------+---------+---------+--
                                -2500         0      2500      5000
```

Group = K-13 subtracted from:

```
Group    Lower   Center   Upper  -------+---------+---------+---------+--
K-A      211,2    816,3  1421,3                   (-*--)
K-HU   -1636,1  -1031,1  -426,1            (--*-)
K-SC   -1362,7   -757,7  -152,7              (-*-)
                              -------+---------+---------+---------+--
                                 -2500         0      2500      5000
```

Group = K-A subtracted from:

```
Group    Lower   Center    Upper  -------+---------+---------+---------+--
K-HU   -2452,4  -1847,4  -1242,3         (--*-)
K-SC   -2178,9  -1573,9   -968,9          (--*-)
                               -------+---------+---------+---------+--
                                  -2500         0      2500      5000
```

Group = K-HU subtracted from:

```
Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-SC   -331,6   273,4  878,4                  (-*--)
                            -------+---------+---------+---------+--
                               -2500         0      2500      5000
```

One-way ANOVA: 1-Heptanol versus Group

```
Source  DF       SS      MS      F      P
Group    6  10284,0  1714,0  73,05  0,000
Error   14    328,5    23,5
Total   20  10612,5

S = 4,844   R-Sq = 96,90%   R-Sq(adj) = 95,58%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev   +---------+---------+---------+---------
E-A      3  108,91   7,31                                   (--*--)
E-Laff   3   45,08   4,01   (--*--)
E-LT-SC  3   58,23   5,21         (--*--)
K-13     3   88,44   3,81                       (--*--)
K-A      3   51,87   4,82      (--*--)
K-HU     3   48,14   3,31    (--*--)
K-SC     3   57,76   4,35         (--*--)
                           +---------+---------+---------+---------
                          40        60        80       100

Pooled StDev = 4,84


Grouping Information Using Tukey Method

Group    N     Mean  Grouping
E-A      3  108,914  A
K-13     3   88,444     B
E-LT-SC  3   58,229      C
K-SC     3   57,757      C
K-A      3   51,871      C
K-HU     3   48,142      C
E-Laff   3   45,080      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,58%


Group = E-A subtracted from:

Group      Lower   Center    Upper  --+---------+---------+---------+------
-
E-Laff   -77,342  -63,834  -50,326  (---*---)
E-LT-SC  -64,192  -50,685  -37,177      (---*--)
K-13     -33,978  -20,470   -6,962              (---*---)
```

```
K-A      -70,551  -57,043  -43,535    (---*---)
K-HU     -74,279  -60,771  -47,263   (---*--)
K-SC     -64,665  -51,157  -37,649      (--*---)
                                  --+---------+---------+---------+------
-
                                 -70       -35         0        35
```

Group = E-Laff subtracted from:

```
Group      Lower  Center   Upper  --+---------+---------+---------+-------
E-LT-SC   -0,358  13,149  26,657                      (---*---)
K-13      29,856  43,364  56,872                               (--*---)
K-A       -6,717   6,791  20,299                    (---*---)
K-HU     -10,445   3,063  16,570                   (---*---)
K-SC      -0,831  12,677  26,185                      (---*--)
                               --+---------+---------+---------+-------
                               -70       -35         0        35
```

Group = E-LT-SC subtracted from:

```
Group    Lower   Center   Upper  --+---------+---------+---------+-------
K-13    16,707   30,214  43,722                          (---*--)
K-A    -19,866   -6,359   7,149               (---*---)
K-HU   -23,595  -10,087   3,421              (---*---)
K-SC   -13,980   -0,472  13,035                 (---*---)
                            --+---------+---------+---------+-------
                            -70       -35         0        35
```

Group = K-13 subtracted from:

```
Group    Lower   Center    Upper  --+---------+---------+---------+-------
K-A    -50,081  -36,573  -23,065         (---*--)
K-HU   -53,809  -40,301  -26,793        (--*---)
K-SC   -44,195  -30,687  -17,179          (---*---)
                            --+---------+---------+---------+-------
                            -70       -35         0        35
```

Group = K-A subtracted from:

```
Group    Lower  Center   Upper  --+---------+---------+---------+-------
K-HU   -17,236  -3,728   9,780                  (---*---)
K-SC    -7,622   5,886  19,394                     (---*---)
                          --+---------+---------+---------+-------
                          -70       -35         0        35
```

Group = K-HU subtracted from:

```
Group   Lower  Center   Upper  --+---------+---------+---------+-------
K-SC   -3,894   9,614  23,122                     (---*---)
                         --+---------+---------+---------+-------
                         -70       -35         0        35
```

One-way ANOVA: (Z)-3-Hexene-1-ol versus Group

```
Source  DF      SS      MS      F      P
Group    5  9011,3  1802,3  90,54  0,000
Error   12   238,9    19,9
Total   17  9250,2

S = 4,462   R-Sq = 97,42%   R-Sq(adj) = 96,34%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  ---+---------+---------+---------+------
E-A     3  53,361  4,272             (-*--)
E-Laff  3  91,122  8,929                               (-*--)
K-13    3  32,996  1,982      (-*-)
K-A     3  45,120  2,686           (-*-)
K-HU    3  22,216  1,591  (-*-)
K-SC    3  32,644  2,791      (-*-)
                          ---+---------+---------+---------+------
                            25        50        75       100

Pooled StDev = 4,462


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-Laff  3  91,122  A
E-A     3  53,361    B
K-A     3  45,120    B C
K-13    3  32,996      C D
K-SC    3  32,644        D
K-HU    3  22,216        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:

Group     Lower   Center    Upper  ------+---------+---------+---------+---
E-Laff   25,525   37,761   49,997                        (--*-)
K-13    -32,600  -20,365   -8,129           (--*-)
K-A     -20,477   -8,241    3,995              (-*--)
K-HU    -43,381  -31,145  -18,910         (--*-)
K-SC    -32,953  -20,717   -8,482           (--*-)
                                  ------+---------+---------+---------+---
                                      -50         0        50       100


Group = E-Laff subtracted from:

Group    Lower   Center    Upper  ------+---------+---------+---------+---
```

```
K-13   -70,361  -58,125  -45,890    (-*--)
K-A    -58,238  -46,002  -33,766      (--*-)
K-HU   -81,142  -68,906  -56,670  (-*--)
K-SC   -70,714  -58,478  -46,242    (-*--)
                                 ------+---------+---------+---------+---
                                     -50         0        50       100
```

```
Group = K-13 subtracted from:

Group    Lower   Center   Upper  ------+---------+---------+---------+---
K-A     -0,112   12,124  24,359                (-*--)
K-HU   -23,017  -10,781   1,455            (--*-)
K-SC   -12,589   -0,353  11,883              (--*-)
                                 ------+---------+---------+---------+---
                                    -50         0        50       100
```

```
Group = K-A subtracted from:

Group    Lower   Center    Upper  ------+---------+---------+---------+---
K-HU   -35,140  -22,904  -10,669          (-*--)
K-SC   -24,712  -12,476   -0,240            (--*-)
                                 ------+---------+---------+---------+---
                                     -50         0        50       100
```

```
Group = K-HU subtracted from:

Group   Lower  Center   Upper  ------+---------+---------+---------+---
K-SC   -1,808  10,428  22,664                (-*--)
                               ------+---------+---------+---------+---
                                   -50         0        50       100
```

One-way ANOVA: (E)-3-Hexene-1-ol versus Group

```
Source  DF      SS     MS      F      P
Group    5  452,61  90,52  12,17  0,000
Error   12   89,26   7,44
Total   17  541,87

S = 2,727   R-Sq = 83,53%   R-Sq(adj) = 76,66%
```

```
                        Individual 95% CIs For Mean Based on
                        Pooled StDev
Level   N    Mean  StDev  ---+---------+---------+---------+------
E-A     3  34,834  3,275                (-----*-----)
E-Laff  3  34,934  3,112                 (----*-----)
K-13    3  37,915  2,796                     (-----*-----)
K-A     3  39,994  3,174                         (-----*----)
K-HU    3  25,418  0,657  (----*-----)
K-SC    3  40,238  2,429                         (-----*-----)
                        ---+---------+---------+---------+------
                        24,0      30,0      36,0      42,0

Pooled StDev = 2,727
```

Grouping Information Using Tukey Method

Group	N	Mean	Grouping
K-SC	3	40,238	A
K-A	3	39,994	A
K-13	3	37,915	A
E-Laff	3	34,934	A
E-A	3	34,834	A
K-HU	3	25,418	B

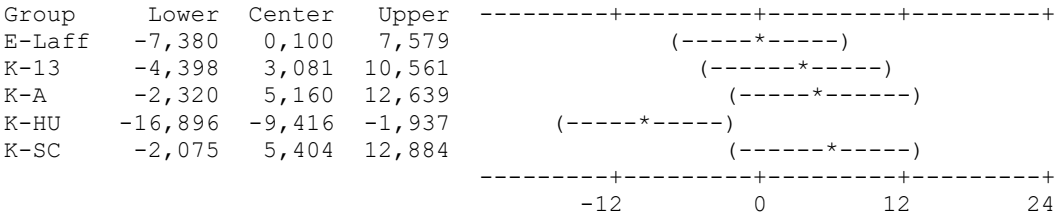
Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%

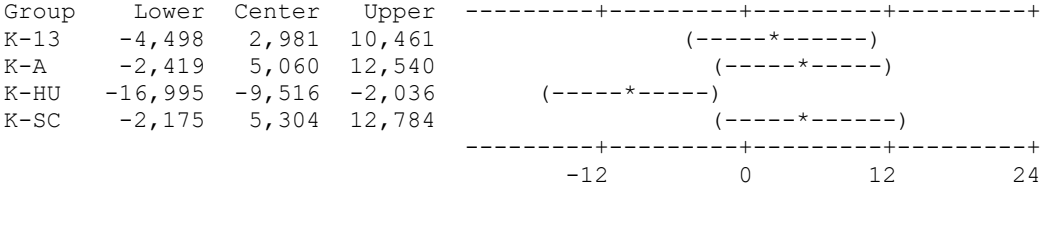
Group = E-A subtracted from:

Group	Lower	Center	Upper
E-Laff	-7,380	0,100	7,579
K-13	-4,398	3,081	10,561
K-A	-2,320	5,160	12,639
K-HU	-16,896	-9,416	-1,937
K-SC	-2,075	5,404	12,884



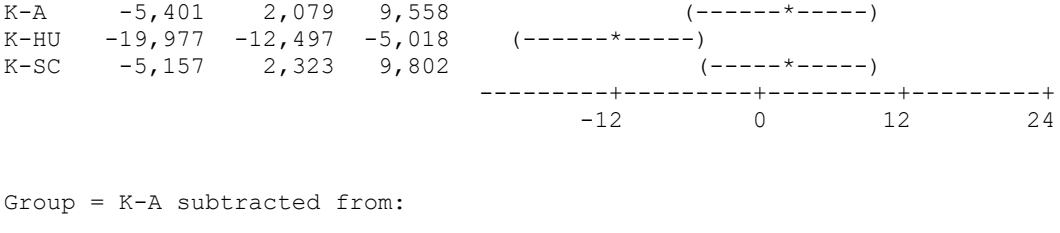
Group = E-Laff subtracted from:

Group	Lower	Center	Upper
K-13	-4,498	2,981	10,461
K-A	-2,419	5,060	12,540
K-HU	-16,995	-9,516	-2,036
K-SC	-2,175	5,304	12,784



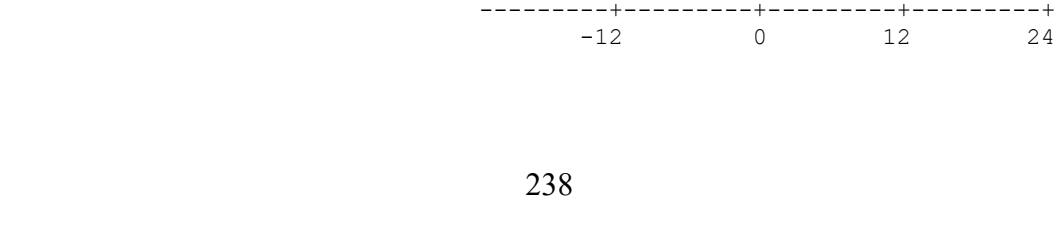
Group = K-13 subtracted from:

Group	Lower	Center	Upper
K-A	-5,401	2,079	9,558
K-HU	-19,977	-12,497	-5,018
K-SC	-5,157	2,323	9,802



Group = K-A subtracted from:

Group	Lower	Center	Upper
K-HU	-22,056	-14,576	-7,096
K-SC	-7,235	0,244	7,724



```
Group = K-HU subtracted from:

Group  Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   7,341  14,820  22,300                          (-----*------)
                             ---------+---------+---------+---------+
                                    -12         0        12        24
```

One-way ANOVA: 2-(Methylthio)ethanol versus Group

```
Source  DF      SS      MS      F      P
Group    7  7339,7  1048,5  55,14  0,000
Error   15   285,3    19,0
Total   22  7625,0

S = 4,361   R-Sq = 96,26%   R-Sq(adj) = 94,51%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N   Mean  StDev  ---+---------+---------+---------+------
E-A      3  40,93   4,26   (-*--)
E-Laff   3  39,79   2,30  (--*--)
E-LT-SC  2  63,78   3,58              (--*--)
E-SC     3  46,87   2,66      (-*--)
K-13     3  75,72   2,39                    (--*--)
K-A      3  62,38   2,90              (-*--)
K-HU     3  94,76   7,14                                (-*--)
K-SC     3  66,59   6,37                (-*--)
                          ---+---------+---------+---------+------
                            40        60        80       100

Pooled StDev = 4,36


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-HU     3  94,764  A
K-13     3  75,723    B
K-SC     3  66,589    B C
E-LT-SC  2  63,784    B C
K-A      3  62,381      C
E-SC     3  46,870        D
E-A      3  40,934        D
E-Laff   3  39,795        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:
```

```
Group      Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff   -13,578  -1,140  11,298                (---*--)
E-LT-SC    8,944  22,849  36,755                       (---*---)
E-SC      -6,503   5,935  18,373                  (---*--)
K-13      22,351  34,789  47,227                          (---*--)
K-A        9,009  21,447  33,885                     (--*---)
K-HU      41,392  53,830  66,267                              (--*---)
K-SC      13,217  25,654  38,092                      (--*---)
                                  ---------+---------+---------+---------+
                                         -35         0        35        70
```

Group = E-Laff subtracted from:

```
Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-LT-SC  10,083  23,989  37,895                    (---*---)
E-SC     -5,363   7,075  19,513                 (---*---)
K-13     23,491  35,929  48,367                      (--*---)
K-A      10,149  22,587  35,025                   (--*---)
K-HU     42,532  54,969  67,407                            (---*--)
K-SC     14,356  26,794  39,232                    (---*--)
                                  ---------+---------+---------+---------+
                                         -35         0        35        70
```

Group = E-LT-SC subtracted from:

```
Group    Lower   Center   Upper  ---------+---------+---------+---------+
E-SC   -30,820  -16,914  -3,008          (---*---)
K-13    -1,966   11,939  25,845                  (---*---)
K-A    -15,308   -1,402  12,503                (---*---)
K-HU    17,074   30,980  44,886                        (---*---)
K-SC   -11,101    2,805  16,711                 (---*---)
                                  ---------+---------+---------+---------+
                                         -35         0        35        70
```

Group = E-SC subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-13   16,416  28,854  41,291                     (--*---)
K-A     3,074  15,512  27,950                  (--*---)
K-HU   35,457  47,894  60,332                          (---*--)
K-SC    7,281  19,719  32,157                   (---*--)
                               ---------+---------+---------+---------+
                                      -35         0        35        70
```

Group = K-13 subtracted from:

```
Group    Lower   Center   Upper  ---------+---------+---------+---------+
K-A    -25,780  -13,342  -0,904            (--*---)
K-HU     6,603   19,041  31,478                    (--*---)
K-SC   -21,572   -9,135   3,303             (--*---)
                                  ---------+---------+---------+---------+
                                         -35         0        35        70
```

Group = K-A subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-HU   19,945  32,383  44,820                          (--*---)
K-SC   -8,230   4,207  16,645                 (--*---)
                              ---------+---------+---------+---------+
                                     -35         0        35        70


Group = K-HU subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-SC   -40,613  -28,175  -15,737         (---*---)
                                ---------+---------+---------+---------+
                                       -35         0        35        70
```

One-way ANOVA: 1,2-Propanediol versus Group

```
Source  DF      SS      MS      F      P
Group    5  7317,8  1463,6  60,34  0,000
Error   12   291,1    24,3
Total   17  7608,9

S = 4,925   R-Sq = 96,17%   R-Sq(adj) = 94,58%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev   +---------+---------+---------+---------
E-A     3   46,65   2,41   (--*--)
E-Laff  3   53,22   3,61       (--*--)
K-13    3   77,45   6,88                  (--*--)
K-A     3  103,08   5,39                              (---*--)
K-HU    3   54,70   3,13       (--*--)
K-SC    3   85,13   6,37                    (---*--)
                           +---------+---------+---------+---------
                          40        60        80       100

Pooled StDev = 4,93


Grouping Information Using Tukey Method

Group   N     Mean  Grouping
K-A     3  103,077  A
K-SC    3   85,129    B
K-13    3   77,447    B
K-HU    3   54,702      C
E-Laff  3   53,216      C
E-A     3   46,652      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%
```

```
Group = E-A subtracted from:

Group    Lower  Center   Upper  --------+---------+---------+---------+-
E-Laff  -6,942   6,564  20,071                  (---*---)
K-13    17,288  30,795  44,302                         (---*---)
K-A     42,918  56,425  69,931                                (---*---)
K-HU    -5,456   8,050  21,557                  (---*---)
K-SC    24,971  38,478  51,984                           (---*---)
                                --------+---------+---------+---------+-
                                      -35         0        35        70


Group = E-Laff subtracted from:

Group    Lower  Center   Upper  --------+---------+---------+---------+-
K-13    10,724  24,231  37,737                       (---*---)
K-A     36,354  49,860  63,367                              (---*---)
K-HU   -12,021   1,486  14,993                 (--*---)
K-SC    18,407  31,913  45,420                         (---*---)
                                --------+---------+---------+---------+-
                                      -35         0        35        70


Group = K-13 subtracted from:

