GENETIC DIVERSITY OF SHEEP BREEDS FOCUSING ON CONSERVATION RESEARCH IN TURKEY

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ABSTRACT

GENETIC DIVERSITY OF SHEEP BREEDS FOCUSING ON CONSERVATION RESEARCH IN TURKEY

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In the first part of the present study, samples of 13 native Turkish sheep breeds (n=628) were examined, individually and comparatively, with respect to their 19 microsatellite loci to characterize them by employing various statistical analyses. Low F_{ST} values, high mean number of alleles and allelic richness as well as results of Factorial Correspondence Analysis and Structure analyses showed the degree of admixture between native sheep breeds of Turkey, IVE and SAK were observed as the most distincts of the breeds and possible introgressions were detected in other breeds. The 2-BAD, a software to examine the admixtures, was employed to estimate the time of the admixtures and the MSVAR software was employed to detect past demographic histories. In the second part, evaluations based on their genetic characteristics were made in relation to their prioritization in conservation studies. By employing four different approaches, it has been concluded that IVE, SAK, KRY, KIV, HEM and breed from Central Anatolia should be included in a conservation program for the preservation of optimum genetic diversity. In the last part of the thesis breeds were also characterized with respect to their relative risk of extinctions and their merits, which were used to estimate the utilities of the breeds. Non-genetic factors, collected based on the existing literature and surveys throughthe questionnaires filled by the field specialists, were incorporated into genetic factors to estimate the utilities of the breeds under different scenarios. In this approach, it is concluded that NOR, AKK, SAK, IVE and HEM should be included in the conserved set of breeds.

By the present study, it is believed that specific genetic features of the natıve Turkish sheep breeds were documented, effects of sampling on the population genetic studies was discussed, the need for a reliable data (genetic and nongenetic, for characterizing the risks and merits of the breeds) for the prioritization of the breeds in the long term sustainable conservation ofthem was emphasized.

Keywords: Turkish native sheep breeds, microsatellites, conservation, priority setting, genetic diversity, risk of extinction, utility

ÖZ

KOYUN IRKLARININ TÜRKİYE’DE KORUMA ARAŞTIRMALARI ODAKLI GENETİK ÇEŞİTLİLİĞİ

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Mevcut çalışmanın ilk kısmında, 13 Türk Koyun ırkının (n=628) örnekleri, tek tek ve karşılaştırmalı olarak, 19 mikrosatelit lokusu baz alınarak incelenmiş ve çeşitli istatistiksel yöntemler uygulanarak karakterize edilmiştir. Düşük FST değerleri, yüksek ortalama alel sayısı ve alelik zenginlik yanı sıra FCA ve STRUCTURE analizleri yerli Türk koyun ırkları arasındaki karışım derecesini göstermiştir. IVE ve SAK ırkları en farklı ırklar olarak öne çıkmış ve diğer ırklarda muhtemel dışarıdan gen katkısı tespiğt edilmiştir. 2-BAD programı karışım zamanlarını, msvar programı da ırkların demografik geçmişlerine ışık tutmak için kullanılmıştır. Çalışmanın ikinci bölümünde, genetic karakterler temel alırnarak, koruma çalışmalarında önceliklendirme yapılmıştır. Dört farklı yaklaşım kullanarak, IVE, SAK, KRY, KIV, HEM ve Orta Anadolu’dan bir ırkın korunması ile ideal genetik çeşitliliğin korunabileceği kararına varılmıştır. Çalışmanın son kısmında, ırkların göreceli soyu tükenme tehlikeleri ve değerleri de tanımlanmış ve bunlar kullanılarak faydaları değerlendirilmiştir. Genetik olmayan etmenler, saha uzmanları tarafından cevaplanan anketlerle toplanmış ve genetik etmenlerle birlikte, değişik senaryolarda ırkların faydalarını ölçmekte kullanılmıştır. Bu yaklaşımda NOR, AKK, SAK, IVE ve HEM ırklarının korunan ırklar kümesinde olmasına karak verilmiştir.

Sunulan çalışma ile Türk yerli koyun ırklarının bazı genetik özellikleri belgelendi,populasyon genetiği çalışmlarında öeneklemenin önemi tartışıldı, uzun dönemli sürdürülebilir koruma çalışmalarında ırkların önceliklendirilmelerinde güvenilir veri (genetik, riskleri ve mezıyetlerını karakterize etmek için gerekli genetik olmayan verilerin) gerekliliği vurgulanmıştır.

Anahtar Kelimeler: Yerli Türk koyun ırkları, mikrosatelitler, koruma, önceliklendirme, genetic çeşitlilik, neslin tükenme tehlikesi, fayda

To My Family,

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CHAPTER 1

INTRODUCTION

Distribution areas of native Turkish sheep breeds are very close to the earliest domestication site. Therefore, they may harbor unique genotypes which do not exist in anywhere else. Thus, their characterization and conservation may have prime importance to secure the food source of the humans. In this study, characterization of the Turkish sheep breeds to a certain extent and an attempt in priority setting for the breeds is carried out. In the following, an introduction for the study is given.

1.1 Domestication Centers for Sheep, Goat, Cattle and Pigs

Nearly 11.000 years before present, hunter gatherers erected monoliths at Göbekli Tepe, an archaeological site, 15 kilometers southeast of the town of Şanlıurfa in the Southeastern Turkey as depicted in the Figure 1.1. The age of the 7 ton limestone slabs that were cut, dragged and erected without metal tools predates the first signs of agriculture and domestication of animals. It has been thought that, the site is the oldest place of worship known so far. Also, the need for organization and support for maintaining a work force that big for building such a site may have sparked the settled communities. Another important point regarding Göbekli Tepe is the abundance of animal remnants found at the site. The remnants were bones of gazelle, boar, red deer and sheep; wild game that was abundant at the area at that time but not yet domesticated (Curry, 2008).

Figure 1.1 The location of Göbekli Tepe. Image taken from http://www.smithsonianmag.com/history-archaeology/gobekli-tepe.html visited on 2/5/2012

“Domestication is the adaptation of an animal or a plant to live in intimate association with and to the advantage of humans” (Merriam-Webster). The association may create such a dependency that the domesticated organisms may lose their ability to live in the wild. The practices that were carried regarding the animals at Göbeklitepe might have been the initial steps in the domestication process of animals. It has been speculated until the late 90’s, morphological changes like a sharp decrease in the size of the animals, were the signs of the domestication (Zeder, 2006). However, as the information from new archaeological sites accumulated, it was accepted that the domestication may have taken place before the size change. In a managed flock with animals that can be considered as domesticated, sex ratio would have been tipped off from one in favor of females. Similarly, if in old age group of females outnumber the males, presumably because the females were kept in the flock to give new birth and milk, it can be again considered as the signature of flock management and hence domestication of the animals. Archaeozoologists now accepted these as the signs of early domestication. The recent archaeological information was reviewed and summarized by Zeder (2008) and the centers of domestication of sheep, goat, pigs and cattle were reassigned in accordance with the new understanding. The map showing the domestication sites of these four species was presented in the Figure 1.2. When compared with Figure 1.1, Göbekli Tepe is found at the intersection points of sheep, pigs and cattle that is at the heart of domestication centers supporting the idea that it may be the earliest site where animal domestication have started.

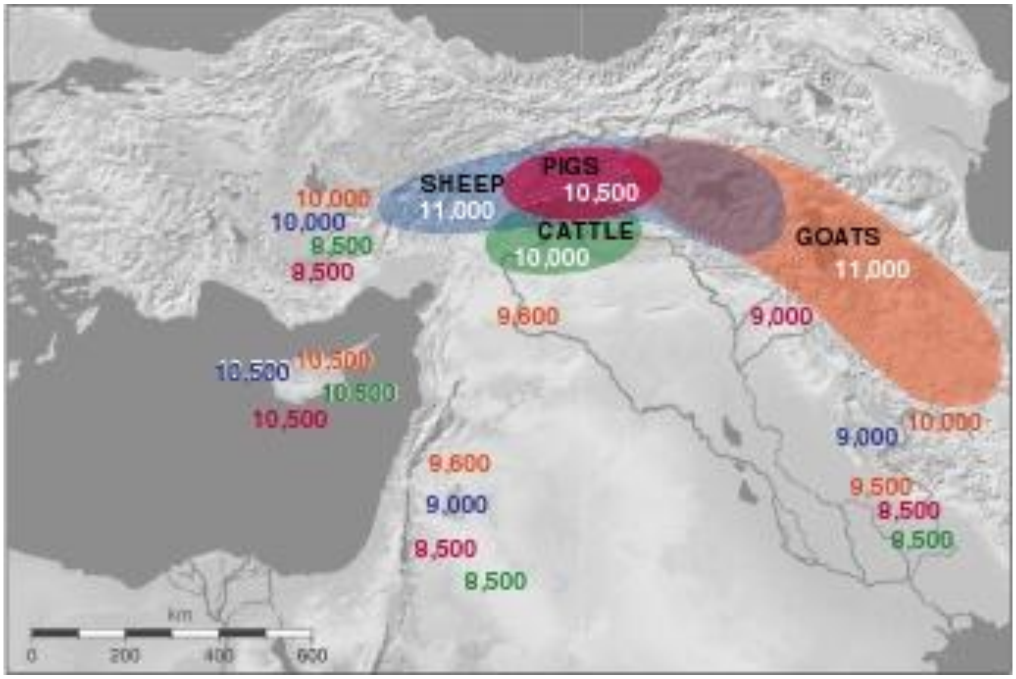

Figure 1.2 The domestication sites of sheep, goat, pigs and cattle in the fertile crescent taken from Zeder (2008). The numbers inside the colored area shows the estimates of how many years before present the initial domestications took place. The numbers outside the colored areas shows the propagation times of domestication before present in years. Blue is for sheep, orange is for goats, red is for pigs, green is for cattle.

1.2 Evolution of the Breeds

Human settlements, agriculture and domestication of livestock marked the beginning of Neolithic Age. Now instead of constant pursuing of wild game and harvesting resources which fluctuate, humans could permanently reside at the same site, relying on the abundant domesticated animals and plants. The farming and animal husbandry is believed to cause a surplus of energy per capita than that of the hunter-gatherer's time, causing an expansion in the population size of the humans. Eventually, the carrying capacity of the region was reached and the human migrations began to Europe through Anatolia (Price, 2000), North Africa (Barker, 2002) and West and Central Asia (Harris, 1996). During the migration of the early farmers in small groups: "Neolithic Demic Diffusion" as was formerly defined by Ammermann and Cavalli-Sforza (1973) both the knowledge of farming and domesticated animals must also migrate. However, with each step of migration, only a fraction of the gene pool was transferred to the new location; therefore the genetic diversity was thinned at the periphery. Thus, it can be anticipated that as well as the richest genetic diversity, the most unique genes can be found in the earliest centers of domestication. For instance according to scholars, the Anatolian native domestic sheep being close to the first domestication center, exhibiting high genetic diversity (Pedrosa *et al.,* 2005; Peter *et al.,* 2007; Lawson-Handley *et al.,* 2007)*,* may still harbor valuable genetic diversity and must have higher priority in conservation (Bruford *et al.,* 2003; Zeder, 2008).

The great variety of livestock breeds that are observed today is the result of an immense history of domesticated animals intertwined with the history of men, comprising colonization, migrations and trade (Groeneveld *et al*, 2010). Since the beginning of domestication, farmers managed the livestock in different environments, this in turn gave rise to the differentiation of the groups of animals that were adapted to different local conditions. During the 10.000 years period, the livestock experienced occasional introgressions and admixture; and constant mutations, drift and selection – both artificial and natural. About two hundred years ago, the concept of breed, animals with similar phenotypes, emerged and selection pressure over the livestock increased for more production at the cost of reduced diversity (Ajmone, 2010). A graphical representation summarizing the factors affecting the emergence of present biodiversity was presented in the Figure 1.3.

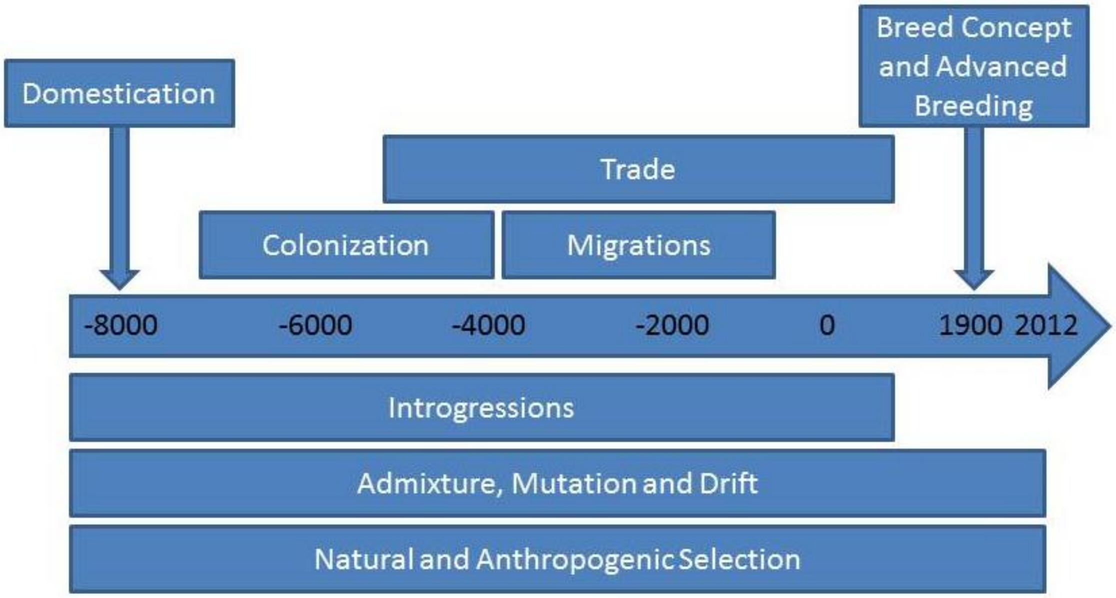

Figure 1.3 Understanding the current biodiversity. The biodiversity that is observed today is the result of constant admixture, mutation, drift, selection and occasional introgressions since the beginning of domestication. Human colonizations, migrations and trades mediated such events. The figure was adapted from Ajmone (2011).

1.3 Definition of Breed

The definition of a breed varies according to the stakeholders' view. Numerous definitions can be found in the literature (for reviews see for instance Wooliams and Toro, 2007).

In Animal Science, a breed is a group of individuals that have uniform values for the characteristics standardized by an authority, and differs from other such groups within the same species (Soysal and Özkan, 2002)

In the views of the breeders, “a breed is a group of domestic animals, defined as such by common consent of the other breeders… a term which arouse among breeders of livestock, created one might say, just for their own use, and no one is warranted in assigning to this word a specific definition and in calling the breeders wrong when they deviate from the formulated definition. It is their word and the breeders’ common usage is what we must accept as the correct definition” (Lush, 1994)

All the definitions stress out three common issues; i) breed is a subjective and often cultural term; ii) members of a breed shares common ancestry and resemblance; iii) members of different breeds frequently can be distinguished by phenotypic traits.

Even before the domestication, populations were under the effects of natural selection. After the domestication, the distinctness of the populations was increased due to artificial selection. The selection often affected by aesthetic considerations like color and often by particular production purposes like meat, or wool production.

1.4 Evolutionary History of Turkish Native Sheep Breeds

Comparative genetic studies indicated that the first domesticated sheep that might have migrated with the early farmers were “primitive”, and the only relics of them are now found at the Northern and Western extremes of Europe, or as in the case of Mouflon, as isolated feral populations mostly found in islands. In Southwest Asia, perhaps on the lands of modern day Iraq and Iran specialization of sheep for secondary products such as wool began (Chessa *et* *al.*, 2009). The time of this episode is unknown but perhaps it was during the Sumerian times, approximately 5000 years before present. The sheep selected for the secondary products began to expand, eventually replacing primitive sheep in all of Asia and in most of Europe except in the regions mentioned above. This second migration of sheep, as revealed by using retrovirus genome integrated into the sheep genome as molecular markers, offered a way of differentiating the sheep of oldest domestication and hence the old and rare gene pools (Chessa *et al.,* 2009). Anatolian sheep breeds, which did not experience heavy improvement schemes throughout the history, are candidates for harboring at least partially such old and rare gene pools.

Yet, another important episode for the Anatolian sheep breeds was the arrival of nomadic Turks from Central Asia. Nearly a thousand years ago, nomadic Turks entered Anatolia from East and Southeast. As in all nomadic cultures, the lack of settlements and farming made the livestock invaluable for the nomadic Turks. It was estimated that nomadic Turks brought at least 78 million sheep with them (Togan *et al*, 2007), which must have been overlaid on the effects of the second sheep migration that happened four thousand years before that date. However, the invasions of Turks did not cover all of the Anatolia instantaneously. Before the invasion of Western Anatolia they stayed behind the approximate borders shown in the Figure 1.4 for another two hundred years. It could be argued that, the relative contribution of sheep brought by nomadic Turks to the Eastern and Western gene pools of sheep were different.

Figure 1.4 The borders of the Byzantine Empire in the 11th century. The Eastern borders of the empire stayed more or less the same for another two centuries.

1.5 Current Status of the Turkish Sheep

In Turkey, most sheep breeding were done by small enterprises and nearly all of the sheep population is comprised of native breeds (Doğan, 2009). These breeds were not selected intensively for economically important traits, such as meat yield or wool production. Although the native breeds of Turkey are not among the economically important sheep breeds of the world, they definitely are superior in their survival in the marginal environments which are found in many parts of Turkey.

As a general trend in the world, economically improved breeds threaten the primitive breeds either by hybridization or by replacing them altogether. Being developed in the countries away from diversity hot spots and under heavy selection, the economically important breeds lack both the diversity and the ability to adapt different environments, performing well only under intensive care of the breeders. Apart from the threats by hybridization and replacement by exotic breeds, Turkey has been experiencing serious bottleneck in livestock populations. Between 1980 and 2000 47.4% of sheep have been lost and between 2000 and 2004 10.7% decline in sheep population has been observed (Oskam *et al.,* 2005). This decline is partly due to the market's shifting from lamb to beef and poultry and partly due to political and social unrest (Sarıgedik, 2004). When a gene is lost, it is lost forever; therefore appropriate measures should be taken to stop the genetic erosion and to protect the future of animal husbandry (FAO, 2006).

1.6 Global Plan of Action

Most livestock breeds worldwide are threatened by the loss of genetic resources (FAO, 2007). It has been estimated that 12% of sheep breeds became extinct in the last 100 years (Hall and Ruane, 1993). Although farm animals are not threatened by a total extinction as wild-life species, native breeds with low market values may be replaced by more feasible breeds, or genetic drifts may occur resulting an irreversible loss of genetic material. The pressure by the economically important breeds on the primitive breeds is at such a level that, Food and Agriculture Organization of the United Nations (FAO) appraises that 32% of the sheep breeds will go extinct in the next 20 years. It has been indicated that the risk of extinctions were seen mostly in regions with highly specialized livestock industries with fast structural changes (FAO, 2010b). Three threats that were the most significant in the erosion of livestock genetic diversity were, i) economic and market drivers; ii) the lack of good livestock policies; iii) lack of good conservation strategies (FAO, 2009b). Of the 33 sheep breeds, which are not considered as economically important breeds, reported for Turkey (DAD-IS, 2012), Karakaçan, Ödemiş and Halkalı have been extinct already (Ertuğrul *et al.*, 2000; Kaymakçı *et al.,* 2000)

Conservation of genetic resources are not limited to preserving endangered breeds but also about ensuring, especially in developing countries where intensive breeding programs were not practiced, sustainable development (Ruane, 2000). By sustainable development it is meant that the development should equally include environmental protection which also includes biodiversity, economic growth and social equity both within and between generations (Hoffmann, 2011). In other words, the welfare of the present generation should be ensured without sacrificing the welfare of the future generations.

The Global Plan of Action for Animal Genetic Resources were signed by 169 countries in 2007, including Turkey, was developed for fighting against the erosion of genetic diversity. The plan contains 4 strategic priority areas as presented below (FAO, 2007).

1. Classification and characterization of animal genetic resources, the assessment of the trends and the risks threatening the animal genetic resources
2. Ensuring the sustainability of the animal production systems
3. Conserving the genetic diversity and integrity for the welfare of current and future generations
4. Building policies, institutions and enhancing capacities

In the light of these aspects, the need for a long term nationwide conservation program in Turkey is undeniable.

Conservation of all breeds is not possible due to limited resources. Furthermore, it may not be necessary, because breeds may not be genetically different, or a breed may not have a long-term or short-term value (Boettcher, 2010). Therefore, a prioritization of breeds should be undertaken. However, before everything the object of the conservation program must be clearly defined, as it would affect the outcome of the prioritization (Bennewitz *et al.*, 2007), and then the breeds at risk should be identified. Three basic approaches could be applied when deciding on a conservation strategy, i) maximum risk, where the breeds are prioritized according to their extinction risks; ii) maximum diversity, where the breeds are prioritized according to the genetic diversity they possess; iii) maximum utility, where multiple factors, like adaptive traits, the breeds' socio-cultural importances and the economic contributions of the breeds, as well as the risk statuses of the breeds and the genetic diversities they have are considered in prioritization of the breeds.

In Turkey, *in vivo* conservation studies for sheep breeds have been started since 2005 at Marmara Livestock Research Institute for Gökçeada, Sakız and Kıvırcık breeds; and Güney Karaman breed at Bahri Dağdaş International Agricultural Research Institute under the management of The General Directorate of Agricultural Research and Policy (shortly TAGEM in Turkish). Also by “Regarding Building-up Livestock 2005/8503 numbered Ministerial Cabinet Bylaw” conservation practices for Sakız, Çine Çaparı, Gökçeada, Kıvırcık, Herik, Karagül, Norduz, Dağlıç and Hemşin breeds were started as small flocks in their natural range (TAGEM, 2009). For the conservation flocks, individuals were selected by their morphologies in the absence of genetic data. The national project “*In Vitro* Conservation and Preliminary Molecular Identification of Some Turkish Domestic Animal Genetic Resources – I (TURKHAYGEN-I, www.turkhaygen.gov.tr) is one of the biggest conservation projects started in Turkey that has been carried out by the large consortium. The aim of the project is to conserve the native breeds of Turkey via cryoconservation and to explore the genetic diversity of the cryoconserved animals. The aim of the TURKHAYGEN-I project coincides with the first (characterization) and the third (conservation) domains of the Global Plan of Action. The present study uses the output of a part of the studies carried out in TURKHAYGEN-I Project.

1.7 Genetic Data and Statistical Analyses

Since the invention of PCR in 1983 by Mullis which allows the selective amplification of DNA, many genetic markers were developed. The amplified regions can then be studies comparatively between individuals. Most often these amplified regions are either mitochondrial DNA's or microsatellites (Bruford *et al.*, 2003). In the present study microsatellites were used. It has been observed in the genome, that there are regions of repeated units of 1-6 base pairs with typical copy numbers between ten and thirty. These short tandem repeats (STR) or microsatellites are inherited in Mendelian fashion, and so long as they are not very close to coding regions, they are not affected by selection (neutral loci); thus offer unbiased information about the genetic diversity of genome (Jobling *et al.*, 2004).

The mutation rates of the microsatellites are estimated around 10^{-3} to 10^{-4} per locus per generation, which makes them excellent tools for investigating the evolution of livestock breeds which has a short evolutionary history. Moreover microsatellites can be used to assess diversities of livestock breeds. Both the evolutionary history and the diversity revealed by the use of microsatellites can be used in the characterization and conservation of livestock breeds. Peter *et al.* (2007) used 31 loci from 57 European and Middle-eastern sheep breeds to evaluate the genetic diversity and structuring among the breeds and found distinct reservoirs of diversity corresponding to the Eastern and Western breeds of Turkey. Gizaw *et al.* (2008) not only characterized 14 Ethiopian Sheep breeds, but also incorporated a priority setting scheme by using microsatellites as the estimators of genetic diversity. Glowatski-Mullis *et al.* (2009), used 9 Swiss breeds represented by 44 microsatellite markers to evaluate the loss of genetic diversity when breeds go to extinction. Although there are numerous advantages of microsatellites, which made them to be a standard tool in studying livestock diversity, the risk of having high frequencies of null alleles, subjective genotyping and size homoplasy is the disadvantages of studying with microsatellites (Peter *et al,* 2007).

Since the beginning of population genetics studies, mathematical and statistical methods were indispensable tools for making the data meaningful. As the data accumulates, the computational power of the computers grew in parallel, providing new means of analyzing the data. Bayesian methods, supported by Markov Chain Monte Carlo algorithms, maximum likelihood and coalescent analyses are common nowadays, enabling the extraction of population histories, origins, diversities, structures and effective population sizes of the breeds from genetic data.

1.8 Justification and Objectives of the Study

Anatolia, being not only in the first domestication sites, of sheep but also being close to the putative origins of the second migration of sheep, may harbor greater and highly unique genetic diversity than any other country. The possibility of finding unique genetic material and the decline of sheep population of recent past, call for an urgent establishment of a conservation program. However, an efficient conservation program requires reliable genetic data. In this context, 19 microsatellite loci from 13 native sheep breeds of Turkey will be used to analyze the diversities, distinctness of the breeds and their contributions to the gene pool of Turkish sheep breeds. Moreover, past demographic events such as bottlenecks and hybridizations among breeds will also be investigated within the limits of data, available methods and programs. In setting the priority of conservations for the breeds the genetic analyses will be done following the guidelines of FAO for the conservation of pure sheep breeds as well as considering the different genetic zones for the admixed breeds.

Yet, one should always keep in mind that, sheep breeding is an economical process which cannot be solely built on the conservation of genetic diversity. To achieve a viable, self-sufficient breeding program, factors other than genetic data, such as the production values of the sheep breeds, adaptations to local conditions, the demands of the market economy and the economic conditions of the breeders should also be considered. To be able to assess the non-genetic parameters of the decision making procedure, an exhaustive screening of available publications will be performed. Also questionnaires to collect information about the aforementioned traits of sheep breeds (e.g. meat yield, milk yield, mothering instinct, walking ability) will be given to specialists, and the answers will be evaluated together with the genetic data while priorities are being set for conservation program.

The main objective of the present study is to shed some light into how present day Turkish sheep breed populations were formed. Turkey being in the crossroads of continents must have been greatly influenced by the migrations. For this purpose, model based Bayesian admixture analyses will be performed, in the hopes to contribute to the understanding of evolutionary history of sheep in Anatolia.

CHAPTER 2

MATERIALS AND METHOD

2.1 Sampling and the Samples

Blood samples of 628 sheep from 13 sheep breeds were obtained. These breeds were Sakız, Karagül, Hemşin, Çine Çaparı, Norduz, Herik, Dağlıç, Morkaraman, Kıvırcık, Karayaka, Gökçeada, İvesi, Akkaraman. Samples were collected by personnel from the Ministry of Food, Agriculture and Livestock (then called Ministry of Agriculture and Rural Affairs) within the context of the project with acronym TURKHAYGEN-I (www.turkhaygen.gov.tr; Project no: 106G115). To represent the gene pool, only a few individuals (2-3) per flock were sampled. Figure 2.1 shows the sample collection sites in Turkey.

Figure 2.1 The distribution of sample collection sites in Turkey. Map was drawn by A. Doğan

Brief information about the breeds was given in Table 2.1. More information can be found from the web site of General Directorate of Agricultural and Research Policy (http://www.tagem.gov.tr/pdf/english_AnGR.pdf [date of visit: 14.2.2012])

Table 2.1 Breed names (international names in parentheses), the abbreviations used for the breeds, the tail types of the breeds (F stands for fat-tail, T &L stands for thin and long tail, SF stands for semi-fat tail), main purpose of its' raise (in a descending order of importance), its' main characteristics and sample sizes employed.

Breeds (International Names)	Abbreviation	Tail Type	Main Products/Special Characteristics	Sample Size
Sakız (Chios)	SAK	SF	Milk / High litter size	49
Karagül (Karakul)	KRG	F	Meat, milk / Transported in 1929	50
Hemşin	HEM	SF	Meat, milk	48
Çine Çaparı	CIC	F	Meat, milk / Rescued from extinction recently	40
Norduz	NOR	F	Meat, milk, wool / Variety of AKK	46
Herik	HER	SF	Meat, milk, wool / Hybrid of AKK MOR and KRY	49
Dağlıç	DAG	F	Meat, milk	50
Morkaraman	MOR	F	Meat	50
Kıvırcık	KIV	T & L	Meat, milk, wool	45
Karayaka	KRY	T & L	Meat, wool	50
İvesi (Awassi)	IVE	F	Milk, meat	51
Gökçeada (Imbros)	GOK	T & L	Milk, meat	50
Akkaraman	AKK	F	Meat, milk	50

Native sheep breeds of Turkey are well adapted to their respective environments. The sheep breeds can be separated into two main groups as fat-tailed, which are found in Central, Southern and Eastern Anatolia where the environment is harsh and continental climate is dominant which are also believed to have a different evolutionary history than the others (Oner *et al.,* 2010); and thin-tailed, which are encountered mainly on coastal areas where environmental conditions are milder.

General properties of the native Turkish breeds which were summarized by General Directorate of Agricultural Research (TAGEM) are as the followings (TAGEM, 2009)

Akkaraman: A fat-tailed breed with generally white body with black speckles at head, nose, ears and legs. It has a wide range of distribution, which includes Central Anatolia and intersections with neighboring regions. The primary use of the breed is for the meat and the secondary use is for milk. Akkaraman is the breed with the highest population size.

Çine Çaparı: It is a fat-tailed breed, confined in the province of Aydın. The breed was rescued recently from extinction; therefore it experiences a serious bottleneck. The main uses of the breed are for the meat and milk production.

Dağlıç: Dağlıç is a fat-tailed breed distributed mainly along Central Western Anatolia. It’s generally white in color, with occasional black spots around eyes, mouth, ears or legs. Main use is meat production, with milk following it.

Morkaraman: A fat-tailed breed with body colors ranging from red to purple. The breed is found mainly in Eastern Anatolia. Morkaraman is bred mainly for its meat production.

İvesi: It is a fat-tailed breed, distributed in South-east Anatolia. It is a trans-boundary breed, ranging as south as Israel. The main use of the breed is milk, with meat as a secondary product.

Karagül: Karagül is a fat tailed breed with black coat color. The breed is found in Tokat province of Turkey. However the breed is introduced in 1929 from Central Asia (Erol *et al.*, 2009). Although the aimed product is the pelt of newborns, in Turkey this goal was never achieved. Instead, Karagül was bred for meat and milk.

Norduz: Norduz is a fat-tailed breed found exclusively in the Gürpınar district of Van province. The body is generally white. Black spots on neck, head and legs are observed. It is known that Norduz is a variety of Akkaraman. Primary product is meat, then milk and wool production comes.

Sakız: Sakız has a thin tailed breed with some fat at the base. Breed is found mainly in the İzmir province of Turkey and Chios Island of Greece. The body is white with black spots around eyes, mouth, nose tip, ears and feet. Its primary use is for milk and lambing.

Herik: Also called Amasya Heriği, this breed is found in the province of Amasya. The tail is thin with fat deposits at the base. It is a hybrid of Akkaraman/Morkaraman ewes and Karayaka rams. The body is white with black-brown speckles at head and legs. The primary use is the meat production, then it is also reared for the production of milk and wool following.

Hemşin: It's found mainly in the mountainous regions of North-Western Anatolia, especially in the provinces of Artvin and Rize. The body color varies from black to beige. The tail is fat at the base and thin at the tip. It is used mainly for meat and milk production.

Kıvırcık: Kıvırcık is a thin tailed breed, found in Marmara, Thrace and Northern Aegean Region of Anatolia. Body is generally white, and the tail is long and thin. The breed is reared for meat, milk and wool in decreasing importance.

Karayaka: Found mainly in the Northern Anatolia. The tail is thin and long. Body is generally white, with black spots near head and neck. Karayaka is bred for its meat and coarse wool, the special quality of its wool, elasticity, is highly admired.

Gökçeada: Found mainly at the island Gökçeada, and surrounding mainland in the province of Çanakkale. The body is white with some black spots around eyes, mouth, ears and feet. The tail is long and thin. The breed's main uses are milk and meat.

2.2 Genetic Data

In this research 19 microsatellite loci were studied. The microsatellite loci used, the allelic range, origin, the chromosomes that they are located on are and the GeneBank accession numbers are given in Table 2.2.

Table 2.2 The names of the loci that were used in the present study, their GeneBank accession numbers, allelic ranges, origins of the loci and the chromosomes that they are located on.

Locus Name	GeneBank Accession #	Allelic Range	Origin	Chromosome
BM8125	G18475	106 - 128	Bovine	17
DYMS1		157 - 211	Bovine	20
ILSTS005	L23481	174 - 218	Bovine	7
ILSTS011	L23485	256 - 294	Bovine	9
INRA063	X71507	156 - 212	Bovine	14
MAF209	M80358	109 - 142	Ovine	17
MAF33	M77200	116 - 147	Ovine	9
MAF65	M67437	112 - 146	Ovine	15
MCM140	L38979	161 - 198	Ovine	6
OarCP34	U15699	110 - 136	Ovine	3p
OarFCB128	L01532	96 - 130	Ovine	2p

Table 2.2 Continued

Locus Name	GeneBank Accession #	Allelic Range	Origin	Chromosome
OarFCB20	L20004	86 - 130	Ovine	2q
OarFCB226	L20006	118 - 160	Ovine	2
OarFCB304	L01535	145 - 191	Ovine	19
OarFCB48	M82875	136 - 172	Ovine	17
OarHH47	L12557	121 - 163	Ovine	18
OarJMP29	U30893	113 - 167	Ovine	14
OarJMP58	U35058	137 - 177	Ovine	26
OarVH72	L12548	121 - 145	Ovine	25

The DNA from blood samples were extracted and amplified, and the resulting data was collected mainly by H. Acar during the study “Bioinformatic Analyses in Microsatellite-Based Genetic Diversity of Turkish Sheep Breeds”. The earlier version of the data was analyzed to a certain extent by Acar (2010). In the present study, the last version of data is analyzed extensively.

2.3 Methods

2.3.1 Detection of Null Alleles

Null alleles are the alleles that are not amplified during PCR. The non-amplification may be caused by the mutation at the sites of primers. The excessive presence of null alleles causes the locus to deviate from Hardy-Weinberg equation in favor of the homozygotes due to the false reading of heterozygotes as homozygotes in the presence of non-amplified alleles. This phenomenon causes an overestimation of the genetic differentiation between populations (Paetkau *et al,* 1997) and underestimation of genetic diversity within populations (Paetkau and Strobeck, 1995). To detect the presence of null alleles at each locus for all breeds, FreeNA (Chapuis and Estoup, 2007) software was run, using the EM algorithm of Dempster *et al.* (1977). However it should be noted that, the deviations from Hardy-Weinberg equation towards homozygotes may also be caused by other factors, like assorted mating, Wahlund effect or inbreeding. The method that FreeNA uses, assumes that the only cause of deviations from Hardy-Weinberg equation is the presence of null alleles. As suggested by (Dakin and Avise, 2004; Chapuis and Estoup, 2007) the estimated potential frequency of null alleles (r) less than 0.2 causes little adverse effects on analyses, so we have set r=0.2 as the threshold for considering the locus as problematic.

2.3.2 Linkage Disequilibrium

Linkage disequilibrium is the non-random distribution of alleles at two loci, which are not necessarily on the same chromosome. If two loci with two alleles each (AB, Ab, aB and ab) is considered the coefficient of linkage D can be defined as;

$$D = G_1 * G_4 - G_2 * G_3 \tag{1}$$

Where G_1 is the frequency of AB, G_2 is the frequency of Ab, G_3 is the frequency of aB and G_4 is the frequency of ab genotypes respectively.

The population is called in Linkage Equilibrium, if D is equal to 0. To be in linkage equilibrium, the alleles in the population must be associated randomly. If the alleles are not associated randomly, D will not be zero; therefore the population will be considered as in linkage disequilibrium. The loci in this study were not in close proximity with each other, so it was expected that all the loci of all the populations were in linkage equilibrium. However, if the individuals selected were close relatives or if there were recent introgression with different linkage groups than the recipient population then linkage disequilibrium might be observed.

The testing of linkage disequilibrium was performed by Genepop 4.1 Software (Raymond and Rousset, 1995; Rousset, 2008) for all pairwise loci across all populations.

2.3.3 Allelic Richness

One measure to determine the genetic variation is to measure the total number of distinct alleles. This measure is important to find out the evolutionary potential of the populations in long term. However, the number of distinct alleles depends heavily on sample size. To overcome this, allelic richness which is a measure of allelic diversity that considers the sample size (Mousadik and Petit, 1996), can be used. In this method the unequal sample sizes are converted to a standard g, and alleles expected in the random sub-sample of size g drawn from the original sample is calculated.

Allelic richness was estimated by FSTAT V.2.9.3 software (Goudet, 2001).

2.3.4 Private Alleles

The alleles that are found in only one population are called, private alleles. It has been proved that, a linear relation exists between the immigrant entering the population at each generation and the frequency of private alleles in equilibrium. New alleles are developed by mutations. The existence of high number and frequency of private alleles points that there has been a little gene flow between populations. The mutation rate is also a factor determining the frequency of private alleles. As mutation rate increases the proportion of alleles that are private decreases.

The frequencies of private alleles were calculated by a script written in PERL (the Practical Extraction and Report Language; Wall, 1987) by the author of this manuscript.

2.2.5 Hardy-Weinberg Equilibrium

For within population diversity, it is argued that the best general measure is the calculation of expected (Hardy-Weinberg) heterozygosity. Average expected heterozygosity at m loci with n alleles each can be calculated with the formula;

$$H_e = 1 - \frac{1}{m} \sum_{k=1}^{m} \sum_{i=1}^{n} p_i^2 \qquad (2)$$

The last term gives the expected frequency of homozygotes at the k^{th} locus for the i^{th} allele, for all loci from 1 to m. First by taking the average by dividing it to m and then by subtracting the result from one, the expected heterozygosity can be calculated.

Estimation of He is not affected by small sample sizes, if the number of loci examined are sufficiently high. Moreover it is not adversely affected in the presence of null alleles.

Expected heterozygosities (He) are calculated by Genepop 4.1 software (Raymond and Rousset, 1995; Rousset, 2008) for each locus-by-population combination and for each population estimates were obtained. Deviations from Hardy-Weinberg equations are tested for each combination by using 10.000 Markov chain and 1.000 dememorization steps, and significant deviations are marked after applying Bonferroni corrections.

2.3.6 F_{IS} Values

F-statistics, which were first defined by Wright (1965) and extended by Nei (1977), measures the deviations of the gene frequencies in a sub-divided population in three terms, namely F_{IS}, F_{IT} and F_{ST}, which are often called as the F-statistics. They are related to each other as denoted by the formula;

$$1-F_{IT} = (1-F_{IS})x(1-F_{ST}) \tag{3}$$

F_{IT} is the correlation between two uniting gametes relative to the sub-population, F_{IS} is the correlation between two uniting gametes relative to the whole population and F_{ST} is the correlation between two randomly drawn gametes from each sub-population and shows the degree of genetic distance between sub-populations.

Usually populations in nature do not follow Hardy-Weinberg equilibrium, and F-statistics uses these deviations to detect the degree of inbreeding within populations. F_{IS} is the measure of departure from Hardy-Weinberg equilibrium and it is estimated by the formula;

$$F_{IS} = 1 - \frac{H_O}{H_S} \tag{4}$$

where H_O is the mean observed heterozygosity over all sub-populations and H_S is the mean expected heterozygosity over all sub=populations.

Positive F_{IS} values mean that heterozygotes are deficient in the sub-population for instance due to inbreeding, and negative F_{IS} values mean that there are excess heterozygotes possibly because of the non-random mating.

In this study, F_{IS} values were calculated by Genetix Software (Belkhir *et al.,* 1996-2004). The significance of tests was done by applying 1000 random permutations and significant deviations were detected after Bonferroni corrections.

2.3.7 A Method to Understand the Demographic Histories of the Breeds

The idea of using molecular markers to detect past evolutionary histories of populations dates as early as 1919 (Hirszfeld and Hirszfeld, 1919). The current studies, which focus on the deviations from equilibria (Hardy-Weinberg Equilibrium, mutation – drift equilibrium, panmictic populations) follows the ground theories set by Nei (Nei, 1975), Tajima (Tajima, 1989a; 1989b) and Watterson (1975).