Group    Lower   Center   Upper  --------+---------+---------+---------+-
K-A     12,123   25,630  39,136                       (---*---)
K-HU   -36,251  -22,745  -9,238          (---*--)
K-SC    -5,824    7,683  21,189                  (---*---)
                               --------+---------+---------+---------+-
                                     -35         0        35        70


Group = K-A subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-HU   -61,881  -48,374  -34,868  (---*---)
K-SC   -31,454  -17,947   -4,441           (---*---)
                              --------+---------+---------+---------+-
                                    -35         0        35        70


Group = K-HU subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-SC   16,921  30,427  43,934                       (---*---)
                           --------+---------+---------+---------+-
                                 -35         0        35        70
```

One-way ANOVA: 3-Penten-2-ol versus Group

```
Source  DF       SS      MS       F      P
Group    7  1722234  246033  731,52  0,000
Error   15     5045     336
Total   22  1727278

S = 18,34   R-Sq = 99,71%   R-Sq(adj) = 99,57%
```

```
                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---------+---------+---------+---------+
E-A      3  130,83  12,48     (*)
E-Laff   3  298,34  28,67            (*)
E-LT-SC  3  938,13  37,06                                      (*)
E-SC     2  311,43   6,10            (*-)
K-13     3   78,97   3,13   (*)
K-A      3  266,98   7,10           (*)
K-HU     3   52,15   3,90  (*)
K-SC     3  120,11   8,78     (*)
                          ---------+---------+---------+---------+
                                 250       500       750      1000

Pooled StDev = 18,34


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  938,13  A
E-SC     2  311,43    B
E-Laff   3  298,34    B
K-A      3  266,98    B
E-A      3  130,83      C
K-SC     3  120,11      C
K-13     3   78,97      C D
K-HU     3   52,15        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group      Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff    115,21  167,51  219,82                      (*)
E-LT-SC   755,00  807,31  859,61                                   (*)
E-SC      122,12  180,60  239,08                      (-*)
K-13     -104,16  -51,86    0,45                  (*)
K-A        83,85  136,15  188,46                      (*)
K-HU     -130,99  -78,68  -26,37                 (*)
K-SC      -63,03  -10,72   41,59                   (*)
                          ---------+---------+---------+---------+
                               -500         0       500      1000


Group = E-Laff subtracted from:

Group      Lower   Center    Upper  ---------+---------+---------+---------
+
E-LT-SC   587,49   639,79   692,10                                   (*)
E-SC      -45,39    13,09    71,57                    (*)
K-13     -271,67  -219,37  -167,06               (*)
```

```
K-A       -83,67   -31,36    20,94                    (*)
K-HU     -298,50  -246,19  -193,89                (*)
K-SC     -230,54  -178,23  -125,93                 (*)
                                     ---------+---------+---------+---------
+
                                           -500         0       500
1000
```

Group = E-LT-SC subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
E-SC   -685,19  -626,71  -568,23       (*-)
K-13   -911,47  -859,16  -806,86   (*)
K-A    -723,46  -671,16  -618,85       (*)
K-HU   -938,29  -885,99  -833,68  (*)
K-SC   -870,33  -818,03  -765,72    (*)
                                  ---------+---------+---------+---------+
                                        -500         0       500      1000
```

Group = E-SC subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-13   -290,93  -232,45  -173,97               (*-)
K-A    -102,93   -44,45    14,03                   (*)
K-HU   -317,76  -259,28  -200,80               (*)
K-SC   -249,80  -191,32  -132,84                (*)
                                  ---------+---------+---------+---------+
                                        -500         0       500      1000
```

Group = K-13 subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-A    135,70  188,01  240,31                      (*)
K-HU   -79,13  -26,82   25,48                   (*-)
K-SC   -11,17   41,14   93,44                     (*)
                            ---------+---------+---------+---------+
                                  -500         0       500      1000
```

Group = K-A subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-HU   -267,14  -214,83  -162,52               (*)
K-SC   -199,18  -146,87   -94,57                (*)
                                  ---------+---------+---------+---------+
                                        -500         0       500      1000
```

Group = K-HU subtracted from:

```
Group  Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   15,65   67,96  120,27                    (*)
                            ---------+---------+---------+---------+
                                  -500         0       500      1000
```

One-way ANOVA: 2-Hexanol versus Group

```
Source  DF        SS       MS       F      P
Group    7  148534,5  21219,2  466,16  0,000
Error   16     728,3     45,5
Total   23  149262,8

S = 6,747   R-Sq = 99,51%   R-Sq(adj) = 99,30%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ------+---------+---------+---------+---
E-A      3  108,77   6,06              (*-)
E-Laff   3  100,90   3,36            (-*)
E-LT-SC  3  228,55   8,52                                  (*)
E-SC     3  244,79  13,11                                    (-*)
K-13     3   60,07   5,92       (*)
K-A      3   33,78   2,94  (-*)
K-HU     3   32,84   2,80  (*-)
K-SC     3   55,45   4,47      (*-)
                          ------+---------+---------+---------+---
                               60       120       180       240

Pooled StDev = 6,75


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-SC     3  244,79  A
E-LT-SC  3  228,55  A
E-A      3  108,77    B
E-Laff   3  100,90    B
K-13     3   60,07      C
K-SC     3   55,45      C
K-A      3   33,78        D
K-HU     3   32,84        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff   -26,95   -7,86   11,22                  (*-)
E-LT-SC  100,70  119,78  138,87                          (-*-)
E-SC     116,93  136,02  155,11                            (*-)
K-13     -67,79  -48,70  -29,61             (-*-)
K-A      -94,08  -74,99  -55,91           (-*)
K-HU     -95,01  -75,92  -56,84           (-*)
K-SC     -72,41  -53,32  -34,23             (-*)
                         ---------+---------+---------+---------+
```

```
                                    -120         0       120       240
```

Group = E-Laff subtracted from:

```
Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-LT-SC  108,56  127,65  146,74                              (-*)
E-SC     124,80  143,88  162,97                               (-*-)
K-13     -59,92  -40,84  -21,75               (-*)
K-A      -86,22  -67,13  -48,04             (*-)
K-HU     -87,15  -68,06  -48,97             (*-)
K-SC     -64,54  -45,46  -26,37               (*-)
                                 ---------+---------+---------+---------+
                                       -120         0       120       240
```

Group = E-LT-SC subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
E-SC     -2,85    16,23    35,32                     (*-)
K-13   -187,57  -168,49  -149,40     (-*-)
K-A    -213,86  -194,78  -175,69   (-*)
K-HU   -214,80  -195,71  -176,62   (-*)
K-SC   -192,19  -173,10  -154,02     (-*)
                                  ---------+---------+---------+---------+
                                        -120         0       120       240
```

Group = E-SC subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-13   -203,81  -184,72  -165,63    (-*)
K-A    -230,10  -211,01  -191,93  (*-)
K-HU   -231,03  -211,94  -192,86  (*-)
K-SC   -208,42  -189,34  -170,25    (*-)
                                  ---------+---------+---------+---------+
                                        -120         0       120       240
```

Group = K-13 subtracted from:

```
Group   Lower  Center  Upper  ---------+---------+---------+---------+
K-A    -45,38  -26,29  -7,21               (-*)
K-HU   -46,31  -27,22  -8,14               (-*)
K-SC   -23,70   -4,62  14,47                 (-*)
                             ---------+---------+---------+---------+
                                   -120         0       120       240
```

Group = K-A subtracted from:

```
Group   Lower  Center  Upper  ---------+---------+---------+---------+
K-HU   -20,02   -0,93  18,16                 (-*-)
K-SC     2,59   21,67  40,76                   (-*)
                             ---------+---------+---------+---------+
                                   -120         0       120       240
```

Group = K-HU subtracted from:

```
Group  Lower  Center  Upper  ---------+---------+---------+---------+
K-SC    3,52   22,60  41,69                    (-*)
                             ---------+---------+---------+---------+
                                   -120         0       120       240
```

One-way ANOVA: 1-Hexanol versus Group

```
Source  DF    SS   MS     F      P
Group    1   934  934  9,12  0,094
Error    2   205  102
Total    3  1139

S = 10,12   R-Sq = 82,01%   R-Sq(adj) = 73,01%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --------+---------+---------+---------+-
E-LT-SC  2  191,67   3,30             (------------*-----------)
E-SC     2  161,11  13,93  (-----------*------------)
                          --------+---------+---------+---------+-
                                150       175       200       225

Pooled StDev = 10,12


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  2  191,67  A
E-SC     2  161,11  A

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-LT-SC subtracted from:

Group   Lower  Center  Upper  -----+---------+---------+---------+----
E-SC   -74,10  -30,56  12,99  (--------------*-------------)
                              -----+---------+---------+---------+----
                                 -60       -30         0        30
```

One-way ANOVA: 3-Hexanol versus Group

```
Source  DF        SS        MS        F      P
Group    1  1329,547  1329,547  1348,79  0,000
Error    4     3,943     0,986
Total    5  1333,490

S = 0,9928   R-Sq = 99,70%   R-Sq(adj) = 99,63%
```

```
                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  ---------+---------+---------+---------+
E-A     3  22,146  1,056  (*-)
E-Laff  3  51,917  0,925                            (-*-)
                          ---------+---------+---------+---------+
                                  30        40        50        60

Pooled StDev = 0,993


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-Laff  3  51,917  A
E-A     3  22,146    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group    Lower  Center   Upper  --+---------+---------+---------+-------
E-Laff  27,521  29,772  32,023                              (-*-)
                             --+---------+---------+---------+-------
                               0        10        20        30
```

One-way ANOVA: 2-Phenoxyethanol versus Group

```
Source  DF      SS      MS       F      P
Group    1  215,79  215,79  102,76  0,001
Error    4    8,40    2,10
Total    5  224,19

S = 1,449   R-Sq = 96,25%   R-Sq(adj) = 95,32%


                          Individual 95% CIs For Mean Based on Pooled StDev
Level   N    Mean  StDev     +---------+---------+---------+---------
E-A     3  34,423  1,381                            (----*---)
E-Laff  3  22,429  1,514     (----*----)
                             +---------+---------+---------+---------
                          20,0      25,0      30,0      35,0

Pooled StDev = 1,449


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-A     3  34,423  A
```

```
E-Laff  3  22,429    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group     Lower   Center   Upper     -+---------+---------+---------+------
--
E-Laff  -15,279  -11,994  -8,709     (------*------)
                                     -+---------+---------+---------+------
--
                                  -15,0     -10,0      -5,0       0,0
```

One-way ANOVA: Isoamyl acetate versus Group

```
Source  DF        SS       MS       F      P
Group    7  11292154  1613165  232,09  0,000
Error   16    111208     6951
Total   23  11403362

S = 83,37   R-Sq = 99,02%   R-Sq(adj) = 98,60%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  -----+---------+---------+---------+----
E-A      3   460,7   21,0  (-*)
E-Laff   3  1410,1   25,9               (*-)
E-LT-SC  3  2750,0   87,2                                   (*-)
E-SC     3  1768,5   42,6                     (*-)
K-13     3  1743,3   80,6                    (-*)
K-A      3   807,9   59,8       (-*)
K-HU     3  1452,2    9,8               (-*)
K-SC     3  2242,3  186,8                          (*)
                          -----+---------+---------+---------+----
                             700      1400      2100      2800

Pooled StDev = 83,4


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  2750,0  A
K-SC     3  2242,3    B
E-SC     3  1768,5      C
K-13     3  1743,3      C
K-HU     3  1452,2        D
E-Laff   3  1410,1        D
K-A      3   807,9          E
E-A      3   460,7            F
```

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%

Group = E-A subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
E-Laff	713,6	949,4	1185,3	(-*-)
E-LT-SC	2053,5	2289,3	2525,2	(-*-)
E-SC	1072,0	1307,9	1543,7	(-*-)
K-13	1046,8	1282,7	1518,5	(-*-)
K-A	111,4	347,2	583,1	(-*-)
K-HU	755,6	991,5	1227,4	(-*-)
K-SC	1545,8	1781,6	2017,5	(-*-)
				--------+---------+---------+---------+-
				-1200 0 1200 2400

Group = E-Laff subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
E-LT-SC	1104,0	1339,9	1575,7	(-*-)
E-SC	122,6	358,4	594,3	(-*-)
K-13	97,4	333,2	569,1	(-*-)
K-A	-838,1	-602,2	-366,4	(-*-)
K-HU	-193,8	42,0	277,9	(-*-)
K-SC	596,3	832,2	1068,1	(-*-)
				--------+---------+---------+---------+-
				-1200 0 1200 2400

Group = E-LT-SC subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
E-SC	-1217,3	-981,5	-745,6	(-*-)
K-13	-1242,5	-1006,7	-770,8	(-*-)
K-A	-2178,0	-1942,1	-1706,3	(-*-)
K-HU	-1533,7	-1297,8	-1062,0	(-*-)
K-SC	-743,5	-507,7	-271,8	(-*-)
				--------+---------+---------+---------+-
				-1200 0 1200 2400

Group = E-SC subtracted from:

Group	Lower	Center	Upper	--------+---------+---------+---------+-
K-13	-261,1	-25,2	210,7	(-*-)
K-A	-1196,5	-960,7	-724,8	(-*-)
K-HU	-552,2	-316,4	-80,5	(-*-)
K-SC	237,9	473,8	709,6	(-*-)
				--------+---------+---------+---------+-
				-1200 0 1200 2400

```
Group = K-13 subtracted from:

Group    Lower  Center   Upper  --------+---------+---------+---------+-
K-A    -1171,3  -935,5  -699,6          (-*-)
K-HU    -527,0  -291,2   -55,3                (-*-)
K-SC     263,1   499,0   734,8                      (-*-)
                                --------+---------+---------+---------+-
                                    -1200         0      1200      2400


Group = K-A subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-HU    408,4   644,3   880,1                      (-*-)
K-SC   1198,6  1434,4  1670,3                             (-*-)
                               --------+---------+---------+---------+-
                                   -1200         0      1200      2400


Group = K-HU subtracted from:

Group  Lower  Center   Upper  --------+---------+---------+---------+-
K-SC   554,3   790,1  1026,0                       (-*-)
                              --------+---------+---------+---------+-
                                  -1200         0      1200      2400
```

One-way ANOVA: Isopropyl acetate versus Group

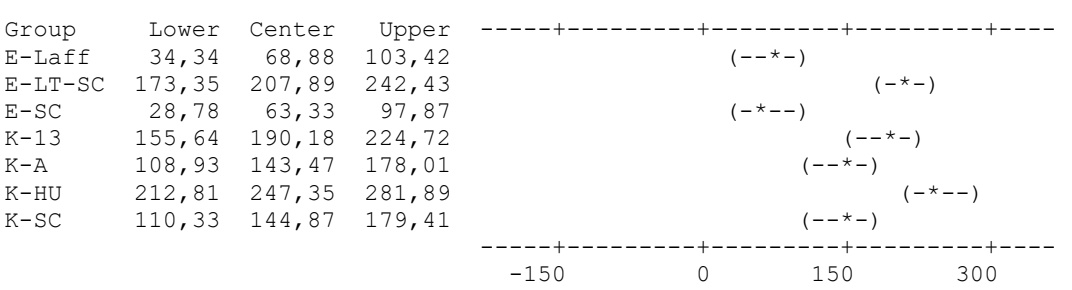
```
Source  DF    SS    MS     F      P
Group    1   2,6   2,6  0,11  0,757
Error    4  94,2  23,6
Total    5  96,8

S = 4,853   R-Sq = 2,66%   R-Sq(adj) = 0,00%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  ------+---------+---------+---------+---
E-A     3  70,878  2,376    (---------------*--------------)
E-Laff  3  69,567  6,439  (---------------*---------------)
                          ------+---------+---------+---------+---
                             65,0      70,0      75,0      80,0

Pooled StDev = 4,853


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-A     3  70,878  A
E-Laff  3  69,567  A

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group
```

```
Individual confidence level = 95,00%


Group = E-A subtracted from:

Group     Lower  Center  Upper     -+---------+---------+---------+--------
E-Laff  -12,314  -1,311  9,691     (------------------*-----------------)
                                   -+---------+---------+---------+--------
                                -12,0      -6,0       0,0       6,0
```

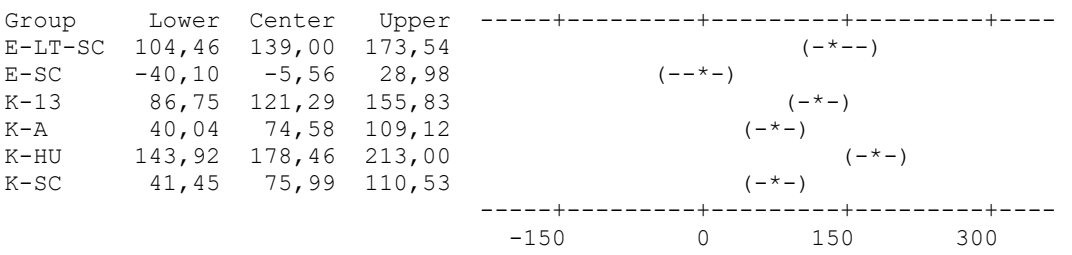
One-way ANOVA: Phenethyl acetate versus Group

```
Source  DF      SS     MS       F      P
Group    7  146571  20939  140,46  0,000
Error   16    2385    149
Total   23  148956

S = 12,21   R-Sq = 98,40%   R-Sq(adj) = 97,70%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev   +---------+---------+---------+---------
E-A      3   82,99   7,38   (-*-)
E-Laff   3  151,88  14,80             (-*-)
E-LT-SC  3  290,88  11,20                                (--*-)
E-SC     3  146,32   4,04             (-*-)
K-13     3  273,17   2,36                                (-*-)
K-A      3  226,46  14,21                           (-*-)
K-HU     3  330,34   7,51                                      (-*-)
K-SC     3  227,86  22,65                           (--*-)
                           +---------+---------+---------+---------
                          70        140       210       280