One such approach is the application MSVAR implemented by Beaumont (Beaumont, 1999). MSVAR analyzes genetic marker data (microsatellites) sampled from multiple loci and detects and quantifies past population size changes. The software employs a Bayesian method which relies on Markov Chain Monte Carlo (MCMC) simulations.

The model assumes that the sampled loci have a genealogical history with coalescence and mutation events dating back to the most common ancestor with size N_1 which gradually changed its size to the current N_0. It is assumed that microsatellites follow Stepwise Mutation Model (SMM).

The outputs of the software were analyzed using R (Ihaka and Gentleman 1996; available via http://www.r-project.org) using Locfit Package (Loader, 1996).

2.4 Methods to Study the Breeds Comparatively

2.4.1 F_{ST} Values

F_{ST}, as stated before, is the measure of genetic differentiation between two sub-populations, which can be used, also as a distance measure to describe the genetic difference between the two populations (breeds). Pairwise F_{ST} values may be calculated by the formula;

$$F_{ST} = 1 - \frac{H_S}{H_T} \tag{5}$$

Where H_S is the mean expected heterozygosity over all sub-populations and H_T is the expected heterozygosity of entire base population assuming random mating among it. By using pairs of sub-populations, one can build a distance matrix of pairwise difference between sub-populations. F_{ST} values ranges from 0 (identical sub-populations) to 1 (complete difference).

However, the F-statistics proposed by Wright, assumes equal and infinite sample sizes. Weir and Cockerham (1984) made revisions to F coefficients to be suited better for small samples.

In this study, F_{ST} values were calculated by Genetix Software (Belkhir *et al.*, 1996-2004). The significance of tests was tested by applying 1000 random permutations and significant deviations were detected after Bonferroni corrections by dividing 0.05 by the number of tests performed.

2.4.2 Genetic Distances

Although F_{ST} values allow us to make pairwise comparisons between sub-populations, it is often needed to depict the distances of all sub-populations with respect to each other. For this purpose several methods to calculate “genetic distances” were proposed. In this study two genetic measures were used to form genetic distance matrices.

The first measure that was used in the study was Nei’s D_A. Nei’s D_A is accepted as the most appropriate method for estimating genetic distances between groups when microsatellites are being studied. The method assumes that the genetic difference occurs because of the two evolutionary forces, drift and mutations. The method is based on infinite allele model and assumes the mutation rates of all of the loci are the same. The calculations are done according to the formula;

$$D_A = 1 - \frac{1}{r}\sum_{j}^{r}\sum_{i}^{m_j}\sqrt{x_{ij}y_{ij}} \qquad (6)$$

Where,

x_{ij} is the frequency of the i^{th} allele at j^{th} locus of sample x,

y_{ij} is the frequency of the i^{th} allele at j^{th} locus of sample y,

m_j is the number of alleles at locus j,

and r is the number of loci studied.

Nei’s D_A ranges from 0 (identical sub-populations) to 1 (no shared allele is present). In this study, Nei’s D_A was calculated by Populations v1.2.30 (Langella, 1999)

The second measure used in this study was Reynold’s Distance. It is another appropriate measure for calculating genetic distances when studying microsatellites. In contrast to Nei’s D_A, Reynold’s Distance assumes only drift as the source of differentiation. It can be calculated by the formula;

$$D^2 = \frac{{}_{m} \quad {}_{i}(x_{mi} - y_{mi})^2}{2 \quad {}_{m}(1 - \quad {}_{i}\, x_{mi} y_{mi})} \qquad (7)$$

Where,

x_{mi} is the frequency of the i^{th} allele at the m^{th} locus of the sample x,

y_{mi} is the frequency of the i^{th} allele at the m^{th} locus of the sample y.

It should be noted that D^2 is expected to rise linearly with accumulated drift.

In our study, the Reynold’s Distances were calculated by using Populations v 1.2.30 software (Langella, 1999).

2.4.3 Neighbor Joining (NJ) Tree

After obtaining the genetic distance matrix of groups of populations, a clustering algorithm is often employed to construct a dendogram for visualizing the genetic similarities of breeds. One of the most widely used clustering algorithms is Neighbor-Joining algorithm of Saitou and Nei (Saitou and Nei, 1987). The advantages of this algorithm are, a) The branch lengths are not ultra-metric (not having the same length) allowing us to deduce additional information about the relationships between populations; b) Being a fast algorithm, it is even suitable for large data sets, and it allow bootstrapping – constructing a number of trees (100 to 1000) instead of one, and determine the statistical error from these samples; c) not assuming the same evolutionary rates, it performs better if there exists non-uniform evolutionary forces acting on different taxa.

Both Reynold’s and Nei’s D_A genetic distances were used to construct NJ trees, by using Populations v 1.2.30 Software (Langella, 1999) with 1000 bootstrapping. The resulting trees are visualized by TreeView v1.6.6 (Page, 2001).

2.4.4 Principal Coordinates Analysis (PCA) for the Centroids of Breeds

Principal Component Analysis (PCA) is a mathematical procedure that aims to represent the patterns in a data set by highlighting the similarities and differences. It was first proposed by Karl Pearson in 1901. Data in real world seldom exists in an easily representable fashion. To overcome the high dimensionality of the data, PCA supplies the user with a lower dimensional figure by eigenvalue decomposition of the covariance matrix of the data. The axis that provides the most variance is selected and the data is presented from its viewpoint, both presentable and without much information loss.

In this study, GenAlex 6.41 (Peakall and Smouse, 2006) was used to depict the data with 2 axes of variance.

2.4.5 Factorial Correspondence Analysis (FCA)

Factorial Correspondence Analysis (FCA) (Lebart *et al,* 1984) was used to see the individuals in multidimensional space and to examine the relationships between individuals. For each allele, a diploid individual may take the value of 0, 1 or 2. The strings of 0,1 or 2’s will represent the individuals with respect to the alleles. Then the most informative three axes (Machugh, *et al.,* 1994), which are the linear combinations of alleles, were selected according to the maximum genetic variation that they explain. The visualization of the independent axes allow how individuals are related to each other, which is an informative way to see the amount of inertia, distinctness and the similarities of the breeds.

In the present study, GENETIX Software (Belkhir *et al.,* 1996-2004) was used to obtain the three dimensional FCA.

2.4.6 Multidimensional Scaling (MDS)

Multidimensional scaling (MDS) analysis (Kruskal, 1964) was carried out to assess the similarities and dissimilarities of the populations. The pairwise F_{ST} values were used as *a priori* distances between breeds in an N-dimensional hypercube. The N-dimensional space was then reduced to M dimensions where M < N while the loss of the individual distances between populations were kept at minimum.

The MDS analysis were performed in two dimensions by using R (Ihaka and Gentleman 1996; available via http://www.r-project.org)

2.4.7 Mantel Test

The Mantel Test, named after Nathan Mantel (Mantel, 1967) is a statistical test of correlation between two matrices of equal rank. The test can be applied to population genetics by forming two matrices, one containing the genetic distances between populations, and the other containing the geographical distances between populations.

Slatkin (1993) showed that if the mutation rate is smaller than the migration rate, there exists a negative correlation between $\log((1-F_{ST})/4F_{ST})$ and log(geographical distance). To find the geographical distances between sampling sites, were calculated by applying the Haversine formula to the pairs of midpoints of sample collection sites for each breed by a script written in Python language by the author of this manuscript. The matrices of F_{ST} and pairwise geographical distances were given as inputs to Arlequin v3.5 Software (Excoffier *et al*., 2006). The existence of the correlation was checked using 10.000 permutations.

2.5 Bayesian Clustering Analysis:

2.5.1 Number of Main Clusters (K)

Recent advances in computer technology made diverse methodologies readily available. One such methodology is clustering in Bayesian statistical framework which has proven to be very useful in population genetics (Mank & Avise, 2004). The software STRUCTURE (Pritchard, 2000) is used to detect population sub-structures by assigning individuals probabilistically to K ancestral populations' clusters (where K may be unknown). In the presence of admixture, one individual may be assigned to two or more clusters. The genetic differentiation between real subpopulations represented in the meta-population plays an important role in the reliability of the clustering. It can be said that the greater the genetic differentiation between sub-populations, the more robust and hence reliable clustering of the individuals.

The most significant parameters of a STRUCTURE analysis are the burn-in length and the estimation of the most probable K.

Burn-in period is the length that the simulation is run before collecting data. It is needed to minimize the effects of the starting configuration. Generally 10.000 – 100.000 burn-in length is more than adequate (Falush *et al.*, 2003)

The other parameter to consider is the estimation of the best K. There are several methods for the estimation of best K. One is the method proposed by Evanno *et al.* (2005). In this method the maximum value of the second order rate of change of the likelihood function ($\Delta K = m|L''(K)|/s[L(K)]$) with respect to K gives the best K.

Another method to estimate the best K is the method used by Tapio *et al*. (2010) originally proposed by Rosenberg *et al.* (2002). The most probable K is the K where the similarity of the independent runs (similar assignment of individuals to parental populations) is at the highest.

Yet, another approach is to measure the maximum likelihood of the different runs with different K values and assuming the most probable K to that value.

All three models were applied in this study. STRUCTURE Console version 2.3.3 (Pritchard, 2002) was used for Bayesian clustering. The burn-in length was 30.000 with 100.000 MCMC steps following it. The program was run for K=2 to 20, with 10 replicates. The similarity coefficients were calculated by the software CLUMPP v1.1.2 (Jakobsson and Rosenberg, 2007). The graphical images were formed by Distruct v1.1 (Rosenberg *et al.*, 2002). All three softwares are available at:

http://pritch.bsd.uchicago.edu/software (STRUCTURE) and http://www.stanford.edu/group/rosenberglab/software.html (CLUMPP and Distruct).

2.5.2 Admixture Analysis by 2-BAD

Admixture is the mixing of two (or more) genetically differentiated populations which results a hybrid population. Admixture events and the levels of proportions contributed to the hybrid by the parents can be estimated by using genetic data. A few well known methods that try to model the admixture (Chikhi *et al.*, 2002; Wang 2003) were developed. However these methods assume that admixture event happened only once in history, and gene flow between the populations after then are neglected, which is not generally the case in real life populations, especially domestic species (Bray *et al.,* 2010).

2-Event Bayesian Admixture (2-BAD) is a software developed for estimating the admixture populations in more complex settings, allowing two or three parent populations and one or two admixture events by employing approximate Bayesian computing (ABC) (Beaumont, 2002). It has been shown that ABC can be used as an alternative to full-likelihood methods because of its low computational cost and flexibility (Excoffier *et al.*, 2005). The method comprises

5 steps: i) definitions of the prior distributions and the parameters of the model; ii) simulation of datasets with values randomly selected from prior distributions; iii) computation of summary statistics from datasets; iv) comparisons of the observed and the simulated statistics; v) rejection of the parameters which are statistically significant than that of the observed data. After the rejection step, histograms of the parameters that were not rejected were drawn and summary statistics for the accepted datasets were presented in a spreadsheet.

In this study, 4 scenarios were tested. In all of the scenarios, a model with two parents and one admixture event was modeled. The graphical representation of the model was presented in the Figure 2.2. The first two scenarios were tested using the microsatellite data from the current study using 19 loci. In the first scenario, the first parent was designated as Sakız, and the second parent was designated as İvesi. In the second scenario, instead of İvesi, Akkaraman and Morkaraman together were assumed as the second parent. In both scenarios Dağlıç was assumed as the hybrid. For the third and fourth scenarios 21 loci microsatellite data from ECONOGENE Project was used (ECONOGENE). Eleven loci (BM8125, OARCP34, DYMS1, OARFCB128, OARFCB226, OARHH47, ILSTS11, ILSTS5, MAF33, MCM140, OARVH72) out of twenty one were similar with the current study.For the results to be as compatible as it could be, for the first parent, Lesvos and Kymi, two Greek breeds in close proximity with Anatolia, were selected instead of Sakız. Dağlıç was again assumed as the hybrid as was in the first two scenarios. For the third scenario the second parent were designated as the combination of Akkaraman and Morkaraman. For the last scenario instead of İvesi, a combination of Middle-eastern breeds (Ossimi from Egypt; Heri, Naemi and Najdi from Saudi Arabia) were selected as the second parent. The program was run for 1.000.000 simulations with a tolerance level of 0.001.

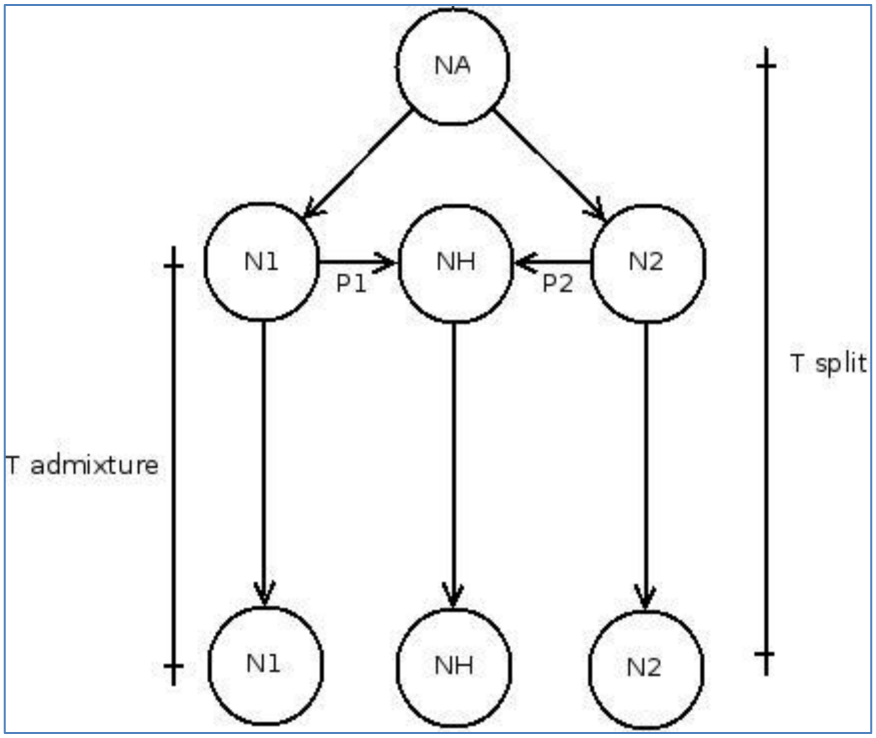

Figure 2.2 The graphical representation of the two parent, one admixture event model. Tsplit is the time since the split of the original ancestral population into two parental populations (in generations). Tadmixture is the time since the admixture event (in generations). P1 and P2 are the percent contributions of the parental populations to the hybrid (admixed) population. NA, N1, N2 and NH are the effective population sizes of ancestral population, first parental population, second parental population and the hybrid population respectively.

2.6 Priority Setting for the Breeds in Their Conservation Studies

2.6.1 Priority Setting For Conservation of Breeds Based on the Genetic Data

To assess the contributions of populations to the genetic diversity, four approaches were used.

2.6.1.1 Contribution to Allelic Richness

To determine the best contributors of diversity, Petit *et al.* (1998) proposed to measure the allelic richness of the populations. Technique of rarefaction (Hurlbert, 1971) is applied to standardize the unequal sample sizes. The genetic diversity is broken down into two components, a) the level of diversity of the population; and b) the uniqueness of the population.

The calculations of contributions to genetic diversity in terms of allelic richness were done by Molkin v3.0.

2.6.1.2 Weitzman Approach

Proposed by Weitzman (1992, 1993) this approach uses a recursive algorithm to determine the relative importance of elements (species, breeds, individuals) to the total diversity using genetic distances. It has four criteria; I) The total amount of diversity should not increase when an element is removed from set; II) The addition of an element which is identical to one (or more) element in a set does not increase diversity; III) A small change in distance measure should not result in a large change in diversity measure; IV) The diversity of the total set increases if the distance between elements increase.

Weitzman criteria sets a good diversity measure, however, due to the nature of the genetic distances, it disregards the genetic variation within elements. As a result the most distinct (may result from inbreeding) elements are given the top priority.

The calculations of Weitzman Diversities were done by using WeitzPro software (Derban *et al.*, 2002).

2.6.1.3 Metapopulation Approach

Another approach to measure the diversity of a set of breeds is to take into account both within and between population components of the coancestry.

While Weitzman Diversity is suitable for sets with little relations (i.e. different species), the method proposed by Caballero and Toro (2002) was better suited for subdivided populations (i.e. different breeds of the same species). The total genetic diversity GD_T is calculated with the formula;

$$GD_T = GD_B + \lambda GD_W \tag{8}$$

Where, GD_B is the genetic diversity between sub-populations and the GD_W is the genetic diversity within sub-populations. The coefficient λ may vary between 0 (Weitzman Diversity) to 1, depending on the aims of conservation scheme, with varying emphasis on within population diversities.

The calculations of total genetic diversities using this method were done by Metapop v1.0.1 (Perez-Figueroa et al., 2009). Modified analyses to detect optimal sets using this approach were performed by a script written in PERL by the author of this manuscript.

2.6.1.4 Marker Estimated Kinship (MEK) Approach

Core set diversity is based on the coancestries (or kinship coefficients) of the elements within a set (Eding *et al,* 2002; Bennewitz and Meuwissen, 2005; Oliehoek, 2006). It was first defined as the smallest set of lines of plants which encompasses the genetic diversity of whole species (Frankel and Brown, 1984). In this approach, the genetic overlap between elements of the set, which is measured as the coancestries or kinship coefficients, is tried to be minimized. The genetic diversity is maximized and the relative importance of the populations in terms of contribution to genetic diversity can be measured in this method.

Unlike Weitzman Diversity, the subtraction of an element may increase the genetic diversity if kinship is decreased. Conversely, the genetic diversity may increase upon an addition of a population which will increase the coancestry in the set.

The vector c, which contains the contributions to the core set was calculated bt the formula (Bennewitz and Meuwissen, 2005),

$$c = \frac{1}{4}\ M^{-1}F - \frac{1'_N M^{-1}F - 4}{1'_N M^{-1}1_N} . M^{-1}1_N \qquad (9)$$

Where,

c is the vector containing the contributions to the core set,

M is the kinship matrix among breeds,

F is the diagonal of M,

1_N is a vector of 1's of length equal to the number of breeds.

Kinship coefficients were calculated by Molkin v3.0 (Gutierrez *et al.*, 2005). The matrix of kinship coefficients is used to calculate the contributions to core set by using Matlab 2009B (MathWorks Inc., 2009). Again, necessary calculations which were not available in the literature were done by the author of the manuscript. The negative contributions were eliminated using a recursive algorithm that was proposed by Eding (2002), by removing the most negative member and recalculating the contribution until no negative contribution is left.

2.6.2 Priority Setting for Conservation of Breeds Based on Extinction Risk, Genetic Contribution Value and Conservation Value

Conservation of all breeds is not possible, because of the innumerable breeds and the limited financial resources. Moreover conservation of all breeds is not scientifically justified, because breeds may not have any values to be conserved or genetically breeds may be effectively the same (Boettcher, 2010). Therefore a prioritization of the breeds to be conserved must be undertaken to effectively allocate the funds.

To assess the conservation priorities for the breeds, a guideline: In Vivo Conservation of Animal Genetic Resources by the Food and Agriculture Organization of the United Nations (FAO) was developed recently (FAO, 2011). In accordance with the guidelines information in the lines of three components were needed. Those components were; the extinction probability of the breeds, the contribution of each breed to the genetic diversity and the conservation values of the breeds. The Food and Agriculture Organization of the United Nations (FAO) Guidelines for the *In Vivo* Conservation of Animal Genetic Resources (FAO, 2011), which was compiled from the contributions of scientists worldwide, aims to provide technical guidance and decision support for prioritization efforts.

There is not a standard and consistent system to evaluate the level of endangerment of the breeds. Because of the differences in the definition of breed (hence unit of study) and the availability of the information, the risk statuses of the breeds of the developed and developing countries demand different criteria to be applied (Alderson, 2009). Although the numerical, genetic or geographical factors such as effective population sizes, number of breeding females and males, the trend in the change of population sizes, degree of inbreeding, the distribution area of the breeds are emphasized strongly (FAO, 2000; Reist-Marti, 2003; Gizaw, 2008; Alderson, 2009; Boettcher, 2010; FAO, 2011)) as the factors of importance for the risk assessment; factors like changes in the production systems, production environments, producer and market preferences as well as political instabilities were believed to be considered also (Rege and Gibson, 2003; Reist-Marti, 2003; Gizaw, 2008).

Extinction probabilities of the breeds must be defined for each breed, if future trends were to be modeled. For the evaluation of the risk status, indicators from literature (FAO, 2000; Reist-Marti, 2003; Gizaw, 2008); of which some of them were also recommended by the guideline, were compiled and modified for the present study. Our indicators, which were presented in the Table 2.3, comprised of 14 variables which could be broken down to three categories. The first category was about the demography of the breeds, which includes population sizes, average ram number per flock, the area of the population's distribution, and the trend in population size in the last five years. The second category was about the farmers and the attitude of farmers' towards the breed which includes the degree of indiscriminating crossbreeding, the trend in the number of farmers in the last five years. The third category is about the political and/or cultural factors which include the existence of the pure stocks kept by the breeders or kept by the state institutions, the availability of shepherds, existence of a conservation scheme, political situation and other threats specific against a breed (the reduction of pasture lands in touristic regions or extensive hybridization for reduction of fat-tail etc.). Both the qualitative and quantitative answers were classified into classes and assigned values between 0 – no impact on risk – and increased with 0.1 increments with each class in the criteria as suggested by Reist-Martiet al. (2003) and Gizaw et al. (2008) with the only exception of the 0.05 increment in the size of the distribution area.

Table 2.3 Variables, criteria and values for assessing risk of extinction for the breeds. The categories with “1” were adapted from Reist-Marti et al. (2003), the categories with “2” were adapted from Gizaw et al. (2008) and the categories with “3” were adapted from the FAO guideline

Variable	**Criterion and Value**
Population Size[1,2,3]	0.3 < 1000 0.2 = 1001 to 10000 0.1 = 10001 to 100000 0 > 100000 missing value = 0.2
Average # of Rams/Flock[2]	0.3 < 4 0.2 = 5 – 8 0.1 = 9 – 12 0 > 12 missing value = 0.2
Degree of Indiscriminate Crossbreeding[1,2,3]	0.3 = high 0.2 = medium 0.1 = low 0 = none missing value = 0.2
Farmers' Opinions [2,3]	0.2 = leave 0.1 = hybridization 0 = continue missing value = 0.2
% Decrease in the # of Farmers	0.3 > 50% 0.2 = 25% - 50% 0.1 = 10% - 24% 0 < 10% missing value = 0.2
Area of Distribution of the Breed[1,3]	0.3 < 0.1 0.2 = 0.1 - 0.24 0.1 = 0.25 – 1 0.05 = 1 – 2 0 > 2
Trend in the Population Size of the Breed[1,3]	0.2 = rapid decrease 0.1 = decrease 0 = stable/increase missing value = 0.1

Table 2.3 Continued

Variable	**Criterion and Value**
Existence of Pure Stock (Breeders)[2,3]	-0.1 = yes 0 = no
Existence of Pure Stock (State)[2,3]	-0.1 = yes 0 = no
Problem of Shepherd Availability	0.3 = high 0.2 = medium 0.1 = low 0 = none
Organization of Farmers[1,3]	0.1 = no 0 = yes
Existence of a Conservation Scheme[1]	0.1 = no 0 = yes
Political Situation[1,3]	0.1 = unrest 0 = no problem
Specific Threats Against the Breed	0.1 for each threat 0 = no

For the population sizes, estimates of the field specialists were used. The risk categories were arranged following the guidelines of FAO (FAO, 2011). The average rams per flock was calculated using the rams of the pure flocks either kept by the breeds or kept by the state. The risk factors were assigned by allocating the numbers in equally sized classes. For the evaluation of the size of the geographic distribution, the specialists were asked to indicate the distributions on the maps, they were digitized first, and then pixels within the areas were counted. Because the areas didn't conform to a uniform distribution as in average number of rams per flock, classes with unequal sizes were used while assigning the risk factors. Factors other than described above were not of continuous nature, thus the answers of the questionnaires were directly assigned into a risk factor.

After assigning individual risks to criterions the values were summed to find the extinction risks of the breeds. The extinction risks were then standardized following Reist-Marti (2003) to range from 0.1 to 0.9 according to the formula;

$$Risk_i = 0.1 + 0.8 * \frac{{}_{n=1}^{14} Risk_i\,(n)}{maxRisk} \qquad (10)$$

Where,

$Risk_i$ is the standardized extinction risk of breed i,

$Risk_i(n)$ is the risk of extinction of breed i from the n^{th} criterion and

maxRisk is the highest possible risk value, which is 2.6 in the current study.

Breed merits include the production values, the adaptation of the breeds to their respective environments, and their socio-cultural importance. For the evaluation of conservation values of the breeds the following formula (Boettcher, 2010) was used where each term is related by a merit of the breed.

$$CV_i = W_{F1} * (F1_i - \mu_1) / \sigma_1 + W_{F2} * (F2_i – \mu_2) / \sigma_2 + \ldots + W_{Fn} * (Fn_i - \mu_n) / \sigma_n \qquad (11)$$

CVi is the conservation value of the breed i, WFn is the weight (i.e. the relative importance) of the factor n, Fni is the value of the factor n for breed i, μn is the average of all the breeds for the factor n, σn is the standard deviation of all breeds for the factor n. The factors which were included in this study were presented in the Table 2.4. Weights in the Table 2.4 was assigned to reflect the importance of meat production against milk production (two times more important), wool production (ten times more important), pelt production (ten times more important) and adaptive abilities (ten times more important).

Table 2.4 The merits: production values, adaptive values and socio-cultural values of the Turkish native sheep breeds . W denotes the weights given for the merits. Negative values for merits indicate the lesser the value of the merit, the favorable it is for the breeder (i.e weaning period, age of maturity, tail weight).

Factor Name	**Relative Importance (Weight)**
Birth Rate	1
Litter Size	1
Average Lambing Period (Yrs)	1
Milk Yield	0.5
Wool Yield	0.1
Weaning Period (Days)	-1
Survival Until Weaning	1
Weight At Birth	1
Weight At Weaning	1
Age Of Maturity (Days)	-1
Daily Weight Gain	1
Feed Conversion	1
Age Of Breeding (Days)	-1
Carcass Weight	1
Tail Weight	-1
Pelt Weight	0.1
Walking Ability	0.1
Grazing Ability	0.1
Herd Instinct	0.1
Mothering Instinct	0.1
Ease Of Milking	0.1
Ease Of Shepherding	0.1
Areas Not Suitable For Animal Breeding	0.1
Special Produce	0.1
Non-Economic Uses	0.1
Traditional Importance	0.1

For the preparation of the list of the production, adaptive and socio-cultural values, recommendations of the personnel of TAGEM (Oya Akın, Nevin Aksümer, Dr. Bekir Ankaralı) and academicians (Prof. Dr. Mehmet Ertuğrul) were used in addition to the attributes found in the breed registries and publications. The attributes from the literature did not include the morphologic traits like height, length or chest depth which were excluded from the analysis thinking that they have no effect on productivity of the breed.

The quantitative traits (i.e. meat yield, milk yield) were incorporated into the formula directly; however the qualitative traits were needed to be converted to numerical values. The conversion was done in a manner similar to the risk assessment following the works of Reist-Marti *et al.* (2003) and Gizaw *et al.* (2008). The factors and the classes were presented in the Table 2.5

Table 2.5 The factors, criteria and values for the conversion of qualitative traits into numeric values.

Variable	**Criterion and Value**
Walking Ability	0.3 = very good 0.2 = good 0.1 = medium 0 = not good
Grazing Ability	0.3 = very good 0.2 = good 0.1 = medium 0 = not good
Herd Instinct	0.3 = very good 0.2 = good 0.1 = medium 0 = not good
Mothering Instinct	0.3 = very good 0.2 = good 0.1 = medium 0 = not good

Table 2.5 Continued

Variable	**Criterion and Value**
Ease Of Milking	0.3 = very good 0.2 = good 0.1 = medium 0 = not good
Ease Of Shepherding	0.3 = very good 0.2 = good 0.1 = medium 0 = not good
Areas Not Suitable For Animal Breeding	0.2 = yes 0.1 = hard 0 = no missing value = 0
Special Products	0.1 = yes 0 = no missing value = 0
Non-Economic Uses	0.1 = yes 0 = no missing value = 0
Traditional Importance	0.1 = yes 0 = no missing value = 0

For the missing values, 0 were assigned to the qualitative traits. For the quantitative traits arithmetic means of the known breeds were calculated, and assigned as the missing values not to affect the outcomes.

Standardized conservation values were calculated with the formula suggested by Gizaw *et al.* (2008);

$$SCV_i = 0.1 + [\ 0.8 * (CV_i - CV_{min}) / (CV_{max} - CV_{min})\ ] \qquad (12)$$

where,

SCV_i is the standardized conservation value of breed i,

CV_i is the conservation value of breed i,

CV_{min} is the minimum conservation value among the breeds,

CV_{max} is the maximum conservation value among the breeds.

According to Formula 12, the breed with the highest conservation value would take the value of 0.9 and the breed with the lowest conservation value would take the value of 0.1, and the rest of the breeds would have intermediate standardized conservation values.

Finally, after the calculation of the standardized conservation values utility of the breed is calculated with the formula (Gizaw *et al.*, 2008),

$$U_i = 2 * (Risk_i * D_i) + SCV_i \qquad (13)$$

Where,

U_i is the utility of breed i, which is the criterion for prioritization,

$Risk_i$ is the standardized risk of breed i calculated by the equation 10,

D_i is the contribution of the breed i to the core set calculated by the equation 9,

SCV_i is the standardized conservation value of breed i calculated by the equation 13.

CHAPTER 3

RESULTS

3.1 Genetic Data

In the present study, genotypes of 628 individuals from 13 native Turkish sheep breeds based on 19 microsatellite loci which were recorded by Acar (2010) were employed as the genetic data.

The loci used were recommended by the Food and Agriculture Organization of the United Nations (FAO) (http://dad.fao.org), and were used by some other previous studies also. The Table 3.1 presented the loci used and the previous studies that employed the same loci.

Table 3.1 Microsatellite loci that were used in the study and previous studies that employed the same loci. In the last row proportion of the same loci employed out of the total loci examined were given as "Total".

Locus	**Peter *et al.* (2007)**	**Gizaw *et al.* (2007)**	**Glowatzki-Mullis *et al.* (2008)**	**Lawson Handley *et al.* (2007)**	**Uzun *et al.* (2006)**
BM8125	✓	✓	✓		✓
DYMS1	✓	✓			
ILSTS005	✓	✓	✓	✓	✓
ILSTS011	✓	✓	✓	✓	✓
INRA063	✓		✓	✓	

Table 3.1 Continued

Locus	**Peter *et al.* (2007)**	**Gizaw *et al.* (2007)**	**Glowatzki-Mullis *et al.* (2008)**	**Lawson Handley *et al.* (2007)**	**Uzun *et al.* (2006)**
MAF209	✓	✓	✓	✓	
MAF33	✓				
MAF65	✓		✓	✓	
MCM140	✓		✓		
OarCP34	✓				
OarFCB128	✓		✓		
OarFCB20	✓	✓	✓	✓	
OarFCB226	✓		✓		
OarFCB304	✓	✓	✓	✓	
OarFCB48			✓	✓	
OarHH47	✓				
OarJMP29	✓	✓		✓	
OarJMP58	✓		✓	✓	
OarVH72	✓	✓	✓		
Total	18/31	9/17	14/44	10/23	3/30

In this study, a total of 273 alleles were detected over the 19 loci. The number of alleles per locus was given in the Table 3.2. The highest number of alleles for a single locus was for OarFCB304 (23) and the lowest number of alleles for a single locus was for OarCP34 (8)

Table 3.2 Total number of observed alleles for the loci used in the study for 13 native Turkish sheep breeds.

Locus	Number of alleles
BM8125	10
DYMS1	18
ILSTS005	11
ILSTS011	10
INRA063	19
MAF209	14
MAF33	14
MAF65	13
MCM140	13
OarCP34	8
OarFCB128	16
OarFCB20	16
OarFCB226	15
OarFCB304	23
OarFCB48	13
OarHH47	14
OarJMP29	18
OarJMP58	19
OarVH72	9

3.2 Descriptive Statistics for the Breeds

3.2.1 Null Alleles

The estimated frequencies of null alleles by the FreeNA software (Chapus and Estoup, 2007) for each locus and breed were given in Table 3.3. Frequencies (r) greater than 0.2 was considered as unacceptable for the further analysis as was suggested by Dakin and Avise, (2004) and Chapuis and Estoup, (2007) were highlighted.

As can be seen from the Table 3.3 IVE at OarFCB226 locus has an estimated null allele frequency greater than 0.2. Therefore, the rest of the analyses were done twice, with and without OarFCB226 and the results done by the exclusion of this locus were presented in Appendix E.

3.2.2 Linkage Disequilibrium

Presence of linkages between pairs of loci across all breeds were checked with Genepop v4.1 (Rousset, 2008). Due to the fact that, the loci studied were on different chromosomes, no linkages were expected to be seen. After Bonferroni corrections 3 loci over 4 breeds (Herik between DYMS1 and HH47, Dağlıç between INRA63 and HH47, Kıvırcık between MAF33 and FCB128, Karayaka between MAF33 & FCB128) out of 2223 pairwise-loci-by-breed combinations are found to be in linkage disequilibrium. Despite the fact that 4 linkage disequilibria were very few, the linkage disequilibrium observed between MAF33 and FCB128 in two breeds (Kıvırcık and Karayaka) was noted.

3.2.3 Allelic Richness

In total 273 alleles were detected using 19 loci. The maximum number of alleles for a single locus is for OarFCB304 (23) and the minimum number of alleles for a single locus is OarCP34 (8). The average number of alleles per locus was 14.37. Average number of alleles per breed was 9.125 while number of alleles for a breed ranged from 9.811 (HER) to 7.872 (SAK).

Table 3.3 Null Allele Frequencies estimated by FreeNA software for 19 microsatellite loci of 13 breeds. The abbreviations of the breeds are SAK for Sakız, KRG for Karagül, HEM for Hemşin, CIC for Çine Çaparı, NOR for Norduz, HER for Herik, DAG for Dağlıç, MOR for Morkaraman, KIV for Kıvırcık, KRY for Karayaka, IVE for İvesi, GOK for Gökçeada and AKK for Akkaraman. The shaded cells indicate r ≥ 0.2 observations.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
MAF65	0.023	0.000	0.000	0.000	0.000	0.000	0.007	0.002	0.000	0.039	0.041	0.021	0.025
OarFCB226	0.000	0.008	0.050	0.056	0.000	0.000	0.000	0.012	0.000	0.000	0.250	0.007	0.000
INRA063	0.000	0.000	0.079	0.041	0.003	0.052	0.035	0.047	0.076	0.039	0.054	0.021	0.032
MAF33	0.000	0.100	0.050	0.021	0.030	0.044	0.000	0.044	0.010	0.014	0.052	0.047	0.000
OarFCB128	0.000	0.000	0.042	0.025	0.000	0.022	0.000	0.074	0.023	0.071	0.181	0.167	0.097
OarCP34	0.032	0.022	0.037	0.013	0.002	0.023	0.058	0.035	0.000	0.000	0.033	0.037	0.041
DYMS1	0.034	0.000	0.006	0.000	0.000	0.038	0.000	0.019	0.018	0.020	0.000	0.029	0.041
OarHH47	0.000	0.010	0.000	0.039	0.000	0.017	0.000	0.035	0.000	0.002	0.000	0.019	0.000
OarVH72	0.051	0.000	0.000	0.110	0.000	0.011	0.011	0.044	0.000	0.000	0.000	0.018	0.131
BM8125	0.057	0.000	0.166	0.150	0.010	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.019
MAF209	0.023	0.000	0.000	0.000	0.021	0.012	0.028	0.003	0.110	0.114	0.115	0.006	0.134
MCM140	0.048	0.000	0.000	0.003	0.008	0.000	0.041	0.000	0.044	0.096	0.029	0.044	0.076
OarJMP29	0.065	0.041	0.049	0.020	0.060	0.092	0.001	0.073	0.000	0.015	0.000	0.000	0.039
OarFCB48	0.011	0.006	0.052	0.014	0.000	0.025	0.010	0.024	0.000	0.007	0.000	0.069	0.043
ILSTS005	0.005	0.036	0.000	0.015	0.002	0.092	0.025	0.046	0.000	0.000	0.006	0.000	0.008
OarJMP58	0.038	0.000	0.059	0.035	0.032	0.000	0.000	0.000	0.000	0.045	0.068	0.046	0.004
OarFCB20	0.032	0.019	0.000	0.029	0.013	0.003	0.000	0.025	0.074	0.013	0.000	0.000	0.010
OarFCB304	0.000	0.000	0.000	0.037	0.000	0.000	0.026	0.023	0.000	0.000	0.001	0.000	0.014
ILSTS011	0.000	0.005	0.068	0.000	0.000	0.000	0.002	0.000	0.058	0.000	0.127	0.000	0.040

Table 3.4 Allelic richnesses were calculated by Fstat v2.9.3 software using n=30 as constant sample population size. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**	**Overall**
MAF65	5.796	4.885	6.606	5.938	8.826	8.286	7.410	9.574	9.478	8.381	10.461	9.806	6.978	7.879
OarFCB226	11.784	10.058	13.826	13.304	12.349	11.651	12.888	10.333	11.139	10.740	11.289	9.141	9.595	11.392
INRA063	6.204	7.139	14.592	12.588	9.786	15.623	14.469	12.487	14.076	12.879	11.950	13.826	16.312	12.456
MAF33	7.054	10.706	11.433	9.173	8.451	9.111	11.000	7.016	7.964	10.266	9.021	8.488	6.973	8.974
OarFCB128	6.755	6.381	10.847	8.553	6.719	12.311	7.000	8.600	8.414	10.086	7.797	10.777	7.601	8.603
OarCP34	6.487	6.841	6.953	6.997	6.881	6.750	7.575	5.998	7.881	6.621	5.985	7.204	7.569	6.903
DYMS1	9.674	11.681	10.139	8.434	12.370	11.255	10.359	11.758	10.888	12.151	11.452	10.206	10.924	10.869
OarHH47	10.601	9.760	11.094	9.575	11.670	12.173	11.362	11.380	12.094	11.101	11.557	12.845	12.137	11.335
OarVH72	7.855	7.633	7.881	6.989	8.528	7.611	8.772	8.575	7.877	5.939	7.579	4.998	6.889	7.471
BM8125	6.775	6.541	7.670	5.940	5.534	7.506	5.796	4.839	5.845	5.940	7.529	6.153	5.617	6.283
MAF209	7.689	5.849	11.284	10.000	8.142	8.281	8.700	8.421	8.784	10.608	8.484	9.363	11.242	8.988
MCM140	7.168	8.901	9.166	8.426	9.501	11.989	11.996	11.262	10.794	10.757	9.727	9.377	10.593	9.974
OarJMP29	8.596	8.626	8.362	8.426	10.315	8.779	7.529	8.377	11.033	10.703	11.147	9.696	10.891	9.422
OarFCB48	6.727	8.987	7.455	6.696	10.945	7.441	8.902	8.767	9.536	8.295	8.963	8.484	7.905	8.393
ILSTS005	5.857	6.177	6.504	3.992	7.210	5.485	6.842	7.859	4.713	6.030	5.689	5.833	5.469	5.974
OarJMP58	7.888	9.946	7.910	8.307	8.769	13.104	10.192	10.612	10.730	11.064	11.581	13.041	11.857	10.385
OarFCB20	8.315	9.409	11.223	7.497	10.861	10.780	11.266	10.852	11.449	7.988	12.551	8.969	12.564	10.286
OarFCB304	12.355	11.620	9.838	7.923	13.119	11.637	11.674	13.972	10.377	12.413	13.854	8.193	10.211	11.322
ILSTS011	5.992	5.536	7.476	7.616	4.869	6.633	7.996	6.130	7.856	7.136	6.883	4.981	4.889	6.461
Overall	7.872	8.246	9.487	8.230	9.202	9.811	9.565	9.306	9.523	9.426	9.658	9.020	9.275	9.125

3.2.4 Private Alleles

The alleles only present in one breed (private alleles) were checked using a script written in Perl language. The results were summarized in the Table 3.5. The frequencies of all private alleles except allele 175 at OarJMP58 locus in GOK were smaller than 0.05. Probably a new mutation in OarJMP58 appeared as a private allele in GOK breed, which is an island breed, and attained a frequency of 0.0676 without propagating to other breeds.

Table 3.5 The frequencies of the private alleles detected in the study. The shaded cell indicates the frequency of the private allele that is greater than 5%.

Breed	**Locus**	**Allele**	**Frequency**
Sakız	DYMS1	167	0.0204
Karagül	BM8125	122	0.0102
Norduz	DYMS1	159	0.0357
Herik	OarJMP58	173	0.0106
Dağlıç	OarFCB304	153	0.03
Morkaraman	OarFCB304	159	0.01
Gökçeada	OarJMP58	171	0.0135
Gökçeada	OarJMP58	175	0.0676
Akkaraman	MAF33	147	0.0208
Akkaraman	OarJMP58	144	0.02

3.2.5 Presence of Hardy-Weinberg Equilibrium in Each Locus

Expected heterozygosities, observed heterozygosities and the deviations from the Hardy-Weinberg (H-W) equilibrium were calculated by Aqlequin v3.5.1.2

(Excoffier, 2006) by using Fisher’s Exact Test. The results are given in the following Table 3.6. Of the 247 breed-locus combinations 13 (5.2%) of them showed significant deviation from H-W equilibrium after Bonferroni corrections ($p < 0.05/247$). Deviations did not accumulate on one breed or locus. The highest number of deviations was observed in the breed HEM (n=3) and in the locus MAF33 (n=4).

The mean number of expected heterozygosity per breed was between 0.73668 (KRG) and 0.79634 (KRY) and the mean number of expected heterozygosity per locus was between 0.61707 (BM8125) and 0.85623 (OarFCB20).

Table 3.6 In each box, expected heterozygosities, significance level of deviations from Hardy-Weinberg (H-W) equilibrium and standard deviations (in parentheses) were given. Shaded cells indicate significant deviations from H-W Equilibrium. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**	**Overall**
MAF65	0.687± (0.0004)	0.560*± (0)	0.750± (0.0004)	0.716± (0.0002)	0.754± (0.0003)	0.724± (0.0002)	0.741± (0.0005)	0.769± (0.0004)	0.820± (0.0006)	0.791± (0.0004)	0.804± (0.0004)	0.716± (0.0003)	0.729± (0.0002)	0.735
OarFCB226	0.700± (0.0003)	0.822± (0.0003)	0.889± (0.0004)	0.889± (0.0001)	0.842± (0.0002)	0.721± (0.0004)	0.806± (0.0003)	0.707± (0.0004)	0.747± (0.0004)	0.789± (0.0003)	0.865*± (0)	0.755± (0.0004)	0.616± (0.0005)	0.780
INRA063	0.675± (0.0003)	0.547± (0.0001)	0.819*± (0)	0.836± (0.0001)	0.799± (0.0001)	0.852± (0.0001)	0.872± (0.0001)	0.867± (0.0002)	0.917± (0.0001)	0.882± (0.0003)	0.846± (0.0003)	0.881± (0.0001)	0.884± (0.0002)	0.821
MAF33	0.752± (0.0004)	0.826*± (0)	0.873± (0.0001)	0.810± (0.0002)	0.754± (0.0004)	0.845± (0.0003)	0.816± (0.0002)	0.739± (0.0002)	0.815*± (0)	0.851*± (0)	0.753± (0.0001)	0.810*± (0)	0.735± (0.0001)	0.798
OarFCB128	0.538± (0.0004)	0.642± (0.0003)	0.804*± (0)	0.628± (0.0002)	0.622± (0.0003)	0.771± (0.0001)	0.852± (0.0002)	0.841± (0.0001)	0.802± (0.0001)	0.836± (0.0001)	0.806*± (0)	0.881*± (0)	0.842± (0.0004)	0.759
OarCP34	0.760± (0.0001)	0.823± (0.0001)	0.813± (0.0001)	0.811± (0.0003)	0.832± (0.0004)	0.827± (0.0005)	0.849± (0.0005)	0.788± (0.0004)	0.842± (0.0002)	0.779± (0.0005)	0.773± (0.0001)	0.818± (0.0004)	0.817± (0.0002)	0.810
DYMS1	0.834± (0.0003)	0.798± (0.0003)	0.816± (0.0001)	0.774± (0.0003)	0.817± (0.0004)	0.785± (0.0003)	0.707± (0.0002)	0.844± (0.0003)	0.834± (0.0004)	0.874± (0.0005)	0.860± (0.0003)	0.835± (0.0003)	0.762± (0.0004)	0.811
OarHH47	0.810± (0.0003)	0.852± (0.0002)	0.788± (0.0002)	0.846± (0.0005)	0.871± (0.0003)	0.858± (0.0003)	0.874± (0.0005)	0.815± (0.0003)	0.852± (0.0004)	0.830± (0.0004)	0.885± (0.0002)	0.873± (0.0004)	0.870± (0.0004)	0.848
OarVH72	0.834± (0.0004)	0.811± (0.0005)	0.843± (0.0003)	0.774± (0.0001)	0.824± (0.0004)	0.807± (0.0004)	0.820± (0.0005)	0.844± (0.0003)	0.822± (0.0002)	0.787± (0.0005)	0.808± (0.0003)	0.563± (0.0004)	0.451*± (0)	0.768
BM8125	0.633± (0.0002)	0.612± (0.0001)	0.754*± (0)	0.781± (0.0001)	0.629± (0.0003)	0.665± (0.0004)	0.524± (0.0005)	0.510± (0.0006)	0.490± (0.0004)	0.724± (0.0005)	0.609± (0.0002)	0.534± (0.0002)	0.555± (0.0004)	0.617
MAF209	0.757± (0.0004)	0.687± (0.0004)	0.866± (0.0001)	0.874± (0.0005)	0.728± (0.0004)	0.790± (0.0005)	0.735± (0.0004)	0.731± (0.0003)	0.777± (0.0001)	0.810± (0.0001)	0.818± (0.0001)	0.838± (0.0004)	0.773*± (0.0001)	0.783
MCM140	0.747± (0.0002)	0.816± (0.0001)	0.708± (0.0005)	0.802± (0.0005)	0.821± (0.0003)	0.861± (0.0002)	0.846± (0.0002)	0.828± (0.0003)	0.814± (0.0003)	0.877± (0.0001)	0.851± (0.0002)	0.786± (0.0002)	0.837± (0.0002)	0.815
OarJMP29	0.738± (0.0003)	0.840± (0.0002)	0.811± (0.0001)	0.808± (0.0004)	0.816± (0.0004)	0.771± (0.0002)	0.787± (0.0003)	0.804± (0.0001)	0.822± (0.0003)	0.852± (0.0005)	0.773± (0.0003)	0.841± (0.0003)	0.824± (0.0001)	0.807
OarFCB48	0.804± (0.0004)	0.689± (0.0003)	0.695± (0.0002)	0.439± (0.0004)	0.768± (0.0002)	0.709± (0.0004)	0.775± (0.0005)	0.796± (0.0003)	0.843± (0.0004)	0.749± (0.0006)	0.668± (0.0002)	0.662± (0.0001)	0.743± (0.0004)	0.718
ILSTS005	0.685± (0.0005)	0.682± (0.0004)	0.547± (0.0003)	0.652± (0.0005)	0.668± (0.0001)	0.597± (0.0001)	0.633± (0.0003)	0.646± (0.0003)	0.612± (0.0005)	0.527± (0.0003)	0.626± (0.0004)	0.694± (0.0005)	0.667± (0.0004)	0.634
OarJMP58	0.831± (0.0005)	0.717± (0.0003)	0.802± (0.0001)	0.757± (0.0002)	0.776± (0.0004)	0.816± (0.0001)	0.831± (0.0002)	0.770± (0.0003)	0.795± (0.0003)	0.780± (0.0003)	0.782± (0.0003)	0.839± (0.0003)	0.797± (0.0002)	0.792
OarFCB20	0.767± (0.0005)	0.854± (0.0004)	0.846± (0.0002)	0.826± (0.0004)	0.867± (0.0003)	0.873± (0.0002)	0.868± (0.0003)	0.864± (0.0004)	0.884± (0.0002)	0.855± (0.0004)	0.876± (0.0001)	0.860± (0.0004)	0.891± (0.0003)	0.856
OarFCB304	0.856± (0.0002)	0.815± (0.0002)	0.709± (0.0003)	0.652± (0.0001)	0.873± (0.0004)	0.802± (0.0003)	0.820± (0.0003)	0.770± (0.0003)	0.703± (0.0004)	0.773± (0.0002)	0.775± (0.0002)	0.509± (0.0003)	0.724± (0.0004)	0.752
ILSTS011	0.733± (0.0005)	0.604± (0.0003)	0.768± (0.0001)	0.760± (0.0003)	0.708± (0.0005)	0.775± (0.0006)	0.771± (0.0002)	0.701± (0.0005)	0.823± (0.0004)	0.765± (0.0005)	0.748± (0.0001)	0.667± (0.0005)	0.669± (0.0005)	0.730
Overall	0.744	0.737	0.784	0.760	0.777	0.782	0.786	0.770	0.790	0.796	0.786	0.756	0.747	

3.2.6 F_{IS} Values:

F_{IS} Values and their significance levels were calculated by GenetixSoftware V4.05 (Belkhir*et al*. 1996–2004; http://univ-montp2.fr/~genetix). HEM, CIC, HER, MOR, KRY, IVE, GOK and AKK deviated significantly from 0 indicating heterozygote deficiency. The results are summarized in the following Table 3.7.

Table 3.7 The shaded cells show significant deviations from zero ($p < 0.5$). Positive values mark heterozygote deficiency and negative values mark heterozygote abundance.

Breed	**N**	**F_{IS}**
Sakız	49	0.01468
Karagül	50	-0.02776
Hemşin	48	0.06019
ÇineÇaparı	40	0.06599
Norduz	46	-0.01238
Herik	49	0.05090
Dağlıç	50	0.02854
Morkaraman	50	0.05590
Kıvırcık	45	0.02442
Karayaka	50	0.05229
İvesi	51	0.10384
Gökçeada	50	0.04749
Akkaraman	50	0.08717

3.2.7 Demographic Histories of the Breeds

The multiloci data was analyzed by msvar v0.9 (Beaumont, 1999) to understand the expansion or contraction events that were experienced by the populations. Figure 3.1 shows the changes in population size in log scale.

Analysis revealed that for all of the breeds there were serious bottlenecks in their history. All breeds gave peak at the negative regions of the graphs, around -2, indicating that effective population sizes today are at most 1/100th of what was used to be before the bottleneck. The most serious bottlenecks were observed in Çine Çaparı and Norduz judging by the area covered by the base of the probability distribution that exceeds -4 in the log scale. However additional analyses are required to detect the time passed since the time of the bottleneck.

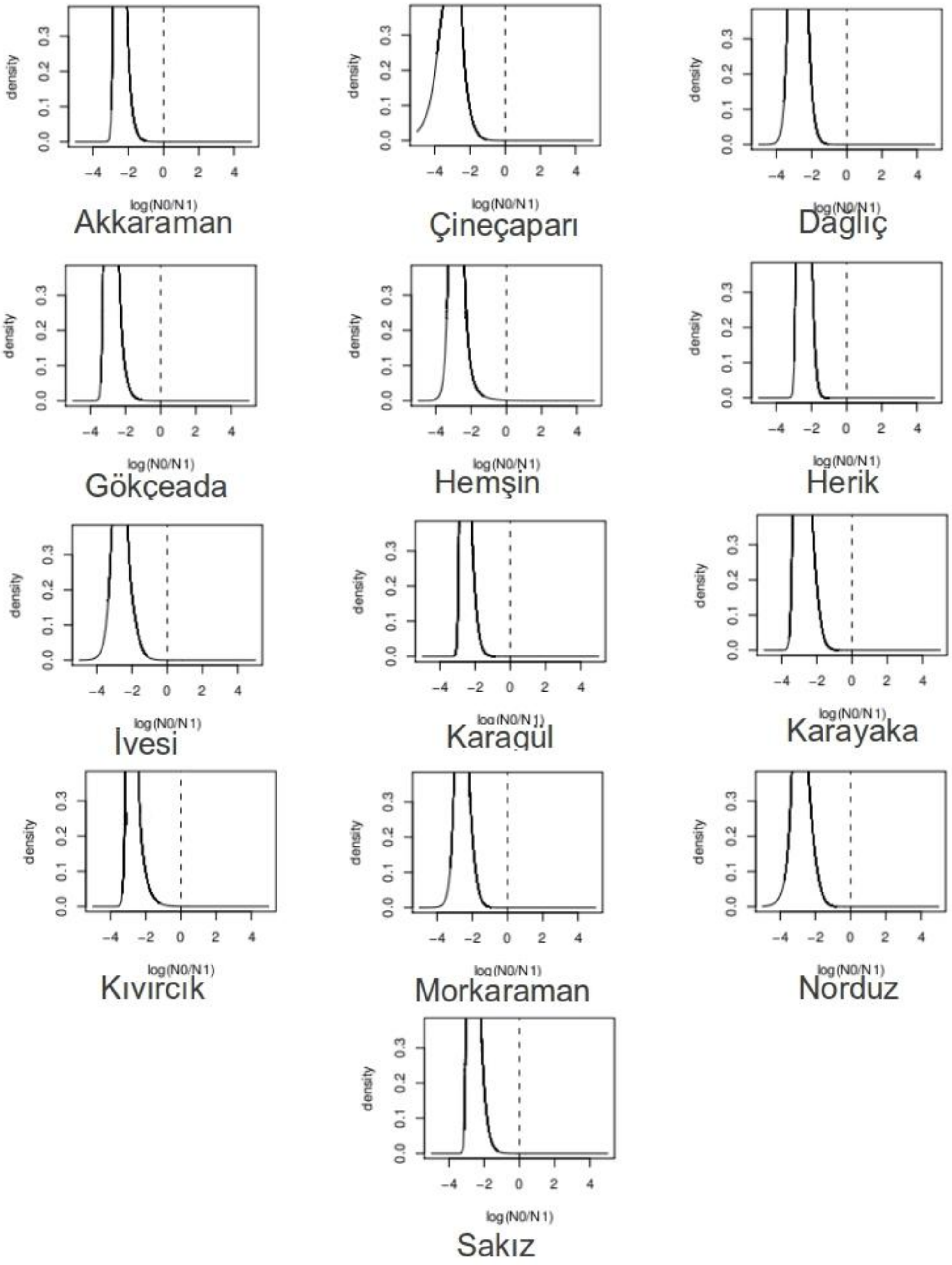

Figure 3.1 The change of population sizes illustrated as the probability distributions. The peaks in the negative region shows the sizes of the populations decreased. The severity of decrease is high in all breeds, exceeding 100 times decrease.

Among the breeds only CIC exhibited a distribution where the proportion of decrease can be more than 10.000.

Until now, the study has focused on the genetic diversities and demographic histories of native sheep breeds of Turkey. The findings thus far could be summarized as; i) Private alleles were not accumulated in all breeds, only one was seen in an island breed; ii) most breeds were heterozygote deficient; iii) linkages were not seen frequently (4/2223); iv) frequencies of null alleles exceeded 0.2 only in one breed, and one locus (İvesi at OarFCB226); v) deviations from Hardy-Weinberg equilibrium were not concentrated in one locus or in one breed; vi) all breeds have experienced serious bottlenecks in the past.

3.3 Comparative Studies for the Breeds

3.3.1 F_{ST} Values

Pairwise F_{ST} values were calculated by FSTAT V.2.9.3 package program (Goudet, 2001). Pairwise F_{ST} values showed that all breeds are differentiated from each other with significance levels smaller than 0.001. The highest level of differentiation was between SAK & GOK (0.08268) and the least differentiation was between MOR & DAG (0.0117). Global F_{ST} was also calculated as 0.0434 and found to be highly significant ($p < 0.001$)

Table 3.8 Pairwise F_{ST} values between breeds.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	-												
KRG	0.059***	-											
HEM	0.059***	0.043***	-										
CIC	0.063***	0.054***	0.034***	-									
NOR	0.047***	0.031***	0.026***	0.027***	-								
HER	0.044***	0.026***	0.025***	0.031***	0.019***	-							
DAG	0.057***	0.049***	0.038***	0.045***	0.026***	0.025***	-						
MOR	0.059***	0.051***	0.045***	0.058***	0.026***	0.031***	0.012***	-					
KIV	0.060***	0.050***	0.032***	0.050***	0.031***	0.019***	0.014***	0.028***	-				
KRY	0.065***	0.050***	0.034***	0.052***	0.037***	0.026***	0.024***	0.024***	0.020***	-			
IVE	0.080***	0.068***	0.046***	0.050***	0.037***	0.047***	0.028***	0.031***	0.044***	0.034***	-		
GOK	**0.083*** **	0.075***	0.047***	0.053***	0.056***	0.036***	0.030***	0.053***	0.019***	0.043***	0.059***	-	
AKK	0.080***	0.077***	0.059***	0.050***	0.048***	0.045***	0.034***	0.036***	0.040***	0.044***	0.054***	0.049***	-

3.3.2 Genetic Distances and Phylogenetic Trees

To construct a phylogenetic tree Reynolds weighted distance and Nei's D_A were chosen because they are regarded as the most appropriate measures for microsatellite data. For calculations Populations 1.2.30 (Langella, 1999) was used. The results were summarized in the Table 3.9. Pairwise Reynold's weighted distances were given above diagonal and Nei's D_A distances were given below the diagonal. It was seen that generally, distances between SAK and others were greater than the pairwise distances between other breeds, suggesting that SAK was genetically more different and/or distinct than the other breeds. The two most distant breeds were SAK-IVE and SAK-GOK.

The resulting trees, Neighbor Joining (NJ) trees, from the distance matrices and their bootstrap values were drawn with Populations 1.2.30 (Langella, 1999) and visualized by Treeview (Page, 2001). The resulting trees were given in the Figures 3.2 and 3.3.

Both of the trees exhibited almost identical topology and a differentiation (not very strong as shown by the bootstrap values) between the two groups of the sheep. The first group is composed of the HER, SAK, KRG, CIC, HEM in the three constructed by Nei's DA and the second group was composed of the rest of the breeds. The rest of the breeds constituted the second group. The topology of the second tree (the tree based on Reynold's distance) was differing in the place of NOR which was also within the first group. It was observed that the first group of sheep breeds corresponds roughly to the local breeds with low population sizes. The second group, however, seems to represent non-local high population size breeds.

Table 3.9 Pairwise distances between the breeds. The lower triangle is for Nei's DA and the upper triangle is for Reynold's distance. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	-	0.061	0.062	0.065	0.049	0.046	0.060	0.062	0.062	0.068	0.085	0.087	0.085
KRG	0.160	-	0.044	0.056	0.032	0.027	0.051	0.053	0.052	0.051	0.071	0.078	0.081
HEM	0.160	0.129	-	0.035	0.027	0.026	0.040	0.047	0.033	0.035	0.048	0.049	0.062
CIC	0.173	0.167	0.119	-	0.028	0.033	0.047	0.061	0.052	0.054	0.053	0.056	0.053
NOR	0.167	0.126	0.115	0.108	-	0.020	0.027	0.027	0.032	0.038	0.039	0.058	0.050
HER	0.140	0.107	0.089	0.118	0.103	-	0.026	0.032	0.020	0.028	0.050	0.038	0.048
DAG	0.169	0.148	0.129	0.142	0.109	0.105	-	0.013	0.015	0.026	0.030	0.032	0.035
MOR	0.175	0.140	0.140	0.147	0.084	0.112	0.080	-	0.029	0.025	0.033	0.056	0.037
KIV	0.172	0.132	0.129	0.161	0.123	0.093	0.077	0.117	-	0.020	0.046	0.020	0.041
KRY	0.180	0.140	0.131	0.161	0.133	0.099	0.104	0.107	0.093	-	0.036	0.045	0.046
IVE	0.219	0.185	0.153	0.162	0.130	0.145	0.124	0.116	0.145	0.136	-	0.063	0.057
GOK	0.197	0.171	0.152	0.156	0.160	0.126	0.113	0.144	0.100	0.125	0.152	-	0.051
AKK	0.188	0.177	0.158	0.146	0.123	0.133	0.114	0.111	0.110	0.114	0.143	0.130	-

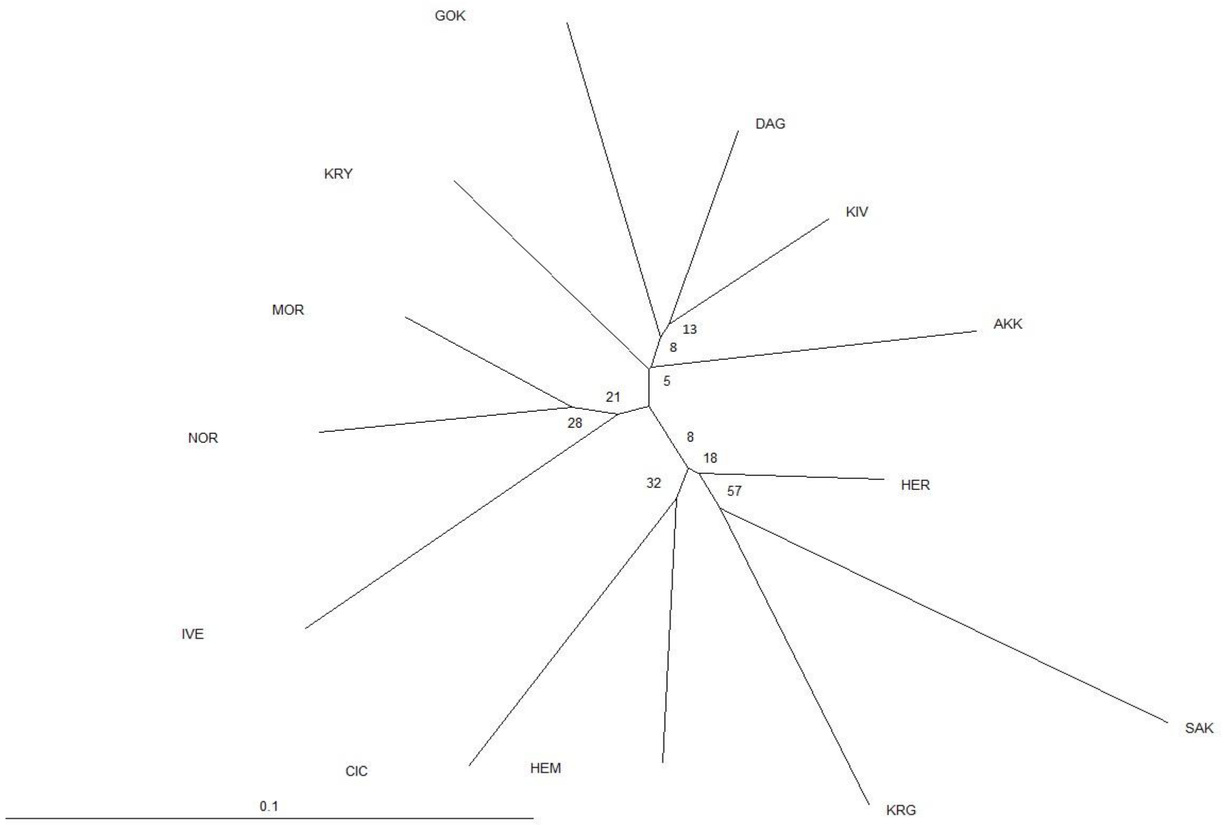

Figure 3.2 The Neighbor-Joining tree drawn using Nei's D_A with bootstrap values with 1000 replications. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

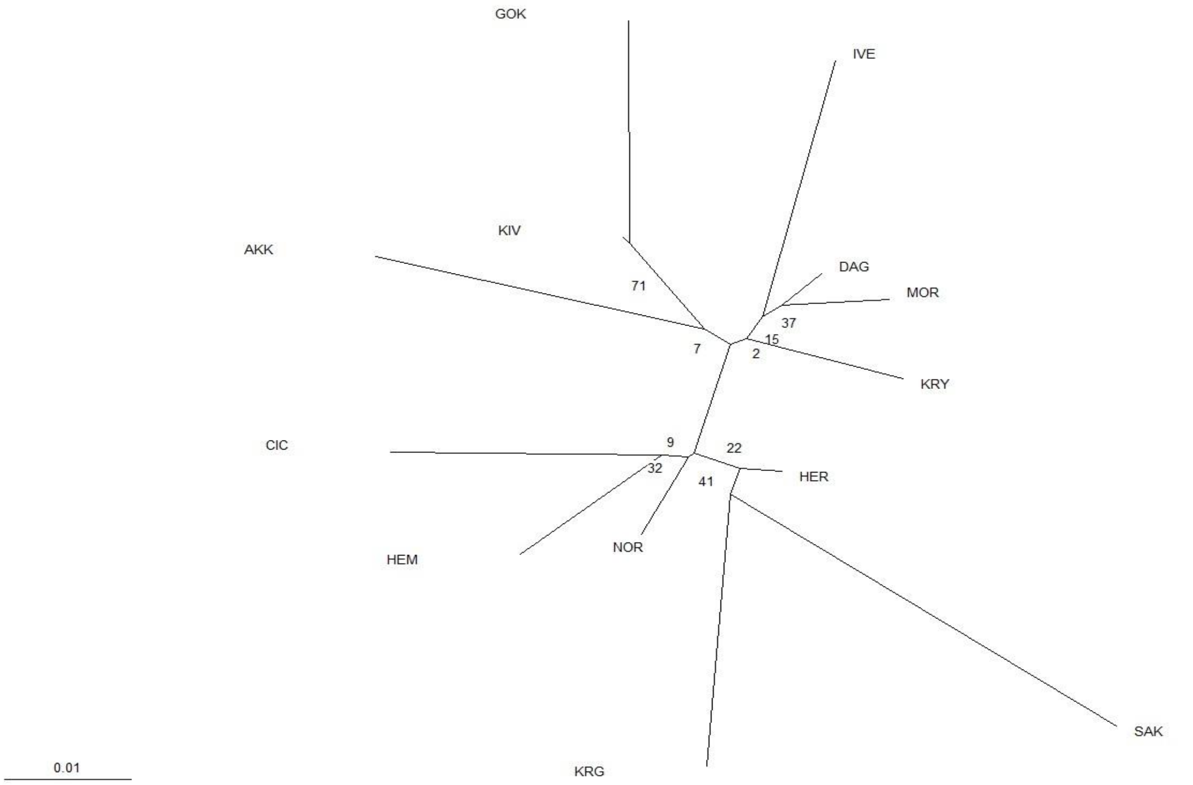

Figure 3.3 The Neighbor-Joining tree drawn using Reynold's Distance with bootstrap values 1000 replications. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

3.3.3 Principal Coordinates Analysis (PCA) for the Centroids of Breeds

PCA for the centroids of breeds were performed by GenAlEx (Peakall and Smouse, 2006)The first axis which accounts for the 27.86% of the variation divided the breeds into the same two groups, first displayed by the NJ tree with Reynold's distance. The second axis which accounted for the 18.22% of the variation displayed the divergence of Eastern Anatolian (MOR and IVE) breeds and Western Anatolian (GOK and CIC) breeds. However, on the two dimensional space of the PCA, SAK and HEM were not in accordance with their geographic locations.

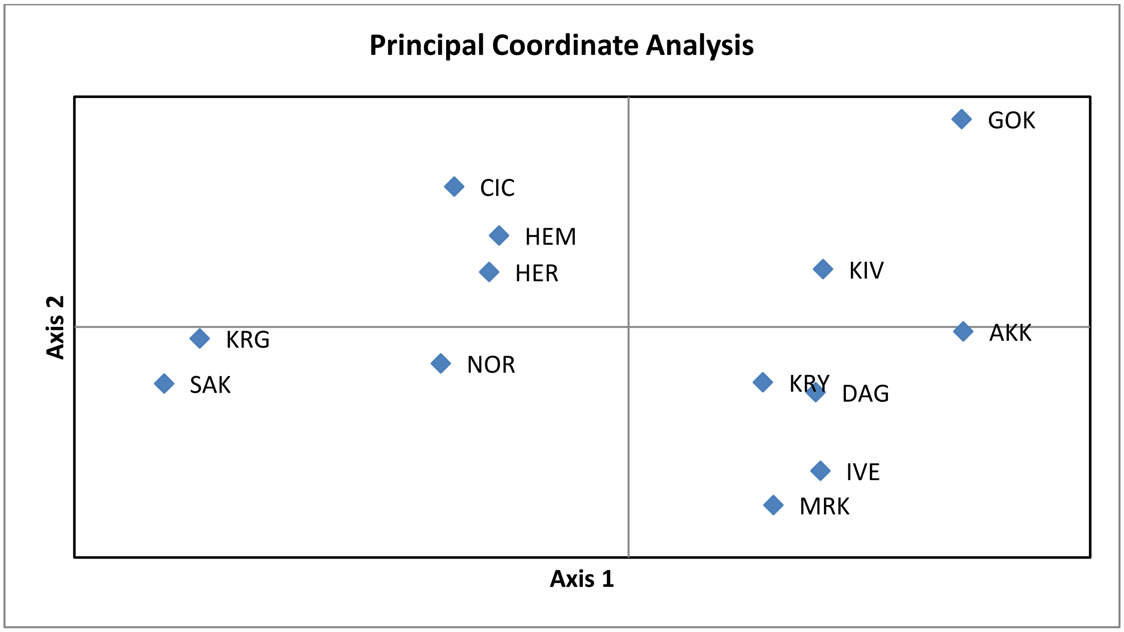

Figure 3.4 The PCA for the centroids of the breeds. Axis 1 accounted for 27.86% of the variation and Axis 2 accounted for 18.22% of the variation. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

3.3.4 Factorial Correspondence Analysis (FCA)

FCA was used to visualize the individuals in a multidimensional space and to detect the relationships between and among breeds.

Genetix v4.05 (Belkhir *et al*. 1996–2004) was used to perform FCA and a 3-Dimensional graphics with different triple combinations of the first 4 factors was drawn by the software and was presented in the Figure 3.5.

The first three axes were accounted for the 40.6% (the maximum of all triple combinations) of the variation. Although the individuals comprising the breeds were close to each other which means that the breeds have a high inertia, the overlaps between the breeds made it impossible to distinguish breeds from each other. Two exceptions are SAK and IVE which stood clearly apart from other breeds.

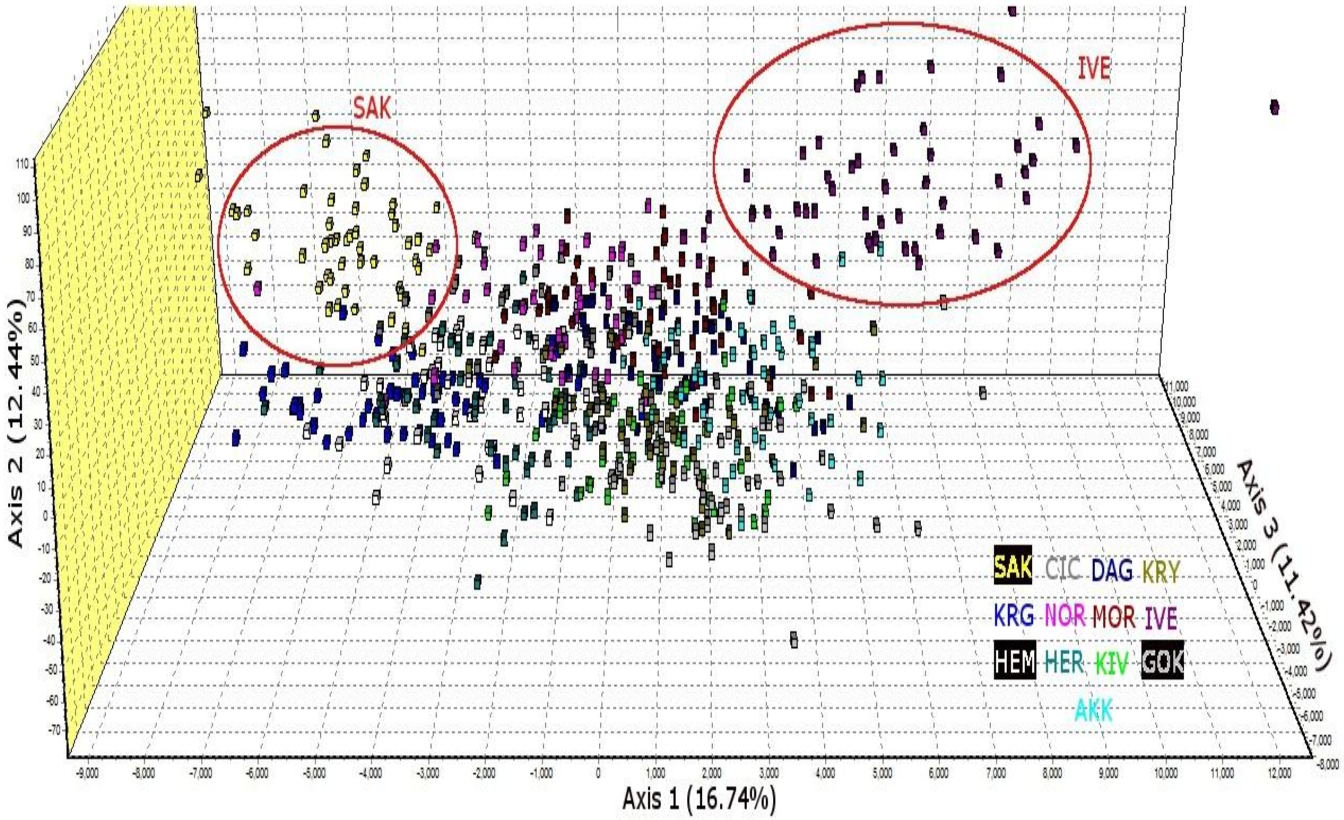

Figure 3.5 The factorial correspondence analysis for the breeds which showed the relationships between and among breeds. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman. The colored dots corresponds to the individuals from breeds given in the legend. Breed names and the color used to indicate their individuals are shown on the lower right hand corner of the Figure.

3.3.5 Multidimensional Scaling (MDS)

Multidimensional Scaling (MDS) (Kruskal, 1964) was done to visualize the similarities and dissimilarities of populations in two dimensions.

R Statistical Package (Ihaka and Gentleman 1996; available via http://www.r-project.org) was used to visualize the two-dimensional map presented in Figure 3.6.

The breeds HEM and HER and the breeds DAG and KRY were observed to be the closest breeds, where SAK – GOK, SAK – AKK and SAK – IVE pairs were found to be the most distant ones.

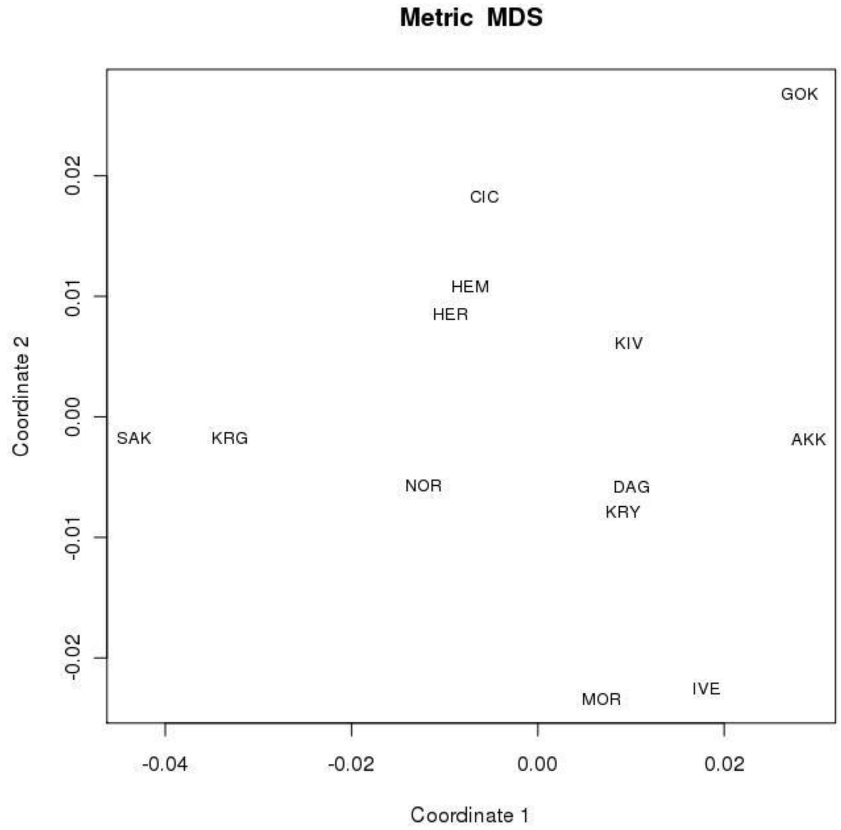

Figure 3.6 The metric MDS in 2 dimensions.

3.3.5 Mantel Test

Mantel tests (Manly, 1991) were performed to search for the presence of association between genetic differentiation measured by F_{ST} and geographical distances. Arlequin v3.5 was used to carry out the analysis. The geographical distances were calculated by applying the Haversine formula to the pairs of midpoints of sample collection sites for each breed by a script written in Python language. The resulting distance matrix was given in Table 3.10.

Table 3.10 The pairwise geographical distances between the midpoints of sample collection sites in kilometers. The distances were calculated as straight lines between points, disregarding geographical barriers (if any).

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	0	890	1376	149	1497	832	357	1345	409	916	1123	214	571
KRG	890	0	486	797	667	86	552	469	758	26	436	882	406
HEM	1376	486	0	1281	369	549	1035	152	1209	460	527	1358	865
CIC	149	797	1281	0	1375	749	245	1237	472	823	991	329	444
NOR	1497	667	369	1375	0	751	1140	243	1424	648	410	1530	931
HER	832	86	549	749	751	0	508	547	676	103	516	810	393
DAG	357	552	1035	245	1140	508	0	993	458	578	768	436	218
MOR	1345	469	152	1237	243	547	993	0	1223	446	392	1351	804
KIV	409	758	1209	472	1424	676	458	1223	0	779	1122	227	633
KRY	916	26	460	823	648	103	578	446	779	0	431	906	431
IVE	1123	436	527	991	410	516	768	392	1122	431	0	1187	551
GOK	214	882	1358	329	1530	810	436	1351	227	906	1187	0	649
AKK	571	406	865	444	931	393	218	804	633	431	551	649	0

Significances of the correlations between F_{ST} and geographic distances were checked using 10000 permutations. We failed to detect a correlation between F_{ST} and geographic distances ($p = 0.2762$)

To sum the pairwise tests between breeds, it could be said that native Turkish breeds were statistically different from each other. However overlap between the individuals of the breeds was high and hence breeds were not distinct. Pairwise F_{ST} values, Nei's DA and Reynolds Distances showed that Sakız and Karagül are quite distinct from other native sheep breeds of Turkey. Trees and PCA suggested that when the groups as a whole were considered it was observed that generally, there were two groups of sheep in Turkey, the first group composed of SAK, KRG, HEM, HER, CIC, NOR where they have relatively small distribution areas and the others. Mantel Test showed that, the differentiation was not in accordance with geographical distances.

3.4 Bayesian Clustering Analysis

3.4.1 Number of Main Clusters (K)

The population substructure and the level of admixture within breeds were analyzed by Structure-console (Pritchard, *et al*. 2000). Three methods were applied to reveal the most probable K. The first method was the method proposed by Evanno *et al*. (Evanno *et al*, 2005) by checking the second order rate of the likelihood function ($\Delta K = m|L''(K)|/\ s[L(K)]$). When this method was employed, the most probable K was found as 2. The resulting graph was given in Figure 3.6

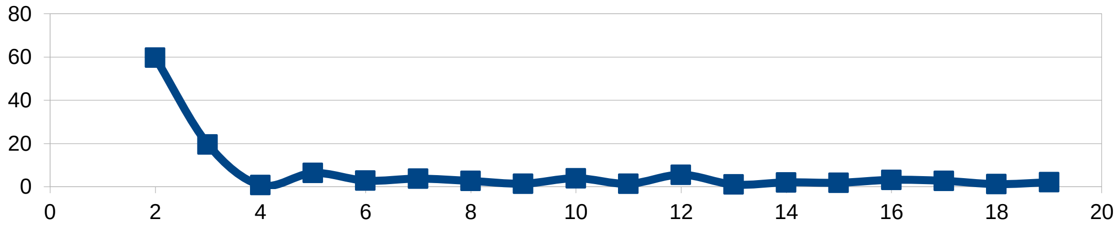

Figure 3.7 The second order rate of the likelihood function against K graph. The peak at K=2 indicates the most probable K. The small peaks at K=5 and K=12 should also be noted.