Pooled StDev = 12,21


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-HU     3  330,34  A
E-LT-SC  3  290,88    B
K-13     3  273,17    B
K-SC     3  227,86      C
K-A      3  226,46      C
E-Laff   3  151,88        D
E-SC     3  146,32        D
E-A      3   82,99          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%
```

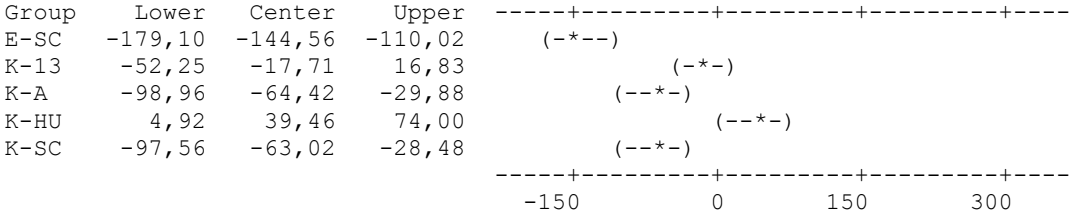
Group = E-A subtracted from:



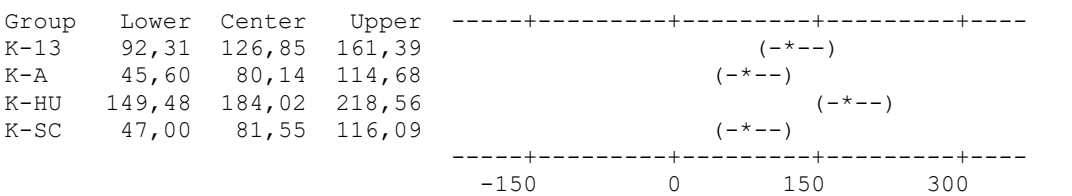
Group = E-Laff subtracted from:



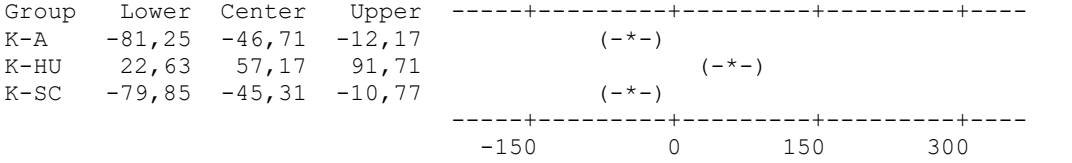
Group = E-LT-SC subtracted from:



Group = E-SC subtracted from:



Group = K-13 subtracted from:



```
Group = K-A subtracted from:

Group   Lower  Center   Upper  -----+---------+---------+---------+----
K-HU    69,34  103,88  138,42                      (-*-)
K-SC   -33,14    1,40   35,94               (-*-)
                            -----+---------+---------+---------+----
                              -150         0       150       300


Group = K-HU subtracted from:

Group    Lower   Center   Upper  -----+---------+---------+---------+----
K-SC   -137,02  -102,48  -67,94        (-*-)
                                -----+---------+---------+---------+----
                                  -150         0       150       300
```

One-way ANOVA: Propyl acetate versus Group

```
Source  DF     SS     MS     F      P
Group    1  206,3  206,3  9,47  0,037
Error    4   87,2   21,8
Total    5  293,4

S = 4,668   R-Sq = 70,30%   R-Sq(adj) = 62,87%


                          Individual 95% CIs For Mean Based on Pooled StDev
Level   N    Mean  StDev    -+---------+---------+---------+--------
E-A     3  53,629  5,532                    (----------*---------)
E-Laff  3  41,902  3,603    (----------*----------)
                            -+---------+---------+---------+--------
                          35,0      42,0      49,0      56,0

Pooled StDev = 4,668


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-A     3  53,629  A
E-Laff  3  41,902    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group     Lower   Center   Upper  --+---------+---------+---------+-------
E-Laff  -22,309  -11,727  -1,144  (---------*----------)
                                  --+---------+---------+---------+-------
                                  -20       -10         0        10
```

One-way ANOVA: Ethyl lactate versus Group

```
Source  DF       SS       MS       F      P
Group    7  7366342  1052335  423,53  0,000
Error   16    39754     2485
Total   23  7406097

S = 49,85   R-Sq = 99,46%   R-Sq(adj) = 99,23%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  -------+---------+---------+---------+--
E-A      3   218,8   21,5  (*-)
E-Laff   3   202,8   19,9  (*)
E-LT-SC  3   565,1   18,2         (*-)
E-SC     3   485,5   24,1       (-*)
K-13     3   611,2   19,3          (*)
K-A      3  2059,5  125,8                                      (*)
K-HU     3   694,0   14,7             (*)
K-SC     3   436,3   41,3       (*)
                          -------+---------+---------+---------+--
                               500      1000      1500      2000

Pooled StDev = 49,8


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  2059,5  A
K-HU     3   694,0    B
K-13     3   611,2    B C
E-LT-SC  3   565,1    B C D
E-SC     3   485,5      C D
K-SC     3   436,3        D
E-A      3   218,8          E
E-Laff   3   202,8          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper      +---------+---------+---------+-------
--
E-Laff   -157,0   -16,0   125,0                         (-*)
E-LT-SC   205,4   346,4   487,4                             (*-)
E-SC      125,8   266,8   407,8                           (-*)
```

```
K-13      251,5   392,5   533,5                            (*)
K-A      1699,8  1840,8  1981,8
(*-)
K-HU      334,2   475,2   616,2                            (-*)
K-SC       76,5   217,5   358,5                          (*-)
                                  +---------+---------+---------+-------
--
                                -2000     -1000         0      1000
```

```
Group = E-Laff subtracted from:

Group     Lower  Center   Upper      +---------+---------+---------+-------
--
E-LT-SC   221,4   362,4   503,4                            (-*)
E-SC      141,7   282,8   423,8                           (-*)
K-13      267,4   408,5   549,5                             (*)
K-A      1715,7  1856,8  1997,8
(-*)
K-HU      350,2   491,2   632,2                              (*)
K-SC       92,5   233,5   374,5                           (*-)
                                  +---------+---------+---------+-------
--
                                -2000     -1000         0      1000
```

```
Group = E-LT-SC subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
E-SC   -220,6   -79,6    61,4                       (*-)
K-13    -94,9    46,1   187,1                        (*-)
K-A    1353,4  1494,4  1635,4                                      (*)
K-HU    -12,2   128,8   269,8                         (*-)
K-SC   -269,9  -128,9    12,2                      (-*)
                              +---------+---------+---------+---------
                            -2000     -1000         0      1000
```

```
Group = E-SC subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
K-13    -15,3   125,7   266,7                        (*-)
K-A    1433,0  1574,0  1715,0                                     (-*)
K-HU     67,4   208,4   349,4                          (*)
K-SC   -190,3   -49,2    91,8                       (-*)
                              +---------+---------+---------+---------
                            -2000     -1000         0      1000
```

```
Group = K-13 subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
K-A    1307,3  1448,3  1589,3                                    (*-)
K-HU    -58,3    82,7   223,7                         (-*)
K-SC   -316,0  -174,9   -33,9                       (*-)
                              +---------+---------+---------+---------
                            -2000     -1000         0      1000
```

```
Group = K-A subtracted from:
```

```
Group    Lower   Center    Upper      +---------+---------+---------+------
---
K-HU   -1506,6  -1365,6  -1224,6           (*-)
K-SC   -1764,3  -1623,2  -1482,2         (-*)
                                   +---------+---------+---------+------
---
                                -2000     -1000         0      1000


Group = K-HU subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
K-SC   -398,7  -257,7  -116,7                    (*-)
                                  +---------+---------+---------+---------
                               -2000     -1000         0      1000
```

One-way ANOVA: Ethyl octanoate versus Group

```
Source  DF      SS     MS       F      P
Group    7  201252  28750  257,45  0,000
Error   14    1563    112
Total   21  202815

S = 10,57   R-Sq = 99,23%   R-Sq(adj) = 98,84%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---+---------+---------+---------+------
E-A      3  178,13  13,64            (*)
E-Laff   3  256,35  12,38                   (-*)
E-LT-SC  2  338,60   7,76                           (-*)
E-SC     2  409,85   1,13                                   (-*-)
K-13     3  133,47   6,96       (*-)
K-A      3  150,67   6,74         (*)
K-HU     3   81,48  12,96  (*)
K-SC     3  229,78  12,24                 (*)
                          ---+---------+---------+---------+------
                           100       200       300       400

Pooled StDev = 10,57


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-SC     2  409,85  A
E-LT-SC  2  338,60    B
E-Laff   3  256,35      C
K-SC     3  229,78      C
E-A      3  178,13        D
K-A      3  150,67        D E
K-13     3  133,47          E
K-HU     3   81,48            F

Means that do not share a letter are significantly different.
```

```
Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group      Lower  Center   Upper  --------+---------+---------+---------+-
E-Laff     47,77   78,22  108,66                      (-*)
E-LT-SC   126,43  160,47  194,51                          (-*-)
E-SC      197,68  231,72  265,76                              (-*)
K-13      -75,11  -44,66  -14,22              (-*)
K-A       -57,90  -27,46    2,99              (-*)
K-HU     -127,09  -96,65  -66,20            (*-)
K-SC       21,21   51,65   82,10                    (-*)
                                --------+---------+---------+---------+-
                                     -200         0       200       400


Group = E-Laff subtracted from:

Group      Lower   Center    Upper  --------+---------+---------+---------
+-
E-LT-SC    48,21    82,25   116,29                       (-*-)
E-SC      119,47   153,51   187,54                           (-*)
K-13     -153,32  -122,88   -92,43            (-*)
K-A      -136,12  -105,67   -75,23            (-*)
K-HU     -205,31  -174,86  -144,42          (*-)
K-SC      -57,01   -26,56     3,88                 (-*)
                                  --------+---------+---------+---------
+-
                                       -200         0       200       400


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
E-SC     33,97    71,25   108,54                      (-*)
K-13   -239,17  -205,13  -171,09        (-*)
K-A    -221,97  -187,93  -153,89         (-*)
K-HU   -291,15  -257,12  -223,08     (-*-)
K-SC   -142,85  -108,81   -74,78             (-*)
                                --------+---------+---------+---------+-
                                     -200         0       200       400


Group = E-SC subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-13   -310,42  -276,38  -242,35    (-*-)
K-A    -293,22  -259,18  -225,14     (-*-)
K-HU   -362,41  -328,37  -294,33  (-*)
K-SC   -214,11  -180,07  -146,03         (-*-)
                                --------+---------+---------+---------+-
                                     -200         0       200       400


Group = K-13 subtracted from:
```

```
Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-A    -13,24   17,20   47,65                  (-*)
K-HU   -82,43  -51,98  -21,54              (*-)
K-SC    65,87   96,32  126,76                     (-*)
                           --------+---------+---------+---------+-
                                -200         0       200       400


Group = K-A subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-HU   -99,63  -69,19  -38,74             (-*)
K-SC    48,67   79,11  109,56                    (-*)
                           --------+---------+---------+---------+-
                                -200         0       200       400


Group = K-HU subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-SC   117,86  148,30  178,75                         (*-)
                           --------+---------+---------+---------+-
                                -200         0       200       400
```

One-way ANOVA: Ethyl-3-hydroxybutyrate versus Group

```
Source  DF      SS     MS      F      P
Group    7  103220  14746  67,09  0,000
Error   16    3517    220
Total   23  106737

S = 14,83   R-Sq = 96,71%   R-Sq(adj) = 95,26%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ------+---------+---------+---------+---
E-A      3   90,16   7,27  (---*---)
E-Laff   3   86,90   5,75  (--*---)
E-LT-SC  3  182,24  15,36                   (--*---)
E-SC     3   96,76   8,53    (--*---)
K-13     3  206,56  18,13                        (--*---)
K-A      3  245,64  24,47                               (---*---)
K-HU     3  249,24   8,90                                (---*--)
K-SC     3  218,02  18,90                             (---*--)
                          ------+---------+---------+---------+---
                              100       150       200       250

Pooled StDev = 14,83


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-HU     3  249,24  A
K-A      3  245,64  A B
K-SC     3  218,02  A B C
```

```
K-13     3  206,56    B C
E-LT-SC  3  182,24      C
E-SC     3   96,76        D
E-A      3   90,16        D
E-Laff   3   86,90        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-Laff   -45,20   -3,26   38,68              (---*--)
E-LT-SC   50,14   92,08  134,03                      (---*--)
E-SC     -35,34    6,60   48,54               (---*--)
K-13      74,46  116,40  158,34                        (---*--)
K-A      113,54  155,48  197,42                           (---*--)
K-HU     117,13  159,08  201,02                            (--*---)
K-SC      85,91  127,86  169,80                         (---*--)
                                -------+---------+---------+---------+--
                                    -120         0       120       240


Group = E-Laff subtracted from:

Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-LT-SC   53,40   95,34  137,29                      (---*--)
E-SC     -32,08    9,86   51,80               (---*--)
K-13      77,72  119,66  161,61                        (---*--)
K-A      116,80  158,74  200,68                            (--*---)
K-HU     120,39  162,34  204,28                            (---*--)
K-SC      89,17  131,12  173,06                         (---*--)
                                -------+---------+---------+---------+--
                                    -120         0       120       240


Group = E-LT-SC subtracted from:

Group    Lower  Center   Upper  -------+---------+---------+---------+--
E-SC   -127,43  -85,49  -43,54       (---*--)
K-13    -17,62   24,32   66,26                 (--*---)
K-A      21,45   63,40  105,34                    (--*---)
K-HU     25,05   66,99  108,93                    (---*--)
K-SC     -6,17   35,77   77,71                 (---*--)
                               -------+---------+---------+---------+--
                                   -120         0       120       240


Group = E-SC subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-13    67,86  109,81  151,75                       (--*---)
K-A    106,94  148,88  190,83                          (--*---)
K-HU   110,54  152,48  194,42                          (---*--)
```

```
K-SC    79,32  121,26  163,20                          (--*---)
                                  -------+---------+---------+---------+--
                                      -120         0       120       240


Group = K-13 subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-A     -2,86   39,08  81,02                  (--*---)
K-HU     0,73   42,67  84,62                  (---*--)
K-SC   -30,49   11,45  53,39               (---*--)
                              -------+---------+---------+---------+--
                                  -120         0       120       240


Group = K-A subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-HU   -38,35    3,60  45,54               (--*---)
K-SC   -69,57  -27,63  14,32            (---*--)
                              -------+---------+---------+---------+--
                                  -120         0       120       240


Group = K-HU subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-SC   -73,16  -31,22  10,72            (--*---)
                              -------+---------+---------+---------+--
                                  -120         0       120       240
```

One-way ANOVA: Ethyl 9-decenoate versus Group

```
Source  DF     SS     MS     F      P
Group    1  13,76  13,76  5,86  0,073
Error    4   9,40   2,35
Total    5  23,17

S = 1,533   R-Sq = 59,41%   R-Sq(adj) = 49,27%


                          Individual 95% CIs For Mean Based on Pooled StDev
Level   N    Mean  StDev     +---------+---------+---------+---------
E-A     3  24,447  0,709     (-----------*-----------)
E-Laff  3  27,476  2,049                (-----------*-----------)
                             +---------+---------+---------+---------
                           22,0      24,0      26,0      28,0

Pooled StDev = 1,533


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-Laff  3  27,476  A
E-A     3  24,447  A

Means that do not share a letter are significantly different.
```

```
Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group    Lower  Center  Upper  ----+---------+---------+---------+-----
E-Laff  -0,446   3,029  6,505             (-------------*-------------)
                           ----+---------+---------+---------+-----
                            -2,5       0,0       2,5       5,0
```

One-way ANOVA: Diethyl succinate versus Group

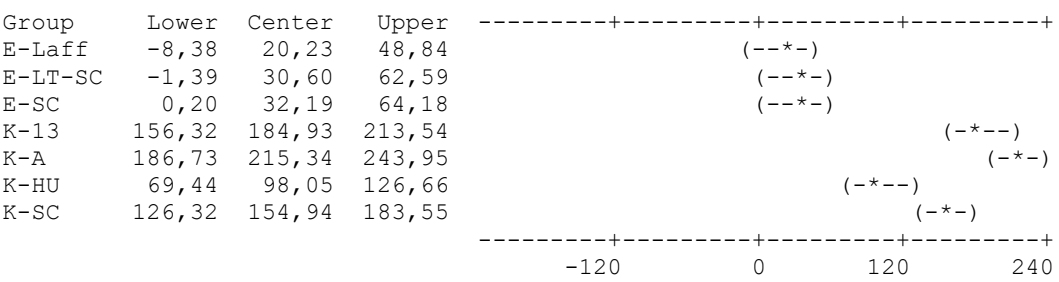
```
Source  DF        SS       MS       F      P
Group    7  138402,6  19771,8  200,46  0,000
Error   14    1380,8     98,6
Total   21  139783,4

S = 9,931   R-Sq = 99,01%   R-Sq(adj) = 98,52%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  -----+---------+---------+---------+----
E-A      3   44,04   2,40  (-*-)
E-Laff   3   64,27   4,59      (-*-)
E-LT-SC  2   74,64   2,48       (-*--)
E-SC     2   76,24   4,24       (--*-)
K-13     3  228,97   7,69                                  (-*-)
K-A      3  259,39  19,84                                       (-*-)
K-HU     3  142,10  12,56                    (-*-)
K-SC     3  198,98   6,41                              (-*-)
                          -----+---------+---------+---------+----
                              60       120       180       240

Pooled StDev = 9,93


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  259,39  A
K-13     3  228,97    B
K-SC     3  198,98      C
K-HU     3  142,10        D
E-SC     2   76,24          E
E-LT-SC  2   74,64          E F
E-Laff   3   64,27          E F
E-A      3   44,04            F