The second method was comparing the similarities between independent structure runs according to the method used by Tapio *et al*. (Tapio *et al*., 2010) by using the software CLUMPP (Jakobsson *et al*., 2007). The most probable K suggested by CLUMPP was 2, giving the similarity coefficient 0.991719051. In the Figure 3.6 Similarity Coefficient vs. K graph was given. The similarity coefficient was maximum at K=2. At K=5 there was another peak. As was ΔK, there was a small peak at K=12

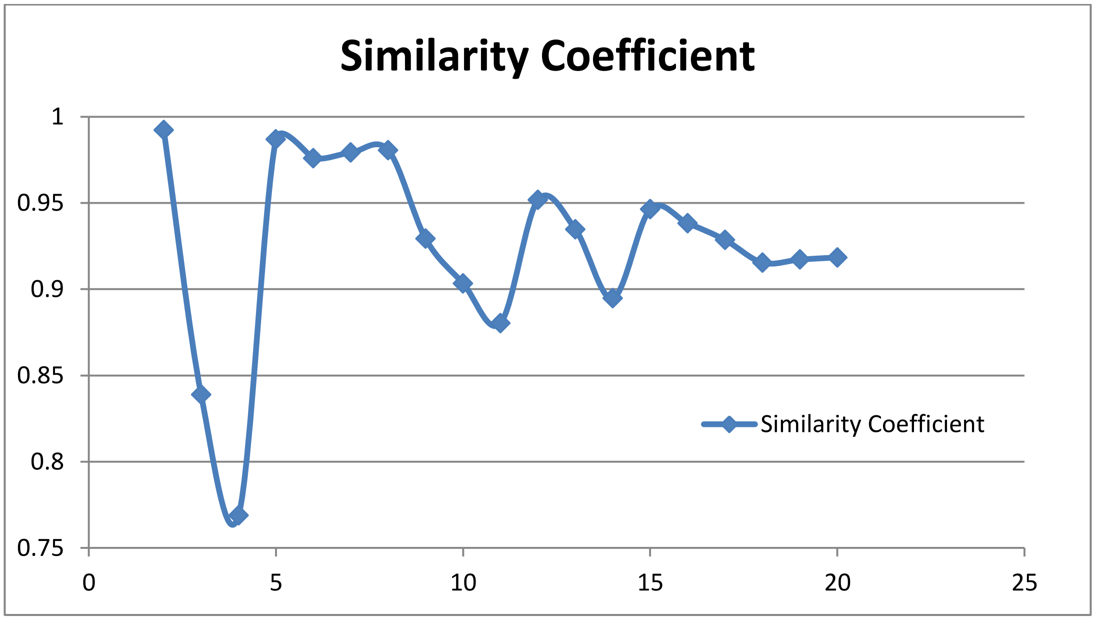

Figure 3.8 The similarity coefficient against K graph.

The third method used was to check for the maximum value of the log likelihood. It was found that at K=12 the log likelihood was maximum. The chart showing the log likelihoods and the mean membership coefficients for individuals for their most probable clusters was given in the Figure 3.7

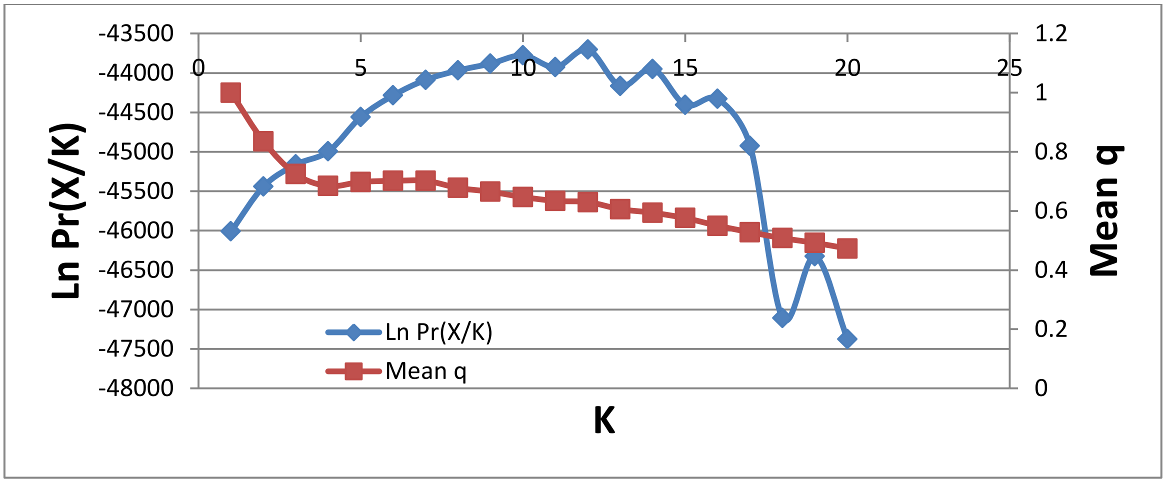

Figure 3.9 Log likelihoods (LnPr(X/K)) against K values and mean membership coefficients (q) against K values. After K=12 log likelihoods began to decrease. The mean membership coefficients dropped rapidly to until K=4 and decreased slowly thereafter.

The visualization of the output of Structure – console was done using Distruct software version 1.1 (Rosenberg, 2004). The results for K=2, K=5 and K=12 were in the Figure 3.8. The rest of the results were given in Appendix B.

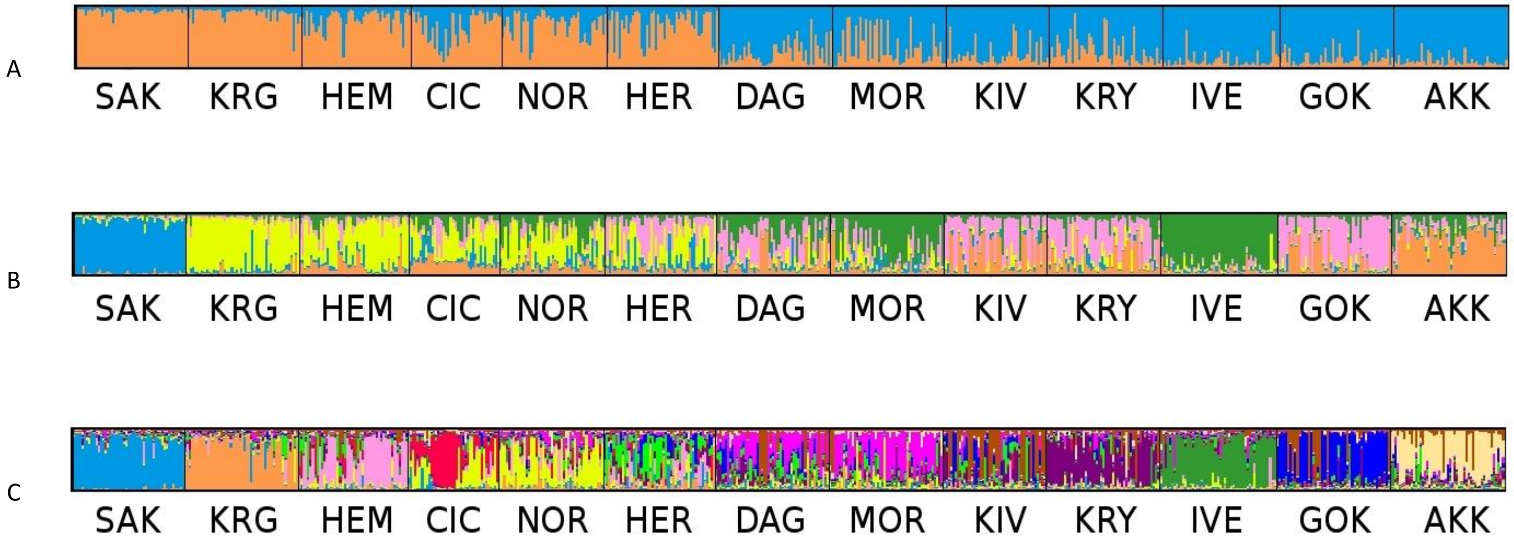

Figure 3.10 The visualization of the outputs of STRUCTURE-Console. A) K=2 B) K=5 C) K=12

Membership coefficients for three different clusters: K=2, K=5, K=12 as calculated by a perl script written by S. C. Açan were given in the Tables 3.11, 3.12 and 3.13.

Table 3.11 The membership coefficients of the breeds to predefined clusters where K=2. Shaded cells shows the cluster with the maximum membership coefficient for a breed. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

BREED	**Cluster 1**	**Cluster 2**
SAK	0.9393	0.0607
KRG	0.9010	0.0990
HEM	0.7995	0.2005
CIC	0.6770	0.3230
NOR	0.7036	0.2964
HER	0.7097	0.2903
DAG	0.2478	0.7522
MOR	0.3370	0.6630
KIV	0.2088	0.7912
KRY	0.2785	0.7215
IVE	0.1160	0.8840
GOK	0.1524	0.8476
AKK	0.1061	0.8939

Table 3.12 The membership coefficients of the breeds to predefined clusters where K=5. Shaded cells shows the cluster with the maximum membership coefficient for a breed. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

BREED	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
SAK	0.0278	0.8858	0.0356	0.0263	0.0244
KRG	0.0445	0.0755	0.7803	0.0596	0.0401
HEM	0.1445	0.0696	0.5905	0.1135	0.0820
CIC	0.1966	0.1327	0.3782	0.1392	0.1533
NOR	0.1292	0.1069	0.4145	0.0905	0.2589
HER	0.0984	0.1448	0.3640	0.3145	0.0783
DAG	0.1906	0.0777	0.0936	0.3394	0.2988
MOR	0.1040	0.0770	0.1081	0.1662	0.5447
KIV	0.3388	0.0522	0.0665	0.4442	0.0982
KRY	0.2348	0.0575	0.1181	0.4611	0.1285
IVE	0.0617	0.0323	0.0512	0.0472	0.8076
GOK	0.2361	0.0378	0.0488	0.6048	0.0726
AKK	0.6003	0.0447	0.0420	0.1379	0.1751

Table 3.13 The membership coefficients of the breeds to predefined clusters where K=12. Shaded cells shows the cluster with the maximum membership coefficient for a breed. SAK stands for Sakız, KRG stands for Karagül, HEM stands for Hemşin, CIC stands for Çine Çaparı, NOR stands for Norduz, HER stands for Herik, DAG stands for Dağlıç, MOR stands for Morkaraman, KIV stands for Kıvırcık, KRY stands for Karayaka, IVE stands for İvesi, GOK stands for Gökçeada and AKK stands for Akkaraman.

BREED	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**	**Cluster 8**	**Cluster 9**	**Cluster 10**	**Cluster 11**	**Cluster 12**
SAK	0.0186	0.8146	0.0236	0.0300	0.0095	0.0132	0.0131	0.0180	0.0152	0.0166	0.0131	0.0146
KRG	0.7193	0.0436	0.0337	0.0369	0.0173	0.0205	0.0149	0.0412	0.0177	0.0228	0.0131	0.0192
HEM	0.0256	0.0258	0.0634	0.5152	0.0212	0.0292	0.0821	0.1229	0.0191	0.0258	0.0164	0.0534
CIC	0.0206	0.0482	0.2563	0.0479	0.0191	0.0170	0.4531	0.0347	0.0294	0.0235	0.0322	0.0181
NOR	0.0680	0.0288	0.4439	0.0835	0.0277	0.0385	0.0506	0.0556	0.0217	0.1090	0.0433	0.0294
HER	0.0986	0.0809	0.0761	0.1335	0.0201	0.0720	0.0524	0.2806	0.0865	0.0472	0.0224	0.0297
DAG	0.0315	0.0339	0.0527	0.0257	0.0447	0.0801	0.0225	0.1122	0.0983	0.3205	0.0362	0.1417
MOR	0.0519	0.0254	0.0920	0.0192	0.0440	0.0674	0.0222	0.0758	0.0382	0.4624	0.0623	0.0392
KIV	0.0268	0.0243	0.0239	0.0286	0.0290	0.1340	0.0310	0.1112	0.1538	0.0667	0.0282	0.3424
KRY	0.0264	0.0238	0.0266	0.0269	0.0383	0.5560	0.0229	0.0512	0.0381	0.0469	0.0533	0.0895
IVE	0.0191	0.0157	0.0374	0.0285	0.6915	0.0342	0.0201	0.0287	0.0182	0.0581	0.0223	0.0263
GOK	0.0142	0.0127	0.0143	0.0177	0.0391	0.0462	0.0241	0.0297	0.5797	0.0157	0.0254	0.1812
AKK	0.0169	0.0175	0.0255	0.0153	0.0452	0.0372	0.0242	0.0471	0.0362	0.0471	0.5907	0.0971

The partitioning at K=2 (SAK, KRG, HEM, CIC, NOR, HER vs. DAG, MOR, KIV, KRY, IVE, GOK, AKK) revealed a very similar partitioning of breeds that was depicted by the first axis of PCA based on the centroids of the breeds (Figure 3.4) and the N-J tree drawn using Reynold's distances which separates the local breeds from the major breeds, and except NOR, results were similar to those displayed by the N-J tree drawn using Nei's DA. At K=5 SAK (Western Anatolia), KRG (Central – North Anatolia), GOK (Northwestern Anatolia), AKK (Central – South Anatolia) and IVE (Southeastern Anatolia) seemed to be the purest breeds and everything else looked as the admixtures of two or more of them. The partitioning at K=12 reveals that, the breeds are highly admixed with low average membership coefficients. The top three pure breeds were SAK, KRG and IVE with membership coefficients 81%, 72% and 69% respectively.

It should be noted that, although admixtures sometimes occurred between breeds with close proximities for instance between MOR IVE at K=5 or MOR HEM at K=12; many times there were exceptions, like the similarity between DAG and MOR and their dissimilarities to AKK which was geographically located between DAG and MOR. Moreover structure at K=12 revealed some clusters which were not the dominant ones in any breeds, but shared by some (i.e. brown in DAG, KIV, KRY, GOK, AKK or light green in HER, AKK, KRG, DAG), which might indicate introgressions from non-native sheep breeds like.

AKK was relatively distinct with no resemblance to NOR (known as a variety of AKK) to HER (hybrid of AKK) or to MOR (found to be similar in a previous study by Peter *et al*., (2007)).

3.4.2 Admixture Analysis by 2-BAD

2-BAD Software v1.2 (Bray *et al*., 2009) was used to gain insight on the population histories of native Turkish sheep breeds so that history can be used as a parameter for the priority setting for conservation studies.

As was presented in Chapter 2, the model consists of an ancestral population splitting up into two parental populations, which in turn reunited in different percentages to form a hybrid population. All three populations (2 parents and the hybrid), were then isolated and evolved separately until present. By the data from the modern populations (population surviving at current times), the times of split and admixture in the past, contributions of the parents to the hybrid population, effective population sizes of the ancestor, parents and the hybrid populations and the mutation rates were estimated.

Two scenarios were considered for the admixture analysis using data from TURKHAYGEN-I and two other scenarios were tested using data from ECONOGENE for comparisons. In the first two scenarios, Sakız sheep was assumed to be the representative of the early sheep in Anatolia. In the first scenario, İvesi was assumed to be the representative of the second parent, whereas Akkaraman and Morkaraman were assumed to be the representative of the second parent in the second scenario. In all scenarios, Dağlıç was assumed to be the hybrid perhaps as of pre-nomadic Turks and post-nomadic Turks mixture of Anatolian sheep breeds. In the third and fourth scenarios, Kymi and Lesvos, breeds from Greece that were in close proximity to Anatolia, were selected as the representatives of the first parent. In the third scenario, Akkaraman and Morkaraman was assumed to be the second parent, while in the fourth scenario, Middle Eastern breeds were assumed to be the second parent.

Scenario 1:

In this scenario Sakız was assigned as the first parent, and İvesi was assigned as the second parent. As the hybrid population Dağlıç represented by the samples of TURKHAYGEN-I project was used. The model which was used was 2-parent, 1-admixture event model which was given in the Figure 2.2.

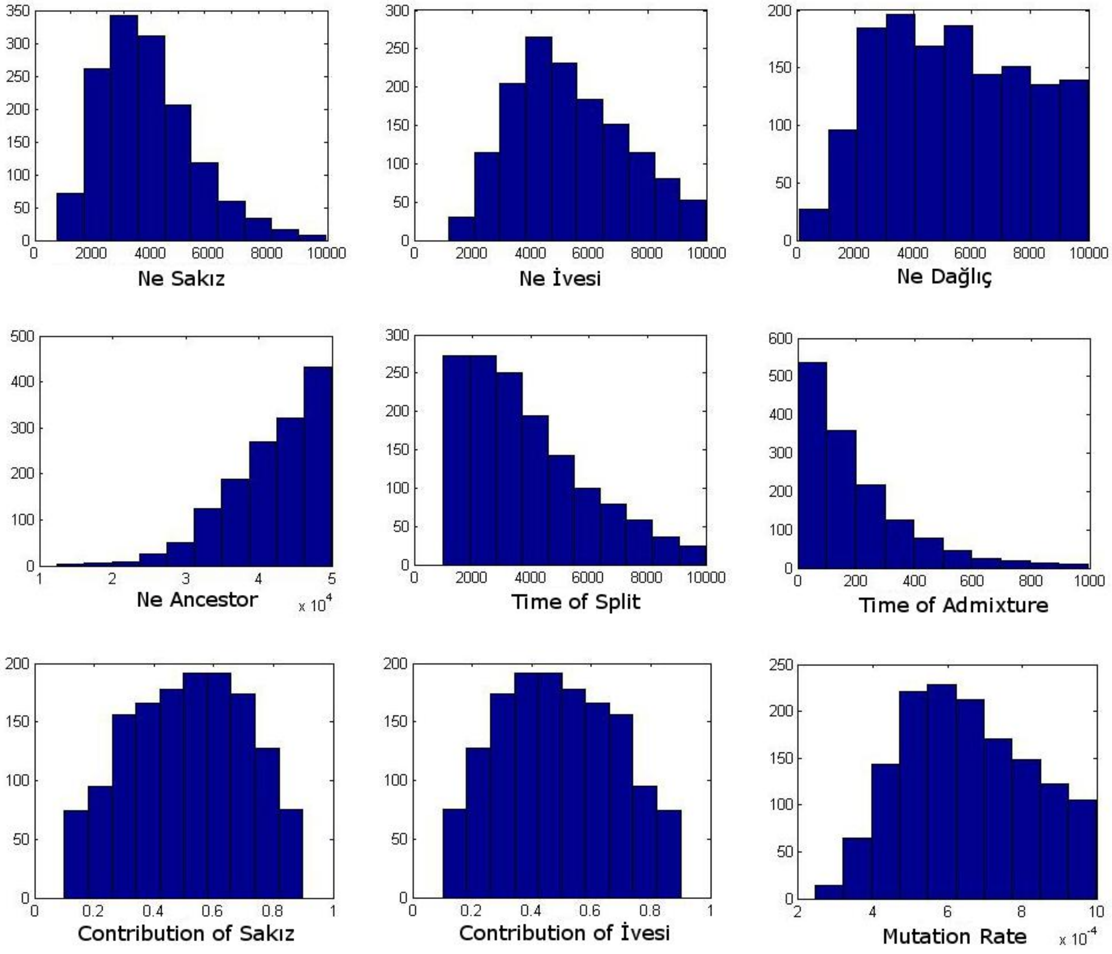

Figure 3.11 The histograms of the posterior distributions after the rejection step after 1.000.000 simulations. (Tolerance level 0.001)

The mean of the effective population size of the first parent Sakız is at 3832.32 with a standard deviation of 1602.32. The effective population size of the second parent İvesi averaged 5314.35 with a standard deviation of 1945.12. The effective population size of the hybrid was estimated 5319.28 with 2484.31 as the standard deviation. Both the Figure and the high standard deviation suggest that, the Ne estimation of the hybrid is less reliable than that of parent populations. The Ne of the ancestral population was estimated as 41749.6, with a standard deviation of 6369.74.

The mutation rate was estimated as 6.5x10-4. The number of generations since the time of admixture was found to be 199.966 and the standard deviation of 183.489 might hint at the recent unrecorded hybridization practices employed by breeders and state. The time of split dated back to 3835.21 generations ago, with a standard deviation of 2076.4. The contributions to the admixed population from parent populations were estimated as 51% Sakız and 49% İvesi, with the standard deviation of 0.19, indicating more or less the same amounts of contribution.

After the regression step, the mean Ne of Sakız was reduced to 1778.03 with a standard deviation of 585.251. The Ne of İvesi was reduced to 3013.32 with 1235.39 as the standard deviation. The effective population size of the hybrids was increased to 8539.29 with the standard deviation of 1639.5. The effective population size of the ancestral population stayed relatively the same, 44334.2 as mean and 8024.41 as standard deviation.

The mutation rate was estimated as 3.2x10-4. The estimated time of the admixture was now more recent, only 24.79 generations with a standard deviation of 38.97. Time of split was again reduced to 1043.18 generations with a standard deviation of 206.169. The contribution of Sakız was raised to 55.7% and contribution of İvesi was lowered to 44.3% with standard deviation of 0.098.

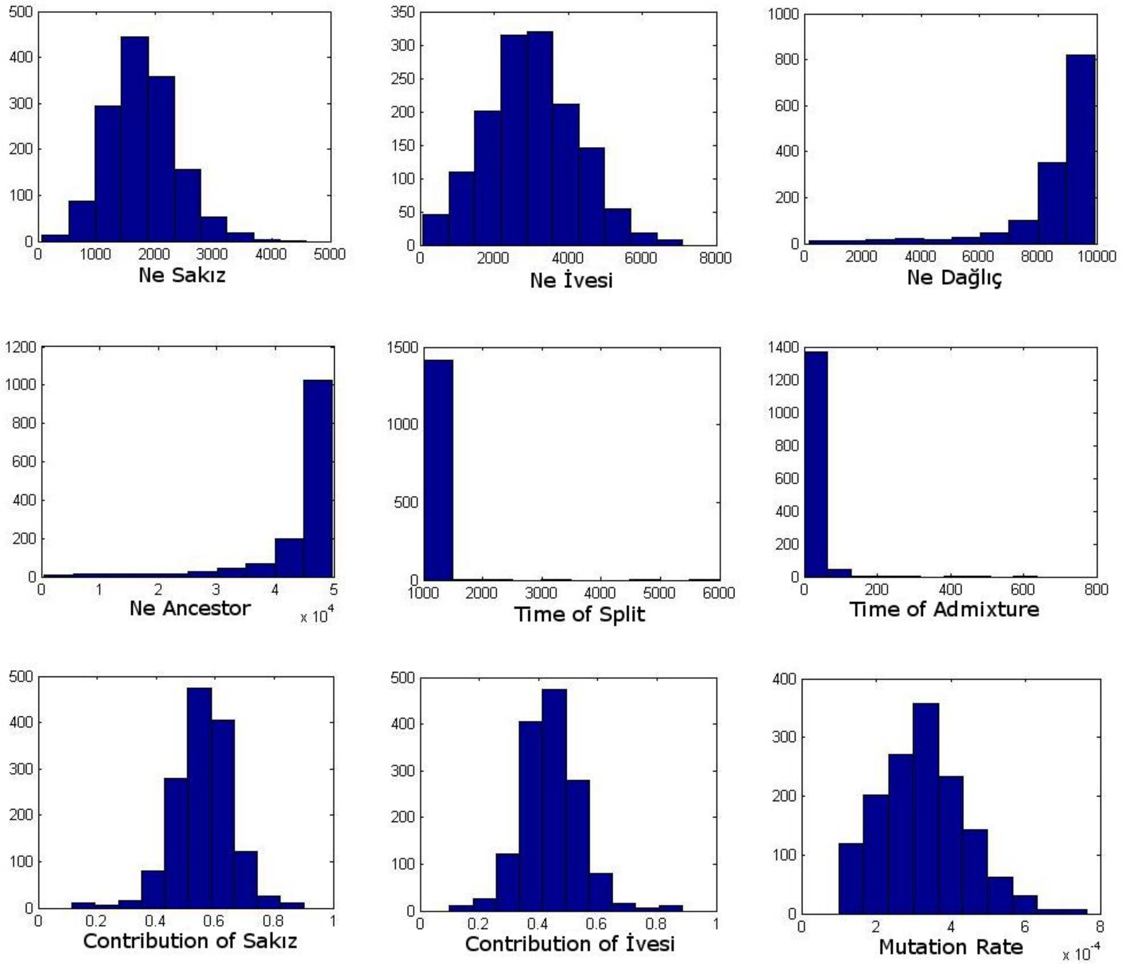

Figure 3.12 The histograms of the posterior distributions after the regression step. Parent 1 is Sakız, parent 2 is İvesi and the hybrid is Dağlıç.

The means, medians and standard deviations after the rejection step and the regression step were given in the Table 3.14

Table 3.14 The means, medians and standard deviations after the rejection step and the regression step. Ne SAK stands for the effective population size of Sakız, Ne IVE stands for the effective population size of İvesi, Ne DAG stands for the effective population size of Dağlıç, Ne Anc. stands for the effective population size of the ancestral population, Mut. Rate stands for the mutation rate, Split stands for the number of generations since the split of the ancestral populations into parent populations, Admixture stands for the number of generations since the admixture event, Cont. SAK stands for the contribution of Sakız to the hybrid population (Dağlıç) and Cont. IVE stands for the the contribution of İvesi to the hybrid population.

	After Rejection			After Regression		
	Mean	St. Dev.	Median	Mean	St. Dev.	Median
Ne SAK	3832.32	1602.32	3608	1778.03	585.251	1741.71
Ne IVE	5314.35	1945.12	5062.5	3013.32	1235.39	2991.2
Ne DAG	5391.28	2484.31	5256	8539.29	1639.5	9106.76
Ne Anc.	41749.6	6369.74	43042.5	44334.2	8024.41	47375.3
Mut. Rate	$6.5x10^{-4}$	$1.7 x10^{-4}$	$6.4 x10^{-4}$	$3.3 x10^{-4}$	$1.2 x10^{-4}$	$3.2 x10^{-4}$
Split	3835.21	2076.4	3394	1043.18	206.169	1018.08
Admixture	199.966	183.489	145	24.79	38.9787	17.1366
Cont. SAK	0.510551	0.196977	0.520795	0.557272	0.098135	0.563089
Cont. IVE	0.489449	0.196977	0.479205	0.442728	0.098135	0.436911

Scenario 2:

In this scenario again Sakız was assigned as the first parent. Likewise, Dağlıç was used as the hybrid population. Akkaraman and Morkaraman breeds together were assigned as the second parent population. The model which was used was 2-parent, 1-admixture event model which was given in the Figure 2.2.

When Sakız was selected as the first parent and Akkaraman and Morkaraman together were selected as the second parent, and Dağlıç was selected as the hybrid population, the Ne of Sakız averaged 4327.24 with a standard deviation of 1775.02 which conformed to the results of the first scenario. The Ne of the other parent Morkaraman + Akkaraman were calculated as 6047.14 with a standard deviation of 2037.97. The effective population size of the hybrid was estimated as 5022.78 with a standard deviation of 2539.8 which again supported the outcomes of the first scenario. The ancestral population's Ne was again high, 41095.9 with a standard deviation of 6787.77.

The mutation rate was estimated as 6.5x10-4 again. The admixture event was calculated to be taken place at 189.004 generations before present. The time of split dated back to 4023.69 generations ago. The contributions to the admixed population by the parents were 49% for Sakız and 51% for Akkaraman and Morkaraman.

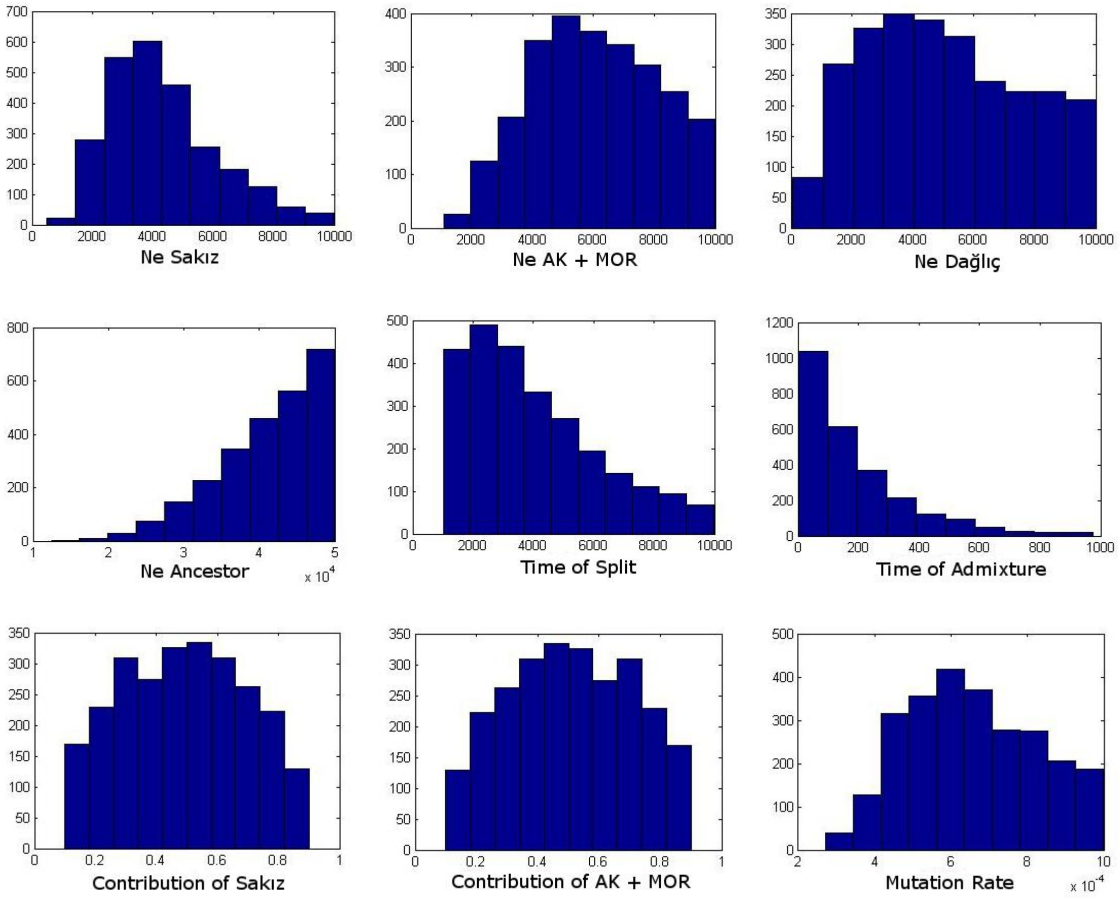

Figure 3.13 The histograms of the posterior distributions after the rejection step after 1.000.000 simulations. (Tolerance level 0.001). Parent 1 is Sakız, parents 2 are Akkaraman and Morkaraman together and the hybrid is Dağlıç.

After the regression step, the effective population size of Sakız was reduced to 1881.2 and the effective population size of Morkaraman and Akkaraman were reduced to 3437.2 with standard deviations of 696.772 and 1525.49 respectively. The Ne of the hybrid was estimated as 4259.6 with a standard deviation of 2147.59. The effective population size of the ancestral population was estimated as 44370 with a standard deviation of 8194.29.

The mutation rate was lowered to 3.9x10-4. According to the estimations of the regression step, the admixture event took place only 3.7591 generations ago. The time of split was estimated as 1008.36 generations ago with a standard deviation of 21.2907.

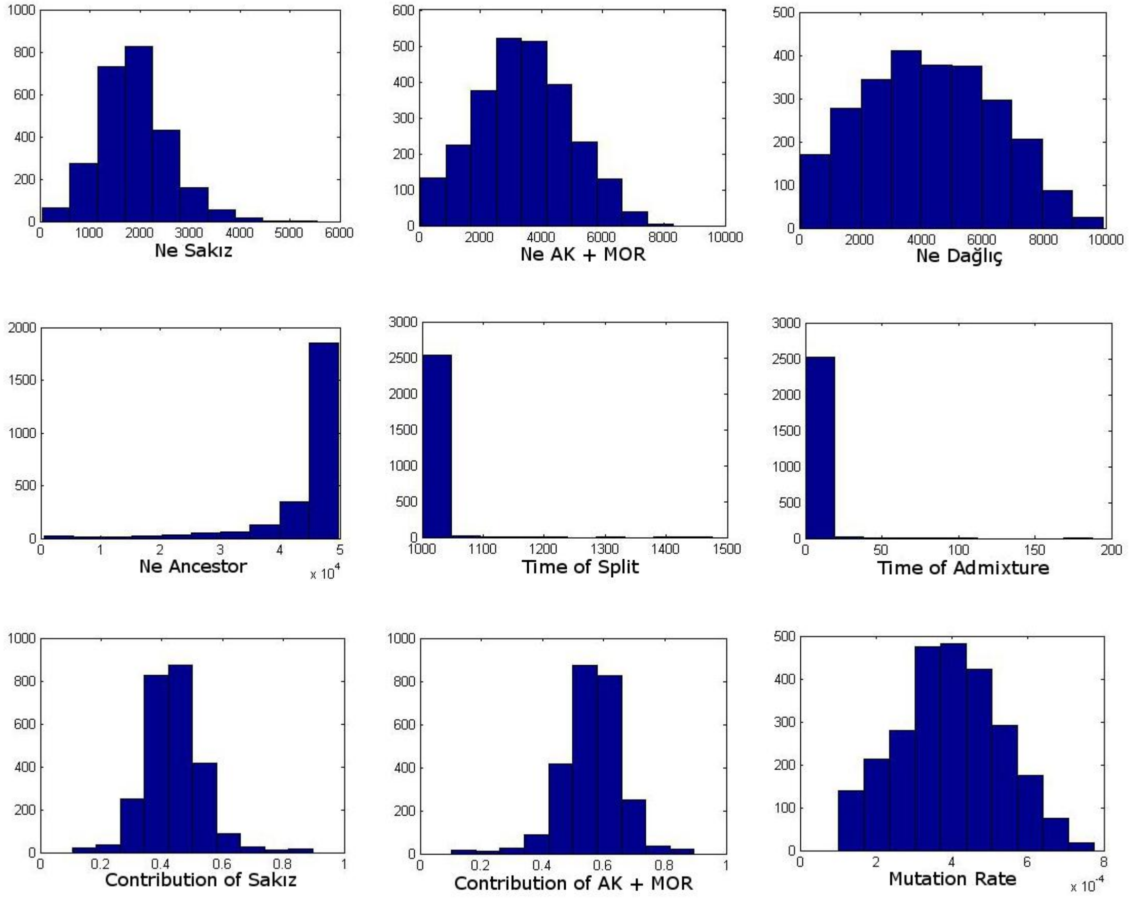

Figure 3.14 The histograms of the posterior distributions after the regression step. Parent 1 is Sakız, parents 2 are Akkaraman and Morkaraman together and the hybrid is Dağlıç.

The means, medians and the standard deviations obtained after the rejection and regression steps were presented in the Table 3.15 for a better comparison.

Table 3.15 The means, standard deviations and medians after the rejection and regression steps. Ne SAK stands for the effective population size of Sakız, Ne AK+MOR stands for the effective population sizes of Akkaraman and Morkaraman, Ne DAG stands for the effective population size of Dağlıç, Ne Anc. Stands for the effective population size of the ancestral population, Mut. Rate stands for the mutation rate, Split stands for the number of generations since the split of the ancestral populations into parent populations, Admixture stands for the number of generations since the admixture event, Cont. SAK stands for the contribution of Sakız to the hybrid population (Dağlıç) and Cont. AK+MOR stands for the the contributions of Akkaraman and Morkaraman to the hybrid population.

	After Rejection			After Regression		
	Mean	St. Dev.	Median	Mean	St. Dev.	Median
Ne SAK	4327.24	1775.02	4037	1881.2	696.772	1834.57
Ne AK+MOR	6047.14	2037.97	5988	3437.2	1525.49	3415.09
Ne DAG	5022.78	2539.8	4808	4259.6	2147.59	4171.66
Ne Anc.	41095.9	6787.77	42463	44370	8194.29	47499.6
Mut. Rate	6.6×10^{-4}	1.7×10^{-4}	6.4×10^{-4}	4.0×10^{-4}	1.4×10^{-4}	3.9×10^{-4}
Split	4023.69	2177.2	3522	1008.36	21.2907	1004.69
Admixture	189.004	181.104	131	3.7591	6.78134	2.38856
Cont. SAK	0.491583	0.20311	0.493691	0.438655	0.096421	0.433839
Cont. AK+MOR	0.508417	0.20311	0.506309	0.561345	0.096421	0.566161

Scenario 3:

In this scenario again 2-parent 1-time admixture event model was used. This time data from a former study (ECONOGENE) was used. As the first parent Akkaraman together with Morkaraman were used. As the second parent, Kymi and Lesvos, two Greek breeds which are close to Anatolia, was selected. Dağlıç was again assigned as the hybrid.

When Akkaraman and Morkaraman together were assigned as the first parent, and Kymi and Lesvos together were assigned as the second parent, with Dağlıç as the hybrid population, the N_e of Akkaraman and Morkaraman was estimated to be 4270.92 with a standard deviation of 1809.76. The N_e of the Greek breeds was estimated as 4790.03 with a standard deviation of 1937.13. The effective population size of the hybrid was estimated as 4558.27 with a standard deviation of 2488.26. The ancestral population's N_e was found to be 42369.6 with a standard deviation of 6155.54.

The mutation rate was estimated as 6.6×10^{-4}. The admixture event was calculated to be taken place at 256.48 generations before present. The time of split dated back to 3593.35 generations ago. The contributions to the admixed population by the parents were 54% for Akkaraman and Morkaraman and 46% for the Greek breeds Kymi and Lesvos.

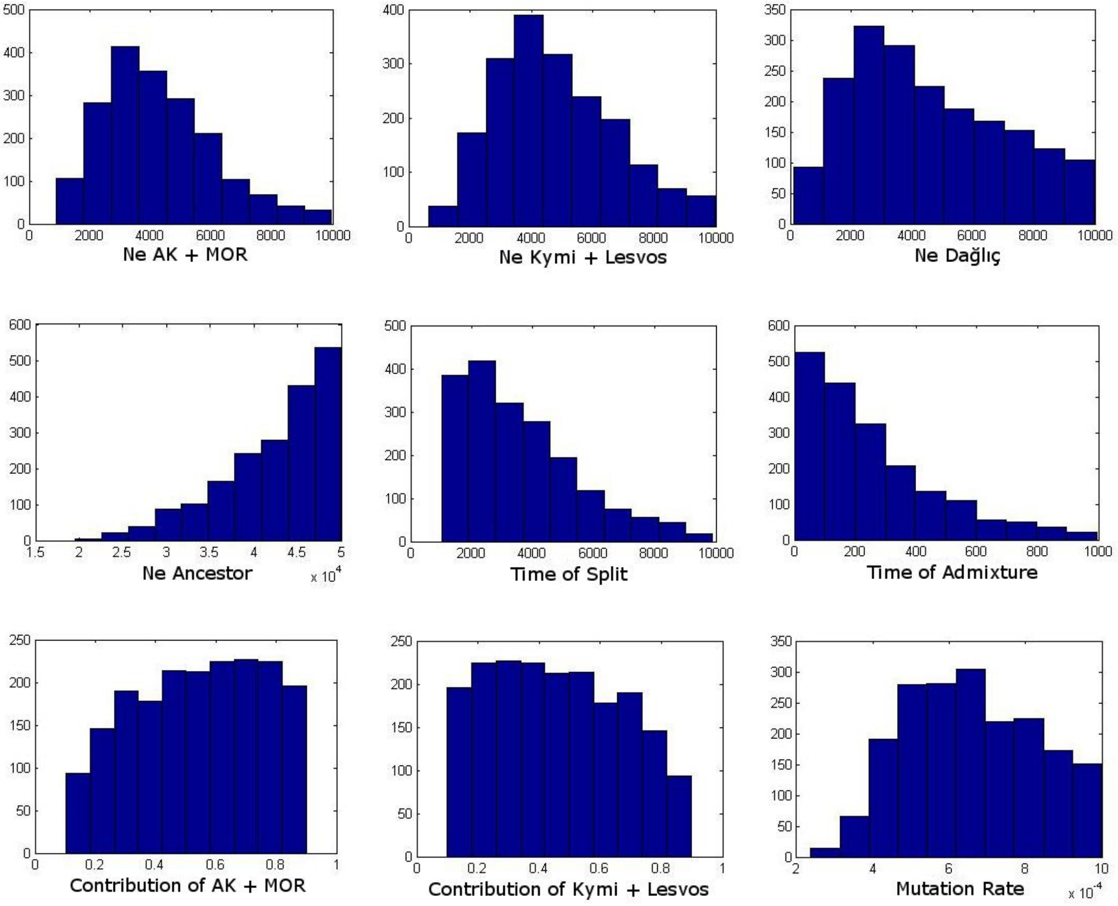

Figure 3.15 The histograms of posterior distributions after rejection step. First parents are Akkaraman and Morkaraman, second parents are Kymi and Lesvos and the hybrid population is Dağlıç.

After the regression step, the effective population size of Akkaraman and Morkaraman was reduced to 941.824 and the effective population size of Kymi and Lesvos was reduced to 539.823 with standard deviations of 347.928 and 212.359 respectively. The N_e of the hybrid was estimated as 2000.78 with a standard deviation of 1325.09. The effective population size of the ancestral population was estimated as 35851.9 with a standard deviation of 12216.

The mutation rate was lowered to 6.0×10^{-4}. According to the estimations of the regression step, the admixture event took place 2.82772 generations ago. The time of split was estimated as 1001.56 generations ago with a standard deviation of 4.05929.

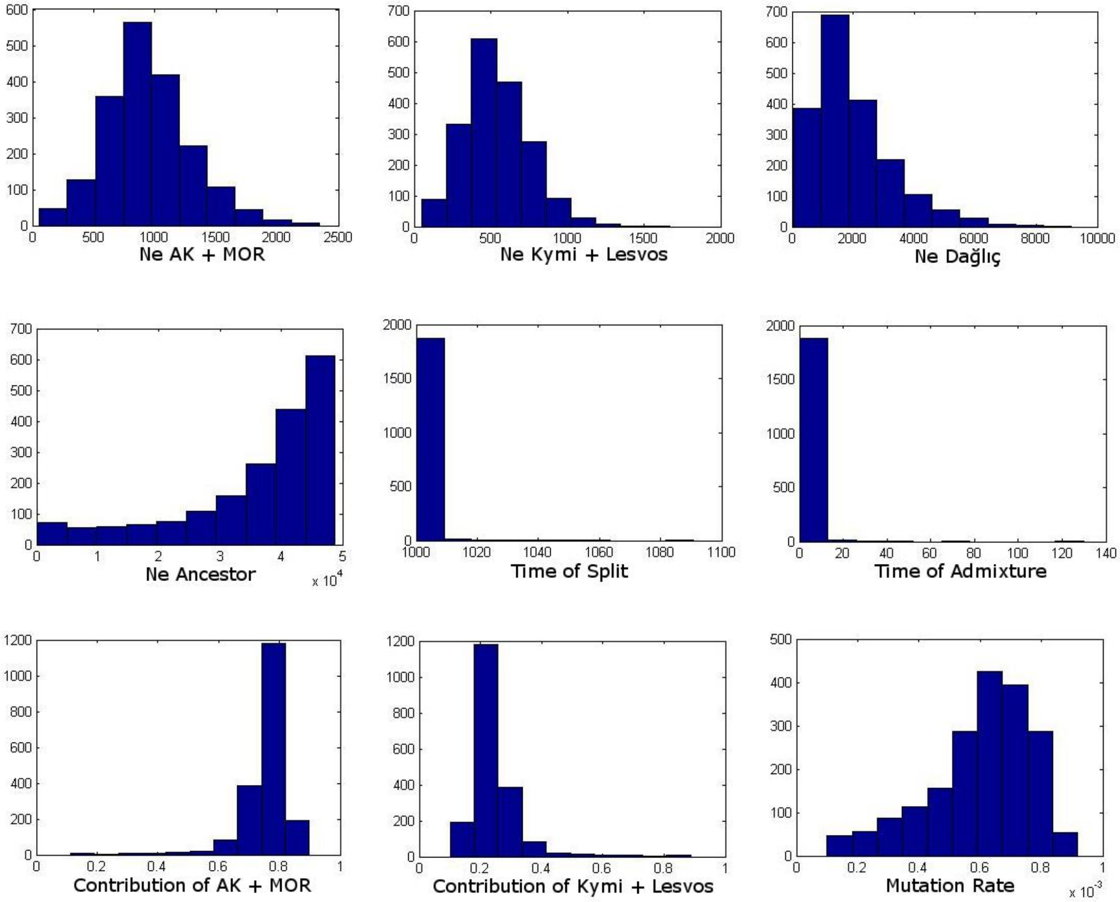

Figure 3.16 The histograms of posterior distributions after regression step. First parents are Akkaraman and Morkaraman, second parents are Kymi and Lesvos and the hybrid population is Dağlıç.

Table 3.16 The means, standard deviations and medians after rejection and regression steps.Ne AK+MOR stands for the effective population size of Akkaraman and Morkaraman, Ne KYM+LES stands for the effective population sizes of Kymi and Lesvos, Ne DAG stands for the effective population size of Dağlıç, Ne Anc. Stands for the effective population size of the ancestral population, Mut. Rate stands for the mutation rate, Split stands for the number of generations since the split of the ancestral populations into parent populations, Admixture stands for the number of generations since the admixture event, Cont. AK+MOR stands for the contribution of Akkaraman and Morkaraman to the hybrid population (Dağlıç) and Cont. KYM+LES stands for the the contributions of Kymi and Lesvos to the hybrid population.

	After Rejection			After Regression		
	Mean	St. Dev.	Median	Mean	St. Dev.	Median
Ne AK+MOR	4270.92	1809.76	3985	941.824	347.928	913.229
Ne KYM+LES	4790.03	1937.13	4495	539.823	212.359	520.98
Ne DAG	4558.27	2488.26	4088	2000.78	1325.09	1693.85
Ne Anc.	42369.6	6155.54	44078	35851.9	12216	40594.2
Mut. Rate	$6.6\text{x}10^{-4}$	$1.7\text{x}10^{-4}$	$6.5\text{x}10^{-4}$	$6.0\text{x}10^{-4}$	$1.7\text{x}10^{-4}$	$6.3\text{x}10^{-4}$
Split	3593.35	1909.56	3178	1001.56	4.05929	1000.83
Admixture	256.48	214.629	197	2.82772	5.87648	1.91346
Cont. AK+MOR	0.539552	0.212772	0.547212	0.754546	0.083612	0.770135
Cont. KYM+LES	0.460448	0.212772	0.452788	0.245454	0.083612	0.229865

Scenario 4:

In this scenario Ossimi from Egypt and Heri, Naemi and Najdi from Saudi Arabia, which comprises the Middle Eastern breeds in the ECONOGENE project, together assigned as the first parent. As the second parent again Kymi and Lesvos were assigned. Dağlıç was assigned as the hybrid as before.

The mean of the effective population size of the first parent group from Middle East was estimated as 4468.54 with a standard deviation of 1883.29. The effective population size of the second parent group from Greece was averaged 4386.62 with a standard deviation of 1822.37. The effective population size of the hybrid was estimated 3667.45 with 2291.34 as the standard deviation. The

N_e of the ancestral population was estimated as 43005.2, with a standard deviation of 5429.14.

The mutation rate was estimated as 7.0x10^{-4}. The number of generations since the time of admixture was found to be 291.842 with the standard deviation of 228.189. The time of split dated back to 3186.5 generations ago, with a standard deviation of 1657.8. The contributions to the admixed population from parent populations were estimated as 44.9% for the Middle Eastern breeds and 55.1% for the Greek breeds.

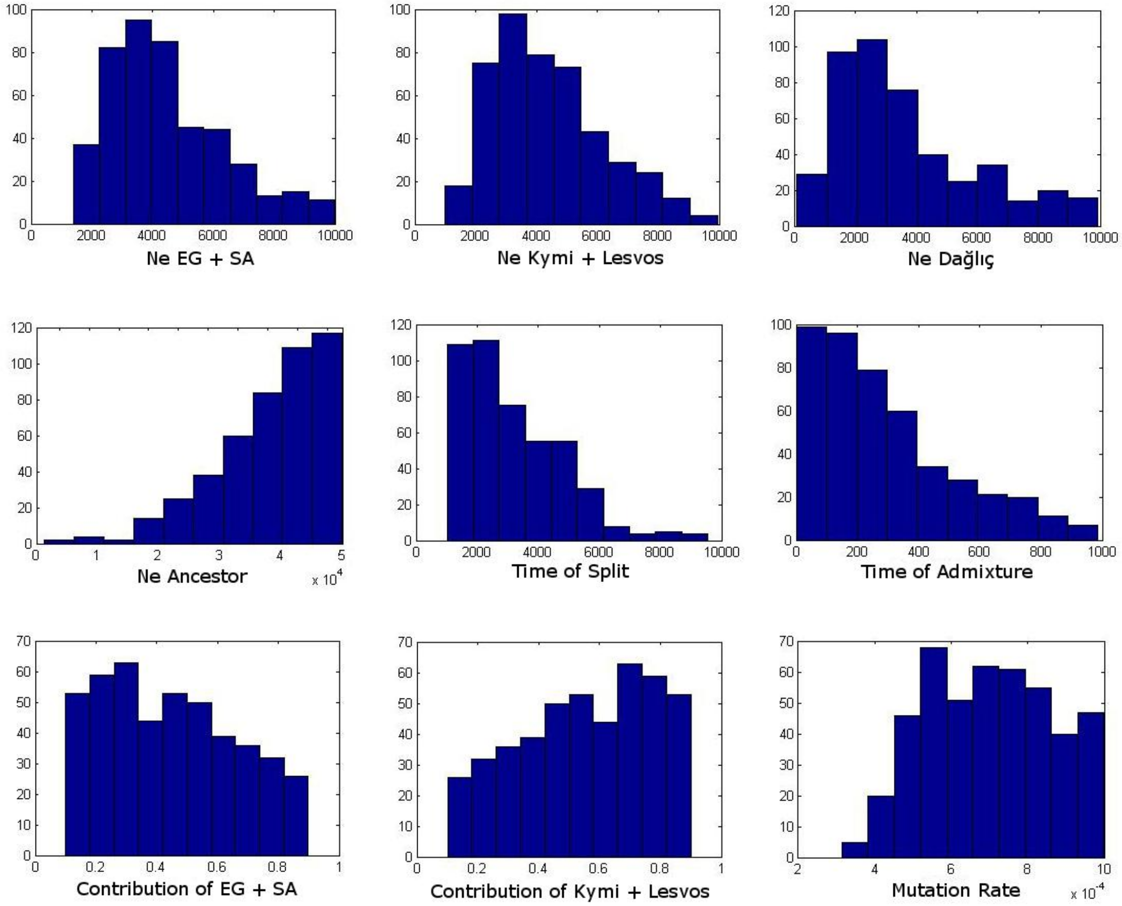

Figure 3.17 Histograms after rejection step. First parents comprise Ossimi from Egypt and Heri, Naemi and Najdi from Saudi Arabia. The hybrid is Dağlıç.

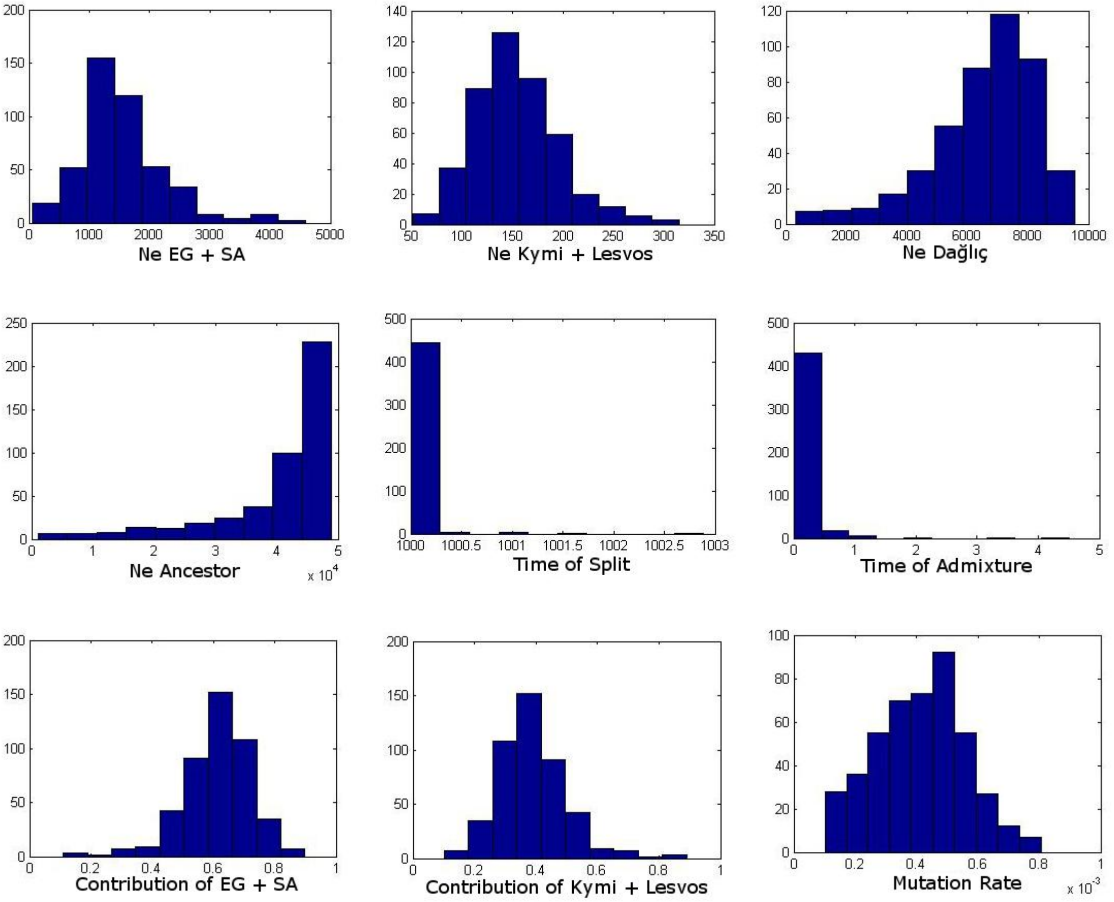

Figure 3.18 Histograms after regression step. First parents comprise Ossimi from Egypt and Heri, Naemi and Najdi from Saudi Arabia. The hybrid is Dağlıç.

Table 3.17 The means, standard deviations and medians after rejection and regression steps.Ne EG+SA stands for the effective population size of the Egyptian and Saudi Arabian breeds of Ossimi, Heri, Naemi and Najdi, Ne KYM+LES stands for the effective population sizes of Kymi and Lesvos, Ne DAG stands for the effective population size of Dağlıç, Ne Anc. Stands for the effective population size of the ancestral population, Mut. Rate stands for the mutation rate, Split stands for the number of generations since the split of the ancestral populations into parent populations, Admixture stands for the number of generations since the admixture event, Cont. EG+SA stands for the contribution of Egyptian and Saudi Arabian breeds to the hybrid population (Dağlıç) and Cont. KYM+LES stands for the the contributions of Kymi and Lesvos to the hybrid population.

	After Rejection			After Regression		
	Mean	St. Dev.	Median	Mean	St. Dev.	Median
Ne EG+SA	4468.54	1883.29	4116	1541.67	696.527	1417.19
Ne KYM+LES	4386.62	1822.37	4031	154.379	42.195	149.705
Ne DAG	3667.45	2291.34	3009	6543.79	1770.59	6882.77
Ne Anc.	43005.2	5429.14	44118	40009.2	10201.9	44176.7
Mut. Rate	7.0×10^{-4}	1.6×10^{-4}	7.0×10^{-4}	4.1×10^{-4}	1.5×10^{-4}	4.2×10^{-4}
Split	3186.5	1657.8	2820	1000.07	0.22465	1000.03
Admixture	291.842	228.189	230	0.202077	0.305942	0.148506
Cont. EG+SA	0.449185	0.218561	0.432597	0.614264	0.109877	0.621262
Cont. KYM+LES	0.550815	0.218561	0.567403	0.385736	0.109877	0.378738

In relation to the results of 2-BAD although two independent data sets (ECONOGENE and HAYGEN) were examined results within “after rejection” results within “after regression” were very consistent. In the group of after rejection parents and hybrids had Ne values 3667 (DAG in the 4th scenario) - 6047 (AKK+MOR) in the second scenario. For the Ne of ancestors estimates were always nearly 41000. Again split times were estimated as nearly between 3200- 4000. Estimates for time since the admixture were in between 189-256. When the results of “after regression” were compared, although the estimates between the scenarios were similar, now Ne values for the breeds were lower although Ne estimates for ancestor were still around 40 000. However, time of admixture dropped to very low values (0.2- 25) and time since the split were around 1000 generations. Weight of contribution of the parent to DAG was dependent on the relative geographic distance of the parent to DAG. Mutation rate was always in the order of 10-4.

3.5 Conservation Studies

3.5.1 Priority Setting For Conservation of Breeds Based on the Genetic Data

In all of the evaluations presented below breeds were treated as gene pools which were unique and it was assumed that their genetic diversity was captured by the current study (i.e their genetic characteristics were independent of sampling).

To identify the breed(s) which have high contribution to genetic diversity of Turkish sheep gene pool different approaches suggested by different researchers have been employed.

3.5.1.1 Contribution to Allelic Richness

In the first approach contribution of each breed was judged based on the measure of allelic richness as proposed by Petit *et al*. (1998). The contributions were calculated by MolKin v3.0 (Gutiérrez *et al*., 2005) and given in the Table 3.18. All the values given were in percentages. The largest contribution to the total variation were by IVE and then HEM. The highest contribution to the between-breeds genetic diversity was through SAK. This result was expected because of the high genetic distance between SAK and other breeds and the highest contribution to within-breeds diversity was by HER which was a highly admixed breed with high number of alleles. Negative values mean that the presence of the breeds are lowering the allelic richness of within, between or total diversities.

Table 3.18 The contributions of Turkish breeds to the gene pool, based on allelic richness. Negative values indicate the detrimental effect of the breed on diversity.

Breed	Within Breed (%)	Between Breeds (%)	Total Contribution (%)
SAK	-1.1063	1.0027	-0.1036
KRG	-0.7761	0.4975	-0.2787
HEM	0.3204	0.2728	0.5931
CIC	-0.7901	0.3983	-0.3918
NOR	0.0687	-0.0877	-0.0190
HER	0.6061	-0.4308	0.1753
DAG	0.3885	-0.2793	0.1092
MOR	0.1601	-0.2211	-0.0610
KIV	0.3515	-0.1830	0.1684
KRY	0.2664	-0.0213	0.2451
IVE	0.4710	0.6497	1.1206
GOK	-0.0924	0.1953	0.1029
AKK	0.1324	-0.1201	0.0123

3.5.1.2 Weitzman Approach

Another approach to determine the contribution of each breed to the genetic diversity was Weitzman Approach. In this approach distinctness of the breeds plays the prime role in priority setting. For this approach WeitzPro (Derban, 2002) software was used. As the distance method Reynold's distance was employed. The results were given in the Table 3.19. The most diversity loss was encountered when SAK was removed from the set. Again this result was anticipated because SAK was the most distinct one among the breeds as was observed throughout the study as for instance depicted by genetic distance analyses. The top three breeds that contribute to the genetic diversity (SAK, KRG, IVE) were the ones with high membership coefficients in STRUCTURE analysis. Because of the assumptions of the model, there are no detrimental effects to the genetic pool by any breed.

Table 3.19 The contributions of breeds to the genetic diversity based on Weitzman Approach.

Breed	Total - Breed	Diversity Loss	Diversity Loss (%)
Total	0.485		
SAK	0.4235	0.0615	12.68
KRG	0.4316	0.0534	11.01
HEM	0.4491	0.0359	7.4
CIC	0.4392	0.0458	9.44
NOR	0.4592	0.0258	5.32
HER	0.4611	0.0239	4.93
DAG	0.4672	0.0178	3.67
MOR	0.4634	0.0216	4.45
KIV	0.461	0.024	4.95
KRY	0.4521	0.0329	6.78
IVE	0.4322	0.0528	10.89
GOK	0.4365	0.0485	10
AKK	0.4381	0.0469	9.67

3.5.1.3 Metapopulation Approach

Yet another approach for determining the contribution of breeds to the genetic diversity, was to consider the within breed variation as well as the between breeds variation as proposed by Caballero and Toro (Caballero & Toro, 2002). Metapop v1.0.3 (Pérez-Figueroa, 2009) was used to calculate the contributions of breeds to genetic diversity and the loss of diversity when one breed was removed from the set. It was observed that the highest genetic loss was encountered when IVE was removed from the breed. When two breeds were removed, for the KRY – IVE pair the loss was the highest. It was also observed that upon the removal of HEM – KRY – IVE triplet, the total genetic loss was maximum.

Conversely, the total genetic diversity that would be observed if different number of breeds in different combinations were retained, were also calculated by a Perl script written by S. C. Açan. For each different number of breeds the combination of the breeds revealing that maximum contribution to the total genetic diversity was presented in Table 3.20. The results showed that if one breed was present the most genetic diversity was attained with the presence of KRY, if two breeds were present the most genetic diversity was attained with the presence of KIV and IVE, and if three breeds were present the most genetic diversity was attained with the presence of HEM – KRY and IVE. It should also be noted that the genetic diversity of the set composed of HEM – KRY – IVE surpassed the total genetic diversity harbored by whole set.

Table 3.20 The gain (+) or loss (-) of diversity when breeds were removed from the set, and the total genetic diversity when only a number of breeds were present. The priorities changed not only with the number of breeds to be conserved, but also with the method (addition or subtraction) to be employed.

GAIN (+) OR LOSS (-) OF DIVERSITY WHEN ONE BREED IS REMOVED								**TOTAL GENETIC DIVERSITY WHEN ONLY n BREED(S) ARE PRESENT**			**TOTAL GENETIC DIVERSITY WHEN n BREED(S) ARE REMOVED**		
	Total Genetic Diversity	**Total Difference**	**Percent**	**Between Breed Diversity**	**Percent**	**Within Breed Diversity**	**Percent**	**One Breed**	**Two Breeds**	**Three Breeds**	**One Breed**	**Two Breeds**	**Three Breeds**
Total	0.8019			0.0406		0.7613							
SAK	0.8011	-0.0008	-0.0998	0.0377	-7.1429	0.7635	0.289						
KRG	0.8034	0.0015	0.1871	0.0391	-3.6946	0.7642	0.3809						
HEM	0.8007	-0.0012	-0.1496	0.0406	0	0.7601	-0.1576			0.8067 (>100%)			0.7952 (99.1%)
CIC	0.802	0.0001	0.0125	0.0398	-1.9704	0.7622	0.1182						
NOR	0.8023	0.0004	0.0499	0.0415	2.2167	0.7608	-0.0657						
HER	0.8024	0.0005	0.0624	0.042	3.4483	0.7604	-0.1182						
DAG	0.8019	0	0	0.042	3.4483	0.7599	-0.1839						
MOR	0.8025	0.0006	0.0748	0.0412	1.4778	0.7613	0						
KIV	0.8019	0	0	0.0406	0	0.7613	0		0.8015 (99.9%)				
KRY	0.8001	-0.0018	-0.2245	0.0411	1.2315	0.7591	-0.289	0.7874 (98%)		0.8067 (>100%)		0.7971 (99.4%)	0.7952 (99.1%)
IVE	0.7995	-0.0024	-0.2993	0.0394	-2.9557	0.76	-0.1708		0.8015 (99.9%)	0.8067 (>100%)	0.7995 (99.7%)	0.7971 (99.4%)	0.7952 (99.1%)
GOK	0.8018	-0.0001	-0.0125	0.0392	-3.4483	0.7627	0.1839						
AKK	0.8026	0.0007	0.0873	0.0393	-3.202	0.7632	0.2496						

The maximum diversities attained with n breeds where n ranges between one and thirteen were calculated by a script written in Perl again written by S. C. Açan. The resulting diversities and the sets of breeds that account for the corresponding diversity were given in the Table 3.21.

Table 3.21 Total genetic diversity captured by the combinations of the breeds. The maximum diversity is attained with 5 breeds, with a set of SAK, HEM, KIV, KRY and IVE as shown in the shaded cells.

# of Breeds	**Total Diversity**	**SET OF BREEDS**
1	0.7874	KRY
2	0.8015	KIV IVE
3	0.8067	HEM KRY IVE
4	0.8089	HEM KIV KRY IVE
5	0.8101	SAK HEM KIV KRY IVE
6	0.8090	SAK HEM DAG KIV KRY IVE
7	0.8084	SAK HEM CIC DAG KIV KRY IVE
8	0.8071	SAK HEM CIC HER DAG KIV KRY IVE
9	0.8062	SAK HEM CIC NOR DAG KIV KRY IVE GOK
10	0.8053	SAK HEM CIC NOR HER DAG KIV KRY IVE GOK
11	0.8044	SAK HEM CIC NOR HER DAG MOR KIV KRY IVE GOK
12	0.8033	SAK HEM CIC NOR HER DAG MOR KIV KRY IVE GOK AKK
13	0.8019	SAK KRG HEM CIC NOR HER DAG MOR KIV KRY IVE GOK AKK

3.5.1.4 Marker Estimated Kinship (MEK) Approach

The last approach used for the evaluation of breeds in relation to their contribution to the genetic variation was by using the coefficients of kinship. The difference between kinship based diversity measures and genetic distances is that, kinship based measures conserve the founder population allele frequencies, while genetic distances would give the priorities to those with the most distinct allele frequencies. The coefficients of kinship were calculated by MolKin v3.0 (Gutiérrez *et al*., 2005) and results were given in the Table 3.22.

Within-breed coefficients (the diagonal) ranged from 0.3491 (KRG) to 0.4217 (IVE). In relation to between breeds, the most distant breeds were SAK and IVE (0.4713) and the least distant breeds were KRG and NOR (0.3943).

The contributions of breeds to the set composed of all breeds were calculated using the kinship matrix by a Matlab M-File. The top three contributors were IVE (31%), SAK (22.6%) and GOK (16%). The results were presented in the Table 3.22. The negative contributions were eliminated iteratively as proposed by (Eding *et al*. 2002).

Table 3.22 The kinship coefficients calculated by MolKin v3.0. The diagonal is the within breed kinship coefficients.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	0.3683	0.4117	0.4443	0.4407	0.4163	0.4261	0.4364	0.4393	0.4395	0.4519	0.4713	0.4546	0.4568
KRG	0.4117	0.3491	0.4203	0.4228	0.3943	0.4024	0.4194	0.4235	0.4231	0.4286	0.4508	0.4386	0.4439
HEM	0.4443	0.4203	0.4064	0.4365	0.4209	0.4327	0.4400	0.4475	0.4371	0.4442	0.4618	0.4454	0.4581
CIC	0.4407	0.4228	0.4365	0.3940	0.4159	0.4303	0.4401	0.4529	0.4460	0.4533	0.4596	0.4434	0.4452
NOR	0.4163	0.3943	0.4209	0.4159	0.3744	0.4107	0.4144	0.4148	0.4201	0.4315	0.4381	0.4374	0.4338
HER	0.4261	0.4024	0.4327	0.4303	0.4107	0.4003	0.4278	0.4334	0.4244	0.4347	0.4597	0.4338	0.4447
DAG	0.4364	0.4194	0.4400	0.4401	0.4144	0.4278	0.3946	0.4130	0.4156	0.4297	0.4399	0.4244	0.4318
MOR	0.4393	0.4235	0.4475	0.4529	0.4148	0.4334	0.4130	0.3976	0.4287	0.4312	0.4426	0.4448	0.4339
KIV	0.4395	0.4231	0.4371	0.4460	0.4201	0.4244	0.4156	0.4287	0.3969	0.4287	0.4554	0.4164	0.4380
KRY	0.4519	0.4286	0.4442	0.4533	0.4315	0.4347	0.4297	0.4312	0.4287	0.4090	0.4522	0.4444	0.4470
IVE	0.4713	0.4508	0.4618	0.4596	0.4381	0.4597	0.4399	0.4426	0.4554	0.4522	0.4217	0.4655	0.4631
GOK	0.4546	0.4386	0.4454	0.4434	0.4374	0.4338	0.4244	0.4448	0.4164	0.4444	0.4655	0.3846	0.4387
AKK	0.4568	0.4439	0.4581	0.4452	0.4338	0.4447	0.4318	0.4339	0.4380	0.4470	0.4631	0.4387	0.3984

Table 3.23 The contributions of breeds to the set of breeds (C) were calculated in Matlab®. Because of the assumptions of the approach, negative contributions were eliminated iteratively one by one starting from the most negative element, until no more negative contribution were left, and presented in the row C Corrected.

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
C	0.3128	0.1722	0.1486	0.1452	-0.3334	-0.1737	-0.4032	0.1657	0.0020	0.0576	0.4285	0.2672	0.2106
C Corrected	0.2255	0.0106	0.0850	0.0459	-	-	-	-	-	0.0081	0.3098	0.1605	0.1546

The contributions of breeds to the set of breeds (C) were calculated in Matlab®. Because of the assumptions of the approach, negative contributions were eliminated iteratively, starting from the most negative element, until no more negative contributions were left and presented in the C Corrected. The results are given in the Table 3.23. According to this approach IVE contributes 30.98% to the diversity, followed by SAK with 22.55% and GOK with 16.05% of the diversity. The vector C-Corrected will be used later in the study while determining the priority of the breeds based on extinction risk, genetic contribution value and conservation value.

To sum up the findings so far, all of the approaches presented IVE in the top three breeds to be conserved. SAK, KRY and HEM appeared as one of the top three breeds to be conserved in half of the approaches. If the most distinct breeds were to be conserved, the top priorities should be given to SAK and KRG with IVE, and if the most genetic diversity or allelic richness were to be conserved the priorities should be given to KRY and HEM with IVE. If the most genetic diversity was the aim of the conservation program IVE, KRY, HEM, SAK and KIV should be conserved. If the aim was to conserve the founder population's alleles, then IVE, SAK and GOK should be conserved.

3.5.2 Priority Setting for Conservation of Breeds Based on Extinction Risk, Genetic Contribution Value and Conservation Value

For setting priorities for conservation of breeds, three parameters were considered as recommended by the guideline of FAO. These were the extinction risk of the breed, the contribution of the breed to the genetic variation, and the standardized conservation value of the breed. To assess the extinction risks and standardized conservation values, first the available data, which includes breed registries from the Official Gazette (www.resmigazete.gov.tr), publications from the Ministry of Food, Agriculture and Animal Husbandry (TAGEM, 2009) and contemporary literature (Soysal, 2010) were evaluated.

Then questionnaires with the help of advices of Prof. Dr. Mehmet Ertuğrul, Dr. Bekir Ankaralı, A. Oya Akın and Nevin Aksümer were prepared. A sample questionnaire was presented in Appendix C. For the surveys, questionnaires were handed out to field specialists of the breeds. The specialists were highly educated personnel, each holding at least a university degree from Veterinary or Animal Science. For the genetic contributions of the breed to the total set, the vector C-Corrected, which was calculated earlier in this study with the help of kinship coefficients, was used.

While assigning risks, an extension of Reist-Marti *et al*.'s (2002) and Gizaw *et al*.'s (2008) approaches were used. As they have suggested, answers were grouped into risk classes as, population size, degree of indiscriminate crossbreeding that has been experienced by the breed, the opinions of farmers on sheep breeds, the trend in the number of farmers, size of distribution area of the breeds, trends in the population size, the existence of pure stock, availability of shepherds, the existence of farmer organizations, the existence of a conservation scheme, the political situation, and existence of specific threats towards the breed. Organized raw data for the surveys of the each breed were given in Appendix D.

Prior to the research, sizes of the distribution areas for the breeds were unknown. The distribution areas were estimated using counting the pixels from the digitized images of the maps given in the Appendix D, which were drawn by the field specialists who answered the questionnaires. The areas were then classified into risk statuses, with respect to the size differences relative to each other as mentioned in section 2.6.2.

If there exists a pure stock of the breed, the breed was assigned -0.1 to its extinction risk. Other discrete answers to the questionnaire were divided into 4 categories, 0 being none, 0.1 being mild, 0.2 medium, and 0.3 severe. The extinction risks were summed up and standardized according to the equation 10 mentioned in section 2.6.2 to range between 0.1 and 0.9.

The variables used in the present study and the estimated values of each of the variables used for the estimation of risk status of the breeds were presented in the Table 3.24.

Table 3.24 The calculation of standardized extinction risks of breeds. * denotes missing values and assumed as medium risk. The risk classes were presented in the Table 2.3 and the questionnaires are included inAppendix C

RISKS	AKK	CIC	DAG	GOK	HEM	HER	IVE	KIV	KRG	KRY	MOR	NOR	SAK	AVG
Pop. Size	0	0.3	0.2	0.1	0.1	0.3	0	0.1	0.3	0	0	0.1	0.3	0.14
Cross Breeding	0.2	0	0.3	0.1	0.1	0.2	0	0.2	0.2	0.1	0.1	0.1	0.1	0.13
Farmers' Opinions	0.1	0	0.1	0	0	0.2	0	0.1	0	0.1	0	0	0	0.05
Trend in Farmers Nb.	0.3	0	0.2	0	0	0.3	0.2	0.3	0.2*	0.1	0.1	0.3	0.1	0.16
Population Dist.	7.9472	0.0564	2.0218	0.8010	1.202	0.2772	0.9364	0.4873	0.0737	0.3700	9.5061	0.4414	0.2385	1.87
	0	0.3	0	0.1	0.05	0.1	0.1	0.1	0.3	0.1	0	0.1	0.2	0.11
Trend in Pop. Size	0	0	0.2	0	0	0.2	0.2	0.1	0	0.1	0.1	0	0	0.07
Pure Stock (public)	0	-0.1	-0.1	-0.1	-0.1	-0.1	0	-0.1	-0.1	0	0	-0.1	-0.1	-0.07
Pure Stock (state)	-0.1	0	0	0	-0.1	0	-0.1	0	0	-0.1	-0.1	0	0	-0.04
Shepherd	0.2	0.2	0.2	0	0.1	0.1	0.3	0.2	0.2	0	0.3	0.2	0.2	0.17
Farmers Org.	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.10
Conservation Sch.	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
Political Sit.	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0.01
Specific Threats	0.1	0.1	0	0.1	0	0.1	0.1	0.1	0.1	0	0	0	0.1	0.06
EXTINCTION RISK	0.9	0.9	1.2	0.4	0.25	1.5	0.9	1.2	1.3	0.5	0.6	0.9	1	0.89
Standardized Risk	0.4130	0.4130	0.5174	0.2391	0.1870	0.6217	0.4130	0.5174	0.5522	0.2739	0.3087	0.4130	0.4478	0.41

It should be noted that, these values were not the absolute extinction risks, but rather extinction risks relative to other breeds. The most prominent problems were found to be the difficulties in finding shepherds, the negative trend in the number of farmers, the population sizes of the breeds, and the degrees of indiscriminate crossbreeding. According to Table 3.23, the breeds with the highest risks of extinction were HER, KRG, KIV and DAG. The breeds with the lowest risks of extinction were HEM, KRY, GOK and MOR. Except MOR they are geographically isolated and apparently have relatively little problem in relation to risk of extinction. The rest of the breeds had extinction probabilities close to the average.

For the estimation of standardized conservation values (SCV) of the breeds, part 2 of the questionnaire presented in the Appendix C were used. The raw data collected in production values, which include birth rate, litter size, average lambing period, milk yield, wool yield, weaning period, survival of the lambs until weaning, weight at birth, weight at weaning, age of maturity, daily weight gain, feed conversion, age of breeding, carcass weight, tail weight, pelt weight were given in the Appendix D. They were used directly in the equation 11 given in section 2.6.2, and similarly production environment variables given in questionnaire that are discrete values which consists of walking ability, grazing ability, herd instinct, mothering instinct, ease of milking, ease of shepherding, the utilization of areas not suitable for the breeding of other species, the presence of special products provided by the breed, the presence of a non-economical uses of the breed and traditional importance of the breed were given in the raw data form in Appendix D.

Evaluations of the breeds in relation to production values, production environment and the conservation values in accordance by the equation 12 which was presented in Chapter 2 were given in the Table 3.24

Table 3.25 The production values, adaptive values and socio-cultural values of the Turkish native sheep breeds. “*” denotes the missing values which were estimated by the average of known values. W denotes the weights given for the merits. Negative values for merits indicate the lesser the value of the merit, the favorable it is for the breeder.

	AKK	**CIC**	**DAG**	**GOK**	**HEM**	**HER**	**IVE**	**KIV**	**KRG**	**KRY**	**MOR**	**NOR**	**SAK**	**W**
birth rate	87.90	92.50	88.00	90.00	88.02	90.00	86.97	87.00	95.00	85.40	90.45	88.02	75.00	1
litter size	1.30	1.10	1.04	1.23	1.10	1.10	1.14	1.20	1.00	1.10	1.02	1.10	2.00	1
average lambing period (yrs)	7.00	6.57	9.00	8.00	6.57	6.57	5.00	6.00	6.57	5.00	6.57	6.57	6.00	1
milk yield	51.30	47.70	57.06	120.39	110.00	40.00	172.41	110.00	88.44	34.90	59.16	137.20	163.35	0.5
wool yield	1.24	0.87	1.31	1.46	0.85	0.95	1.56	1.01	1.13	1.30	0.78	1.13	1.12	0.1
weaning period (days)	90.00	146.00	110.00	90.00	108.88	108.88	105.00	120.00	108.88	120.00	108.88	75.00	90.00	-1
survival until weaning	95.00	93.58	97.06	98.00	93.58	93.58	93.58	95.00	95.00	90.00	93.58	92.00	85.00	1
weight at birth	4.00	3.80	3.50	3.75	3.30	3.40	3.52	3.25	3.20	3.50	3.52	4.20	3.50	1
weight at weaning	21.00	20.89	22.48	18.70	22.44	22.44	22.44	32.50	22.44	20.00	22.44	29.89	21.50	1
age of maturity (days)	225.00	269.56	225.50	365.00	269.56	269.56	410.00	309.00	269.56	180.00	225.00	269.56	217.00	-1
daily weight gain	250.00	211.00	241.05	190.48	197.50	230.75	230.75	275.00	230.75	275.00	230.75	279.00	206.00	1
feed conversion	0.20	0.19	0.21	0.14	0.19	0.19	0.19	0.15	0.19	0.26	0.19	0.18	0.17	1
age of breeding (days)	515.00	540.00	467.00	337.00	540.00	540.00	450.00	528.00	450.00	547.00	532.00	548.00	240.00	-1
carcass weight	9.79	9.27	9.87	7.15	8.75	8.75	10.51	8.60	8.75	8.85	10.47	11.33	8.33	1
tail weight	3.50	1.95	2.72	1.95	1.95	1.95	2.91	0.20	1.95	0.87	3.17	1.95	0.30	-1
pelt weight	5.00	4.65	4.65	3.60	4.65	4.65	4.65	4.30	4.65	6.50	6.13	8.86	4.65	0.1
walking ability	0.30	0.20	0.30	0.30	0.30	0.20	0.30	0.30	0.20	0.30	0.30	0.20	0.00	0.1
grazing ability	0.30	0.30	0.30	0.20	0.30	0.20	0.30	0.30	0.20	0.30	0.30	0.20	0.20	0.1
herd instinct	0.20	0.30	0.20	0.30	0.30	0.10	0.20	0.30	0.00	0.20	0.30	0.30	0.00	0.1
mothering instinct	0.20	0.30	0.20	0.30	0.30	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.00	0.1
ease of milking	0.10	0.20	0.10	0.10	0.20	0.30	0.20	0.20	0.10	0.10	0.20	0.20	0.20	0.1
ease of shepherding	0.30	0.30	0.20	0.00	0.30	0.00	0.30	0.20	0.00	0.00	0.30	0.20	0.00	0.1
areas not suitable for animal breeding	0.10	0.00	0.10	0.00	0.20	0.00	0.00	0.10	0.00	0.20	0.00	0.00	0.00	0.1
special product	0.10	0.00	0.00	0.10	0.10	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.00	0.1
non-economic uses	0.00	0.00	0.00	0.10	0.10	0.00	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.1
traditional importance	0.00	0.00	0.10	0.10	0.10	0.00	0.10	0.00	0.00	0.00	0.10	0.10	0.10	0.1

In the last part of priority setting for the breeds their genetic contribution to the core set, their relative risk of extinctions and merits (production, adaptability, socio-cultural importance) were considered collectively to calculate their Utility values (Gizaw *et al*., 2008)

Three different scenarios were considered while calculating the Utilities (Ui) of the breeds. In the first scenario the merits of the breeds were weighted according to the conservation program which would consider meat production having 2 times more important than milk and 10 times more important than wool and pelt production. The weights of this scenario were presented in the Table 3.25.