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
```

All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%

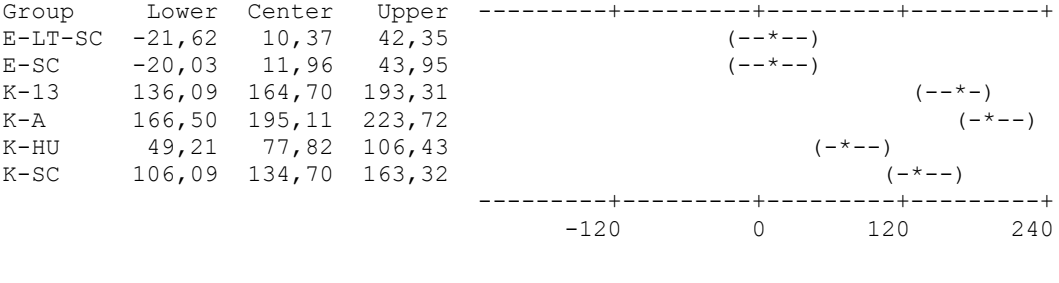
Group = E-A subtracted from:

Group	Lower	Center	Upper
E-Laff	-8,38	20,23	48,84
E-LT-SC	-1,39	30,60	62,59
E-SC	0,20	32,19	64,18
K-13	156,32	184,93	213,54
K-A	186,73	215,34	243,95
K-HU	69,44	98,05	126,66
K-SC	126,32	154,94	183,55



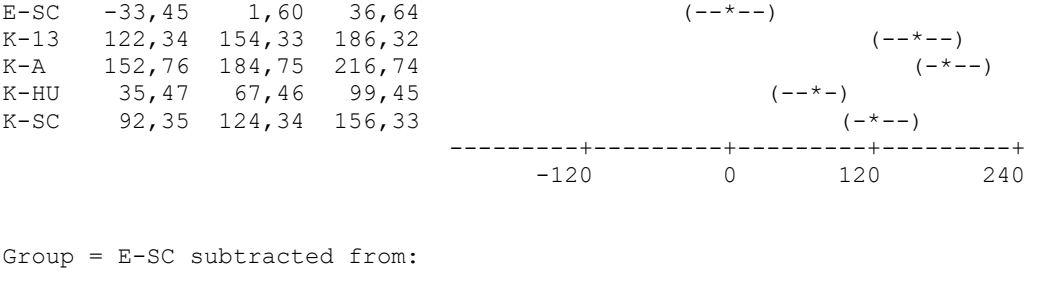
Group = E-Laff subtracted from:

Group	Lower	Center	Upper
E-LT-SC	-21,62	10,37	42,35
E-SC	-20,03	11,96	43,95
K-13	136,09	164,70	193,31
K-A	166,50	195,11	223,72
K-HU	49,21	77,82	106,43
K-SC	106,09	134,70	163,32



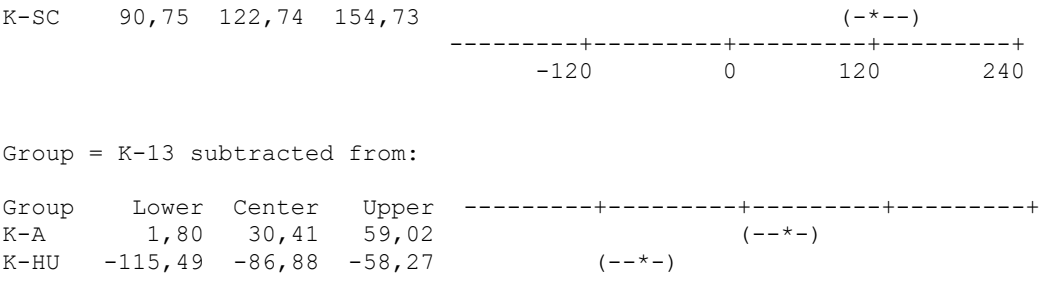
Group = E-LT-SC subtracted from:

Group	Lower	Center	Upper
E-SC	-33,45	1,60	36,64
K-13	122,34	154,33	186,32
K-A	152,76	184,75	216,74
K-HU	35,47	67,46	99,45
K-SC	92,35	124,34	156,33



Group = E-SC subtracted from:

Group	Lower	Center	Upper
K-13	120,75	152,74	184,73
K-A	151,16	183,15	215,14
K-HU	33,87	65,86	97,85
K-SC	90,75	122,74	154,73



Group = K-13 subtracted from:

Group	Lower	Center	Upper
K-A	1,80	30,41	59,02
K-HU	-115,49	-86,88	-58,27

```
K-SC    -58,61  -29,99   -1,38                (--*-)
                                  ---------+---------+---------+---------+
                                         -120         0       120       240


Group = K-A subtracted from:

Group    Lower   Center   Upper  ---------+---------+---------+---------+
K-HU   -145,90  -117,29  -88,68         (-*--)
K-SC    -89,02   -60,41  -31,80              (-*-)
                                  ---------+---------+---------+---------+
                                        -120         0       120       240


Group = K-HU subtracted from:

Group  Lower  Center  Upper  ---------+---------+---------+---------+
K-SC   28,27   56,88  85,49                      (--*-)
                             ---------+---------+---------+---------+
                                   -120         0       120       240
```

One-way ANOVA: Ethyl 4-hydroxybutanoate versus Group

```
Source  DF        SS       MS       F      P
Group    7  17561306  2508758  214,96  0,000
Error   16    186730    11671
Total   23  17748036

S = 108,0   R-Sq = 98,95%   R-Sq(adj) = 98,49%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --------+---------+---------+---------+-
E-A      3  1264,8   69,8    (-*)
E-Laff   3  1480,2  106,3       (-*)
E-LT-SC  3  1314,6   37,4     (*-)
E-SC     3  1124,6   52,8  (-*-)
K-13     3  2922,6  103,6                          (-*)
K-A      3  3684,7  129,9                                   (-*-)
K-HU     3  2344,8   66,2                    (*-)
K-SC     3  2058,8  202,6               (-*)
                          --------+---------+---------+---------+-
                               1600      2400      3200      4000

Pooled StDev = 108,0


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  3684,7  A
K-13     3  2922,6     B
K-HU     3  2344,8       C
K-SC     3  2058,8       C
E-Laff   3  1480,2         D
E-LT-SC  3  1314,6         D E
E-A      3  1264,8         D E
```

```
E-SC     3  1124,6          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff    -90,2   215,4   521,0                    (-*-)
E-LT-SC  -255,8    49,8   355,4                  (-*-)
E-SC     -445,9  -140,2   165,4                (-*-)
K-13     1352,2  1657,8  1963,4                            (-*-)
K-A      2114,2  2419,9  2725,5                                 (-*-)
K-HU      774,4  1080,0  1385,6                       (-*-)
K-SC      488,3   793,9  1099,6                    (-*-)
                         ---------+---------+---------+---------+
                              -1500         0      1500      3000


Group = E-Laff subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-LT-SC  -471,2  -165,6   140,0                (-*-)
E-SC     -661,3  -355,6   -50,0              (-*-)
K-13     1136,8  1442,4  1748,0                         (-*-)
K-A      1898,8  2204,5  2510,1                              (-*-)
K-HU      559,0   864,6  1170,2                    (-*-)
K-SC      272,9   578,5   884,2                  (-*-)
                         ---------+---------+---------+---------+
                              -1500         0      1500      3000


Group = E-LT-SC subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
E-SC   -495,7  -190,0   115,6              (-*-)
K-13   1302,4  1608,0  1913,6                       (-*-)
K-A    2064,4  2370,1  2675,7                            (-*-)
K-HU    724,6  1030,2  1335,8                    (-*-)
K-SC    438,5   744,1  1049,8                  (-*-)
                        ---------+---------+---------+---------+
                             -1500         0      1500      3000


Group = E-SC subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-13   1492,4  1798,0  2103,7                       (-*-)
K-A    2254,5  2560,1  2865,7                            (-*-)
K-HU    914,6  1220,2  1525,9                    (-*-)
K-SC    628,6   934,2  1239,8                  (-*-)
                        ---------+---------+---------+---------+
                             -1500         0      1500      3000
```

```
Group = K-13 subtracted from:

Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-A      456,4   762,1  1067,7                      (-*-)
K-HU    -883,4  -577,8  -272,2             (-*-)
K-SC   -1169,5  -863,9  -558,2          (-*-)
                                ---------+---------+---------+---------+
                                     -1500         0      1500      3000


Group = K-A subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-HU   -1645,5  -1339,9  -1034,2         (-*-)
K-SC   -1931,5  -1625,9  -1320,3       (-*-)
                                ---------+---------+---------+---------+
                                    -1500         0      1500      3000


Group = K-HU subtracted from:

Group   Lower  Center  Upper  ---------+---------+---------+---------+
K-SC   -591,7  -286,1   19,6              (-*-)
                           ---------+---------+---------+---------+
                                -1500         0      1500      3000
```

One-way ANOVA: Monoethyl succinate versus Group

```
Source  DF       SS       MS      F      P
Group    6  9018316  1503053  79,68  0,000
Error   12   226370    18864
Total   18  9244686

S = 137,3   R-Sq = 97,55%   R-Sq(adj) = 96,33%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level    N    Mean  StDev  --+---------+---------+---------+-------
E-A      3   659,1   41,3  (--*--)
E-LT-SC  2  1046,1   42,9        (--*---)
E-SC     2   722,3   30,4   (--*---)
K-13     3  2610,7  248,7                                    (--*-)
K-A      3  2107,1  177,6                             (--*--)
K-HU     3  1157,7   84,9          (--*--)
K-SC     3  1700,6   97,3                   (--*--)
                         --+---------+---------+---------+-------
                         600      1200      1800      2400

Pooled StDev = 137,3


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-13     3  2610,7  A
K-A      3  2107,1    B
```

```
K-SC     3  1700,6      C
K-HU     3  1157,7        D
E-LT-SC  2  1046,1        D E
E-SC     2   722,3        D E
E-A      3   659,1          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,56%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-LT-SC   -51,8   387,0   825,9                    (--*---)
E-SC     -375,6    63,2   502,1                 (---*--)
K-13     1559,1  1951,6  2344,1                                  (--*---)
K-A      1055,4  1448,0  1840,5                            (--*--)
K-HU      106,1   498,6   891,1                      (--*--)
K-SC      649,0  1041,5  1434,0                          (---*--)
                                 ---------+---------+---------+---------+
                                     -1200         0      1200      2400


Group = E-LT-SC subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
E-SC   -804,6  -323,8   156,9            (---*---)
K-13   1125,7  1564,6  2003,4                               (---*---)
K-A     622,1  1060,9  1499,8                         (---*--)
K-HU   -327,3   111,5   550,4                 (---*---)
K-SC    215,6   654,5  1093,3                      (--*---)
                               ---------+---------+---------+---------+
                                   -1200         0      1200      2400


Group = E-SC subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-13   1449,5  1888,4  2327,2                                 (---*--)
K-A     945,9  1384,7  1823,6                           (---*--)
K-HU     -3,5   435,4   874,2                    (---*--)
K-SC    539,4   978,3  1417,1                        (---*---)
                               ---------+---------+---------+---------+
                                   -1200         0      1200      2400


Group = K-13 subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-A     -896,2   -503,6   -111,1             (--*--)
K-HU   -1845,6  -1453,0  -1060,5      (--*--)
K-SC   -1302,6   -910,1   -517,6          (--*---)
                                ---------+---------+---------+---------+
                                    -1200         0      1200      2400
```

```
Group = K-A subtracted from:

Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-HU   -1341,9  -949,4  -556,9          (--*--)
K-SC    -799,0  -406,5   -13,9              (---*--)
                                ---------+---------+---------+---------+
                                     -1200         0      1200      2400


Group = K-HU subtracted from:

Group  Lower  Center  Upper  ---------+---------+---------+---------+
K-SC   150,4   542,9  935,4                      (---*--)
                             ---------+---------+---------+---------+
                                  -1200         0      1200      2400
```

One-way ANOVA: Ethyl butyrate versus Group

```
Source  DF    SS   MS     F      P
Group    1   616  616  2,16  0,216
Error    4  1140  285
Total    5  1756

S = 16,88   R-Sq = 35,06%   R-Sq(adj) = 18,82%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level   N    Mean  StDev  ----+---------+---------+---------+-----
E-A     3  259,37   3,43  (-------------*------------)
E-Laff  3  279,63  23,63            (-------------*------------)
                         ----+---------+---------+---------+-----
                           240       260       280       300

Pooled StDev = 16,88


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-Laff  3  279,63  A
E-A     3  259,37  A

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group    Lower  Center  Upper  -----+---------+---------+---------+----
E-Laff  -18,02   20,26  58,54          (--------------*--------------)
                           -----+---------+---------+---------+----
```

```
                                -25         0        25        50
```

One-way ANOVA: Ethyl-3-hydroxypropionate versus Group

```
Source  DF      SS      MS       F      P
Group    5  9808,3  1961,7  128,21  0,000
Error   12   183,6    15,3
Total   17  9992,0

S = 3,912   R-Sq = 98,16%   R-Sq(adj) = 97,40%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  ---------+---------+---------+---------+
E-A     3  26,605  1,392  (-*--)
E-Laff  3  26,393  1,794  (-*--)
K-13    3  88,554  1,186                                (-*--)
K-A     3  65,190  5,028                      (--*-)
K-HU    3  65,986  5,534                       (-*-)
K-SC    3  73,374  5,417                          (--*-)
                          ---------+---------+---------+---------+
                                  40        60        80       100

Pooled StDev = 3,912


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
K-13    3  88,554  A
K-SC    3  73,374     B
K-HU    3  65,986     B
K-A     3  65,190     B
E-A     3  26,605       C
E-Laff  3  26,393       C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:

Group     Lower  Center   Upper  --------+---------+---------+---------+-
E-Laff  -10,939  -0,212  10,516                (--*--)
K-13     51,222  61,950  72,677                              (-*--)
K-A      27,858  38,585  49,312                         (--*-)
K-HU     28,654  39,381  50,108                         (--*--)
K-SC     36,042  46,769  57,497                           (--*-)
                         --------+---------+---------+---------+-
                               -40         0        40        80
```

```
Group = E-Laff subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-13   51,434  62,161  72,889                                  (--*-)
K-A    28,069  38,797  49,524                            (--*-)
K-HU   28,865  39,593  50,320                            (--*--)
K-SC   36,253  46,981  57,708                              (--*-)
                           --------+---------+---------+---------+-
                                 -40         0        40        80


Group = K-13 subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-A    -34,092  -23,365  -12,637           (--*--)
K-HU   -33,296  -22,569  -11,841            (-*--)
K-SC   -25,908  -15,180   -4,453              (-*--)
                                --------+---------+---------+---------+-
                                      -40         0        40        80


Group = K-A subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-HU   -9,931   0,796  11,523                 (-*--)
K-SC   -2,543   8,184  18,912                  (--*--)
                           --------+---------+---------+---------+-
                                 -40         0        40        80


Group = K-HU subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-SC   -3,339   7,388  18,116                (--*--)
                           --------+---------+---------+---------+-
                                 -40         0        40        80
```

One-way ANOVA: Ethyl2-hydroxy3phenylpropanoate versus Group

```
Source  DF      SS      MS      F      P
Group    2  6121,1  3060,6  47,37  0,000
Error    6   387,7    64,6
Total    8  6508,8

S = 8,038   R-Sq = 94,04%   R-Sq(adj) = 92,06%


                        Individual 95% CIs For Mean Based on
                        Pooled StDev
Level  N    Mean  StDev  -----+---------+---------+---------+----
K-13   3   92,33   5,08        (----*---)
K-A    3  135,76  11,14                          (---*----)
K-SC   3   73,47   6,62  (---*----)
                        -----+---------+---------+---------+----
                            75       100       125       150

Pooled StDev = 8,04
```

```
Grouping Information Using Tukey Method

Group  N     Mean  Grouping
K-A    3  135,755  A
K-13   3   92,331    B
K-SC   3   73,468    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 97,80%


Group = K-13 subtracted from:

Group    Lower   Center   Upper  ------+---------+---------+---------+---
K-A     23,282   43,424  63,566                      (---*---)
K-SC   -39,004  -18,863   1,279          (---*---)
                                ------+---------+---------+---------+---
                                    -50         0        50       100


Group = K-A subtracted from:

Group    Lower   Center    Upper  ------+---------+---------+---------+---
K-SC   -82,429  -62,287  -42,145  (---*---)
                                  ------+---------+---------+---------+---
                                      -50         0        50       100
```

One-way ANOVA: Methyl 4-hydroxybutanoate versus Group

```
Source  DF       SS      MS       F      P
Group    3  2931,83  977,28  460,90  0,000
Error    8    16,96    2,12
Total   11  2948,79

S = 1,456   R-Sq = 99,42%   R-Sq(adj) = 99,21%


                        Individual 95% CIs For Mean Based on
                        Pooled StDev
Level  N    Mean  StDev  --------+---------+---------+---------+-
K-13   3  20,687  1,036      (*-)
K-A    3  56,393  1,686                                  (-*-)
K-HU   3  28,973  1,659             (*-)
K-SC   3  16,071  1,346  (*-)
                        --------+---------+---------+---------+-
                               24        36        48        60

Pooled StDev = 1,456


Grouping Information Using Tukey Method
```

```
Group  N    Mean  Grouping
K-A    3  56,393  A
K-HU   3  28,973    B
K-13   3  20,687      C
K-SC   3  16,071        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,74%


Group = K-13 subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-A    31,898  35,707  39,515                              (*-)
K-HU    4,478   8,286  12,095                    (*-)
K-SC   -8,424  -4,615  -0,807                (*-)
                              --------+---------+---------+---------+-
                                    -25         0        25        50


Group = K-A subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-HU   -31,229  -27,420  -23,612        (*-)
K-SC   -44,130  -40,322  -36,513  (-*)
                                  --------+---------+---------+---------+-
                                        -25         0        25        50


Group = K-HU subtracted from:

Group    Lower   Center   Upper  --------+---------+---------+---------+-
K-SC   -16,710  -12,901  -9,093            (-*)
                                --------+---------+---------+---------+-
                                      -25         0        25        50
```

One-way ANOVA: Ethyl decanoate versus Group

```
Source  DF      SS      MS       F      P
Group    3  503145  167715  608,39  0,000
Error    7    1930     276
Total   10  505075

S = 16,60   R-Sq = 99,62%   R-Sq(adj) = 99,45%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---------+---------+---------+---------+
E-A      3   40,52   3,11  (-*)
E-Laff   3   55,40   0,82   (-*)
E-LT-SC  3  463,98  29,26                                (-*)
E-SC     2  496,05  14,03                                  (-*-)
```

```
                          ---------+---------+---------+---------+
                                 150       300       450       600

Pooled StDev = 16,60


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-SC     2  496,05  A
E-LT-SC  3  463,98  A
E-Laff   3   55,40    B
E-A      3   40,52    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,70%


Group = E-A subtracted from:

Group     Lower  Center   Upper     +---------+---------+---------+--------
-
E-Laff   -29,99   14,87   59,74                       (-*)
E-LT-SC  378,59  423,46  468,32                                    (-*)
E-SC     405,38  455,53  505,69                                    (*-)
                                +---------+---------+---------+--------
-
                              -500      -250         0       250