In the second scenario milk production was considered to have an equal importance with the meat production. Wool and pelt production were again inferior to milk and meat production by a factor of ten.

In the third scenario, milk and meat production were considered to have equal weight. In addition to those, adaptive traits and socio-cultural values of the breeds were considered to be as important as the economic traits, and calculations were done accordingly. All results were presented in the Table 3.26

Table 3.26 The utility values for the breeds for different scenarios. Shaded cells show the top three breeds in each scenario

	AKK	**CIC**	**DAG**	**GOK**	**HEM**	**HER**	**IVE**	**KIV**	**KRG**	**KRY**	**MOR**	**NOR**	**SAK**
Scenario 1 (Meat = 2xMilk)	0.679	0.138	0.580	0.343	0.168	0.113	0.406	0.395	0.249	0.308	0.312	0.900	0.522
Scenario 2 (Milk = Meat)	0.647	0.138	0.550	0.380	0.207	0.107	0.487	0.415	0.266	0.284	0.303	0.900	0.584
Scenario 3 (Adaptability)	0.737	0.343	0.593	0.566	0.748	0.100	0.758	0.604	0.133	0.422	0.703	0.900	0.354

To sum up, according to the answers of the questionnaires, regardless of the scenario, NOR should be included in the conservation program. When adaptability or the socio-cultural values were not of the issue, SAK was the one to be included in such a program. If local adaptations and socio-cultural importance of the breeds were considered along with their economic values, IVE and HEM should be included in the conservation program.

In all scenarios HER, KRG and CIC scored relatively poorly, ranking in the bottom three, suggesting that they probably shouldn’t be considered for any conservation scheme.

As a summary, within the limits of data, if genetic diversity measures are the criteria IVE, SAK, KRY and HEM must have priorities, if risk of endangerment is the criteria KIV and DAG (after hybrid breed HER and imported breed KRG) should have high priorities, if the utilities are the criteria under different scenarios NOR, AKK, SAK , HEM, IVE were the breeds that must have high priorities in conservation studies.

CHAPTER 4

DISCUSSION

In this study data based on 19 microsatellite loci from 628 sheep from 13 native Turkish sheep breeds were investigated. In the first part of the study, the genetic data was used evaluate the descriptive statistics of the breeds, their genetic similarities and differences and their histories. In the second part of the study, genetic data was again used to determine the contributions of the breeds to the Turkish sheep gene pool and with the combination of non-genetic data in a framework of decision support for setting priorities in conservation practices was tried to be formulized.

4.1 Revisiting the Genetic Data

Molecular data used in this study were collected as a part of "*In Vitro* Conservation and Preliminary Molecular Identification of Some Turkish Domestic Animal Genetic Resources – I" (TURKHAYGEN – I project). The samples were collected by the field specialists of the Ministry of Food, Agriculture and Livestock (then called the Ministry of Agriculture and Rural Affairs). Sample collection sites were chosen to reduce the effects of admixture between neighboring breedsand hence were relatively narrow with respect to the known distribution areas of the breeds (Akçapınar, 2002). Few samples per flock were collected to prevent the representation of the breed by close relatives.

4.2 Results of Descriptive Statistics, Bottleneck Analysis

The molecular data, which was mainly the same as used by Acar (2010), was analyzed once more after discrepancies were detected. In the study, out of 19 loci only OarFCB226 locus only in İvesi showed an estimated null allele frequency greater than the tolerable value of 0.2 and therefore it might have caused significant problems in analyses (Dakin and Avise, 2004; Chapuis and Estoup, 2007). In the similar studies by Peter *et al*. (2007) and Glowatzki-Mullis *et al*. (2009) didn't report null alleles in the OarFCB226 locus. As well as the analysis where this locus was included all of the analyses were repeated by excluding the locus. Some of these analyses analyses were given in Appendix E. These, analyses revealed that exclusion of OarFCB did not change the presence of two groupings among the samples but the distinctness of IVE was reduced. As a result, contribution of IVE to core set was reduced from 31% to 23% and its rank of contribution became 5th in the final prioritization of the breeds.

The loci that were analyzed in the study were not on the same chromosome. Hence, alleles of different loci were expected to be randomly associated in the populations. The population is said to be in linkage equilibrium if the alleles of the any two loci are found to be associated randomly. High degree of inbreeding might cause linkage disequilibrium (LD) in a population (for instance if highly related individuals were collected then this would be detected by the presence of LD in the analysis) or the signs of recent introgression could be detected by the presence of LD. In the study, out of 171 pairwise interactions of loci among 13 populations, totalling 2223 combinations only 4 combinations were found to be in LD. Moreover, the linkage disequilibriums were not concentrated in any breed. The low number of LD suggested that during the sampling close relatives were not included. However, the presence of LD between MAF33 and FCB128 in both Karayaka and Kıvırcık suggested that both of them might be introgressed by an exotic breed for instance Merino. In other words, if as suspected, Merino genome was recently introduced and it did not have time (in terms of generations) to randomly disperse in the gene pools of KIV and KAR it could be the reason of observing LD in these two breeds.

All loci were polymorphic, and the number of alleles ranged from 23 (OarFCB304) to 8 (OarCP34) with an average of 14.37. When compared with the similar studies for European breeds, Lawson-Handly *et al*. (2007) reported 19.9 alleles per locus, Peter *et al*. (2007) reported an average of 18.19 alleles per locus and Glowatzki-Mullis *et al*. (2009) reported 12.95 alleles per locus. The first two studies from Europe covered breeds not only from Europe but also from Middle East therefore observation of higher number of alleles than what was observed in the present study was expected. However, although number of alleles from a relatively small Switzerland (Glowatzki-Mullis *et al*. 2009) was lower than those of the present study still the difference was not high enough. Perhaps because these loci were chosen mainly based on the European sheep breeds hence there is an ascertainment biased or as was stated by the recent paper based on nearly 50.000 SNP (Kijas *et al*, 2012) sheep breeds exhibited large variation in general.

The similar trend with respect to another measure of genetic diversity: allelic richness was observed. In our study, mean allelic richness was found as 9.12, while Sakız had the lowest with 7.87 and Herik had the highest with 9.81. It should be noted that, sample sizes affect allelic richness greatly; therefore rarefaction procedure (Mousadik and Petit, 1998), which is the standardization of sample sizes to a fixed sub-sample size of g, drawn randomly from the original sample, must be performed first. In our study the sub-sample size g was determined as 30. The reported allelic richness from other studies, except the one which was done by using breeds from Europe - Middle East spectrum (Lawson – Handley *et al*. 2007) were lower than that of our study which were presented in the table 4.1. However it should be noted that the sample sizes differ in the studies. Glowatzki-Mullis *et al*. (2007) stated that the standard sample size was equal to the size of the lowest sample which was 18. Although it was not mentioned in the manuscripts what the sub-sample g of the other studies, Gizaw *et al*. used uniform sample sizes of 48 and the lowest sample size of Tapio *et al*. was 18. The average number of individuals per breed was 30 for Peter *et al*. and 28 for Lawson Handley *et al*.

Table 4.1 Average allelic richness per breed reported by the similar studies, and the number of common loci shared with the study and the current study.

Study	Average Allelic Richness	Number of Common Loci
Peter *et al.* (2007)	6.42	18
Gizaw *et al.* (2007)	6.79	9
Glowatzki – Mullis *et al.* (2008)	6.48	14
Lawson – Handley *et al.* (2007)	9.07	10
Tapio *et al.* (2010)	3.89 – 6.98	8
Current Study	9.12	

The high number of allelic richness, which is a measure of diversity, confirmed the expectation of high genetic diversity near the centers of domestication. However, the high allelic richness might imply high level of admixture, as the breed with the highest allelic richness was found to be the most admixed breed (HER), and the breed with the lowest allelic richness was found to be the most distinct breed (SAK), which will be discussed further in this chapter. Nevertheless, even the breed with the lowest allelic richness in this study still surpassed all but one of the reported allelic richnesses.

Heterozygosity, like allelic richness, is another measure which reveals the within breed variation which takes into account the frequency of alleles. In addition statistical differences between observed and expected heterozygosities marks deviations from Hardy - Weinberg equilibrium principle, making the the expected heterozygosity as the most widely used measure to describe within group variation.

The breeds Karagül and Sakız had the minimum two expected heterozygosities, while Karayaka and Kıvırcık had the maximum two. Karagül was imported in the 1930's, and never reached to a population size as much as the native sheep breeds of Turkey, and Sakız is a breed which was distributed in a small geographical area. Both breeds have relatively small populations, which would justify the low expected heterozygosities. However, the third lowest expected heterozygosity was in Akkaraman, which is the most populous breed of Turkey. The low expected heterozygosity might be due to the limited coverage of the total genetic diversity of AKK during the sampling procedure. The lowest observed heterozygosity was detected in CIC, which was rescued from the brink of extinction and hence went through a severe bottleneck which might have caused the low observed heterozygosity of this breed.

Deviations from Hardy – Weinberg equilibrium didn't accumulate on one breed or loci. The breed with the most deviations was Hemşin, in three loci, exhibited an excess of homozygotes in all cases, which could be attributed to the breeding style of Hemşin. Being bred in the mountainous regions of the Northwest Anatolia, Hemşin populations generally exist as isolated sub-populations, in other words the excess homozygotes of Hemşin might be due to Wahlund Effect. The locus that exhibited the most frequent Hardy – Weinberg deviations was MAF33. It was significantly deviant in the breeds KRG, KIV, KRY and GOK. KIV and KRY had linkage disequilibrium between MAF33 and OarFCB128. GOK had also a high, albeit non-significant, degree of linkage disequilibrium between MAF33 and OarFCB128, and shown significant deviations from Hardy – Weinberg equilibrium both in MAF33 and OarFCB128 loci. Since Merino introgression is also experienced by GOK and KRG might alsobe affected by being close to KRY deviations for MAF might be related with recent introgression of Merino.

In the study, 10 private alleles were encountered in 8 different breeds. Only one, 175 allele at OarJMP58 locus in Gökçeada was above the frequency of 5%. It is known that sample sizes affect the presence of private alleles. Rarefaction was not applied in this study because sample sizes were close to each other. The presence of 2 private alleles, one exceeding frequencies of 5% in Gökçeada breed, was not surprising, because Gökçeada is an island breed, which is one of the most isolated breeds of Turkey. Emergence of a new mutation in a locus without propagating to other breeds was more probable for Gökçeada than any other Turkish breeds where ram exchanges between breeds is a common practice among breeders.

Overall F_{IS} values for the breeds showed that 11 breeds out of 13 experienced heterozygote deficiencies and 8 breeds out of 11 showed significance. This result was concordant with the study of Peter *et al.* (2007) which revealed positive values for all of the studied 57 breeds (4 non-significant breeds). Also another study by Koban *et al.* (unpublished) reported Hemşin, Morkaraman and Karayaka indicating the positive F_{IS} values were not due to sampling errors but rather they are the facts of the breeds. The non-existence of isolations among the most sheep populations in Turkey makes the Wahlund Effect a low probability (although in some cases it may exist as we saw for HEM), but it suggests the presence of inbreeding in most of the sheep breeds of Turkey.

The cause of the inbreeding might be due to the employment of few rams for producing offspring. Although much care has been taken not to include close relatives during the sampling procedure, it has been expressed by the specialists that “Although we know the mother of the lamb, we have no means to be sure which ram sired the lamb”. It could be possible that the few dominant rams could have mated with the most of the ewes. High degree of distortion in the sex ratio lowers the effective population size appreciably and this of course increases the inbreeding level which is a general problem in livestock.

The second plausible cause for the inbreeding could be the bottlenecks that the breeds have experienced. According to microsatellite data, all breeds have experienced severe bottlenecks, their population sizes reduced by a factor of 100, even some breeds (CIC and NOR) had their population sizes reduced by a factor of 10.000. The reduced pool of possible mates might have triggered inbreeding. Nonetheless, population size reductions to this extent might have caused loss of genetic diversity, the reasons of bottlenecks must be considered seriously to avert such incidents in the future.

4.3 In search for a pattern for the genetic diversity of breeds

4.3.1 F_{ST} values

The useful and informative F-Statistics developed by Wright in 1965 were not commonly used until lately. The computational power nowadays enabled the permutations for the testing of significance of the Wright’s F-Statistics. The population pairwise F_{ST} values gave insights on the genetic differentiation between the breeds. The global F_{ST} value was calculated as 0.04, which was lower compared to the previous studies which reported 0.06 – 0.13 for European sheep breeds (Lawson-Handley, *et al*., 2007; Tapio, *et al*., 2010). The low degree of differentiation might be caused by the lack of barriers between the breeds of Turkey. However small, the differentiation was significant with p values smaller than 0.001. Despite the lack of barriers, all breeds have shown significant differentiation ($p < 0.001$) when pairwise F_{ST} values were considered. Sakız had particularly high values of F_{ST}’s suggesting that, it is quite different than the rest of the native sheep breeds of Turkey. Another point of interest was, the highest differentiation was between SAK and GOK, which occupy neighboring geographical zones. Although, the main reason is not known isolatedness of the two breeds, as well as different evolutionary history/ random drift can be invoked as some of the reasons of differentiation. mtDNA (maternally inherited DNA) indicates that GOK is very different than SAK (TURKHAYGEN-I 6th Progress Report, Project No. 106G005, TUBITAK)

4.3.2 Phylogenetic Trees

For the construction of phylogenetic trees, Nei's D_A and Reynold's distance were used. Nei's D_A assumes the differentiation occurs because of genetic drift and mutations, whereas Reynold's Distance assumes the only source of differentiation is the genetic drift. When the phylogenetic trees based on these two distances were constructed, their topologies were observed to be similar. Both trees exhibited dichotomy, implying the breeds form two genetically distinct groups. However low bootstrap values suggest that, as the F_{ST} values, the differentiation was not high and robust. The highest bootstrap value was on the branch of SAK, implying again its distinctness among the native sheep breeds of Turkey.

The phylogenetic tree constructed by Nei's D_A placed Akkaraman, Kıvırcık, Dağlıç, Gökçeada, Karayaka, Morkaraman, Norduz and İvesi together as the first group and Çine Çaparı, Hemşin, Karagül, Sakız and Herik together as the second group. The first group, except Norduz, was composed of the major breeds of Turkey, which have relatively larger areas of distributions and larger population sizes. The breeds which are geographically closer to each other (Dağlıç, Akkaraman, Karayaka, Kıvırcık, Gökçeada, which are western breeds vs. Morkaraman, Norduz, İvesi which are eastern breeds) were placed together. In Peter *et al.* (2007), however, Morkaraman and Akkaraman were placed together in the breeds of Middle East, and Dağlıç and Karayaka were placed in the breeds of Europe. The study of Uzun *et al.* (2006) reported similar results, placing Akkaraman and Morkaraman in close proximity. Also it has been reported that Norduz was actually a variety of Akkaraman (Kopuzlu and Bingöl, 2010). So it was surprising to see Morkaraman and Akkaraman apart, yet Morkaraman and Norduz close to each other. There might be two explanations for this phenomenon. Firstly, as it was said before, the sampling might not have captured the whole genetic diversity harbored by the breeds, especially for Akkaraman; and secondly, the scales (geographic span) of the studies differ. As the support for the second argument other studies did not have all of the breeds considered in this study.

The phylogenetic tree constructed using Reynold's Distance were quite similar to the one constructed with Nei's D_A, with the only exception of NOR being placed with CIC, HEM, KRG, SAK and HER. Again MOR and DAG were placed together, with IVE, and then KIV and GOK relative to others, which are neighboring breeds seemed to have a common ancestor (radiated from a common node) but also very different from each other as depicted by the long branches. Again with respect to Nei's D_A, AKK and MOR were not close to each other.

4.3.3 Evaluation of the results of Principle Component Analysis (PCA), Factorial Correspondence Analysis (FCA), Multidimensional Scaling (MDS) and Mantel Test

Both PCA and FCA were performed for the visualization of the study materials in multidimensional space. In PCA the study material was the centroid of the breeds, while FCA examined the individuals.

The first axis of the PCA was accounted for the 27.86% of the variation. The separation of the first axis was similar with the dichotomy expressed by the neighbor joining tree constructed using Reynold's Distance. The second axis of the PCA accounted for 18.22% of the variation.

The result of FCA, which depicted the individuals in a multidimensional space, once again showed that the breeds were not differentiated. The only breeds that showed significant differentiation were IVE and SAK. The rest of the breeds were clustered together. It should be noted that, no matter how intertwined the breeds were, the individuals belonging to breeds were still placed (packed) close to each other, supporting the low but significant differences of pairwise F_{ST} values evaluated earlier in the study.

MDS was applied to represent the distances between breeds in a 2-dimensional space. The F_{ST} values were used as *a priori* distances between breeds, and the result was similar to that of F_{ST} results. The distance between GOK and SAK was the highest. The most closely related breeds were HEM – HER and DAG – KRY breeds. As observed before, SAK, GOK, AKK, IVE and to a degree MOR was observed to be the breeds which are the most distant ones.

Mantel test was performed to detect if there were any correlations between the genetic distances which were measured as F_{ST} values and the geographical distances. Although it was expected to see higher F_{ST} values with increasing geographical distances, it was not the case in our study. Absence of correlation between geographic and genetic distances within Turkey seems to be the part of a global trend observed for sheep breeds even when studied based on about 50.000 SNP (Kijas *et al*. 2012).

4.3.4 Genetic Landscape of the Turkish breeds

In a recent study (which is done by S. Demirci and it is in progress) pairwise F_{ST} values were subjected to multidimensional scaling (MDS) and the scores of the populations on the first dimension of MDS was visualized as the synthetic map with the ArcGIS (desktop 10)

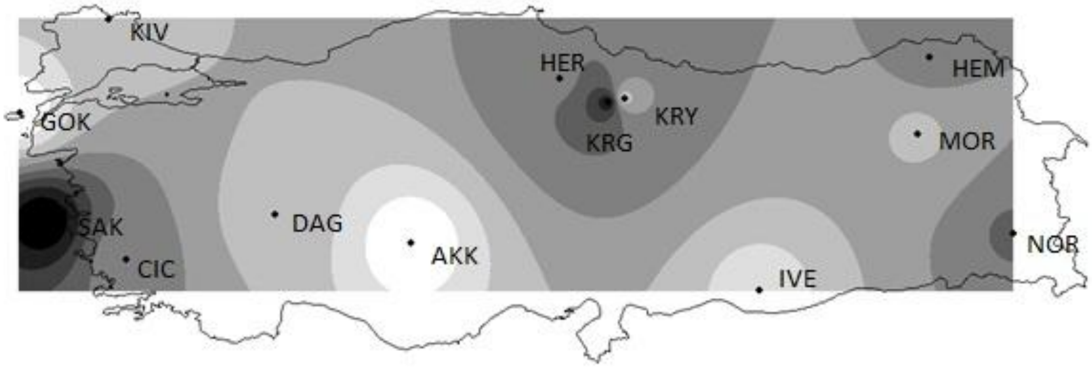

Figure 4.1 Synthetic map (ArcGIS Desktop10) showing spatial distribution of pairwise F_{ST} values. Pairwise F_{ST} values are calculated by using micosatellites. Black points indicate the centroids of the breed samples. Symbols for the breeds were given in Table 2.1. Figure is used with the courtesy of S. Demirci.

As it can be seen from the shades on the map there is no East-West or South-North cline. But 4 light shades of the synthetic map correspond to the first group of the second NJ tree and the 4 dark ones to the second group of breeds of the same tree. However, the second synthetic map, now interpolations based on the scores of the second dimension of multidimensional scaling is given in Figure 4.2.

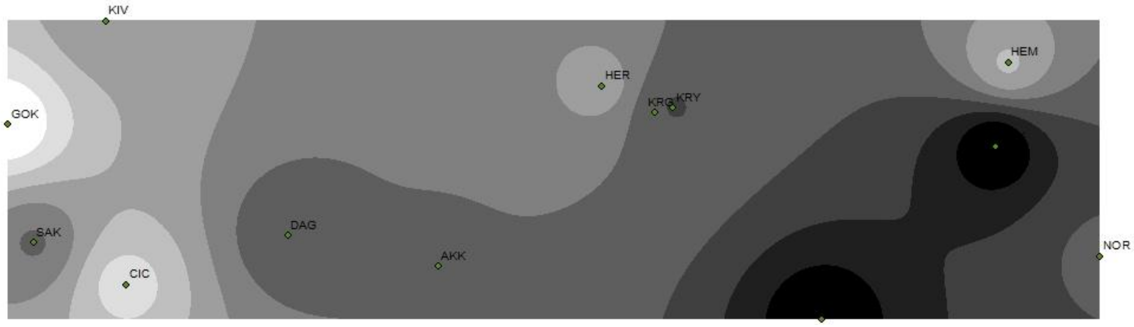

Figure 4.2 Synthetic map (ArcGIS Desktop10) based on pairwise F_{ST} of microsatellites, scores of breeds on second dimension of MDS plot were used for the interpolation. Black points indicate the centroids of the breed samples. Symbols for the breeds are as given in table 2.1. Figure is used with the courtesy of S. Demirci.

The figure, suggested the presence of Southeast- Northwest trend in the line of second expansion of “improved” sheep and also in the line of nomadic sheep arriving to Anatolia from the South and Southeast Anatolia. It is very tempting to assume that there is “a trend” as unraveled by the second synthetic map, but confounded by the recent, heavy male mediated exchange between the breeds in Turkey.

4.3.5 Clustering Analysis and Admixture

Bayesian clustering analysis was employed to detect the population substructures using Structure-console (Pritchard *et al*., 2000). Both the peak of the second order rate of the likelihood function (Evanno *et al.,* 2005) and the peak at the similarity coefficient (Tapio *et al.,* 2010) suggested that the most probable number of clusters was 2. At K=2, the clustering was the same as the neighbor joining tree constructed with Reynold’s Distance and the Axis 1 of the PCA and finally the dark versus light shades on the first synthetic map were in accordance with the two groups.

When compared to similar studies (Peter *et al.,* 2007; Tapio *et al.*, 2010; Glowatzki-Mullis *et al.*, 2009), the high degree of admixture in the populations of Turkish sheep breeds was evident. Figure 4.3 presents the comparison of the outcomes of structure results of the present study and the work of Glowatzki-Mullis *et al*.’s (2009).

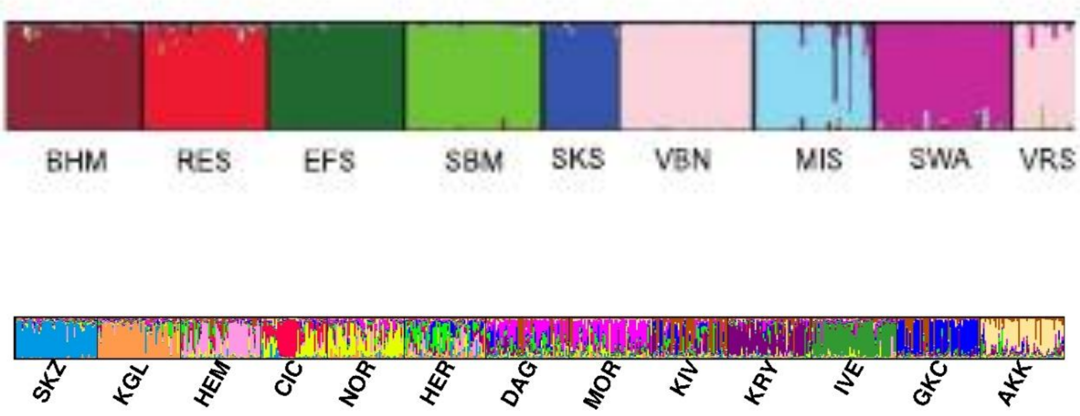

Figure 4.3 Comparison of the STRUCTURE results of the work of Glowatzki-Mullis *et al*. (2009), as the upper part; with the present study, as the lower part. K=9 for the work of Glowatzki-Mullis *et al*.'s (2009) and K=12 for the present study. BHM stands for Brown Headed Meat Sheep, RES stands for Red Engadine Sheep, EFS stands for East Friesian, SBM stands for Swiss Black Brown Mountain Sheep, SKS stands for Skudde, VBN stands for Valais Bloacknose, MIS stands for Mirror Sheep, SWA stands for Swiss White Alpine and VRS stands for Valais Red, all native sheep breeds of Switzerland.

- When two results were compared, for the Swiss breeds, each breed was identified by one color (one cluster), with very minor touches of a second color, depicting the genetic uniformity of the breeds. However, in the case of Turkish breeds, almost all breed samples are represented with mixture of colors indicating that they were highly admixed. The least admixed breeds were SAK, KRG and IVE. This result was expected, because there are no herd books, exchanging rams regardless of the breed is a common and highly praised practice among breeders. Breeders expect heterosis by this practice. Furthermore many foreign breeds (German Meat Merino, Black Headed Mutton, East Friesian, Ile de France, Rambouillet, Hampshire Down, Leicester, Lincoln, Dorset, Texel, Suffolk, Romanov) were known to be introduced into Anatolia in the past (Kaymakçı and Taşkın, 2008).

Introgression seems to be experienced mostly by the breeds of western part of Anatolia but it seemed to be that it was also applied in Central Anatolia and Eastern (MOR) and Southeastern of Anatolia (IVE), may be with an exception of HEM and NOR.

- The blocks of single color on the breeds in Figure 4.3, they either represent pure individuals of the breeds or they may represent recent introgression from other breeds especially if they exist in multiple breeds.
- The common color brown in the figure 4.3 for K=12 suggest that they have a common introgression since it is known that Merinos is introgressed to KIV, also, to KRY and GOK it is higly likely that the brown color represents the contribution of Merinos gene pool to these breeds.

LD observed for MAF33 and OARFCB128, also deviation of MAF33 from Hardy Weinberg equlibrium in these breeds are supporting this proposition. Unfortunately, in the present study there is not a sample from an exotic breed. For the next study samples of Merino which is widely used, is going to be employed.

Another inference drawn from the results of the study was that, even though animals may resemble to a phenotype, they may exhibit a genotype which is very different than the genotype typically associated with the phenotype. This is a well-known fact. For instance in a recent study published on dogs (von Holdt *et al*., 2010) it was observed that some of the toy dogs do resemble to the genomes of Mastiff dogs.

For the European breeds because they have a uniform genetic structure, the outlook and the typical breed genotype correlate most of the time. Even there, some exceptions were observed as found by the different colors on the color of the breed in Figure 4.3 top part. Despite the best efforts of the ministry officials, our analysis showed that highly admixed individuals were included in the samplings.

Turkish sheep (maybe with the exception of Sakız), should be considered as landraces rather than breeds in Western understanding. A landrace is an indigenous population which has evolved mostly by natural processes. It has a greater potential to resist the biotic and abiotic factors, resulting a better performance under a low input agricultural system (Zeven, 1998). As opposed to purebreeds landraces are usually more diverse in both physically and genetically.

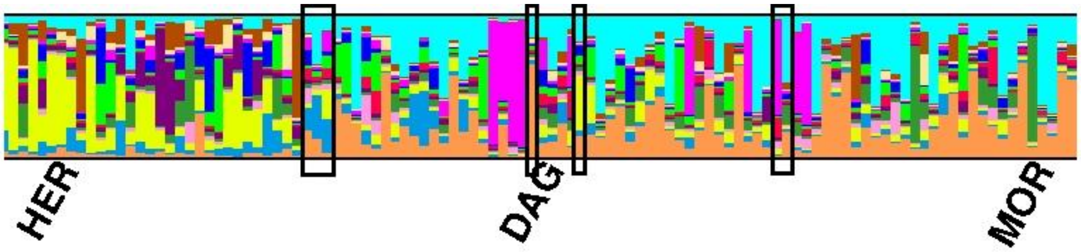

Figure 4.4 The bar plot from STRUCTURE illustrating the Dağlıç samples. The individuals inside the rectangles were the individuals from conservation flocks.

- The figure 4.4 shows an enlarged portion (bar chart) of the figure 4.3 bottom part, which concentrates on the Dağlıç breed. Few (n=7) of these were samples from the conservation flocks. They were boxed in Figure 4.4. The degree of admixture (mixture of colors) even in the individuals of the conservation flocks were found to be high. Even more, the lack of a dominant color in the conservation flock individuals implied that there existed no standard genotype which has been agreed upon, that could be called as "Dağlıç Genotype". Then, existence of conservation flocks – at least for Dağlıç – does not guarantee the conservation of the breed. Furthermore, from the structure analysis it could be seen that, except for few, (e.g. dominantly magenta individuals) individuals were generally composed of fragments of more than two colors suggesting that admixture had been continuing for a long time and admixture was between multiple breeds rather than the two. For the blocks of single color they either represent pure individuals of the breeds or they may represent recent introgression from other breeds if they exist in multiple breeds.

4.4 Origins of the Turkish Breeds, Sampling Effect On the Results of Genetic Data, Genetic Diversity Trends in Anatolia

Origins of Turkish sheep breeds can be discussed in the light of recent genetic studies. First of all, earliest (11.500) domestication (Zeder, 2007) does not seem to have effect in at least Eastern Turkish breeds as was shown by the complete absence of R0 and R1 retrotypes (Chessa, *et al*., 2009). The second expansion of sheep (for Turkey in the direction of Southeast - Northwest) is dominating all over the world except the peripheral breeds of Europe (including Cyprus). Presence of the two groups of sheep in Eastern Anatolia and Western Anatolia was recognized independently first based on microsatellites by Peter *et al*., (2007), then based on Y-chromosome haplotypes by Oner *et al*.,(2010) and very recently based on very high number of SNP by Kijas *et al*., (2012). The differentiation was attributed to the arrival of high number (n>78 million) of sheep from the Asia by the nomadic Turks (Togan *et al*, 2007). Thus, a hypothesis was proposed as follows: SAK, at least largely, can be considered as the sheep before the nomads in Anatolia and IVE or MOR – AKK (or mostly fat tail sheep) can be considered as the representative of the “sheep arriving together with Turks”.Therefore, in the 2-BAD studies parents were selected from East or West of Turkey. The hybrid was a sample of a breed (DAG) which has a native distribution in between these two zones. Perhaps, there were some fat tailed sheep in Anatolia before the arrival of Turks, but during their arrival an enhanced flux of sheep arrival from East of Anatolia can be anticipated.

Whatever the reason of this differentiation is, it must be taken into account in the genetic dimension of the priority setting for the breeds. However, this differentiation need not be manifested by the presence of sharply separated two homogenous groups of sheep in Turkey. Samples representing the breeds seemed to be admixed for sure. It is highly likely that in the next sampling the landscape observed by the ArcGIS may change. Furthermore, in the present study since the samples were obtained from a small geographic area they might be representing gene pools suffering from local drift (as it may be for AKK) and perhaps local introgression (may be DAG introgressed by MOR as it is observed in one of the NJ trees and in Structure Analysis) might be displaying a distorted landscape of the microsatellite based genetic diversity of Turkish sheep breeds. In relation to absence of East-West differentiation in the present data, it can be proposed that sampling from small areas is at least one of the reasons. Thus, while sampling in search of the genetic diversity distribution of the breeds, or sheep in general, sampling from the whole Turkey may be a better strategy. In the previous sampling (Peter *et al*., 2007) sampling was covering almost the whole native distributions of the involved breeds. Then, East - West differentiation was observed. Collection site of DAG in the present study was perhaps 1/5 th of the previous study; similarly collection site of AKK was even 1/8 th of the previous study.

If the samples from the wide area together with the samples of exotic breeds will be studied, the breeds will be characterized better in terms of their degree of admixture. Thereby, their pure representatives (if exist) can be located to be used in their conservation studies. Under the present scheme of sampling neither the general trend in sheep diversity nor the characteristics of the breeds could be obtained reliably. With this strategy the distribution areas of the breeds can also be defined. One last proposition in relation to sampling and genetic data would be to increase the sample sizes and number of loci used in a similar study.

Finally, it was very surprising to see no trend in the first synthetic map but a Southeast-Northwest trend in the second synthetic map. Maybe contribution of the breeds arriving from the East, generated a cline in the direction of Southeast-Northwest. While this cline was smoothed out over the centuries it still existed as clearly observed by the synthetic map of mtDNA haplogroups (from S. Demirci's study in progress). Yet, may be it was blurred by the more recent, local, small scale, accumulating, male mediated exchanges between the breeds. Therefore, in the first synthetic map the more recent genetic diversities were caught which were superimposed on the second cline like diversity pattern as observed by the second synthetic map.

4.5 Pairwise Admixture Analyses

In the process of priority setting evolutionary history of breeds play an important role (FAO Guideline, 2010). Therefore, plausibility of the hypothesis (i.e. existence of the sheep breed groups as before the Turks, after the Turks and hybrids in Turkey) was wanted to be tested by the admixture analysis.

The admixture analysis which can be employed by 2-Event Bayesian Admixture (2-BAD) software (Bray *et al.,* 2009) was performed mainly for two reasons. The first reason was to shed some light on the evolutionary histories of the native sheep breeds of Turkey and the second reason was estimate some parameters like the effective population sizes, mutation rates and the percent contributions of the parent populations to the assumed hybrid population

Four different scenarios were tested. In the first two using data from the present study, and the latter two using the data from ECONOGENE Project for comparisons. In all scenarios DAG was used as the hybrid. In using the ECONOGENE data DAG sample was the sample collected for ECONOGENE however in the context of first two scenarios DAG was the sample collected for

TURKHAYGEN-1. The usage of Approximate Bayesian Computing for estimating admixture events and parameters is a fairly new method, and the results can only be compared with the results of this study.

In all of the scenarios the estimated values of the parameters within the method groups (after rejection and after regression) were similar. Although standard deviations were high, consistency in the results with respect to these three parameters suggested that the data of the two studies were compatible. In Kijas *et al.*,'s (2012) study it was observed that for the sheep breeds Ne are relatively high (around 500) presumably due to the high historic mixture. In the present study, partly depending on the method of estimation but always Ne values were very high (mostly around 4000). In a previous study high diversity and hence high Ne was attributed to continuing migration in goats (Fernandez *et al.*, 2006). Perhaps, because in Turkey all of the breeds are mixed (at least the samples that were used in the present study) and that was why both the Ne and the standard deviations were high. The observation that: weight of contribution of the parent to DAG was dependent on the relative geographic distance of the parent to DAG indicates that as well as the presence of admixture this admixture has a gradual change in relation to East-West of Anatolia in the range of from Greece to Egypt –Saudi Arabia although it might be a week cline which could not be detected with the mantel test and could not be observed by the first synthetic map (Figure 4.1).

Very high Ne for the ancestral populations (Nearly 43000) may again be related with multiple domestication events over the time or continuous introgression from the wild which was possible for the ancestors of first and second sheep expansions since the wild form were and are present in the area. As has been mentioned by Tapio *et al.*, (2006), until very recently, introgression of the wild sheep have been practiced around the Caspian region.

Mutation rates of microsatellites were between 10^{-3} and 10^{-4}. Hence, estimates are compatible with the expectations

Finally, the time of split was estimated as ~1000 generations before present by the after regression method. If the generation time of the sheep can be excepted as ~ 5-6 years (Keightley and Eyre-Walker, 2000), time of the split is about 5000- 6000 YBP well agreeing with the second expansion of sheep (Chessa *et al.*, 2009) hence with the time of separation of Asian and European breeds. But then the time of the admixture is very recent, 1- 125 years (5-6 times 0.2- 25). On the other hand, if after rejection method is considered then split time is very old (nearly 20.000 YBP), which is possible and admixture times then are around the 1100 YBP fairly coinciding with the time of the invasion of Anatolia by the nomadic Turks.

In relation to time estimates, it can be perhaps suggested that just as it was in the synthetic maps there were two patterns (the Northwest - Southeast pattern laying at the background and slightly more dominant effect of high degree of admixture occurring in the recent) that were detected by the two methods of 2-BAD

4.6 Genetic Considerations in the Priority Setting for the Sheep Breeds in Turkey

Although it is impossible to answer the question of “Which breeds should be included in a conservation program?” by only considering the genetic diversity, evaluation and documentation of the genetic resources are essential for conservation practices. In this study, four different approaches were simulated and results were compared.

The first approach was the method proposed by Petit *et al*. (1998). The contribution to the genetic pool was decided based on the contribution of each breed to the allelic richness. Allelic richness, which measures the number of alleles per locus, is highly dependent on effective population size; hence it might hold information about past demographic changes. However, to cope with the uneven sample sizes rarefaction method (Hurlbert, 1971) should be applied. The idea behind measuring allelic richness is that, if a population has high allelic richness at the measured loci, there is a strong possibility that it might have high allelic richness at the other loci as well (Schoen and Brown, 1993). In the present study, it was estimated that İvesi is the top contributor to the allelic richness followed by Hemşin and Karayaka by 1.12%, 0.59% and 0.24% respectively (1.21%, 0.54% and 0.29% respectively without OarFCB226 locus). Although Herik, Dağlıç and Kıvırcık ranked higher when only allelic richness was considered, their contribution to the total was not very high. The contribution for within breeds were high for Herik, Dağlıç and Kıvırcık, but the redundancy of the alleles due to high admixture they received negative scores for between breeds contribution, resulting in mediocre positions. For the between breeds contribution Sakız had the greatest contribution with 1.00%, marking itself as the most distinct breed of Turkey once again.

The second approach was proposed by Weitzman (1992, 1993). This approach compares the diversity of a set of breeds, and the same set minus the breed in consideration. A genetic distance between breeds must be used. In the present study we have chosen Reynold’s Distance for the calculation of Weitzman Diversity. The breeds SAK, KRG and IVE ranked as the top three breeds with 12.68%, 11.01% and 10.89% contributions to diversity respectively (12.42% for SAK, 11.66% for GOK and 11.08% for KRG when OarFCB226 was excluded. IVE ranked 5th with 9.37%.). These three breeds were the breeds with the highest membership coefficients in the STRUCTURE analyses. The Weitzman Diversity, which considers only the genetic distance between breeds, is known to be biased towards the most distinct breeds because it doesn’t consider the variation within the breeds (Caballero and Toro, 2002; Eding and Meuwissen, 2001; Thaon d’Arnoldi *et al*., 1998).

The third approach treats the entities as a part of a larger entity, a meta-population formed by individual populations (Caballero and Toro, 2002). Unlike Weitzman approach, the diversity within the breeds was considered as well. Different studies suggest applying different coefficients for the within breed component of the diversity according to the conservation goal in mind (Piyasatian and Kinghorn, 2003; Eding and Meuwissen, 2005). In the current study we have presented the results with the coefficient of the within breed component as 1. According to our calculations, the top three breeds which would cause the most diversity loss when subtracted from the meta-population was İvesi, Karayaka and Hemşin with the percentages as 0.30%, 0.22% and 0.15%. The percentages are low, yet comparable with the results of Glowatzki-Mullis *et al*., which ranged from 0.9% to 0%. In both studies, the most of the variation were held by the within breed component, however, in Glowatzki-Mullis’s study, the genetic loss from between breed component was considerably higher than that of the present study (-12.2% - 0% vs. -7.14% - 3.45%). This result implied again the existence of heavily admixed and low differentiated breeds. In this approach, diversity even increased when certain breeds were omitted from the set.

The best combinations of breeds which would give the maximum diversity with a fixed number of breeds were also calculated. The findings showed that, according to the samples of the present study, conserving SAK, HEM, KIV, KRY and IVE would give the maximum genetic diversity.

The last approach that was performed to determine the contribution of sheep breeds to the genetic diversity was using the kinship coefficients. Unlike genetic distance methods that would prefer the most distant breeds, kinship based diversity measures tries to conserve the allele frequencies of the founder population. The calculated kinship coefficients were first calculated and then a vector C was formed using the coefficients. Like Weitzman Diversity, the method does not allow negative contributions, which were eliminated iteratively starting from the most negative item. The top three breeds contributed to the set were IVE with 31%, SAK with 23% and GOK with 16% (IVE was lovered to 23% after the exclusion of OarFCB226. In the absence of OarFCB226 the top three breeds were found to be SAK with 25%, IVE with 23% and GOK with 18%). The most admixed breeds, Norduz, Herik, Dağlıç, Morkaraman and Kıvırcık were found to be negative contributors, thus eliminated from the vector C.