Group = E-Laff subtracted from:

Group     Lower  Center   Upper     +---------+---------+---------+--------
-
E-LT-SC  363,72  408,58  453,44                                    (*-)
E-SC     390,50  440,66  490,81                                    (*-)
                                +---------+---------+---------+--------
-
                              -500      -250         0       250


Group = E-LT-SC subtracted from:

Group   Lower  Center  Upper     +---------+---------+---------+---------
E-SC   -18,08   32,08  82,23                     (-*-)
                                +---------+---------+---------+---------
                           -500      -250         0       250
```

One-way ANOVA: Ethyl hexanoate versus Group

```
Source  DF      SS     MS      F      P
Group    7  314372  44910  51,75  0,000
Error   14   12150    868
```

```
Total   21  326522

S = 29,46   R-Sq = 96,28%   R-Sq(adj) = 94,42%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ------+---------+---------+---------+---
E-A      3  469,11  38,40                       (--*--)
E-Laff   3  449,26  32,28                     (--*--)
E-LT-SC  2  444,94  30,92                    (---*---)
E-SC     2  579,79  38,80                              (--*---)
K-13     3  248,64  17,47      (--*--)
K-A      3  249,94  23,04      (--*--)
K-HU     3  209,53  18,46  (--*---)
K-SC     3  396,68  33,93                 (--*--)
                          ------+---------+---------+---------+---
                              240       360       480       600

Pooled StDev = 29,46


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-SC     2  579,79  A
E-A      3  469,11    B
E-Laff   3  449,26    B
E-LT-SC  2  444,94    B
K-SC     3  396,68    B
K-A      3  249,94      C
K-13     3  248,64      C
K-HU     3  209,53      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group      Lower   Center    Upper  ---------+---------+---------+--------+
E-Laff   -104,72   -19,85    65,02                (--*---)
E-LT-SC  -119,06   -24,17    70,72               (---*---)
E-SC       15,79   110,68   205,57                     (--*---)
K-13     -305,34  -220,47  -135,60         (--*---)
K-A      -304,05  -219,17  -134,30         (--*---)
K-HU     -344,46  -259,59  -174,71       (---*--)
K-SC     -157,31   -72,43    12,44               (--*--)
                          ---------+---------+---------+--------+
                                -250         0       250      500

Group = E-Laff subtracted from:

Group      Lower   Center    Upper  ---------+---------+---------+--------+
E-LT-SC   -99,21    -4,32    90,57                (---*---)
```

```
E-SC       35,64   130,53   225,42                      (---*---)
K-13     -285,49  -200,62  -115,75          (--*--)
K-A      -284,20  -199,32  -114,45          (--*--)
K-HU     -324,61  -239,74  -154,86        (--*---)
K-SC     -137,46   -52,58    32,29                (--*--)
                                    ---------+---------+---------+---------+
                                          -250         0       250       500
```

Group = E-LT-SC subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
E-SC     30,90   134,85   238,80                     (---*----)
K-13   -291,19  -196,30  -101,41         (---*---)
K-A    -289,89  -195,00  -100,11         (---*---)
K-HU   -330,30  -235,41  -140,52        (---*--)
K-SC   -143,15   -48,26    46,63               (---*---)
                                   ---------+---------+---------+---------+
                                         -250         0       250       500
```

Group = E-SC subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-13   -426,04  -331,15  -236,26    (---*---)
K-A    -424,74  -329,85  -234,96    (---*---)
K-HU   -465,15  -370,26  -275,37  (---*---)
K-SC   -278,00  -183,11   -88,22          (---*--)
                                   ---------+---------+---------+---------+
                                         -250         0       250       500
```

Group = K-13 subtracted from:

```
Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-A     -83,57    1,30   86,17                  (--*--)
K-HU   -123,99  -39,11   45,76                (--*---)
K-SC     63,16  148,04  232,91                       (--*--)
                                  ---------+---------+---------+---------+
                                        -250         0       250       500
```

Group = K-A subtracted from:

```
Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-HU   -125,28  -40,41   44,46                (--*---)
K-SC     61,87  146,74  231,61                       (---*--)
                                  ---------+---------+---------+---------+
                                        -250         0       250       500
```

Group = K-HU subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   102,28  187,15  272,02                       (--*---)
                                 ---------+---------+---------+---------+
                                       -250         0       250       500
```

One-way ANOVA: Butanoic acid versus Group

```
Source  DF      SS     MS      F      P
Group    5  156287  31257  75,02  0,000
Error   11    4583    417
Total   16  160870

S = 20,41   R-Sq = 97,15%   R-Sq(adj) = 95,86%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev   +---------+---------+---------+---------
E-A      3  107,36   8,42   (--*---)
E-Laff   3  250,49  22,72                   (--*---)
E-LT-SC  3  335,22  27,29                            (--*--)
E-SC     2  345,60   9,32                            (---*---)
K-A      3  161,70  12,85          (--*--)
K-SC     3  353,35  27,40                              (--*--)
                    +---------+---------+---------+---------
                   80        160       240       320

Pooled StDev = 20,41


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-SC     3  353,35  A
E-SC     2  345,60  A
E-LT-SC  3  335,22  A
E-Laff   3  250,49    B
K-A      3  161,70      C
E-A      3  107,36      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,42%


Group = E-A subtracted from:

Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-Laff    86,33  143,13  199,94                        (---*--)
E-LT-SC  171,06  227,86  284,67                             (---*---)
E-SC     174,74  238,24  301,75                              (---*---)
K-A       -2,46   54,35  111,15                   (---*--)
K-SC     189,19  245,99  302,80                               (--*---)
                         -------+---------+---------+---------+--
                             -150         0       150       300


Group = E-Laff subtracted from:

Group      Lower  Center   Upper  -------+---------+---------+---------+--
```

```
E-LT-SC    27,93   84,73  141,53                    (---*--)
E-SC       31,60   95,11  158,62                    (---*----)
K-A      -145,59  -88,79  -31,98         (---*---)
K-SC       46,06  102,86  159,66                     (---*---)
                                  -------+---------+---------+---------+--
                                      -150         0       150       300
```

```
Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
E-SC    -53,13    10,38    73,89              (----*---)
K-A    -230,32  -173,52  -116,71    (--*---)
K-SC    -38,67    18,13    74,93               (---*---)
                                  -------+---------+---------+---------+--
                                      -150         0       150       300
```

```
Group = E-SC subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
K-A    -247,41  -183,90  -120,39   (---*---)
K-SC    -55,76     7,75    71,26              (----*---)
                                  -------+---------+---------+---------+--
                                      -150         0       150       300
```

```
Group = K-A subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-SC   134,84  191,64  248,45                           (---*---)
                             -------+---------+---------+---------+--
                                 -150         0       150       300
```

One-way ANOVA: Hexanoic acid versus Group

```
Source  DF        SS       MS       F      P
Group    7  20292779  2898968  210,36  0,000
Error   16    220495    13781
Total   23  20513274

S = 117,4   R-Sq = 98,93%   R-Sq(adj) = 98,45%
```

```
                          Individual 95% CIs For Mean Based on
                          Pooled StdDev
Level    N    Mean  StDev  -----+---------+---------+---------+----
E-A      3   696,7   38,1    (-*-)
E-Laff   3  1741,7   54,8                (-*-)
E-LT-SC  3  2428,8  147,1                        (*-)
E-SC     3  3339,7   72,7                                   (-*-)
K-13     3   848,9  239,9      (-*)
K-A      3   556,2   50,7  (-*-)
K-HU     3   794,1    3,1     (-*-)
K-SC     3  1528,3  136,8             (-*-)
                          -----+---------+---------+---------+----
                             800      1600      2400      3200
```

Pooled StDev = 117,4

Grouping Information Using Tukey Method

Group	N	Mean	Grouping
E-SC	3	3339,7	A
E-LT-SC	3	2428,8	B
E-Laff	3	1741,7	C
K-SC	3	1528,3	C
K-13	3	848,9	D
K-HU	3	794,1	D
E-A	3	696,7	D
K-A	3	556,2	D

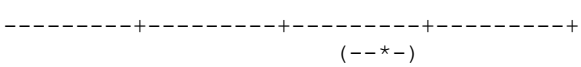
Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%

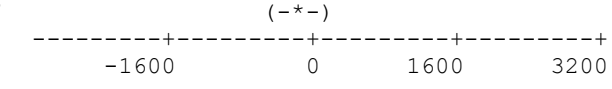
Group = E-A subtracted from:

Group	Lower	Center	Upper
E-Laff	712,9	1045,0	1377,1
E-LT-SC	1400,0	1732,1	2064,2
E-SC	2310,9	2643,0	2975,1
K-13	-179,9	152,2	484,3
K-A	-472,6	-140,5	191,6
K-HU	-234,7	97,4	429,5
K-SC	499,5	831,6	1163,7



Group = E-Laff subtracted from:

Group	Lower	Center	Upper
E-LT-SC	355,0	687,2	1019,3
E-SC	1265,9	1598,0	1930,1
K-13	-1224,9	-892,8	-560,7
K-A	-1517,6	-1185,5	-853,4
K-HU	-1279,7	-947,6	-615,5
K-SC	-545,5	-213,4	118,7



Group = E-LT-SC subtracted from:

Group	Lower	Center	Upper
E-SC	578,8	910,9	1243,0
K-13	-1912,1	-1580,0	-1247,9
K-A	-2204,7	-1872,6	-1540,5
K-HU	-1966,9	-1634,8	-1302,6
K-SC	-1232,6	-900,5	-568,4

```
                                      -1600         0      1600      3200

Group = E-SC subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-13   -2822,9  -2490,8  -2158,7   (-*--)
K-A    -3115,6  -2783,5  -2451,4  (-*-)
K-HU   -2877,7  -2545,6  -2213,5   (-*-)
K-SC   -2143,5  -1811,4  -1479,3        (-*-)
                                  ---------+---------+---------+---------+
                                       -1600         0      1600      3200


Group = K-13 subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-A    -624,8  -292,7    39,4                (-*-)
K-HU   -386,9   -54,8   277,3                  (-*-)
K-SC    347,3   679,4  1011,5                      (-*-)
                               ---------+---------+---------+---------+
                                    -1600         0      1600      3200


Group = K-A subtracted from:

Group  Lower  Center   Upper  ---------+---------+---------+---------+
K-HU   -94,2   237,9   570,0                   (-*--)
K-SC   640,0   972,1  1304,2                        (-*-)
                            ---------+---------+---------+---------+
                                 -1600         0      1600      3200


Group = K-HU subtracted from:

Group  Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   402,1   734,2  1066,3                       (-*-)
                            ---------+---------+---------+---------+
                                 -1600         0      1600      3200
```

One-way ANOVA: Octanoic acid versus Group

```
Source  DF        SS       MS       F      P
Group    7  33177837  4739691  623,81  0,000
Error   15    113970     7598
Total   22  33291806

S = 87,17   R-Sq = 99,66%   R-Sq(adj) = 99,50%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  -------+---------+---------+---------+--
E-A      3  1057,2   50,6        (-*)
E-Laff   3  2251,8   58,5                  (-*)
E-LT-SC  3  3300,3  195,0                            (*)
E-SC     2  3973,7  113,6                                  (-*)
K-13     3   527,0    4,3   (*)
```

```
K-A      3   433,9   35,2  (*)
K-HU     3   548,4   22,4   (*-)
K-SC     3  1317,6   69,0           (*)
                          -------+---------+---------+---------+--
                              1000      2000      3000      4000

Pooled StDev = 87,2


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-SC     2  3973,7  A
E-LT-SC  3  3300,3    B
E-Laff   3  2251,8      C
K-SC     3  1317,6        D
E-A      3  1057,2          E
K-HU     3   548,4            F
K-13     3   527,0            F
K-A      3   433,9            F

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff    946,0  1194,6  1443,2                          (*)
E-LT-SC  1994,5  2243,1  2491,7                               (*)
E-SC     2638,6  2916,5  3194,5                                  (-*)
K-13     -778,8  -530,2  -281,6                (*-)
K-A      -871,9  -623,3  -374,7                (*)
K-HU     -757,4  -508,8  -260,2                (*-)
K-SC       11,8   260,4   509,0                    (*-)
                          ---------+---------+---------+---------+
                               -2000         0      2000      4000


Group = E-Laff subtracted from:

Group      Lower   Center    Upper  ---------+---------+---------+--------+
E-LT-SC    799,9   1048,5   1297,1                         (*)
E-SC      1444,0   1721,9   1999,9                            (-*)
K-13     -1973,4  -1724,8  -1476,2           (*-)
K-A      -2066,5  -1817,9  -1569,3           (*)
K-HU     -1952,0  -1703,4  -1454,8           (*-)
K-SC     -1182,8   -934,2   -685,6               (*-)
                             ---------+---------+---------+--------+
                                  -2000         0      2000     4000


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
```

```
E-SC     395,5    673,4    951,4                        (*-)
K-13   -3021,9  -2773,2  -2524,6      (*)
K-A    -3115,0  -2866,4  -2617,8     (-*)
K-HU   -3000,5  -2751,9  -2503,3      (*)
K-SC   -2231,3  -1982,7  -1734,1          (*)
                                  ---------+---------+---------+---------+
                                       -2000         0      2000      4000
```

```
Group = E-SC subtracted from:

Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-13   -3724,6  -3446,7  -3168,7  (-*)
K-A    -3817,8  -3539,8  -3261,9  (*-)
K-HU   -3703,3  -3425,3  -3147,4  (-*)
K-SC   -2934,1  -2656,1  -2378,2      (-*)
                                  ---------+---------+---------+---------+
                                       -2000         0      2000      4000
```

```
Group = K-13 subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-A    -341,8   -93,2   155,5                  (-*)
K-HU   -227,3    21,3   270,0                   (*)
K-SC    541,9   790,5  1039,2                       (*)
                             ---------+---------+---------+---------+
                                  -2000         0      2000      4000
```

```
Group = K-A subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-HU   -134,1   114,5   363,1                  (-*)
K-SC    635,1   883,7  1132,3                      (*-)
                             ---------+---------+---------+---------+
                                  -2000         0      2000      4000
```

```
Group = K-HU subtracted from:

Group  Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   520,6   769,2  1017,8                       (*)
                           ---------+---------+---------+---------+
                                -2000         0      2000      4000
```

One-way ANOVA: Decanoic acid versus Group

```
Source  DF      SS      MS      F      P
Group    4  9377,3  2344,3  33,17  0,000
Error    8   565,5    70,7
Total   12  9942,8

S = 8,407   R-Sq = 94,31%   R-Sq(adj) = 91,47%

                          Individual 95% CIs For Mean Based on
                          Pooled StDev
```

```
Level    N    Mean  StDev  ----+---------+---------+---------+-----
E-A      3  127,71  10,38                      (---*----)
E-Laff   3  138,02   9,35                          (---*----)
E-LT-SC  2  132,54   8,44                       (----*----)
E-SC     2   78,99   6,42  (-----*----)
K-SC     3   77,44   5,60   (---*---)
                           ----+---------+---------+---------+-----
                              75       100       125       150
```

Pooled StDev = 8,41

Grouping Information Using Tukey Method

```
Group    N    Mean  Grouping
E-Laff   3  138,02  A
E-LT-SC  2  132,54  A
E-A      3  127,71  A
E-SC     2   78,99    B
K-SC     3   77,44    B
```

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,14%

Group = E-A subtracted from:

```
Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-Laff   -13,43   10,31   34,05               (----*----)
E-LT-SC  -21,71    4,83   31,36             (----*----)
E-SC     -75,26  -48,73  -22,19    (----*-----)
K-SC     -74,00  -50,27  -26,53    (----*----)
                                 -------+---------+---------+---------+--
                                      -50         0        50       100
```

Group = E-Laff subtracted from:

```
Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-LT-SC  -32,02   -5,48   21,05            (----*----)
E-SC     -85,58  -59,04  -32,50  (----*-----)
K-SC     -84,32  -60,58  -36,84  (----*----)
                                 -------+---------+---------+---------+--
                                      -50         0        50       100
```

Group = E-LT-SC subtracted from:

```
Group   Lower  Center   Upper  -------+---------+---------+---------+--
E-SC   -82,62  -53,55  -24,48  (-----*-----)
K-SC   -81,63  -55,10  -28,56   (----*----)
                               -------+---------+---------+---------+--
                                    -50         0        50       100
```

```
Group = E-SC subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-SC   -28,08   -1,54  25,00             (-----*----)
                            -------+---------+---------+---------+--
                                 -50         0        50       100
```

One-way ANOVA: Propanoic acid versus Group

```
Source  DF       SS      MS      F      P
Group    7  23271,0  3324,4  85,33  0,000
Error   15    584,4    39,0
Total   22  23855,4

S = 6,242   R-Sq = 97,55%   R-Sq(adj) = 96,41%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --------+---------+---------+---------+-
E-A      3   43,22   3,45  (-*--)
E-Laff   3   53,87   3,08     (--*--)
E-LT-SC  3  106,87   3,01                       (--*-)
E-SC     2   58,65   0,27      (---*--)
K-13     3  134,87  12,61                                (--*--)
K-A      3  124,90   5,71                             (--*-)
K-HU     3   99,56   5,07                        (-*--)
K-SC     3   89,04   6,67                   (--*-)
                          --------+---------+---------+---------+-
                                  60        90       120       150

Pooled StDev = 6,24


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-13     3  134,87  A
K-A      3  124,90  A
E-LT-SC  3  106,87    B
K-HU     3   99,56    B C
K-SC     3   89,04      C
E-SC     2   58,65        D
E-Laff   3   53,87        D
E-A      3   43,22        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group    Lower  Center   Upper  ------+---------+---------+---------+---
```

```
E-Laff   -7,15   10,65   28,45                 (--*--)
E-LT-SC  45,85   63,65   81,45                          (--*--)
E-SC     -4,47   15,43   35,34                 (---*--)
K-13     73,85   91,65  109,45                              (--*--)
K-A      63,88   81,68   99,48                            (--*--)
K-HU     38,54   56,34   74,15                       (--*--)
K-SC     28,02   45,83   63,63                     (--*--)
                                 ------+---------+---------+---------+---
                                     -60         0        60       120
```

Group = E-Laff subtracted from:

```
Group     Lower  Center  Upper  ------+---------+---------+---------+---
E-LT-SC   35,20   53,00  70,80                       (--*--)
E-SC     -15,12    4,78  24,68              (---*--)
K-13      63,20   81,00  98,80                           (--*-)
K-A       53,23   71,03  88,83                         (--*--)
K-HU      27,89   45,69  63,50                     (--*--)
K-SC      17,37   35,17  52,98                   (--*--)
                                 ------+---------+---------+---------+---
                                     -60         0        60       120
```

Group = E-LT-SC subtracted from:

```
Group   Lower  Center   Upper  ------+---------+---------+---------+---
E-SC   -68,12  -48,22  -28,32       (--*--)
K-13    10,20   28,00   45,80                 (--*--)
K-A      0,22   18,03   35,83               (--*--)
K-HU   -25,11   -7,31   10,49            (--*--)
K-SC   -35,63  -17,83   -0,02         (--*--)
                                 ------+---------+---------+---------+---
                                     -60         0        60       120
```

Group = E-SC subtracted from:

```
Group  Lower  Center  Upper  ------+---------+---------+---------+---
K-13   56,32   76,22  96,12                       (---*--)
K-A    46,34   66,25  86,15                     (--*--)
K-HU   21,01   40,91  60,82                  (--*--)
K-SC   10,49   30,39  50,30                (--*--)
                               ------+---------+---------+---------+---
                                  -60         0        60       120
```

Group = K-13 subtracted from:

```
Group   Lower  Center   Upper  ------+---------+---------+---------+---
K-A    -27,77   -9,97    7,83         (--*--)
K-HU   -53,11  -35,31  -17,50      (--*--)
K-SC   -63,63  -45,83  -28,02    (--*--)
                                 ------+---------+---------+---------+---
                                     -60         0        60       120
```

Group = K-A subtracted from:

```
Group   Lower  Center   Upper  ------+---------+---------+---------+---
```

```
K-HU   -43,14  -25,34   -7,53           (--*--)
K-SC   -53,66  -35,85  -18,05         (--*--)
                                -------+---------+---------+---------+---
                                    -60         0        60       120


Group = K-HU subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+---
K-SC   -28,32  -10,52   7,28             (--*--)
                               -------+---------+---------+---------+---
                                   -60         0        60       120
```

One-way ANOVA: Nonanoic acid versus Group

```
Source  DF       SS      MS       F      P
Group    7  45185,7  6455,1  526,46  0,000
Error   14    171,7    12,3
Total   21  45357,3

S = 3,502   R-Sq = 99,62%   R-Sq(adj) = 99,43%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---------+---------+---------+---------+
E-A      3   28,22   2,66      (*)
E-Laff   3   49,46   3,38          (*)
E-LT-SC  2  171,29   8,93                                  (*)
E-SC     2  109,98   4,13                      (*)
K-13     3   43,71   3,93         (*)
K-A      3   22,81   0,73     (*
K-HU     3    9,00   0,44  (*)
K-SC     3   49,81   1,64          (*)
                          ---------+---------+---------+---------+
                                  50       100       150       200

Pooled StDev = 3,50


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  2  171,29  A
E-SC     2  109,98    B
K-SC     3   49,81      C
E-Laff   3   49,46      C
K-13     3   43,71      C
E-A      3   28,22        D
K-A      3   22,81        D
K-HU     3    9,00          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group
```

```
Individual confidence level = 99,67%


Group = E-A subtracted from:

Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-Laff    11,16   21,25   31,33                   (*)
E-LT-SC  131,79  143,07  154,35                             (*)
E-SC      70,48   81,76   93,03                        (*)
K-13       5,40   15,49   25,58                   (*)
K-A      -15,49   -5,41    4,68               (*)
K-HU     -29,31  -19,22   -9,13              (*)
K-SC      11,50   21,59   31,68                   (*)
                              -------+---------+---------+---------+--
                                  -100         0       100       200


Group = E-Laff subtracted from:

Group     Lower  Center   Upper  -------+---------+---------+---------+--
E-LT-SC  110,54  121,82  133,10                             (*)
E-SC      49,23   60,51   71,79                       (*)
K-13     -15,84   -5,75    4,33               (*)
K-A      -36,74  -26,65  -16,56             (*)
K-HU     -50,55  -40,47  -30,38            (*)
K-SC      -9,74    0,35   10,43                (*)
                              -------+---------+---------+---------+--
                                  -100         0       100       200


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
E-SC    -73,67   -61,31   -48,96           (*)
K-13   -138,85  -127,58  -116,30     (*)
K-A    -159,75  -148,47  -137,20   (*)
K-HU   -173,57  -162,29  -151,01  (*)
K-SC   -132,76  -121,48  -110,20     (*)
                               -------+---------+---------+---------+--
                                   -100         0       100       200


Group = E-SC subtracted from:

Group    Lower   Center   Upper  -------+---------+---------+---------+--
K-13    -77,54   -66,26  -54,99          (*-)
K-A     -98,44   -87,16  -75,88        (*)
K-HU   -112,26  -100,98  -89,70       (*)
K-SC    -71,44   -60,17  -48,89           (*)
                              -------+---------+---------+---------+--
                                  -100         0       100       200


Group = K-13 subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-A    -30,99  -20,90  -10,81               (*)
K-HU   -44,80  -34,71  -24,62              (*)
K-SC    -3,99    6,10   16,19                  (*)
                            -------+---------+---------+---------+--
```

```
                                  -100         0       100       200


Group = K-A subtracted from:

Group   Lower  Center  Upper  -------+---------+---------+---------+--
K-HU   -23,90  -13,81  -3,73                (*)
K-SC    16,91   27,00  37,09                    (*)
                              -------+---------+---------+---------+--
                                  -100         0       100       200


Group = K-HU subtracted from:

Group  Lower  Center  Upper  -------+---------+---------+---------+--
K-SC   30,72   40,81  50,90                    (*)
                             -------+---------+---------+---------+--
                                 -100         0       100       200
```

One-way ANOVA: Tetradecanoic acid versus Group

```
Source  DF      SS      MS       F      P
Group    1  1332,4  1332,4  113,52  0,000
Error    4    46,9    11,7
Total    5  1379,3

S = 3,426   R-Sq = 96,60%   R-Sq(adj) = 95,75%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level   N    Mean  StDev  --+---------+---------+---------+-------
E-A     3  39,649  3,694  (----*----)
E-Laff  3  69,452  3,135                       (----*---)
                         --+---------+---------+---------+-------
                          36        48        60        72

Pooled StDev = 3,426


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
E-Laff  3  69,452  A
E-A     3  39,649    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group    Lower  Center   Upper  ------+---------+---------+---------+---
```

```
E-Laff  22,037  29,803  37,570                          (------*-----)
                                  ------+---------+---------+---------+---
                                        0        12        24        36
```

One-way ANOVA: Dodecanoic acid versus Group

```
Source  DF      SS      MS      F      P
Group    1  4075,6  4075,6  87,00  0,001
Error    4   187,4    46,8
Total    5  4263,0

S = 6,844   R-Sq = 95,60%   R-Sq(adj) = 94,51%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  -------+---------+---------+---------+--
E-A     3   56,72   3,54  (----*-----)
E-Laff  3  108,84   9,01                          (----*-----)
                          -------+---------+---------+---------+--
                                60        80       100       120

Pooled StDev = 6,84


Grouping Information Using Tukey Method

Group   N     Mean  Grouping
E-Laff  3  108,842  A
E-A     3   56,717    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group    Lower  Center   Upper  ------+---------+---------+---------+---
E-Laff  36,609  52,125  67,641                       (-----*-----)
                                  ------+---------+---------+---------+---
                                        0        25        50        75
```

One-way ANOVA: Pentanoic acid versus Group

```
Source  DF      SS      MS       F      P
Group    5  847043  169409  167,40  0,000
Error   12   12144    1012
Total   17  859187

S = 31,81   R-Sq = 98,59%   R-Sq(adj) = 98,00%
```

```
                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  -------+---------+---------+---------+--
E-A     3  104,50   9,16  (-*-)
E-Laff  3  374,68   6,30               (-*-)
K-13    3  623,99  24,75                         (-*-)
K-A     3  463,39  43,74                    (-*-)
K-HU    3  405,91   4,83                (-*-)
K-SC    3  804,83  58,30                                   (-*-)
                          -------+---------+---------+---------+--
                               200       400       600       800
```

Pooled StDev = 31,81

Grouping Information Using Tukey Method

Group	N	Mean	Grouping
K-SC	3	804,83	A
K-13	3	623,99	B
K-A	3	463,39	C
K-HU	3	405,91	C D
E-Laff	3	374,68	D
E-A	3	104,50	E

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%

Group = E-A subtracted from:

```
Group    Lower  Center   Upper  -----+---------+---------+---------+----
E-Laff  182,94  270,18  357,42                    (--*-)
K-13    432,25  519,49  606,73                           (--*-)
K-A     271,65  358,89  446,13                      (-*--)
K-HU    214,17  301,41  388,65                     (--*-)
K-SC    613,09  700,33  787,57                                 (-*--)
                          -----+---------+---------+---------+----
                            -350         0       350       700
```

Group = E-Laff subtracted from:

```
Group   Lower  Center   Upper  -----+---------+---------+---------+----
K-13   162,08  249,32  336,56                   (-*--)
K-A      1,47   88,71  175,95               (--*-)
K-HU   -56,01   31,23  118,47              (--*-)
K-SC   342,91  430,15  517,39                        (-*--)
                          -----+---------+---------+---------+----
                            -350         0       350       700
```

Group = K-13 subtracted from:

```
Group    Lower   Center    Upper  -----+---------+---------+---------+----
```

```
K-A    -247,85  -160,61   -73,37          (-*--)
K-HU   -305,32  -218,08  -130,84        (--*-)
K-SC     93,59   180,83   268,07                    (-*--)
                                  -----+---------+---------+---------+----
                                    -350         0       350       700


Group = K-A subtracted from:

Group    Lower  Center   Upper  -----+---------+---------+---------+----
K-HU   -144,72  -57,48   29,76             (-*--)
K-SC    254,20  341,44  428,68                       (--*-)
                           -----+---------+---------+---------+----
                             -350         0       350       700


Group = K-HU subtracted from:

Group   Lower  Center   Upper  -----+---------+---------+---------+----
K-SC   311,68  398,92  486,16                        (-*--)
                          -----+---------+---------+---------+----
                            -350         0       350       700
```

One-way ANOVA: Isobutyric acid versus Group

```
Source  DF       SS      MS       F      P
Group    7  1376941  196706  159,98  0,000
Error   15    18444    1230
Total   22  1395385

S = 35,07   R-Sq = 98,68%   R-Sq(adj) = 98,06%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---------+---------+---------+---------+
E-A      3   72,21   2,67  (-*-)
E-Laff   3  229,30  15,09       (-*-)
E-LT-SC  3  197,95  16,20      (-*-)
E-SC     2  119,39   1,35    (-*-)
K-13     3  491,98  44,86                 (-*)
K-A      3  389,59  29,94              (-*)
K-HU     3  360,52  10,56             (*-)
K-SC     3  885,64  75,52                                 (*-)
                          ---------+---------+---------+---------+
                                 250       500       750      1000

Pooled StDev = 35,07


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-SC     3  885,64  A
K-13     3  491,98     B
K-A      3  389,59       C
K-HU     3  360,52       C
E-Laff   3  229,30         D
```

```
E-LT-SC  3  197,95        D
E-SC     2  119,39        D E
E-A      3   72,21          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group     Lower  Center   Upper  --------+---------+---------+---------+-
E-Laff    57,07  157,08  257,09                    (-*-)
E-LT-SC   25,72  125,73  225,74                    (-*-)
E-SC     -64,64   47,17  158,99                  (-*-)
K-13     319,75  419,76  519,77                        (-*-)
K-A      217,37  317,38  417,39                     (-*-)
K-HU     188,30  288,31  388,32                     (-*-)
K-SC     713,41  813,42  913,43                              (-*-)
                                 --------+---------+---------+---------+-
                                      -500         0       500      1000


Group = E-Laff subtracted from:

Group      Lower   Center   Upper  --------+---------+---------+---------+-
E-LT-SC  -131,36   -31,35   68,66               (-*-)
E-SC     -221,72  -109,91    1,91             (-*-)
K-13      162,67   262,68  362,69                    (-*-)
K-A        60,28   160,30  260,31                 (-*-)
K-HU       31,21   131,23  231,24                 (-*-)
K-SC      556,33   656,34  756,35                          (-*-)
                                 --------+---------+---------+---------+-
                                      -500         0       500      1000


Group = E-LT-SC subtracted from:

Group    Lower  Center   Upper  --------+---------+---------+---------+-
E-SC   -190,37  -78,56   33,26           (-*--)
K-13    194,02  294,03  394,04                   (-*-)
K-A      91,64  191,65  291,66                (-*-)
K-HU     62,57  162,58  262,59                (-*-)
K-SC    587,68  687,69  787,70                         (-*-)
                                 --------+---------+---------+---------+-
                                      -500         0       500      1000


Group = E-SC subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-13   260,77  372,59  484,40                   (-*--)
K-A    158,39  270,20  382,02                (-*--)
K-HU   129,32  241,13  352,95                (-*-)
K-SC   654,43  766,25  878,06                         (-*--)
                                 --------+---------+---------+---------+-
                                      -500         0       500      1000
```

```
Group = K-13 subtracted from:

Group    Lower   Center   Upper  --------+---------+---------+---------+-
K-A    -202,40  -102,38   -2,37               (-*-)
K-HU   -231,47  -131,45  -31,44              (-*-)
K-SC    293,65   393,66  493,67                          (-*-)
                                --------+---------+---------+---------+-
                                     -500         0       500      1000


Group = K-A subtracted from:

Group    Lower  Center   Upper  --------+---------+---------+---------+-
K-HU   -129,08  -29,07   70,94               (-*-)
K-SC    396,03  496,05  596,06                          (-*-)
                               --------+---------+---------+---------+-
                                    -500         0       500      1000


Group = K-HU subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-SC   425,10  525,12  625,13                          (-*-)
                              --------+---------+---------+---------+-
                                   -500         0       500      1000
```

One-way ANOVA: Heptanoic acid versus Group

```
Source  DF      SS      MS       F      P
Group    4  5296,0  1324,0  115,55  0,000
Error   10   114,6    11,5
Total   14  5410,6

S = 3,385   R-Sq = 97,88%   R-Sq(adj) = 97,04%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level    N    Mean  StDev  -------+---------+---------+---------+--
E-LT-SC  3  86,063  4,653                            (-*-)
K-13     3  70,314  3,639                      (-*-)
K-A      3  74,439  1,945                        (-*-)
K-HU     3  62,658  4,212                  (-*--)
K-SC     3  30,372  0,935  (-*-)
                         -------+---------+---------+---------+--
                               40        60        80       100

Pooled StDev = 3,385


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  86,063  A
K-A      3  74,439    B
K-13     3  70,314    B C
```

```
K-HU     3  62,658      C
K-SC     3  30,372        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,18%


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  --+---------+---------+---------+-------
K-13   -24,837  -15,749   -6,661               (--*--)
K-A    -20,712  -11,624   -2,537                (--*--)
K-HU   -32,493  -23,405  -14,318            (--*--)
K-SC   -64,779  -55,692  -46,604  (--*--)
                                  --+---------+---------+---------+-------
                                  -60       -30         0        30


Group = K-13 subtracted from:

Group    Lower   Center    Upper  --+---------+---------+---------+-------
K-A     -4,963    4,125   13,212                    (--*--)
K-HU   -16,744   -7,656    1,431                 (--*--)
K-SC   -49,031  -39,943  -30,855       (--*--)
                                  --+---------+---------+---------+-------
                                  -60       -30         0        30


Group = K-A subtracted from:

Group    Lower   Center    Upper  --+---------+---------+---------+-------
K-HU   -20,869  -11,781   -2,693                (--*--)
K-SC   -53,155  -44,067  -34,980     (--*--)
                                  --+---------+---------+---------+-------
                                  -60       -30         0        30


Group = K-HU subtracted from:

Group    Lower   Center    Upper  --+---------+---------+---------+-------
K-SC   -41,374  -32,286  -23,198         (--*--)
                                  --+---------+---------+---------+-------
                                  -60       -30         0        30
```

One-way ANOVA: Acetic acid versus Group

```
Source  DF        SS       MS       F      P
Group    7  17767320  2538189  481,16  0,000
Error   14     73852     5275
Total   21  17841172

S = 72,63   R-Sq = 99,59%   R-Sq(adj) = 99,38%
```

```
                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ----+---------+---------+---------+-----
E-A      3   652,2   26,7   (*)
E-Laff   3   541,4    1,5  (*)
E-LT-SC  2  1662,2   58,5              (-*)
E-SC     2  1317,8   78,7           (*-)
K-13     3  1522,3  103,4             (*)
K-A      3  3414,6   56,5                                      (*)
K-HU     3   691,2   20,5    (*)
K-SC     3  1379,8  130,8            (*)
                          ----+---------+---------+---------+-----
                            800      1600      2400      3200

Pooled StDev = 72,6


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  3414,6  A
E-LT-SC  2  1662,2    B
K-13     3  1522,3    B C
K-SC     3  1379,8      C
E-SC     2  1317,8      C
K-HU     3   691,2        D
E-A      3   652,2        D
E-Laff   3   541,4        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%


Group = E-A subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-Laff   -320,0  -110,7    98,5                  (*-)
E-LT-SC   776,1  1010,1  1244,0                       (*-)
E-SC      431,7   665,6   899,5                    (*-)
K-13      660,9   870,2  1079,4                     (*-)
K-A      2553,2  2762,5  2971,7                                (*-)
K-HU     -170,2    39,0   248,3                   (*-)
K-SC      518,4   727,6   936,9                      (-*)
                          ---------+---------+---------+---------+
                               -1600         0      1600      3200


Group = E-Laff subtracted from:

Group     Lower  Center   Upper  ---------+---------+---------+---------+
E-LT-SC   886,9  1120,8  1354,8                         (*)
E-SC      542,4   776,3  1010,3                      (-*)
K-13      771,7   980,9  1190,2                        (*)
K-A      2664,0  2873,2  3082,5                                 (*)
```

```
K-HU      -59,5   149,8   359,0                     (*)
K-SC      629,1   838,4  1047,6                        (*-)
                                  ---------+---------+---------+---------+
                                       -1600         0      1600      3200
```