If we would sum up, all approaches pointed out that İvesi from South-Eastern Anatolia is a breed that contributes a lot to the genetic resources of Turkish sheep breeds. Furthermore Sakız from Western Anatolia stood out as the most distinct breed of the native Anatolian breeds. When accompanied with Hemşin from North-eastern Anatolia, Karayaka from Northern Anatolia and Kıvırcık from Thrace, the maximum diversity is attained.Furthermore, prioritized breeds by different approaches were included into this set. Furthermore. Breeds both from the East and West were covered by the set. If a breed from the regions (such as AKK) where steppe climate reigns was included to the set, all climatic regions and various geographic regions of the Anatolia would have been covered. Then by conserving these 6 breeds (SAK, IVE, HEM, KRY, KIV and AKK) may be different adaptations which were not measured by the neutral alleles would have been also covered by the conservation studies

However, it must be emphasized that results on the genetic data must be considered with caution because of the limited coverage of the genetic diversity and because only the limited number (n=19) of and all neutral loci were used.

4.7 Utilities of the Studied Turkish Sheep Breeds

For a conservation program to be successful, not only the genetic diversity but also the extinction risks, adaptability of the breeds, possession of unique traits of economic or scientific interest and socio-cultural importance should also be considered (Ruane, 2000; Gandini and Villa, 2003). Therefore questionnaires were prepared to gather non-genetic data, which would be used together with genetic data, for setting priorities in a conservation program.

Earlier studies, (Canon *et al*., 2001; Mateus *et al*., 2004, Tapio *et al*., 2006, Glowatzki-Mullis *et al*., 2009) decided about the priorities of the breeds solely on the bases if genetic diversity. A few studies (Reist-Marti *et al*., 2006; Gizaw *et al*., 2008) blended non-genetic criteria with the contributions of breeds to the genetic diversity following the framework of Ruane (2000). In the current study, we applied a maximum utility approach suggested by Simianer *et al*. (2003) and refined by Gizaw *et al*. (2008).

For the evaluation of the utility of the breeds, three components were needed; i) contribution of the breed to the genetic diversity; ii) risk of extinction of the breed; iii) conservation value of the breed.

For the contribution of the breed to the genetic diversity, microsatellite data was used to calculate the contribution of each breed to the core set earlier in the study.

For the estimation of risk status, the extinction risk for each breed was tried to be estimated. The factors affecting the risk status were selected following the guidelines of World Watch List 3rd Edition (FAO, 2000) and the draft of FAO Guidelines for the In Vivo Conservation of Animal Genetic Resources (FAO, 2011). Ordered categories were established for each factor and values were assigned to breeds according to the effect on risk. The risk categories were assigned 0 for no risk and 0.3 for high risk and intermediate values in between.

The extinction risks were standardized to fit in the range between 0.1 and 0.9. The breeds that had extinction risks above average were Herik, Karagül, Kıvırcık, Dağlıç and Sakız. The main reason for the high risk is the already low population sizes, extensive hybridization, the small area of distribution and most importantly the low esteem of the farmers for the breed. It should be noted that all risks considered were of equal weight; however in reality some factors may affect the welfare of the breed differently than those of other factors. Nevertheless, it could be argued that, better performing breeds (İvesi, Morkaraman), or breeds with high adaptability to marginal environment (Gökçeada, Karayaka, Hemşin) have lower risks of extinctions.

As part of the prioritization process of the breeds their relative merits in terms of, the economic values of the breeds, the adaptive values of the breeds and the socio-cultural importance of the breeds were considered. The adaptive and socio-cultural values were assigned to categories as were the risk factors, and economic values were used directly. Three scenarios were tested. In the first scenario, where meat production was twice as important as milk production, Norduz, Akkaraman and Sakız were the top three breeds. This result was surprising, because both Akkaraman and Norduz have never been outstanding breeds so far in the study. Norduz, which had no contribution to the genetic diversity, had only the conservation value component of the utility function, yet managed to score the first place. Akkaraman's and Norduz's success lies in the high feed conversion, fast maturity and the heavy carcass weights, combined with hardiness and high adaptability of the breeds to their respective environments.

In the second scenario, milk production was considered as important as meat production. In this scenario, again Norduz, Akkaraman and Sakız ranked as the top three. Sakız, with high milk production closed the gap between Akkaraman, however the fast maturation and carcass weight factors of Norduz and Akkaraman dominated again, ranking at the first and second place respectively.

In the third scenario, adaptive and socio-cultural values had the same weights with the production values. With those parameters, Norduz ranked first as with the first two scenarios. However Hemşin ranked the second and Akkaraman ranked the third. Sakız, which was known to be a delicate breed with low adaptive skills ranked as the ninth.

In all of the scenarios, Herik, Karagül and Çine Çaparı scored badly, suggesting that they should not be considered in a conservation program.

If utilities of the breeds are the criteria for conservation, NOR, AKK, SAK, HEM, IVE seemed to be the breeds that should have priorities. This set is largely overlapping with the set proposed based on the genetic diversities. In this set, breeds both from East and West of Anatolia are observed. However, most of the breeds exhibiting relatively high risk (HER, KRG, DAG and SAK) were not in the proposed set.

However, the data used in the study may be incomplete, or may be irrelevant of the study. As Ruane (1999) indicated, since microsatellite loci are neutral loci, they might not reflect the presence or absence of a few but important selected loci that creates the phenotypic differences in different breeds. Also despite the best efforts of the ministry personnel, the samples collected might not represent the whole breed. This phenomenon is most probable in the case of AKK and DAG, where samplings were performed in a small percentage of the breeds' natural distribution areas. Moreover, 19 loci may not be enough to characterize the breeds whose evolutionary history is encompassed by migrations and admixtures.

In addition to the shortcomings of the genetic data, the non-genetic factors were also imperfect. Although there have been numerous publication on native Turkish sheep breeds, data is still far from being complete. Moreover, the publications, being published by different field specialists and academicians with different research questions in mind; are not standard in regards to the variety of information they contained. Also the breed registries were not complete – HEM, HER and KRG were not published at the time of the writing of this manuscript – and the ones that were present were not standard in manner mentioned before.

Also, during the study all stakeholders couldn’t be contacted which would give different insights on the breeds that were being studied. Despite the specialists that have been contacted were probably the most knowledgeable people regarding their respective breeds and the breeders, it would be better if people with different perspectives (i.e. breeders, academicians, government officials) could be contacted.

4.8 Conclusive Comments

As the studies clearly show, in the absence of breed associations, herdbook keeping and willingness of breeders to isolate the breeds, Turkish breeds are and will continue to be admixed. With the global F_{ST} value 0.04 for the Turkish breeds number of migrants (mN) in each generation, can be estimated to be nearly 10>mN>5 (Allendorf and Luikart, 2007). Perhaps, all of the sheep breeds of the world are admixed but among them, studied Turkish breeds are highly admixed. In Western Europe there is an inclination to accept that unless the breed is “pure” (admixture is less than 12.5%) it need not be considered as a breed and need not be conserved separately. Why do we want to have the “pure” breed? Mainly because its’ high merit(s) will then be observed uniformly in almost every member (there will not be a large scatter in the distribution of the merit of the individuals). For the Turkish breeds membership coefficients can be a measure for the measurement of admixture. Then, perhaps except SAK none of the breeds are qualifying for the individual conservation. However, their features in adaptation to marginal environmental conditions are empirically evident as evidenced by the observation that economically important breeds cannot survive in Anatolia under the rearing conditions practiced in Anatolia. Furthermore, they have morphological identity, they have distinct merits (for instance wool quality, meat quality, adaptability for walking, climbing). Hence, they are “breeds”. Furthermore they are very valuable breeds especially because they seemed to have resistance to parasites and can thrive on poor quality forage. Despite the fact that their genetic diversities are characterized in some neutral (present study) or non-neutral (for instance Un *et al*., 2008) markers, they are still poorly characterized in their adaptive and productive traits.**Therefore, there must be a strong argument to conserve all the breeds until they are characterized reasonably well.** However, it must be realized that fully subsidized conservation cannot continue forever.

Between the stage of “conservation of all the breeds” and “conservation of breeds in accordance of their priorities” there must be important steps to be taken, as some of them were listed below. The items marked with “P” are believed to be related with the type of the studies carried out in the present study.

1. Exercises for priority setting (as was presented here) must be made to have a better understanding for priority setting, “P”.
2. Isolation of the breeds can be enhanced and if isolation brings improvements in the merits of the breeds it can be advertised to generate a positive feedback.
3. In conservation efforts, genetic studies must be integrated.
    a. For instance in testing the individuals for their appropriateness before their inclusion to the conservation flock. However, test criteria may vary from one “breed” to another because, for some of the breeds, breed identity may be very low,”P”.
    b. During the conservation genetic monitoring can be done to ensure that the Ne was kept between 25- 500. Otherwise the high level of

    genetic erosion will be inevitable and insignificant part of the breed’s gene pool will be conserved, “P”.

    c. As a part of “risk status indicators” calculation of Ne and rate of loss of genetic diversity is used. In the absence of well-established herdbook system, genetic studies can be used to estimate these parameters“P”.
    d. Especially for a highly admixed breeds studies must be done with higher number of loci. For the efficient quick and cheap genetic characterization of the individuals .a SNP chip design must be considered.

4. Also the question ”Can the stocks held for the breed improvement be considered as the conservation of the breed?” must be discussed.
5. The trends, developments in the methods of priority setting for the breeds must be followed closely and measures such as collection of statistics, must be taken.

As it is known there is no single publication where prioritization was done based on the utility or genetic ranking of the breeds. Currently, most of the prioritization studies are for the academic purposes (Boettcher, 2010). By the present study, it is believed that specific genetic features of the Turkish breeds were documented, effects of sampling on the genetic studies was discussed, theneed for a reliable data (genetic, discrete and numerical data characterizing the risks and merits of the breed) for the prioritization of the breeds in the long term sustainable conservation of them was emphasized.

CHAPTER 5

CONCLUSIONS

In the first part of the present study samples of 13 native Turkish sheep breeds (n=628) were examined, individually and comparatively, with respect to their 19 microsatellite loci and by many statistical methods and softwares to characterize them. Then, some evaluations based on their genetic characteristics were made in relation to their prioritization in conservation studies. In the last part of the thesis breeds were also characterized with respect to their relative risk of extinctions and their merits. Finally within the limits of data the utility of the breeds were estimated and ranked. The results and conclusions of the study can be listed as follows:

1. By the study it is documented that, based on the employed samples of the breeds, Turkish sheep breeds seem to be highly admixed as indicated by: high mean number alleles and allelic richness within breeds but low global F_{ST}; results of FCA analysis; membership coefficients of Structure-console and visual representations of Structure analysis.

2. Admixture within the breeds might have being continuing for a long time (~1000 years) but might have been enhanced in the recent years (~12 years). These conclusions are tentatively drawn by the evaluation of synthetic maps and results of 2-BAD.

3. In relation to breeds it seems that as well as the admixture between the native breeds, perhaps introgression of the exotic breed (MERINO) was

documented for KIV, KRY, GOK, DAG, HER by the analysis of linkage disequilibrium, Hardy - Weinberg Equilibrium, Structure analysis.

4. In the study, with the good intensions, sampling areas were confined to a limited area. The ill effect of this sampling strategy might be detected mostly in sample of AKK. Although, AKK has the highest population size it exhibited low He, on the contrary to expectations, it has no resemblances to MOR, NOR and HER.

5. Although there is no genetic barrier between AKK and DAG as was previously observed (may be because of the sampling effect) still distinctness and differentiation between an Eastern breed (IVE) and a Western breed (SAK) was evident in the study. Confirming the hypothesis that there are at least two distinct sets of breeds differing in their evolutionary histories

6. In relation to the breeds, all samples displayed positive F_{IS} values may be due to the involvement of few males in their mating. More over HEM seems to exhibit Wahlund effect, GOK displays isolation that would be expected from an island population and all the breeds seem to have gone through 100 fold population size decrease in their past where it seems to be higher for CIC.

7. The present study indicated that genetic studies when necessary with high throughput technics (e.g. whole genome coverage with SNP chips) must be introduced to conservation studies in setting the conservation flocks and in monitoring them

8. In four different approaches of priority setting for the breeds in their conservation based on only genetic data revealed that with respect to allelic richness IVE, HEM, KRY, SAK; with respect to Weitzman approach, SAK, KRG, IVE; in Meta population consideration SAK, KIV, KRY and IVE

seemed to capture the maximum diversity (and even higher than the observed one) and in the kinship-core set approach IVE, SAK, GOK were the breeds that were suggested to have priority. As a conclusion, IVE, SAK, KRY, KIV, HEM and a breed from the central Anatolia (may be AKK) would be the optimum set to cover total genetic diversity including allelic richness, distinctness, products of different evolutionary histories, different geographies and perhaps different environmental adaptations.

9. To measure the relative risk of extinctions of the breeds a questionnaire was prepared by the guidance of personnel of the General Directorate of Agricultural Research (TAGEM) and (Prof. Dr. Mehmet Ertuğrul) by using the guideline “In Vivo Conservation of Animal Genetic Resources” prepared by the Food and Griculture Organization of the United Nations (FAO) . Evaluations were done mostly in accordance of FAO guideline indicated that Herik, Karagül, Kıvırcık, Dağlıç and Sakız were the breeds that had extinction risks above average.

10. To document the merits of the breeds (their economic values, adaptive values and socio-cultural importance) another questionnaire was prepared again by the guidance of the personnel of TAGEM and Prof. Dr. Mehmet Ertuğrul and by using FAO guideline and previous work of Gizaw *et al*. (2008). Evaluations were done mostly in accordance of FAO guideline.

11. When merits, risks and genetic data were evaluated under different scenarios NOR seemed to have highe(st) utility AKK, SAK, IVE, HEM also were among the highly ranking breeds.

12. It seems that at the end of the study the proposed set for the conservation can be NOR, AKK, SAK, IVE, HEM.

13. However, in relation to results, it is believed that data has limitations hence results must be considered with caution. Nevertheless, study helped us to

gain insights about the genetic characteristics of Turkish sheep breeds, problems related with sampling, the missing data needed in priority setting for the breeds in their conservation studies.

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APPENDIX A

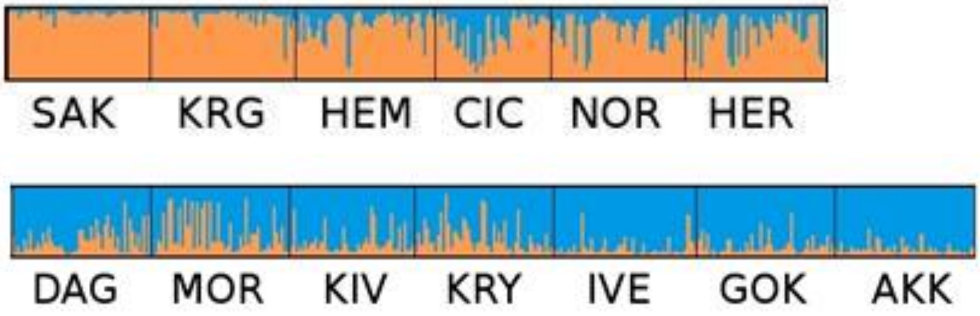
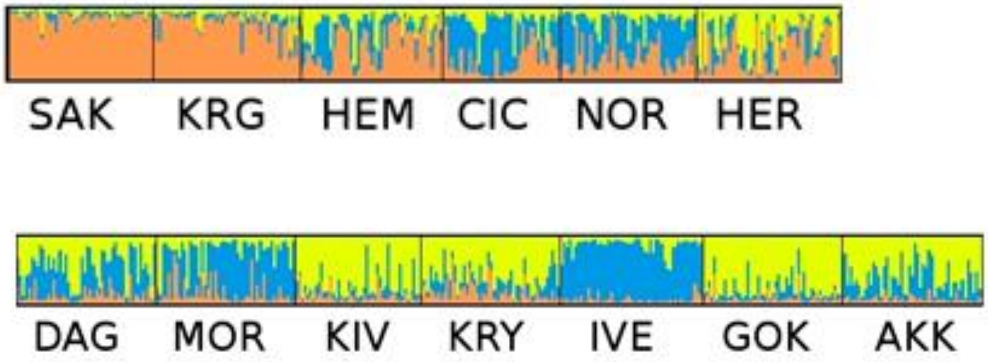
LIST OF SOFTWARE AND SCRIPTS USED IN THE STUDY

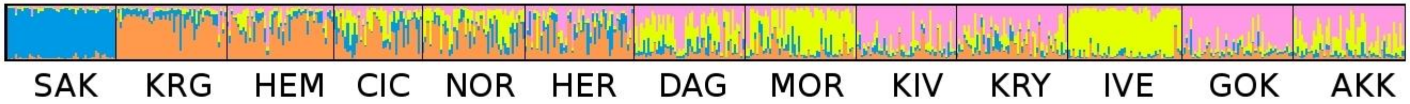
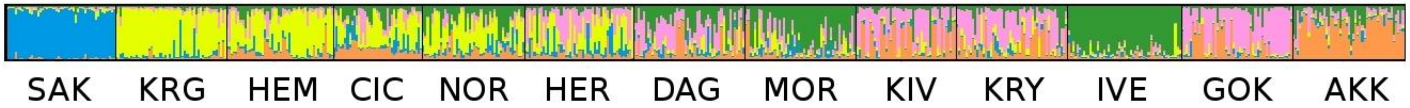
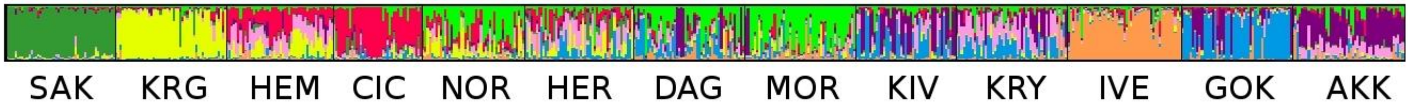
SOFTWARE	USAGE
2-BAD	Population Admixture
Arlequin 3.2	Heterozygosity, Mantel Test
CLUMPP	Similarity Between Structure Runs
FreeNA	Null allele estimation
FStat 2.9.3.2	allelic richness
GenAlEx	PCA
Genepop v4.1	Linkage Disequilibrium
Genetix 4.0.5	$F_{ST,}$, $F_{IS,}$ FCA
Metapop 1.0.3	Contribution to gene pool
Molkin 3.0	Contribution to allelic richness, Kinship coefficients
Msvar v0.9	Demographic History
Populations v1.2.30	Nei' D_A distance, Reynold's Distance NJ tree
R Statistical Package	Analysis of Msvar outputs, MDS
Structure-console	examine the presence of population structure
WeitzPro	Weitzman Diversity

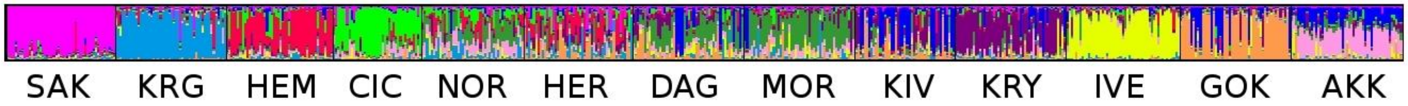
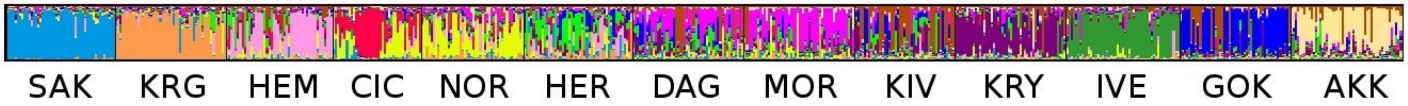
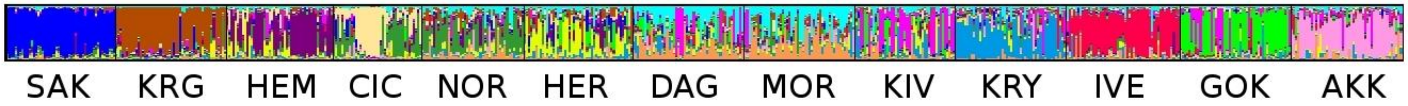
SCRIPTS	**USAGE**
Perl Script No 1	Detection of private alleles
Perl Script No 2	Detect optimal sets of breeds with a fixed number of breeds
Perl Script No 3	Parsing of the output files of CLUMPP to calculate the membership coefficients for breeds to a cluster
Matlab ® M-File	Calculation of the vector of contributions of breeds to the core set
Python Script No 1	Calculation of the geographical distances between sample collection sites

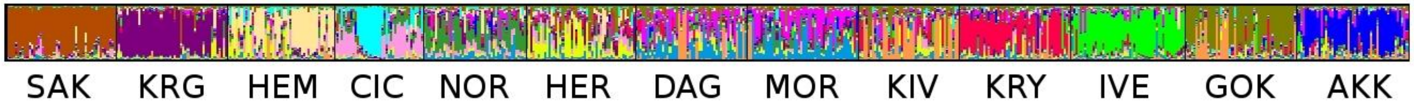
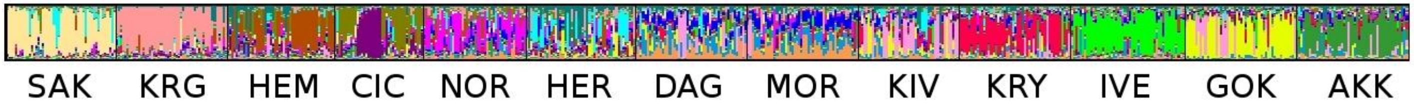
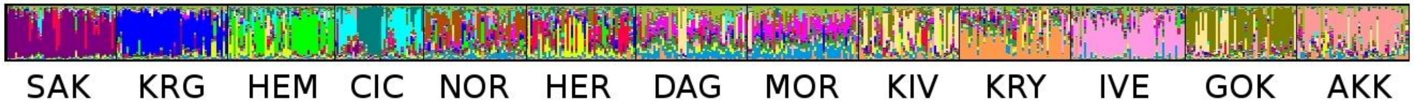
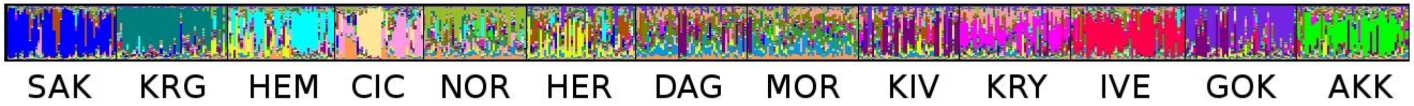
APPENDIX B

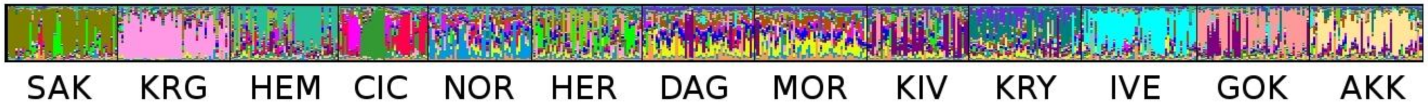
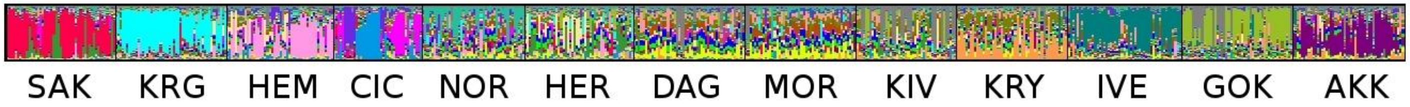
STRUCTURE OUTPUTS OF K=2 TO K=20

K	STRUCTURE OUTPUT REGARDING TO K
2	
3	

K	**STRUCTURE OUTPUT REGARDING TO K**
4	
5	
6	
7	
8	

K	STRUCTURE OUTPUT REGARDING TO K
9	
10	
11	
12	
13	

K	STRUCTURE OUTPUT REGARDING TO K
14	
15	
16	
17	
18	

K	STRUCTURE OUTPUT REGARDING TO K
19	
20	

APPENDIX C

SAMPLE SURVEY FOR EVALUATION EXTINCTION PROBABILITY AND MERITS OF BREED

1. Evaluation of Extinction Probability

1. State the other (local) names of the breed if there are any
2. Show the distribution of the breed on the map.

   (local / regional / widespead / transboundary)

3. What is the main purpose of breeding?

   A. Product: Mean / Milk / Wool / Dual purpose

   B. Economical: Commercial / Supplementary Income / Subsistence / Transhumance

4. What is the general farm size and farm structure of the breed?

   A. (Sheep only / Livestock only / Livestock + Agriculture / Other)

   B. < 20 / 20 – 50 / 50 – 100 / 100+

   C. Extensive / Semi-intensive / Intensive

5. Have there been a change in the product in the recent years? If yes

towards which direction? Why?

6. What do the farmers do to increase market value?
7. What is the general opinion of the farmers on the breed?

(continue breeding / hybridization / change the breed / quit breeding)

8. For how many generations do the farmers keep their flocks?
9. Are there any farmers who quitted breeding in the area? What is the percentage?
10. Why farmers quit sheep breeding?
11. What is the population size of the breed?

(< 1000 / 1000 – 10000 / 10000 – 100000 / 100000+)

12. How was the change in the population size in the last 5 years?

(Increase / Stable / Decrease / Fast decrease)

13. What is the farmer's tendency of hybridizing the breed?

(None / Low / Medium / High)

14. Between which breeds farmers do hybridization? Why? Which localities (mark on the map)?
15. What are the hybrids called?
16. Do you know any breeds that were relocated to the area of this breed?
17. Are there any conservation flocks in the hands of public? How many flocks? How many breeders? When did it start?
18. With how many sheep did the conservation flocks in the hands of public start? How many of them were rams?
19. How many sheep are there in the conservation flocks in the hands of public?

20. How many breeding females are there in the conservation flocks in the hand of public?
21. How many breeding males are there in the conservation flocks in the hand of public?
22. How many breeding males in the conservation flocks in the hand of public are from the first flock? How many of them are relatives of the first rams?
23. On what criteria are the rams selected in the conservation flocks in the hand of public?
24. Are the any conservation flocks held by agricultural institutes? How many? When did it start?
25. With how many sheep did the conservation flocks held by agricultural institutes? How many of them were rams?
26. How many sheep are there in the conservation flocks held by agricultural institutes?
27. How many breeding females are there in the conservation flocks held by agricultural institutes?
28. How many breeding males are there in the conservation flocks held by agricultural institutes?
29. How many breeding males in the conservation flocks held by agricultural institutes are from the first flock? How many of them are relatives of the first rams?
30. On what criteria are the rams selected in the conservation flocks held by agricultural institutes?
31. Are the any development flocks? How many? When did it start?
32. With how many sheep did the development flocks? How many of them were rams?
33. How many sheep are there in the development flocks?
34. How many breeding females are there in the development flocks?
35. How many breeding males are there in the development flocks?

36. How many breeding males in the development flocks are from the first flock? How many of them are relatives of the first rams?
37. On what criteria are the rams selected in the development flocks?
38. Is there a breeders association for the breed? If yes what is the contact information for it?
39. Is finding a shepherd a problem?
40. Are there any specific threats for this breed?

(fat tail / small size / low prolificacy / changing trends in animal husbandry etc)

2. Evaluation of Production, Adaptation and Socio-cultural Values

I) Production Values

1. Birth rate
2. Prolificacy
3. For how many years it can be used for breeding?
4. Milk yield (lactation period yield / milking yield)
5. Type of wool? Weight and yield
6. Weaning age of lambs (Male / Female)
7. What is the percentage of living lambs until weaning?
8. Weight at birth
9. Weight at weaning
10. Age of adolescence
11. Daily weight gain
12. Feeding conversion
13. Age at the first breeding (Male / Female)
14. Carcass weight and yield (Warm / Cold)
15. Weight of tail
16. Meat / Bone / Fat percentages
17. Weight of pelt

II) Adaptation Values

1. Walking ability
2. Grazing ability
3. Herd instinct
4. Ease of milking
5. Maternal instinct
6. Ease of administration
7. Are there any special abilities/traits for the breed? If yes, what?

(resistance to parasites/dieseases/allergens , shape of lips, wool structure etc)

8. What is the sheltering conditions of the breed? (fold / pastures / transhumance etc.)
9. How is the breed fed? Is extra money spend for feeding during the year?
10. How much money is spent on veterinary services during the year?
11. The properties of the region

(climate / pastures / sheltering / terrain / steepness / temperature in the winter / temperature in the summer / humidty etc.)

12. Are there any regions in the range of the breed where only sheep breeding can be done?
13. Are there any special produces for the breed?

III) Sociocultural Values

1. Are there any uses from the breed beside economical uses? (Touristic etc.)
2. How much place does the breed take place in the traditions of the region (Dowry, religious etc.)

APPENDIX D

STANDARDIZED EXTINCTION RISKS AND MERITS OF THE BREEDS

	AKK	**CIC**	**DAG**	**GOK**	**HEM**	**HER**	**IVE**	**KIV**	**KRG**	**KRY**	**MOR**	**NOR**	**SAK**
Risks													
Pop size	0	0.3	0.2	0.1	0.1	0.3	0	0.1	0.3	0	0	0.1	0.3
Avg. ram number	6.25	15	4	16	14	14	Missing	13	16	7	Missing	1	2
Cross-breeding	0.2	0	0.3	0.1	0.1	0.2	0	0.2	0.2	0.1	0.1	0.1	0.1
farmers opinions	0.1	0	0.1	0	0	0.2	0	0.1	0	0.1	0	0	0
trend in number of farmers	0.3	0	0.2	0	0	0.3	0.2	0.3	0.2	0.1	0.1	0.3	0.1
pop distribution	7.95	0.06	2.02	0.8	1.2	0.28	0.94	0.49	0.07	0.37	9.51	0.44	0.24
trend in pop. Size	0	0	0.2	0	0	0.2	0.2	0.1	0	0.1	0.1	0	0
pure stock (breeders)	0	-0.1	-0.1	-0.1	-0.1	-0.1	0	-0.1	-0.1	0	0	-0.1	-0.1
pure stock (state)	-0.1	0	0	0	-0.1	0	-0.1	0	0	-0.1	-0.1	0	0
shepherd availability	0.2	0.2	0.2	0	0.1	0.1	0.3	0.2	0.2	0	0.3	0.2	0.2
Organization of farmers	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1
Conservation scheme	0	0	0	0	0	0	0	0	0	0	0	0	0
political situation	0	0	0	0	0	0	0	0	0	0	0	0.1	0
special threats	0.1	0.1	0	0.1	0	0.1	0.1	0.1	0.1	0	0	0	0.1

	AKK	CIC	DAG	GOK	HEM	HER	IVE	KIV	KRG	KRY	MOR	NOR	SAK
Merits													
Production Values													
birth rate	87.9	92.5	88	90	88.02	90	86.97	87	95	85.4	90.45	88.02	75
litter size	1.3	1.1	1.04	1.23	1.1	1.1	1.14	1.2	1	1.1	1.02	1.1	2
average lambing period (yrs)	7	6.57	9	8	6.57	6.57	5	6	6.57	5	6.57	6.57	6
milk yield	51.3	47.7	57.06	120.39	110	40	172.41	110	88.44	34.9	59.16	137.2	163.35
wool yield	1.24	0.87	1.31	1.46	0.85	0.95	1.56	1.01	1.13	1.3	0.78	1.13	1.12
weaning period (days)	90	146	110	90	108.88	108.88	105	120	108.88	120	108.88	75	90
survival until weaning	95	93.58	97.06	98	93.58	93.58	93.58	95	95	90	93.58	92	85
weight at birth	4	3.8	3.5	3.75	3.3	3.4	3.52	3.25	3.2	3.5	3.52	4.2	3.5
weight at weaning	21	20.89	22.48	18.7	22.44	22.44	22.44	32.5	22.44	20	22.44	29.89	21.5
age of maturity (days)	225	269.56	225.5	365	269.56	269.56	410	309	269.56	180	225	269.56	217
daily weight gain	250	211	241.05	190.48	197.5	230.75	230.75	275	230.75	275	230.75	279	206
feed conversion	0.2	0.19	0.21	0.14	0.19	0.19	0.19	0.15	0.19	0.26	0.19	0.18	0.17
age of breeding (days)	515	540	467	337	540	540	450	528	450	547	532	548	240
carcass weight	9.79	9.27	9.87	7.15	8.75	8.75	10.51	8.6	8.75	8.85	10.47	11.33	8.33
tail weight	3.5	1.95	2.72	1.95	1.95	1.95	2.91	0.2	1.95	0.87	3.17	1.95	0.3
pelt weight	5	4.65	4.65	3.6	4.65	4.65	4.65	4.3	4.65	6.5	6.13	8.86	4.65
Production Environment													
walking ability	0.3	0.2	0.3	0.3	0.3	0.2	0.3	0.3	0.2	0.3	0.3	0.2	0
grazing ability	0.3	0.3	0.3	0.2	0.3	0.2	0.3	0.3	0.2	0.3	0.3	0.2	0.2
herd instinct	0.2	0.3	0.2	0.3	0.3	0.1	0.2	0.3	0	0.2	0.3	0.3	0
mothering instinct	0.2	0.3	0.2	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.3	0.2	0
ease of milking	0.1	0.2	0.1	0.1	0.2	0.3	0.2	0.2	0.1	0.1	0.2	0.2	0.2
ease of shepherding	0.3	0.3	0.2	0	0.3	0	0.3	0.2	0	0	0.3	0.2	0

	AKK	**CIC**	**DAG**	**GOK**	**HEM**	**HER**	**IVE**	**KIV**	**KRG**	**KRY**	**MOR**	**NOR**	**SAK**
special traits	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation	local adaptation
sheltering environment	Transhumance	Missing	Transhumance	Transhumance	Transhumance	Transhumance	Transhumance	Transhumance	Transhumance	Transhumance	Transhumance	Transhumance	closed shelter
feeding expenses	before/after birth	Missing	before/after birth	before/after birth	before/after birth	before/ after birth	before/after birth	before/after birth	before/after birth	before/after birth	before/after birth	before/after birth	nearly all year
vet. Expenses	Protective	Protective	Protective	Protective	Protective	Protective	Protective	Protective	Protective	Protective	Protective	Protective	Protective
Habitat Properties													
areas not suitable for animal breeding (Y/N)	0.1	0	0.1	0	0.2	0	0	0.1	0	0.2	0	0	0
special produce	0.1	0	0	0.1	0.1	0	0.1	0.1	0.1	0.1	0.1	0.1	0
Sociocultural Importance													
non-economic uses	0	0	0	0.1	0.1	0	0	0	0	0	0.1	0.1	0.1
traditional importance	0	0	0.1	0.1	0.1	0	0.1	0	0	0	0.1	0.1	0.1

APPENDIX E

RESULTS WITHOUT OARFCB226 LOCUS

Linkage Disequilibrium:

After the elimination of the OarFCB226 locus, 6 loci pairs out of 1989 loci pairs across 13 populations (KRG → BM8125 & FCB304, HEM → FCB128 & FCB304, HER → FCB304 & ILST1, DAG → INRA63 & FCB128, KIV → MAF33 & FCB128, KIV → VH72 & FCB48) were found to be in linkage disequilibrium. The tables for overall genotypic disequilibrium were given in the table E.1.

Allelic Richness:

After excluding OarFCB226 a total of 258 alleles were detected with an average of 8.999 per breed. The maximum number of alleles was harbored by HER (9.709) and the minimum number of alleles was found in SAK (7.655). The table E.2 was provided for a more complete viewing.

Hardy-Weinberg Equilibrium:

After the exclusion of OarFCB226, only 1 locus-by-breed deviation was subtracted making the total number of non H-W equilibrium sites 12 out of 234 (5.1%). The mean number of expected heterozygosities per breeds didn’t change, however the mean number of expected heterozygosities ranged between 0.73197 (KRG) and 0.79675 (KRY). The table E.3 was given for viewing.