Group = E-LT-SC subtracted from:

```
Group    Lower  Center   Upper  ---------+---------+---------+---------+
E-SC    -600,8  -344,5   -88,2                (-*)
K-13    -373,8  -139,9    94,1                  (*-)
K-A     1518,4  1752,4  1986,3                            (-*)
K-HU   -1205,0  -971,0  -737,1            (-*)
K-SC    -516,4  -282,4   -48,5                 (*-)
                                  ---------+---------+---------+---------+
                                       -1600         0      1600      3200
```

Group = E-SC subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-13    -29,4   204,6   438,5                    (*-)
K-A    1862,9  2096,9  2330,8                              (*-)
K-HU   -860,5  -626,6  -392,6               (*-)
K-SC   -171,9    62,0   296,0                   (*-)
                                  ---------+---------+---------+---------+
                                       -1600         0      1600      3200
```

Group = K-13 subtracted from:

```
Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-A     1683,0  1892,3  2101,5                              (*)
K-HU   -1040,4  -831,2  -621,9            (-*)
K-SC    -351,8  -142,6    66,7                 (*)
                                  ---------+---------+---------+---------+
                                       -1600         0      1600      3200
```

Group = K-A subtracted from:

```
Group    Lower   Center    Upper  ---------+---------+---------+---------+
K-HU   -2932,7  -2723,4  -2514,2   (*)
K-SC   -2244,1  -2034,8  -1825,6       (*-)
                                  ---------+---------+---------+---------+
                                       -1600         0      1600      3200
```

Group = K-HU subtracted from:

```
Group  Lower  Center  Upper  ---------+---------+---------+---------+
K-SC   479,4   688,6  897,8                       (*-)
                              ---------+---------+---------+---------+
                                   -1600         0      1600      3200
```

One-way ANOVA: Diethyl dl-malate versus Group

```
Source  DF      SS     MS      F      P
Group    3  204,07  68,02  15,69  0,001
Error    8   34,69   4,34
Total   11  238,76

S = 2,082   R-Sq = 85,47%   R-Sq(adj) = 80,02%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level  N    Mean  StDev  ---------+---------+---------+---------+
K-13   3  35,801  2,195                      (------*-----)
K-A    3  36,581  2,274                        (-----*------)
K-HU   3  29,202  2,138       (------*------)
K-SC   3  27,015  1,670  (------*-----)
                          ---------+---------+---------+---------+
                                28,0      32,0      36,0      40,0

Pooled StDev = 2,082


Grouping Information Using Tukey Method

Group  N    Mean  Grouping
K-A    3  36,581  A
K-13   3  35,801  A
K-HU   3  29,202    B
K-SC   3  27,015    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,74%


Group = K-13 subtracted from:

Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-A     -4,666   0,780   6,226              (------*------)
K-HU   -12,045  -6,599  -1,153      (------*------)
K-SC   -14,232  -8,786  -3,340   (------*------)
                               ---------+---------+---------+---------+
                                     -8,0       0,0       8,0      16,0


Group = K-A subtracted from:

Group    Lower  Center   Upper  ---------+---------+---------+---------+
K-HU   -12,825  -7,379  -1,933     (------*------)
K-SC   -15,012  -9,566  -4,120  (------*------)
                               ---------+---------+---------+---------+
                                     -8,0       0,0       8,0      16,0
```

```
Group = K-HU subtracted from:

Group   Lower  Center  Upper  ---------+---------+---------+---------+
K-SC   -7,633  -2,187  3,259           (------*------)
                             ---------+---------+---------+---------+
                                   -8,0       0,0       8,0      16,0
```

One-way ANOVA: γ-butyrolactone versus Group

```
Source  DF       SS      MS       F      P
Group    7  3073759  439108  584,57  0,000
Error   16    12019     751
Total   23  3085778

S = 27,41   R-Sq = 99,61%   R-Sq(adj) = 99,44%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  --+---------+---------+---------+-------
E-A      3   283,2   25,3  (*-)
E-Laff   3   339,4   22,0    (*)
E-LT-SC  3   522,3   29,1          (*-)
E-SC     3   578,7    4,2            (*)
K-13     3  1216,7   30,8                                  (-*)
K-A      3  1176,0   30,3                                 (*)
K-HU     3  1074,4   20,6                               (*)
K-SC     3   495,7   41,5         (-*)
                          --+---------+---------+---------+-------
                          300       600       900      1200

Pooled StDev = 27,4


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-13     3  1216,7  A
K-A      3  1176,0  A
K-HU     3  1074,4     B
E-SC     3   578,7      C
E-LT-SC  3   522,3      C D
K-SC     3   495,7        D
E-Laff   3   339,4          E
E-A      3   283,2          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%


Group = E-A subtracted from:

Group    Lower  Center   Upper  ---------+---------+---------+---------+
```

```
E-Laff   -21,3    56,2   133,7                    (*-)
E-LT-SC  161,6   239,1   316,6                       (-*)
E-SC     218,0   295,5   373,0                        (-*)
K-13     856,0   933,5  1011,1                                 (-*)
K-A      815,3   892,8   970,3                               (-*)
K-HU     713,6   791,2   868,7                            (-*)
K-SC     135,0   212,5   290,1                       (*-)
                                 ---------+---------+---------+---------+
                                       -500         0       500      1000
```

Group = E-Laff subtracted from:

```
Group    Lower  Center  Upper  ---------+---------+---------+---------+
E-LT-SC  105,4   182,9  260,4                      (-*)
E-SC     161,8   239,3  316,8                       (-*)
K-13     799,8   877,3  954,9                                (-*)
K-A      759,1   836,6  914,1                             (-*)
K-HU     657,5   735,0  812,5                          (-*)
K-SC      78,8   156,4  233,9                       (*-)
                              ---------+---------+---------+---------+
                                    -500         0       500      1000
```

Group = E-LT-SC subtracted from:

```
Group   Lower  Center  Upper  ---------+---------+---------+---------+
E-SC    -21,1    56,4  133,9                   (*-)
K-13    616,9   694,4  772,0                            (-*)
K-A     576,2   653,7  731,2                            (*-)
K-HU    474,6   552,1  629,6                         (-*-)
K-SC   -104,1   -26,5   51,0                 (*-)
                             ---------+---------+---------+---------+
                                   -500         0       500      1000
```

Group = E-SC subtracted from:

```
Group   Lower  Center  Upper  ---------+---------+---------+---------+
K-13    560,5   638,0  715,6                               (-*)
K-A     519,8   597,3  674,8                             (-*)
K-HU    418,1   495,7  573,2                          (-*)
K-SC   -160,5   -82,9   -5,4                (*-)
                             ---------+---------+---------+---------+
                                   -500         0       500      1000
```

Group = K-13 subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-A    -118,3   -40,7    36,8                 (*-)
K-HU   -219,9  -142,3   -64,8               (*-)
K-SC   -798,5  -721,0  -643,4     (-*)
                             ---------+---------+---------+---------+
                                   -500         0       500      1000
```

Group = K-A subtracted from:

```
Group   Lower  Center   Upper  ---------+---------+---------+---------+
```

```
K-HU   -179,2  -101,6   -24,1                  (-*-)
K-SC   -757,8  -680,3  -602,7       (*-)
                                 ---------+---------+---------+---------+
                                       -500         0       500      1000


Group = K-HU subtracted from:

Group   Lower  Center   Upper  ---------+---------+---------+---------+
K-SC   -656,2  -578,6  -501,1        (*-)
                                 ---------+---------+---------+---------+
                                       -500         0       500      1000
```

One-way ANOVA: Pantolactone versus Group

```
Source  DF      SS     MS      F      P
Group    7  2823,5  403,4  19,72  0,000
Error   15   306,7   20,4
Total   22  3130,2

S = 4,522   R-Sq = 90,20%   R-Sq(adj) = 85,63%


                           Individual 95% CIs For Mean Based on
                           Pooled StDev
Level    N    Mean  StDev  ---+---------+---------+---------+------
E-A      3  62,268  6,142            (----*----)
E-Laff   3  50,401  0,912  (----*----)
E-LT-SC  3  72,874  5,175                     (----*---)
E-SC     2  54,405  4,546     (----*-----)
K-13     3  65,245  6,428               (---*----)
K-A      3  77,345  3,878                        (---*----)
K-HU     3  64,533  3,690              (----*---)
K-SC     3  86,679  2,778                                 (---*----)
                           ---+---------+---------+---------+------
                             48        60        72        84

Pooled StDev = 4,522


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-SC     3  86,679  A
K-A      3  77,345  A B
E-LT-SC  3  72,874    B C
K-13     3  65,245    B C D
K-HU     3  64,533    B C D
E-A      3  62,268      C D E
E-SC     2  54,405        D E
E-Laff   3  50,401          E

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group
```

```
Individual confidence level = 99,67%


Group = E-A subtracted from:

Group      Lower   Center   Upper    +---------+---------+---------+-------
E-Laff   -24,765  -11,868   1,030              (----*----)
E-LT-SC   -2,292   10,606  23,504                       (----*----)
E-SC     -22,283   -7,863   6,557               (-----*-----)
K-13      -9,921    2,977  15,874                    (----*----)
K-A        2,180   15,077  27,975                         (----*----)
K-HU     -10,633    2,265  15,163                    (----*----)
K-SC      11,514   24,411  37,309                              (----*----)
                              +---------+---------+---------+-------
                            -50       -25         0        25


Group = E-Laff subtracted from:

Group      Lower  Center   Upper    +---------+---------+---------+--------
E-LT-SC    9,576  22,474  35,371                          (----*----)
E-SC     -10,415   4,005  18,425                 (-----*----)
K-13       1,947  14,844  27,742                      (----*----)
K-A       14,047  26,945  39,842                           (----*----)
K-HU       1,235  14,133  27,030                      (-----*----)
K-SC      23,381  36,279  49,177                               (-----*---)
                            +---------+---------+---------+--------
                          -50       -25         0        25


Group = E-LT-SC subtracted from:

Group    Lower   Center   Upper    +---------+---------+---------+---------
E-SC   -32,889  -18,469  -4,049           (-----*----)
K-13   -20,527   -7,629   5,268                (----*----)
K-A     -8,426    4,471  17,369                     (----*----)
K-HU   -21,239   -8,341   4,557                (----*----)
K-SC     0,908   13,805  26,703                          (-----*----)
                              +---------+---------+---------+---------
                            -50       -25         0        25


Group = E-SC subtracted from:

Group   Lower  Center   Upper    +---------+---------+---------+---------
K-13   -3,581  10,839  25,259                    (----*-----)
K-A     8,520  22,940  37,360                        (-----*-----)
K-HU   -4,292  10,128  24,548                   (-----*-----)
K-SC   17,854  32,274  46,694                             (-----*-----)
                            +---------+---------+---------+---------
                          -50       -25         0        25


Group = K-13 subtracted from:

Group    Lower  Center   Upper    +---------+---------+---------+---------
K-A     -0,797  12,101  24,998                      (----*----)
K-HU   -13,609  -0,711  12,186                (----*----)
K-SC     8,537  21,435  34,332                       (-----*----)
                          +---------+---------+---------+---------
```

```
                                -50       -25         0        25


Group = K-A subtracted from:

Group    Lower   Center   Upper    +---------+---------+---------+---------
K-HU   -25,710  -12,812   0,086             (----*----)
K-SC    -3,564    9,334  22,232                       (----*----)
                                  +---------+---------+---------+---------
                                -50       -25         0        25


Group = K-HU subtracted from:

Group  Lower  Center   Upper    +---------+---------+---------+---------
K-SC   9,249  22,146  35,044                         (----*----)
                               +---------+---------+---------+---------
                             -50       -25         0        25
```

One-way ANOVA: 2-Methoxy-4-vinylphenol versus Group

```
Source  DF        SS       MS       F      P
Group    7  188306,9  26901,0  376,28  0,000
Error   16    1143,9     71,5
Total   23  189450,8

S = 8,455   R-Sq = 99,40%   R-Sq(adj) = 99,13%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ----+---------+---------+---------+-----
E-A      3  142,38   9,09              (*-)
E-Laff   3  176,57   5,32                   (*-)
E-LT-SC  3  283,40  18,50                                (*-)
E-SC     3  290,51   5,90                                 (-*)
K-13     3   79,03   1,40      (*-)
K-A      3  153,11   7,84               (-*)
K-HU     3   52,17   4,50  (*-)
K-SC     3  286,06   0,68                                (-*)
                          ----+---------+---------+---------+-----
                             70       140       210       280

Pooled StDev = 8,46


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-SC     3  290,51  A
K-SC     3  286,06  A
E-LT-SC  3  283,40  A
E-Laff   3  176,57    B
K-A      3  153,11    B C
E-A      3  142,38      C
K-13     3   79,03        D
K-HU     3   52,17          E
```

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,68%

Group = E-A subtracted from:

Group	Lower	Center	Upper	-------+---------+---------+---------+--
E-Laff	10,27	34,19	58,11	(*-)
E-LT-SC	117,10	141,02	164,94	(*-)
E-SC	124,21	148,14	172,06	(-*)
K-13	-87,26	-63,34	-39,42	(-*)
K-A	-13,19	10,73	34,65	(-*)
K-HU	-114,12	-90,20	-66,28	(-*-)
K-SC	119,77	143,69	167,61	(-*)

-------+---------+---------+---------+--
-150 0 150 300

Group = E-Laff subtracted from:

Group	Lower	Center	Upper	-------+---------+---------+---------+-
-				
E-LT-SC	82,91	106,83	130,75	(*-)
E-SC	90,02	113,94	137,86	(-*)
K-13	-121,45	-97,53	-73,61	(*-)
K-A	-47,38	-23,46	0,46	(*-)
K-HU	-148,31	-124,39	-100,47	(-*)
K-SC	85,58	109,50	133,42	(*-)

-------+---------+---------+---------+-
-
-150 0 150 300

Group = E-LT-SC subtracted from:

Group	Lower	Center	Upper	-------+---------+---------+---------+--
E-SC	-16,81	7,11	31,03	(*-)
K-13	-228,28	-204,36	-180,44	(*-)
K-A	-154,21	-130,29	-106,37	(*-)
K-HU	-255,14	-231,22	-207,30	(-*)
K-SC	-21,25	2,67	26,59	(*-)

-------+---------+---------+---------+--
-150 0 150 300

Group = E-SC subtracted from:

Group	Lower	Center	Upper	-------+---------+---------+---------+--
K-13	-235,40	-211,48	-187,56	(-*)
K-A	-161,32	-137,40	-113,48	(-*)
K-HU	-262,26	-238,34	-214,42	(*-)
K-SC	-28,37	-4,45	19,47	(-*)

-------+---------+---------+---------+--
-150 0 150 300

```
Group = K-13 subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-A     50,15   74,07   97,99                    (-*-)
K-HU   -50,78  -26,86   -2,94               (*-)
K-SC   183,11  207,03  230,95                              (-*)
                              -------+---------+---------+---------+--
                                  -150         0       150       300


Group = K-A subtracted from:

Group    Lower   Center   Upper  -------+---------+---------+---------+--
K-HU   -124,86  -100,93  -77,01          (*-)
K-SC    109,03   132,95  156,87                         (-*)
                             -------+---------+---------+---------+--
                                 -150         0       150       300


Group = K-HU subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-SC   209,97  233,89  257,81                           (-*)
                              -------+---------+---------+---------+--
                                  -150         0       150       300
```

One-way ANOVA: 4-vinyl-phenol versus Group

```
Source  DF     SS     MS       F      P
Group    3  82716  27572  107,17  0,000
Error    8   2058    257
Total   11  84774

S = 16,04   R-Sq = 97,57%   R-Sq(adj) = 96,66%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  ---------+---------+---------+---------+
E-LT-SC  3  329,95  28,57                                  (--*--)
E-SC     3  254,27  12,56                        (--*--)
K-A      3  100,22   4,13  (--*--)
K-SC     3  213,46   6,17                 (--*---)
                          ---------+---------+---------+---------+
                                 140       210       280       350

Pooled StDev = 16,04


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
E-LT-SC  3  329,95  A
E-SC     3  254,27    B
K-SC     3  213,46    B
K-A      3  100,22      C
```

```
Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,74%


Group = E-LT-SC subtracted from:

Group    Lower   Center    Upper  ---+---------+---------+---------+------
E-SC   -117,63   -75,68   -33,73              (---*--)
K-A    -271,68  -229,72  -187,77  (---*--)
K-SC   -158,44  -116,49   -74,54           (--*---)
                                 ---+---------+---------+---------+------
                                 -240      -120         0       120


Group = E-SC subtracted from:

Group    Lower   Center    Upper  ---+---------+---------+---------+------
K-A    -195,99  -154,04  -112,09        (--*---)
K-SC    -82,76   -40,81     1,14                (---*--)
                                 ---+---------+---------+---------+------
                                 -240      -120         0       120


Group = K-A subtracted from:

Group  Lower  Center   Upper  ---+---------+---------+---------+------
K-SC   71,28  113,24  155,19                              (--*---)
                           ---+---------+---------+---------+------
                           -240      -120         0       120
```

One-way ANOVA: Phenol versus Group

```
Source  DF      SS      MS       F      P
Group    1  216,47  216,47  114,16  0,000
Error    4    7,59    1,90
Total    5  224,06

S = 1,377   R-Sq = 96,61%   R-Sq(adj) = 95,77%


                        Individual 95% CIs For Mean Based on Pooled StDev
Level   N    Mean  StDev     +---------+---------+---------+---------
E-A     3  24,180  1,770                          (---*----)
E-Laff  3  12,167  0,811     (---*----)
                             +---------+---------+---------+---------
                           10,0      15,0      20,0      25,0

Pooled StDev = 1,377


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
```

```
E-A     3  24,180  A
E-Laff  3  12,167    B

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 95,00%


Group = E-A subtracted from:

Group     Lower   Center   Upper      +---------+---------+---------+------
E-Laff  -15,135  -12,013  -8,891      (-----*-----)
                                     +---------+---------+---------+------
                                  -15,0     -10,0      -5,0       0,0
```

One-way ANOVA: Tyrosol versus Group

```
Source  DF       SS      MS       F      P
Group    7  5282953  754708  383,26  0,000
Error   14    27569    1969
Total   21  5310522

S = 44,38   R-Sq = 99,48%   R-Sq(adj) = 99,22%


                           Individual 95% CIs For Mean Based on
                           Pooled StDev
Level    N    Mean  StDev  -------+---------+---------+---------+--
E-A      3  1874,5   36,4                         (*-)
E-Laff   3  1723,0   51,7                       (*-)
E-LT-SC  2  1666,3   25,3                      (*-)
E-SC     2  1208,8    9,3            (*-)
K-13     3   722,4   66,1  (*-)
K-A      3  2217,5   33,1                                  (*)
K-HU     3   906,6   18,3      (*)
K-SC     3  1656,3   60,2                      (*)
                           -------+---------+---------+---------+--
                               1000      1500      2000      2500

Pooled StDev = 44,4


Grouping Information Using Tukey Method

Group    N    Mean  Grouping
K-A      3  2217,5  A
E-A      3  1874,5    B
E-Laff   3  1723,0      C
E-LT-SC  2  1666,3      C
K-SC     3  1656,3      C
E-SC     2  1208,8        D
K-HU     3   906,6          E
K-13     3   722,4            F
```

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%

Group = E-A subtracted from:

Group	Lower	Center	Upper	------+---------+---------+---------+---
E-Laff	-279,4	-151,5	-23,7	(*-)
E-LT-SC	-351,2	-208,2	-65,3	(-*)
E-SC	-808,7	-665,7	-522,8	(*-)
K-13	-1280,0	-1152,1	-1024,3	(*-)
K-A	215,1	343,0	470,8	(*-)
K-HU	-1095,8	-968,0	-840,1	(*-)
K-SC	-346,1	-218,2	-90,4	(*)
				------+---------+---------+---------+---
				-1000 0 1000 2000

Group = E-Laff subtracted from:

Group	Lower	Center	Upper	------+---------+---------+---------+---
E-LT-SC	-199,7	-56,7	86,2	(*-)
E-SC	-657,1	-514,2	-371,3	(-*)
K-13	-1128,4	-1000,6	-872,8	(*)
K-A	366,6	494,5	622,3	(*)
K-HU	-944,3	-816,5	-688,6	(*)
K-SC	-194,6	-66,7	61,1	(*-)
				------+---------+---------+---------+---
				-1000 0 1000 2000

Group = E-LT-SC subtracted from:

Group	Lower	Center	Upper	------+---------+---------+---------+---
E-SC	-614,1	-457,5	-300,9	(*-)
K-13	-1086,8	-943,9	-800,9	(-*)
K-A	408,3	551,2	694,1	(-*)
K-HU	-902,7	-759,7	-616,8	(*-)
K-SC	-152,9	-10,0	132,9	(-*)
				------+---------+---------+---------+---
				-1000 0 1000 2000

Group = E-SC subtracted from:

Group	Lower	Center	Upper	------+---------+---------+---------+---
K-13	-629,3	-486,4	-343,5	(*-)
K-A	865,8	1008,7	1151,6	(*-)
K-HU	-445,2	-302,2	-159,3	(*)
K-SC	304,6	447,5	590,4	(*-)
				------+---------+---------+---------+---
				-1000 0 1000 2000

```
Group = K-13 subtracted from:

Group   Lower  Center   Upper  ------+---------+---------+---------+---
K-A    1367,2  1495,1  1622,9                                  (*)
K-HU     56,3   184,2   312,0                    (*)
K-SC    806,0   933,9  1061,7                          (*-)
                                ------+---------+---------+---------+---
                                  -1000         0      1000      2000


Group = K-A subtracted from:

Group    Lower   Center    Upper  ------+---------+---------+---------+---
K-HU   -1438,8  -1310,9  -1183,1    (*)
K-SC    -689,0   -561,2   -433,4           (*-)
                                   ------+---------+---------+---------+---
                                     -1000         0      1000      2000


Group = K-HU subtracted from:

Group  Lower  Center  Upper  ------+---------+---------+---------+---
K-SC   621,9   749,7  877,6                        (*-)
                             ------+---------+---------+---------+---
                               -1000         0      1000      2000
```

One-way ANOVA: Soleron versus Group

```
Source  DF       SS      MS       F      P
Group    5  15030,2  3006,0  103,02  0,000
Error   12    350,2    29,2
Total   17  15380,4

S = 5,402   R-Sq = 97,72%   R-Sq(adj) = 96,77%


                        Individual 95% CIs For Mean Based on
                        Pooled StDev
Level   N   Mean  StDev  ----+---------+---------+---------+-----
E-A     3  35,13   3,36       (--*--)
E-Laff  3  22,47   0,57  (--*--)
K-13    3  81,84   7,33                          (--*-)
K-A     3  97,06   8,48                                (--*--)
K-HU    3  34,53   3,10       (--*--)
K-SC    3  82,18   5,30                          (--*--)
                        ----+---------+---------+---------+-----
                           25        50        75       100

Pooled StDev = 5,40


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
K-A     3  97,061  A
K-SC    3  82,178    B
K-13    3  81,839    B
```

```
E-A     3  35,134      C
K-HU    3  34,529      C
E-Laff  3  22,473      C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:

Group     Lower   Center   Upper  --------+---------+---------+---------+-
E-Laff  -27,475  -12,661   2,153               (-*--)
K-13     31,891   46,706  61,520                         (--*--)
K-A      47,113   61,928  76,742                            (--*--)
K-HU    -15,419   -0,605  14,209                  (--*--)
K-SC     32,230   47,044  61,859                         (--*--)
                                 --------+---------+---------+---------+-
                                       -50         0        50       100


Group = E-Laff subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-13   44,552  59,366  74,181                         (--*--)
K-A    59,774  74,588  89,403                            (--*--)
K-HU   -2,758  12,056  26,870                  (--*--)
K-SC   44,891  59,705  74,519                         (--*--)
                              --------+---------+---------+---------+-
                                    -50         0        50       100


Group = K-13 subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-A      0,408   15,222   30,036                    (--*--)
K-HU   -62,124  -47,310  -32,496        (--*--)
K-SC   -14,475    0,339   15,153                 (--*--)
                                 --------+---------+---------+---------+-
                                       -50         0        50       100


Group = K-A subtracted from:

Group    Lower   Center    Upper  --------+---------+---------+---------+-
K-HU   -77,346  -62,532  -47,718     (-*--)
K-SC   -29,697  -14,883   -0,069              (--*--)
                                 --------+---------+---------+---------+-
                                       -50         0        50       100


Group = K-HU subtracted from:

Group   Lower  Center   Upper  --------+---------+---------+---------+-
K-SC   32,835  47,649  62,463                           (--*-)
                              --------+---------+---------+---------+-
```

```
                                    -50         0        50       100
```

One-way ANOVA: Guaiacol versus Group

```
Source  DF      SS      MS      F      P
Group    5  5199,3  1039,9  66,91  0,000
Error   12   186,5    15,5
Total   17  5385,8

S = 3,942   R-Sq = 96,54%   R-Sq(adj) = 95,09%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level   N    Mean  StDev  ----+---------+---------+---------+-----
E-A     3  63,043  4,830              (--*-)
E-Laff  3  57,149  1,000           (--*-)
K-13    3  61,301  1,370             (--*-)
K-A     3  94,696  4,785                                (-*--)
K-HU    3  37,137  3,367  (--*-)
K-SC    3  57,411  5,729           (--*-)
                          ----+---------+---------+---------+-----
                             40        60        80       100

Pooled StDev = 3,942


Grouping Information Using Tukey Method

Group   N    Mean  Grouping
K-A     3  94,696  A
E-A     3  63,043     B
K-13    3  61,301     B
K-SC    3  57,411     B
E-Laff  3  57,149     B
K-HU    3  37,137       C

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,43%


Group = E-A subtracted from:

Group     Lower   Center    Upper    +---------+---------+---------+-------
--
E-Laff  -16,705   -5,894    4,917                  (--*--)
K-13    -12,552   -1,741    9,070                   (---*--)
K-A      20,842   31,653   42,464                              (--*--)
K-HU    -36,717  -25,906  -15,095            (--*--)
K-SC    -16,443   -5,632    5,179                  (--*--)
                                  +---------+---------+---------+-------
--
                                -70       -35         0        35
```

```
Group = E-Laff subtracted from:

Group    Lower   Center   Upper    +---------+---------+---------+---------
K-13    -6,658    4,153  14,964                    (--*--)
K-A     26,736   37,547  48,358                              (--*--)
K-HU   -30,823  -20,012  -9,201             (--*--)
K-SC   -10,549    0,262  11,073                   (--*--)
                                +---------+---------+---------+---------
                              -70       -35         0        35


Group = K-13 subtracted from:

Group    Lower   Center    Upper    +---------+---------+---------+--------
K-A     22,583   33,394   44,205                           (---*--)
K-HU   -34,976  -24,165  -13,353             (--*--)
K-SC   -14,702   -3,891    6,921                   (--*--)
                                +---------+---------+---------+--------
                              -70       -35         0        35


Group = K-A subtracted from:

Group    Lower   Center    Upper    +---------+---------+---------+--------
K-HU   -68,370  -57,559  -46,748    (---*--)
K-SC   -48,096  -37,285  -26,473          (--*--)
                                +---------+---------+---------+--------
                              -70       -35         0        35


Group = K-HU subtracted from:

Group  Lower  Center   Upper    +---------+---------+---------+---------
K-SC   9,463  20,274  31,085                        (--*--)
                             +---------+---------+---------+---------
                           -70       -35         0        35
```

One-way ANOVA: Acetoin versus Group

```
Source  DF       SS      MS        F      P
Group    7  3145275  449325  1381,23  0,000
Error   15     4880     325
Total   22  3150154

S = 18,04   R-Sq = 99,85%   R-Sq(adj) = 99,77%


                          Individual 95% CIs For Mean Based on
                          Pooled StDev
Level    N    Mean  StDev  -----+---------+---------+---------+----
E-A      3   190,3   10,7   (*)
E-Laff   3   175,9   16,0  (*)
E-LT-SC  2   168,1    0,2  (*)
E-SC     3   178,7    7,8  (*)
K-13     3   200,7   19,1   (*)
K-A      3  1292,3   26,8                                      (*)
```

```
K-HU     3   270,4   26,7     (*)
K-SC     3   190,8   14,5   (*)
                          -----+---------+---------+---------+----
                             300       600       900      1200
```

Pooled StDev = 18,0

Grouping Information Using Tukey Method

Group	N	Mean	Grouping
K-A	3	1292,3	A
K-HU	3	270,4	B
K-13	3	200,7	C
K-SC	3	190,8	C
E-A	3	190,3	C
E-SC	3	178,7	C
E-Laff	3	175,9	C
E-LT-SC	2	168,1	C

Means that do not share a letter are significantly different.

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 99,67%

Group = E-A subtracted from:

```
Group     Lower  Center   Upper      +---------+---------+---------+-------
--
E-Laff    -65,8   -14,4    37,0                        (*)
E-LT-SC   -79,7   -22,2    35,3                        (*)
E-SC      -63,0   -11,5    39,9                        (*)
K-13      -41,0    10,4    61,8                        (*)
K-A      1050,6  1102,0  1153,4
*)
K-HU       28,6    80,1   131,5                         (*)
K-SC      -50,9     0,5    52,0                        (*)
                                  +---------+---------+---------+-------
--
                                -1200      -600         0       600
```

Group = E-Laff subtracted from:

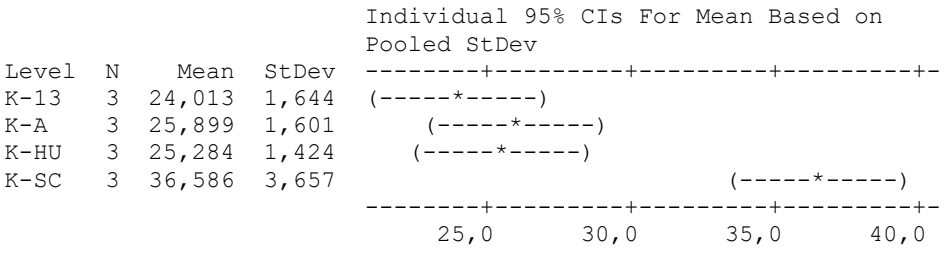
```
Group     Lower  Center   Upper      +---------+---------+---------+-------
--
E-LT-SC   -65,3    -7,8    49,7                        (*)
E-SC      -48,6     2,9    54,3                        (*)
K-13      -26,6    24,8    76,2                         *)
K-A      1065,0  1116,4  1167,9                                        (*)
K-HU       43,0    94,5   145,9                          (*)
K-SC      -36,5    14,9    66,4                        (*)
                                  +---------+---------+---------+-------
                                -1200      -600         0       600
```

```
Group = E-LT-SC subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
E-SC    -46,9    10,7    68,2                        (*)
K-13    -24,9    32,6    90,1                         (*)
K-A    1066,7  1124,2  1181,7
(*)
K-HU     44,8   102,3   159,8                          (*)
K-SC    -34,8    22,7    80,2                        (*)
                                 +---------+---------+---------+---------
                               -1200      -600         0       600


Group = E-SC subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
K-13    -29,5    21,9    73,4                         (*)
K-A    1062,1  1113,5  1165,0                                            (*)
K-HU     40,2    91,6   143,1                          (*)
K-SC    -39,4    12,1    63,5                        (*)
                                 +---------+---------+---------+---------
                               -1200      -600         0       600


Group = K-13 subtracted from:

Group   Lower  Center   Upper      +---------+---------+---------+---------
K-A    1040,2  1091,6  1143,1                                            (*)
K-HU     18,2    69,7   121,1                          (*)
K-SC    -61,3    -9,9    41,6                        (*)
                                 +---------+---------+---------+---------
                               -1200      -600         0       600


Group = K-A subtracted from:

Group    Lower   Center    Upper      +---------+---------+---------+------
K-HU   -1073,4  -1021,9   -970,5        (*)
K-SC   -1152,9  -1101,5  -1050,0       (*
                                      +---------+---------+---------+------
--
                                   -1200      -600         0       600


Group = K-HU subtracted from:

Group   Lower  Center  Upper      +---------+---------+---------+---------
K-SC   -131,0   -79,6  -28,1                       (*)
                                 +---------+---------+---------+---------
                               -1200      -600         0       600
```

One-way ANOVA: Geraniol versus Group

```
Source  DF      SS      MS      F      P
Group    3  304,14  101,38  19,62  0,000
Error    8   41,34    5,17
Total   11  345,49
```

S = 2,273   R-Sq = 88,03%   R-Sq(adj) = 83,55%



Pooled StDev = 2,273

Grouping Information Using Tukey Method

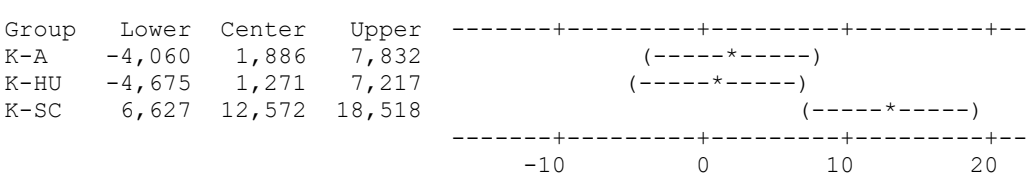
Group	N	Mean	Grouping
K-SC	3	36,586	A
K-A	3	25,899	B
K-HU	3	25,284	B
K-13	3	24,013	B

Means that do not share a letter are significantly different.

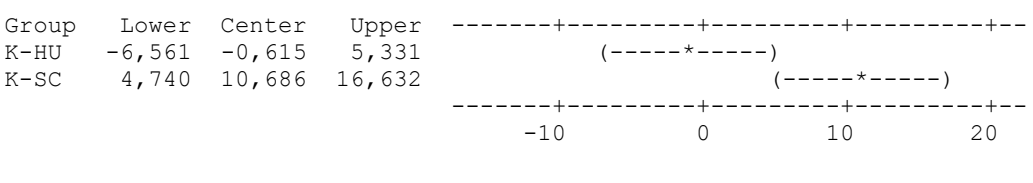
Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,74%

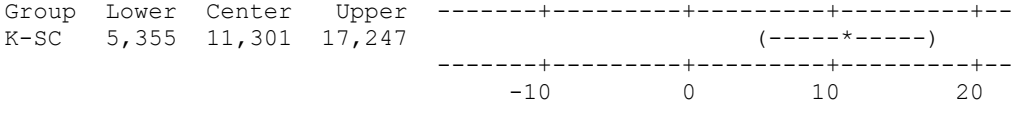
Group = K-13 subtracted from:



Group = K-A subtracted from:



Group = K-HU subtracted from:



One-way ANOVA: Syringol versus Group

```
Source  DF       SS       MS       F      P
Group    3  50904,7  16968,2  452,35  0,000
Error    8    300,1     37,5
Total   11  51204,8

S = 6,125   R-Sq = 99,41%   R-Sq(adj) = 99,19%


                         Individual 95% CIs For Mean Based on
                         Pooled StDev
Level  N    Mean  StDev  ----+---------+---------+---------+-----
K-13   3   61,30   5,05       (*-)
K-A    3  190,72   0,51                                  (*-)
K-HU   3   37,54   1,22  (-*)
K-SC   3  163,61  11,08                           (-*)
                         ----+---------+---------+---------+-----
                            50       100       150       200

Pooled StDev = 6,12


Grouping Information Using Tukey Method

Group  N    Mean  Grouping
K-A    3  190,72  A
K-SC   3  163,61    B
K-13   3   61,30      C
K-HU   3   37,54        D

Means that do not share a letter are significantly different.


Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of Group

Individual confidence level = 98,74%


Group = K-13 subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-A    113,40  129,41  145,43                            (-*-)
K-HU   -39,79  -23,77   -7,75                 (-*)
K-SC    86,29  102,30  118,32                          (*-)
                           -------+---------+---------+---------+--
                               -100         0       100       200


Group = K-A subtracted from:

Group    Lower   Center    Upper  -------+---------+---------+---------+--
K-HU   -169,20  -153,18  -137,16  (-*)
K-SC    -43,13   -27,11   -11,09               (*-)
                           -------+---------+---------+---------+--
                               -100         0       100       200
```

```
Group = K-HU subtracted from:

Group   Lower  Center   Upper  -------+---------+---------+---------+--
K-SC   110,05  126,07  142,09                            (-*)
                              -------+---------+---------+---------+--
                                  -100         0       100       200
```