Table E.1 Allelic Richness after the exclusion of OarFCB226 Locus

	SAK	KRG	HEM	CIC	NOR	HER	DAG	MOR	KIV	KRY	IVE	GOK	AKK	Overall
MAF65	5.796	4.885	6.606	5.938	8.826	8.286	7.410	9.574	9.478	8.381	10.461	9.806	6.978	7.879
INRA063	6.204	7.139	14.592	12.588	9.786	15.623	14.469	12.487	14.076	12.879	11.950	13.826	16.312	12.456
MAF33	7.054	10.706	11.433	9.173	8.451	9.111	11.000	7.016	7.964	10.266	9.021	8.488	6.973	8.974
OarFCB128	6.755	6.381	10.847	8.553	6.719	12.311	7.000	8.600	8.414	10.086	7.797	10.777	7.601	8.603
OarCP34	6.487	6.841	6.953	6.997	6.881	6.750	7.575	5.998	7.881	6.621	5.985	7.204	7.569	6.903
DYMS1	9.674	11.681	10.139	8.434	12.370	11.255	10.359	11.758	10.888	12.151	11.452	10.206	10.924	10.869
OarHH47	10.601	9.760	11.094	9.575	11.670	12.173	11.362	11.380	12.094	11.101	11.557	12.845	12.137	11.335
OarVH72	7.855	7.633	7.881	6.989	8.528	7.611	8.772	8.575	7.877	5.939	7.579	4.998	6.889	7.471
BM8125	6.775	6.541	7.670	5.940	5.534	7.506	5.796	4.839	5.845	5.940	7.529	6.153	5.617	6.283
MAF209	7.689	5.849	11.284	10.000	8.142	8.281	8.700	8.421	8.784	10.608	8.484	9.363	11.242	8.988
MCM140	7.168	8.901	9.166	8.426	9.501	11.989	11.996	11.262	10.794	10.757	9.727	9.377	10.593	9.974
OarJMP29	8.596	8.626	8.362	8.426	10.315	8.779	7.529	8.377	11.033	10.703	11.147	9.696	10.891	9.422
OarFCB48	6.727	8.987	7.455	6.696	10.945	7.441	8.902	8.767	9.536	8.295	8.963	8.484	7.905	8.393
ILSTS005	5.857	6.177	6.504	3.992	7.210	5.485	6.842	7.859	4.713	6.030	5.689	5.833	5.469	5.974
OarJMP58	7.888	9.946	7.910	8.307	8.769	13.104	10.192	10.612	10.730	11.064	11.581	13.041	11.857	10.385
OarFCB20	8.315	9.409	11.223	7.497	10.861	10.780	11.266	10.852	11.449	7.988	12.551	8.969	12.564	10.286
OarFCB304	12.355	11.620	9.838	7.923	13.119	11.637	11.674	13.972	10.377	12.413	13.854	8.193	10.211	11.322
ILSTS011	5.992	5.536	7.476	7.616	4.869	6.633	7.996	6.130	7.856	7.136	6.883	4.981	4.889	6.461
Overall	7.655	8.145	9.246	7.948	9.028	9.709	9.380	9.249	9.433	9.353	9.567	9.013	9.257	8.999

Table E.2 Expected heterozygosities, significance level of deviations from Hardy-Weinberg equilibrium and standard deviations after the exclusion of OarFCB226 Locus

	SAK	KRG	HEM	CIC	NOR	HER	DAG	MOR	KIV	KRY	IVE	GOK	AKK	Overal
MAF65	0.6873± (0.0005)	0.5596*± (0)	0.74971± (0.00038)	0.7156± (0.0002)	0.7542± (0.0004)	0.7239± (0.0003)	0.7406± (0.0004)	0.7688± (0.0006)	0.81973± (0.00044)	0.79087± (0.00053)	0.80375± (0.00041)	0.71616± (0.00024)	0.72929± (0.00026)	0.735
INRA063	0.6749± (0.0003)	0.5475± (0.0001)	0.81897*± (0)	0.8358± (0.0001)	0.7993± (0.0001)	0.8524± (0.0001)	0.8715± (0.0001)	0.8672± (0.0003)	0.91745± (0.00004)	0.88202± (0.00034)	0.84644± (0.00034)	0.88061± (0.00006)	0.88364± (0.00023)	0.821
MAF33	0.7515± (0.0006)	0.8262*± (0.0001)	0.87348± (0.00015)	0.8104± (0.0002)	0.7537± (0.0004)	0.8452± (0.0005)	0.8156± (0.0002)	0.7386± (0.0002)	0.81473*± (0)	0.85071*± (0)	0.75333± (0.00008)	0.80965*± (0)	0.73465± (0.00003)	0.798
OarFCB 128	0.5382± (0.0003)	0.642± (0.0004)	0.80459*± (0)	0.6279± (0.0003)	0.6221± (0.0003)	0.7709± (0.0001)	0.8515± (0.0002)	0.8410± (0.0001)	0.80175± (0.00003)	0.83575± (0.00003)	0.80586*± (0)	0.88071*± (0)	0.84211± (0.00032)	0.759
OarCP34	0.7599± (0.0001)	0.8226± (0.0001)	0.81309± (0.00007)	0.8111± (0.0004)	0.8316± (0.0005)	0.8266± (0.0004)	0.8487± (0.0003)	0.7877± (0.0004)	0.8422± (0.00022)	0.77939± (0.00034)	0.77256± (0.00011)	0.8178± (0.00038)	0.81732± (0.00016)	0.810
DYMS1	0.8399± (0.0003)	0.7978± (0.0003)	0.81557± (0.00008)	0.7746± (0.0003)	0.8170± (0.0002)	0.7853± (0.0003)	0.7069± (0.0003)	0.8435± (0.0003)	0.83421± (0.00024)	0.8744± (0.00035)	0.85972± (0.0004)	0.83487± (0.00025)	0.76206± (0.00027)	0.811
OarHH47	0.8103± (0.0003)	0.8518± (0.0002)	0.78824± (0.00017)	0.8456± (0.0003)	0.8715± (0.0004)	0.8577± (0.0002)	0.8736± (0.0003)	0.8148± (0.0002)	0.85253± (0.0003)	0.83039± (0.00034)	0.88497± (0.0002)	0.87292± (0.00036)	0.87043± (0.00032)	0.848
OarVH72	0.8338± (0.0004)	0.8115± (0.0004)	0.84281± (0.00021)	0.7742± (0.0001)	0.8242± (0.0003)	0.8065± (0.0003)	0.8204± (0.0005)	0.8440± (0.0003)	0.82222± (0.00015)	0.78747± (0.00044)	0.808± (0.00018)	0.56263± (0.00051)	0.45093*± (0)	0.768
BM8125	0.6333± (0.0003)	0.6122± (0.0001)	0.75416*± (0)	0.7807± (0.0001)	0.629± (0.0004)	0.6652± (0.0004)	0.5245± (0.0004)	0.5097± (0.0004)	0.48964± (0.00048)	0.72432± (0.00049)	0.6094± (0.00014)	0.53434± (0.0002)	0.55548± (0.0004)	0.617
MAF209	0.757± (0.0004)	0.6869± (0.0003)	0.8655± (0.00006)	0.8740± (0.0003)	0.7281± (0.0003)	0.7904± (0.0004)	0.7349± (0.0003)	0.7309± (0.0004)	0.77728± (0.00004)	0.81008± (0.00003)	0.81829± (0.00007)	0.83803± (0.00037)	0.77299*± (0)	0.783
MCM140	0.7473± (0.0002)	0.8157± (0.0001)	0.70807± (0.00043)	0.8019± (0.0005)	0.821± (0.0003)	0.8610± (0.0002)	0.846± (0.0002)	0.8285± (0.0004)	0.81398± (0.00027)	0.87665± (0.00006)	0.8509± (0.00028)	0.78571± (0.00025)	0.83695± (0.00018)	0.815
OarJMP29	0.7382± (0.0003)	0.8404± (0.0002)	0.81149± (0.00004)	0.8082± (0.0005)	0.8164± (0.0003)	0.7708± (0.0003)	0.7869± (0.0004)	0.8036± (0.0001)	0.82172± (0.00043)	0.85188± (0.00046)	0.77313± (0.00045)	0.84083± (0.00054)	0.82444± (0.00013)	0.807
OarFCB48	0.8037± (0.0004)	0.6889± (0.0004)	0.6947± (0.00025)	0.4389± (0.0004)	0.7685± (0.0002)	0.7088± (0.0003)	0.7753± (0.0005)	0.7962± (0.0004)	0.84345± (0.00052)	0.74879± (0.00032)	0.66798± (0.00019)	0.66186± (0.00015)	0.74303± (0.00034)	0.718
ILSTS005	0.6847± (0.0005)	0.6824± (0.0004)	0.54701± (0.0004)	0.6519± (0.0005)	0.6687± (0.0001)	0.5969± (0.0001)	0.6329± (0.0003)	0.6463± (0.0003)	0.61216± (0.00046)	0.52687± (0.00024)	0.62613± (0.00041)	0.69366± (0.00043)	0.66689± (0.00059)	0.633
OarJMP58	0.831± (0.0004)	0.7168± (0.0003)	0.80188± (0.00003)	0.7566± (0.0002)	0.7755± (0.0003)	0.8161± (0.0001)	0.8307± (0.0002)	0.7697± (0.0003)	0.79499± (0.00031)	0.7796± (0.0004)	0.78174± (0.00037)	0.83932± (0.0003)	0.79717± (0.00028)	0.792
OarFCB20	0.7671± (0.0004)	0.8535± (0.0004)	0.84605± (0.00032)	0.8259± (0.0004)	0.86718± (0.00036)	0.87334± (0.00018)	0.86768± (0.00041)	0.86444± (0.00047)	0.88414± (0.00015)	0.85475± (0.00033)	0.87575± (0.00013)	0.8604± (0.00043)	0.89071± (0.00037)	0.856
OarFCB304	0.8559± (0.0002)	0.8154± (0.0004)	0.70855± (0.00031)	0.6522± (0.0001)	0.87267± (0.00042)	0.80244± (0.0003)	0.8198± (0.00035)	0.7703± (0.00021)	0.70312± (0.00025)	0.77293± (0.00017)	0.7748± (0.00017)	0.50929± (0.00022)	0.72424± (0.0004)	0.752
ILSTS011	0.7332± (0.00049)	0.6040± (0.0003)	0.76798± (0.00006)	0.7602± (0.0002)	0.70807± (0.00042)	0.77534± (0.00039)	0.77131± (0.00014)	0.70081± (0.00041)	0.82272± (0.00036)	0.76465± (0.00043)	0.74802± (0.00009)	0.66711± (0.00049)	0.66863± (0.00058)	0.730
Overall	0.74707	0.73197	0.77844	0.75254	0.77379	0.78493	0.78438	0.77367	0.79267	0.79675	0.78115	0.75588	0.75394	

F-Statistics (F_{IS})

After removing the OarFCB226 locus from the analysis, KRG is added to the deviated set with a negative F_{IS} indicating an excess heterozygotes. Results were given in the table E.3.

Table E.3 F_{IS} values and their significances after the exclusion of OarFCB226 Locus

Breed	N	F_{IS}
SAK	49	0.01883
KRG	50	-0.03082
HEM	48	0.05416
CIC	40	0.06366
NOR	46	-0.00601
HER	49	0.06033
DAG	50	0.03326
MOR	50	0.05969
KIV	45	0.03732
KRY	50	0.05595
IVE	51	0.07652
GOK	50	0.05198
AKK	50	0.09142

F-Statistics (F_{ST})

After the exclusion of OarFCB226, global F_{ST} is calculated as 0.0435 with a p-value < 0.001. All populations differed from each other significantly ($p < 0.001$). The maximum pairwise F_{ST} is between SAK and GOK (0.08268) and the minimum is between MOR and DAG (0.01172). The results were given in the table E.4

Table E.4 Pairwise F_{ST} values between breeds after the exclusion of OarFCB226 Locus

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	-												
KRG	0.05741 ***	-											
HEM	0.0595 ***	0.04279 ***	-										
CIC	0.06275 ***	0.0552 ***	0.03547 ***	-									
NOR	0.04837 ***	0.03109 ***	0.02746 ***	0.02833 ***	-								
HER	0.04612 ***	0.0237 ***	0.023 ***	0.02993 ***	0.01857 ***	-							
DAG	0.05773 ***	0.05115 ***	0.03769 ***	0.04525 ***	0.02624 ***	0.02428 ***	-						
MOR	0.06025 ***	0.05186 ***	0.04307 ***	0.05767 ***	0.02471 ***	0.0308 ***	0.01207 ***	-					
KIV	0.06172 ***	0.051 ***	0.02985 ***	0.04947 ***	0.03124 ***	0.01952 ***	0.01436 ***	0.02893 ***	-				
KRY	0.06698 ***	0.05171 ***	0.03354 ***	0.053 ***	0.03841 ***	0.02694 ***	0.02506 ***	0.02481 ***	0.02013 ***	-			
IVE	0.07746 ***	0.06904 ***	0.04559 ***	0.0504 ***	0.03557 ***	0.04235 ***	0.02743 ***	0.02781 ***	0.04095 ***	0.0322 ***	-		
GOK	0.08497 ***	0.07712 ***	0.04611 ***	0.05421 ***	0.05704 ***	0.03715 ***	0.03094 ***	0.05465 ***	0.01959 ***	0.04522 ***	0.05803 ***	-	
AKK	0.08289 ***	0.07697 ***	0.05571 ***	0.0475 ***	0.0477 ***	0.04674 ***	0.03394 ***	0.03701 ***	0.04062 ***	0.04498 ***	0.04882 ***	0.05002 ***	-

Genetic Distances:

After the exclusion of OarFCB226, SAK remained as the most distant breed. Similarly the top two pairwise distances are between SAK-IVE and SAK-GOK again. The results are given in the table E.5. The upper triangle is the Reynold's weighted distance and the lower triangle is the Nei's D_A. The resulting trees were given in the figures E.1 and E.2.

Table E.5 Genetic distances (Nei's D_A and Reynold's Distance) between breeds after the exclusion of OarFCB226 Locus

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	-	0.0594	0.0621	0.0655	0.0499	0.0481	0.0601	0.0628	0.0643	0.0700	0.0815	0.0897	0.0874
KRG	0.1558	-	0.0442	0.0572	0.0316	0.0247	0.0528	0.0537	0.0526	0.0535	0.0721	0.0809	0.0807
HEM	0.1631	0.1250	-	0.0373	0.0285	0.0246	0.0393	0.0450	0.0312	0.0352	0.0479	0.0484	0.0585
CIC	0.1751	0.1665	0.1218	-	0.0293	0.0317	0.0472	0.0604	0.0517	0.0556	0.0530	0.0570	0.0500
NOR	0.1714	0.1227	0.1190	0.1072	-	0.0195	0.0270	0.0256	0.0321	0.0397	0.0370	0.0595	0.0496
HER	0.1446	0.1003	0.0882	0.1156	0.1051	-	0.0256	0.0324	0.0208	0.0285	0.0447	0.0392	0.0492
DAG	0.1670	0.1485	0.1257	0.1391	0.1048	0.1010	-	0.0129	0.0151	0.0262	0.0288	0.0324	0.0354
MOR	0.1757	0.1415	0.1357	0.1447	0.0770	0.1078	0.0795	-	0.0301	0.0260	0.0293	0.0573	0.0388
KIV	0.1730	0.1305	0.1227	0.1585	0.1177	0.0892	0.0763	0.1184	-	0.0211	0.0429	0.0208	0.0425
KRY	0.1824	0.1434	0.1295	0.1613	0.1330	0.0980	0.1024	0.1082	0.0915	-	0.0339	0.0474	0.0471
IVE	0.2174	0.1832	0.1500	0.1609	0.1255	0.1384	0.1211	0.1153	0.1391	0.1351	-	0.0611	0.0513
GOK	0.1979	0.1730	0.1480	0.1546	0.1580	0.1236	0.1104	0.1447	0.0971	0.1268	0.1508	-	0.0526
AKK	0.1919	0.1761	0.1541	0.1424	0.1205	0.1322	0.1139	0.1140	0.1084	0.1147	0.1422	0.1318	-

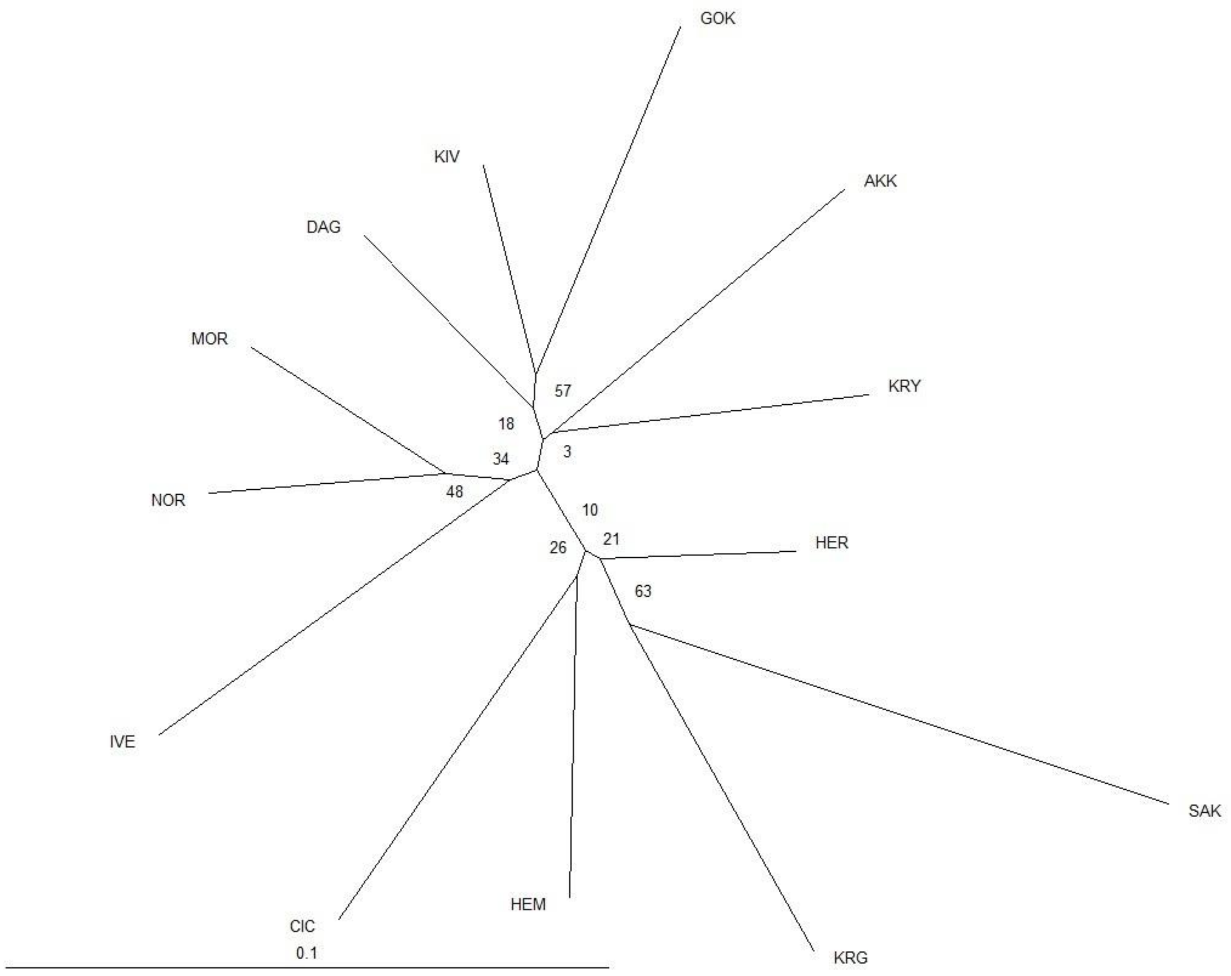


Figure E.1 Neighbor –joining tree constructed using Nei's DA after the exclusion of OarFCB226 Locus

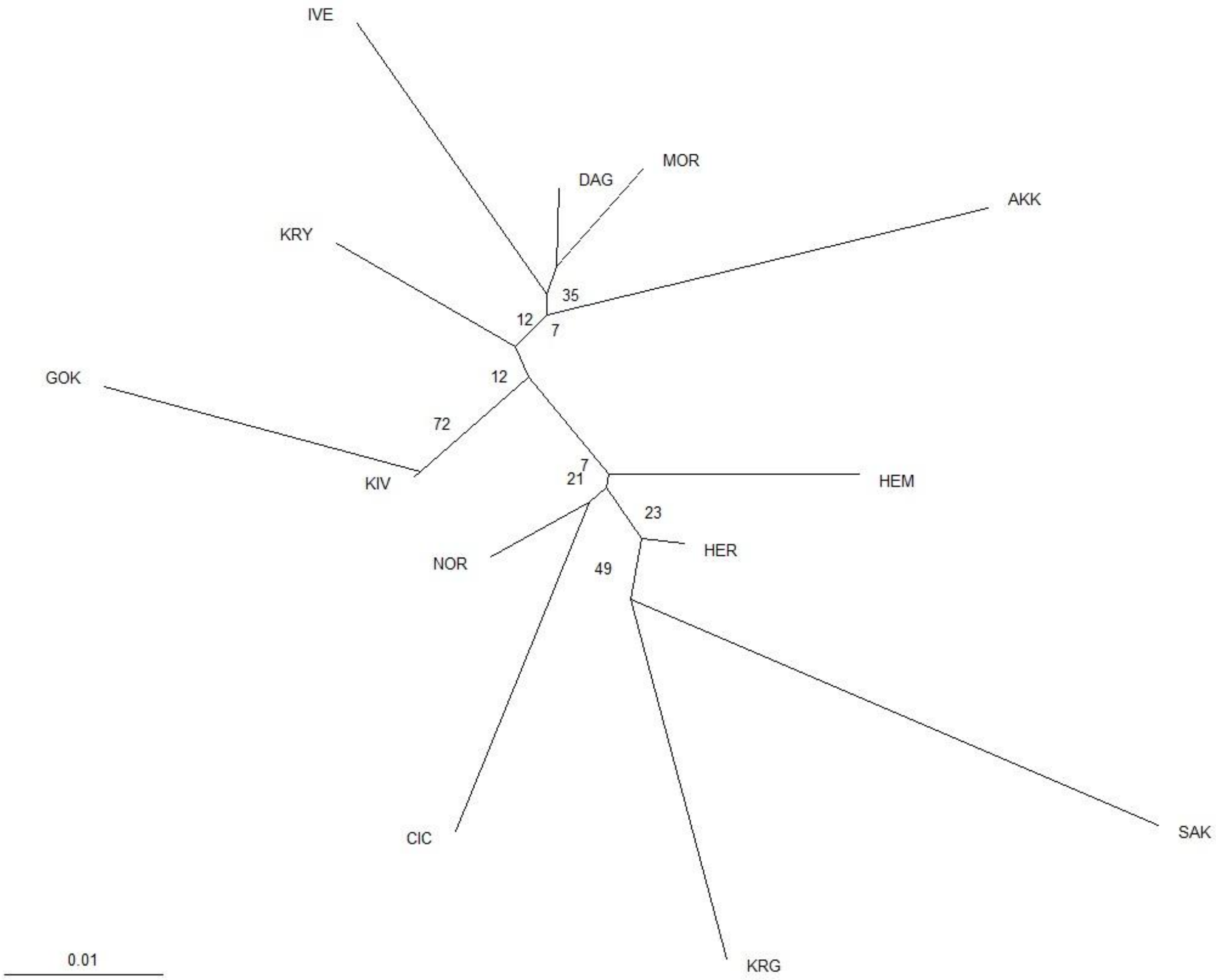


Figure E.2 Neighbor-joining tree constructed using Reynold's Distance after the exclusion of OarFCB226 Locus

Principal Coordinates Analysis:

After the exclusion of FCB226 the first axist which accounts for the 41.27% of the deviation again separates the local and non-local breeds which was given in the figure E.3.

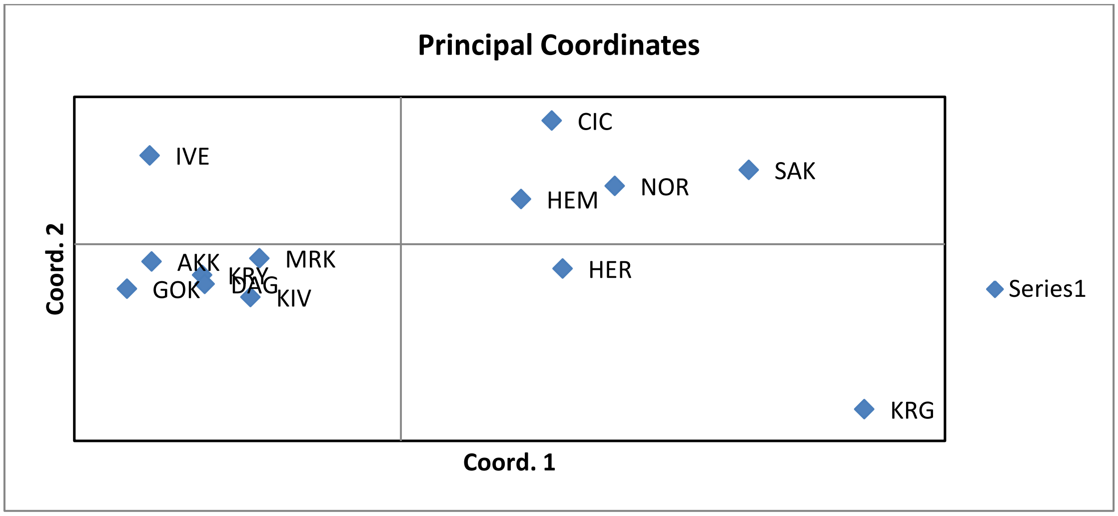


Figure E.3 Principal Coordinates Analysis for the centroids of the breeds after the exclusion of OarFCB226 Locus

Bayesian Clustering Analysis:

Analyses were done after excluding the OarFCB226 locus. The method suggested by Evanno proposed that the most probable K was again 2. Figure E.4 is available for viewing

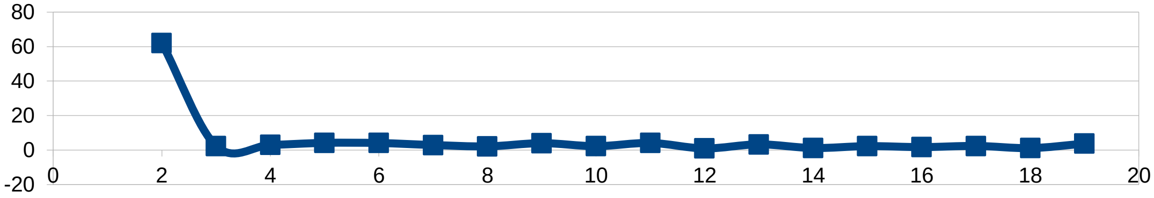


Figure E.4 Second order rate of likelihood function after the exclusion of OarFCB226 Locus

The method that was performed using CLUMPP again suggested that the most probable K was 2 with a similarity coefficient of 0.992323142. The figure E.5 was provided for viewving.

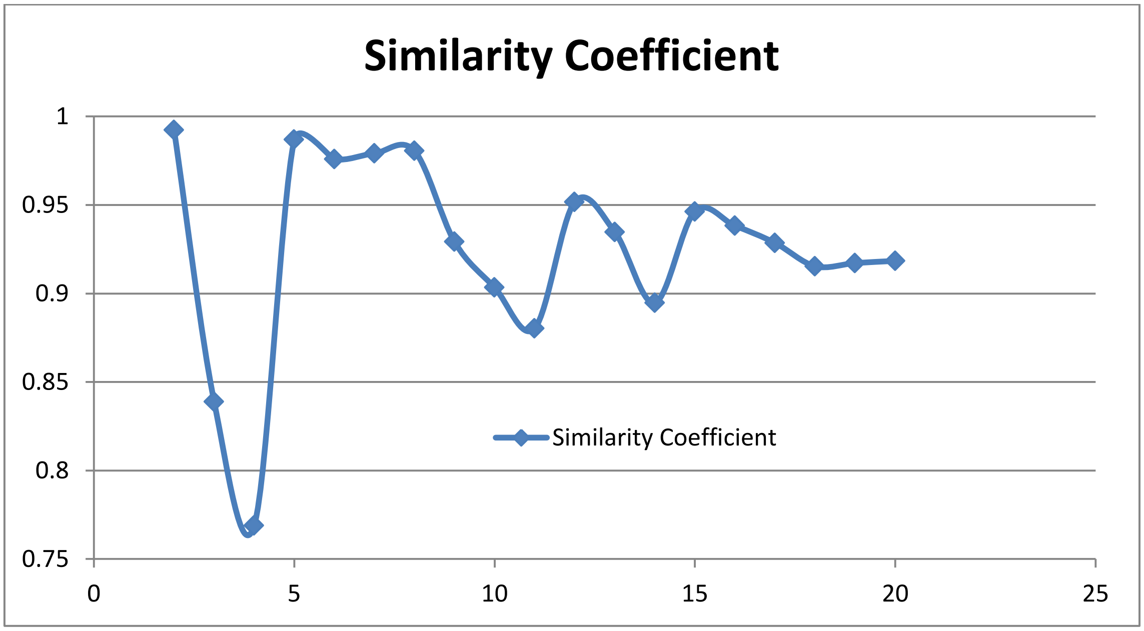


Figure E.5 Similarity coefficient against K graph after the exclusion of OarFCB226 Locus

The maximum value of log likelihood function is attained at K=11. Figure E.6 was provided for viewving.

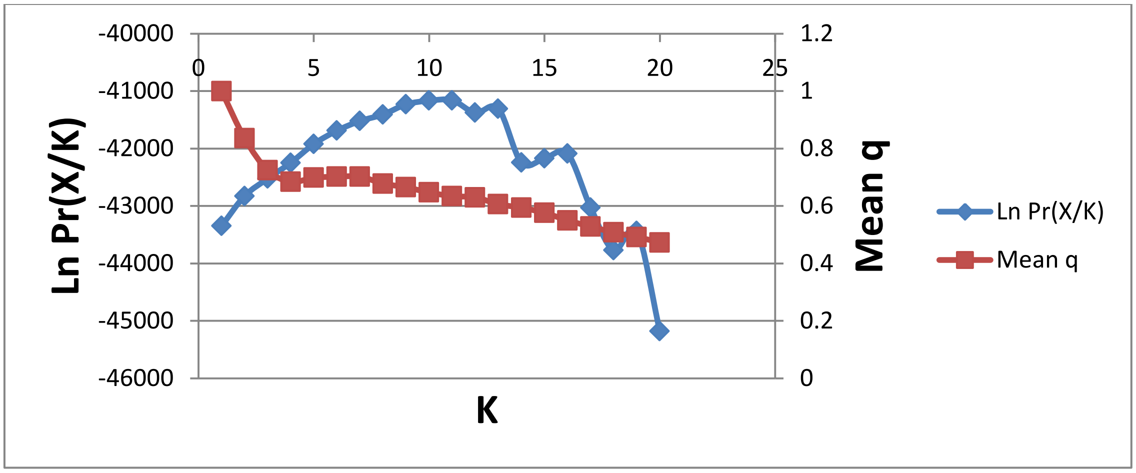


Figure E.6 Log likelihoods (LnPr(X/K and mean membership coefficients (q) against K values after the exclusion of OarFCB226 Locus

The visualization of the Structure – console outputs for K=2 and K=11 were given in the figure E.7.

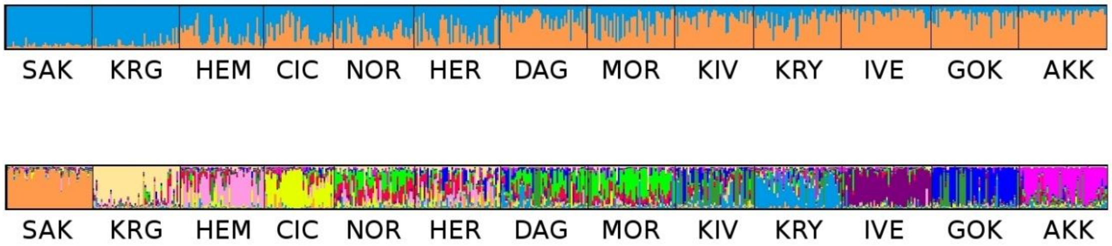


Figure E.7 The visualization of STRUCTURE outputs after the exclusion of OarFCB226 Locus for K=2 and K=11

Mantel Test:

After the exclusion of OarFCB226 the analysis was repeated with 10000 permutations. Again a correlation between FST and geographic distances were not detected (p = 0.2739).

Contribution to Genetic Diversity

After the exclusion of OarFCB226 the overall picture didn't change. IVE was the top contributor with 1.2057%. SAK was again the top contributor for between breeds and HER was the top contributor for within breeds. Table E.6 was provided for viewing

Table E.6 Contributions of breeds to genetic pool based on allelic richness after the exclusion of OarFCB226 Locus

Breed	Within Breed (%)	Between Breeds (%)	Total Contribution (%)
SAK	-1.2041	1.1134	-0.0907
KRG	-0.7647	0.5223	-0.2424
HEM	0.2219	0.3209	0.5428
CIC	-0.9412	0.4173	-0.5239
NOR	0.0259	-0.1055	-0.0796
HER	0.6361	-0.4485	0.1877
DAG	0.3416	-0.3107	0.0309
MOR	0.2241	-0.2183	0.0059
KIV	0.3889	-0.2722	0.1167
KRY	0.3177	-0.0316	0.2861
IVE	0.5094	0.6963	1.2057
GOK	0.0131	0.1499	0.1630
AKK	0.2312	-0.1277	0.1035

After the exclusion of OarFCB226 the first noticed difference was the increase in Total genetic diversity from 0.435 to 0.603. This result suggests that most alleles of OarFCB226 was shared among breeds with some special alleles concentrated in IVE (the contribution of IVE drops to 9.37%). Again SAK was the top contributor. The results were given in the table E.7.

Table E.7 Contributions of breeds to the genetic diversity based on Weitzman approach after the exclusion of OarFCB226 Locus

Breed	Total - Breed	Diversity Loss	Diversity Loss (%)
Total	0.603		
SAK	0.5281	0.0749	12.42
KRG	0.5362	0.0668	11.08
HEM	0.5565	0.0465	7.71
CIC	0.5482	0.0548	9.09
NOR	0.5685	0.0345	5.72
HER	0.573	0.03	4.98
DAG	0.5799	0.0231	3.83
MOR	0.5744	0.0286	4.74
KIV	0.5721	0.0309	5.12
KRY	0.5603	0.0427	7.08
IVE	0.5465	0.0565	9.37
GOK	0.5327	0.0703	11.66
AKK	0.5438	0.0592	9.82

Upon the removal of OarFCB226 the breed that causes the most genetic diversity loss was observed as KRY. IVE – KRY pair was accounted for the most diversity loss when breeds were removed from the set in pairs. When the breeds were removed from the set in trios either SAK or KIV was found to be in league with IVE – KRY pair.

When only one breed was present, the most genetic diversity was attained in the presence of KRY. When two breeds were present, KIV – IVE pair was the top genetic diversity provider. When three breeds are present, SAK – KRY – IVE breeds constitute the most genetic diversity, which again surpasses the diversity of the whole set. The results were given in the table E.8. In the table E.9 total diversity attained when different combinations of breeds were present were given.

Table E.8 The gain (+) or loss (-) of diversity when breeds were removed from the set, and the total genetic diversity when only a number of breeds were present after the exclusion of OarFCB226 Locus

GAIN (+) OR LOSS (-) OF DIVERSITY WHEN ONE BREED IS REMOVED								TOTAL GENETIC DIVERSITY WHEN ONLY n BREED(S) ARE PRESENT			TOTAL GENETIC DIVERSITY WHEN n BREED(S) ARE REMOVED		
	Total Genetic Diversity	Total Difference	Percent	Between Breed Diversity	Percent	Within Breed Diversity	Percent	One Breed	Two Breeds	Three Breeds	One Breed	Two Breeds	Three Breeds
Total	0.8015			0.0406		0.7609							
SAK	0.8003	-0.0012	-0.14972	0.0375	-7.63547	0.7628	0.249704			0.8047 (>100%)			0.7956 (99.2%)*
KRG	0.8033	0.0018	0.22458	0.0391	-3.69458	0.7641	0.42055						
HEM	0.8009	-0.0006	-0.07486	0.0406	0	0.7602	-0.092						
CIC	0.802	0.0005	0.06238	0.0398	-1.97044	0.7622	0.17085						
NOR	0.8021	0.0006	0.07486	0.0414	1.97044	0.7606	-0.03943						
HER	0.8017	0.0002	0.02495	0.042	3.44828	0.7597	-0.15771						
DAG	0.8016	1E-04	0.01248	0.0419	3.20197	0.7596	-0.17085						
MOR	0.8017	0.0002	0.02495	0.0411	1.23153	0.7605	-0.05257						
KIV	0.8006	-0.0009	-0.11229	0.0414	1.97044	0.7591	-0.23656		0.7994 (99.7%)				0.7956 (99.2%)*
KRY	0.7995	-0.002	-0.24953	0.0409	0.73892	0.7586	-0.30227	0.7878 (98.2%)		0.8047 (>100%)	0.7995 (99.7%)	0.7972 (99.4%)	0.7956 (99.2%)
IVE	0.7997	-0.0018	-0.22458	0.0397	-2.21675	0.7599	-0.13142		0.7994 (99.7%)	0.8047 (>100%)		0.7972 (99.4%)	0.7956 (99.2%)
GOK	0.8012	-0.0003	-0.03743	0.039	-3.94089	0.7622	0.17085						
AKK	0.8015	0	0	0.0393	-3.20197	0.7621	0.15771						

Table E.9 Total genetic diversity captured by the combinations of the breeds after the exclusion of OarFCB226 Locus

Diversity	SET OF BREEDS
0.7878	KRY
0.7994	KIV IVE
0.8047	SAK KRY IVE
0.8084	SAK KIV KRY IVE
0.8085	SAK HEM KIV KRY IVE
0.8075	SAK HEM KIV KRY IVE AKK
0.8070	SAK HEM HER KIV KRY IVE AKK
0.8063	SAK HEM HER DAG KIV KRY IVE AKK
0.8052	SAK HEM NOR HER DAG KIV KRY IVE AKK
0.8046	SAK HEM NOR HER DAG KIV KRY IVE GOK AKK
0.8038	SAK HEM NOR HER DAG MOR KIV KRY IVE GOK AKK
0.8032	SAK HEM CIC NOR HER DAG MOR KIV KRY IVE GOK AKK
0.8014	SAK KRG HEM CIC NOR HER DAG MOR KIV KRY IVE GOK AKK

After the exclusion of OarFCB226 the within-breed kinships ranged from 0.3462 (KRG) to 0.4107 (IVE). The most distant breeds were found to be, SAK – IVE and the least distant breeds were found to be KRG and NOR. The results are given in the table E.10.

Table E.10 Kinship coefficients after the exclusion of OarFCB226 Locus

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**	**AKK**
SAK	0.3710	0.4102	0.4436	0.4398	0.4182	0.4322	0.4373	0.4436	0.4458	0.4557	0.4647	0.4594	0.4638
KRG	0.4102	0.3462	0.4164	0.4196	0.3921	0.4015	0.4181	0.4238	0.4250	0.4291	0.4446	0.4398	0.4447
HEM	0.4436	0.4164	0.4017	0.4329	0.4192	0.4316	0.4361	0.4450	0.4362	0.4422	0.4538	0.4430	0.4559
CIC	0.4398	0.4196	0.4329	0.3891	0.4138	0.4292	0.4368	0.4515	0.4467	0.4526	0.4521	0.4423	0.4433
NOR	0.4182	0.3921	0.4192	0.4138	0.3736	0.4130	0.4131	0.4151	0.4229	0.4329	0.4309	0.4393	0.4359
HER	0.4322	0.4015	0.4316	0.4292	0.4130	0.4059	0.4294	0.4383	0.4310	0.4390	0.4529	0.4389	0.4522
DAG	0.4373	0.4181	0.4361	0.4368	0.4131	0.4294	0.3930	0.4142	0.4182	0.4300	0.4326	0.4252	0.4339
MOR	0.4436	0.4238	0.4450	0.4515	0.4151	0.4383	0.4142	0.4010	0.4347	0.4341	0.4361	0.4495	0.4399
KIV	0.4458	0.4250	0.4362	0.4467	0.4229	0.4310	0.4182	0.4347	0.4034	0.4332	0.4501	0.4213	0.4453
KRY	0.4557	0.4291	0.4422	0.4526	0.4329	0.4390	0.4300	0.4341	0.4332	0.4103	0.4454	0.4481	0.4514
IVE	0.4647	0.4446	0.4538	0.4521	0.4309	0.4529	0.4326	0.4361	0.4501	0.4454	0.4107	0.4595	0.4560
GOK	0.4594	0.4398	0.4430	0.4423	0.4393	0.4389	0.4252	0.4495	0.4213	0.4481	0.4595	0.3862	0.4441
AKK	0.4638	0.4447	0.4559	0.4433	0.4359	0.4522	0.4339	0.4399	0.4453	0.4514	0.4560	0.4441	0.4041

The contributions of breeds to the set was again calculated by a Matlab M-File. The negative contributors are eliminated iteratively. The top three contributors are SAK (24.7%), IVE (22.9%) and GOK (17.8%). The results are presented in the table E.11.

Table E.11 The contributions of breeds to the core set after the exclusion of OarFCB226 Locus

	SAK	**KRG**	**HEM**	**CIC**	**NOR**	**HER**	**DAG**	**MOR**	**KIV**	**KRY**	**IVE**	**GOK**
C	0.3137	0.1566	0.0988	0.1507	-0.3098	-0.1541	-0.4356	0.2215	0.0373	0.0909	0.3445	0.4546
C Corrected	0.2471	0.0045	0.0545	0.0422	-	-	-	-	-	0.0667	0.2294	0.4386

APPENDIX F

ANSWERS TO THE QUESTIONNAIRES USED IN THE STUDY

Akkaraman Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?
   karaman koyunu
2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?
   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)
   yurt içi, yaygın.
3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine
   et

B. Ek gelir / Ticari / Göçer / Geçimlik
   ticari

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)
   hayvan + bitki

B. < 20 / 20 – 50 / 50 – 100 / 100+
   100+

C. Ekstansif / Yarı İntansif / İntansif

ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

   değişmedi

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   birşey yapmıyor

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   melezleme

8. Bu ırk kaç nesildir yetiştiriliyor?

   Anadolu'ya Türklerle beraber geldiği düşünülüyor.

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   var. %50-60

10. Koyunculuk (ırk) neden terkediliyor?

    1. hayvancılık politikalari yetersiz/yanlış, koyunculuk zor, 3. koyunculuk karı düşük

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    100.000'den fazla

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    sabittir

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    orta

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    merinos, ,ivesi, pırlak, genelde kuyruğu inceltmek için

15. Melezlere ne isim verilmekte?

    karapınar merinosu, merinos kırması

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    yok

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?
18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

var. 48 sürü. 2005'te

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    6300 hayvan. 300 koç

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

    yaklaşık 15000

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

    12000

35. Geliştirme sürülerinde kaç baş damızlık koç var?

    600

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    aynı koçtan hiç yok. Aşım yapacak koçun 1/2'si dışarıdan

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

    morfoloji/büyüme gelişme

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    yok

39. Çoban bulma sorunu var mı?

    var. Orta seviye

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

yağlı kuyruk sebebiyle melezleme baskısı var. Tüketici alışkanlıkları sebebi ile

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

   87.9

2. Döl verimi ne kadardır?

   1.3

3. Ortalama kaç yıl döl vermektedir?

7 yıl

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   51.3 / 21.6

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık. 2.2 kg / 56.5%

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   3 ay

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   95%

8. Doğum ağırlığı nedir?

   4 kg

9. Sütten kesim ağırlığı nedir?

   20 – 22 kg

10. Kuzuların ergenliğe ulaşma yaşı nedir?

    210 - 240

11. Günlük canlı ağırlık artışı nedir?

    200 – 300 gram

12. Yem değerlendime değeri nedir?

    5kg’da 1 kg

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    485 - 545

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

    19.7 / 19.5

    49.7 / 47.4

15. Kuyruk ağırlığı nedir?

    3.5

16. Et/Kemik/Yağ oranı nedir?

    53/19.3/18.1

17. Post ağırlığı ne kadardır?

    5

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   Çok iyi

2. Irkın otlama yeteneği nasıldır?

   Çok iyi. dudak yapısı en kısa otu koparır.

3. Irkın sürü içgüdüsü nasıldır?

   iyi

4. Irkın sağılabilirliği nasıldır?

   orta

5. Irkın analık içgüdüsü nasıldır?

   Iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   Çok iyi

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   dudak yapısı en kısa otu koparır, ayak yapısı uzun yürüyüşe elverişli

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   300 – 500 başlık sürüler. Yazın merada, kışın ağılda

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   gebeliğin sonunda ve sonrasında ek yemleme

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    aşılar ve parazitle mücadele

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    bozkır, fakir meralar, ova, yükselti az, kışın soğuk, yazın sıcak, yağış az.

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    bozkırda başka hayvan yetiştirmek zor.

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    kuzu tandır, akkaraman kuzusundan yapılıyor.

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   yok

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   eskiden önemliydi. Çeyizlerde yatak yorgan koyundan oluyor. Halı dokuması yapılıyor

Ek bilgi:
Orta Anadolu meralarında akkaramanla rekabet edemez merinoslar.
Ama tüketici alışkanlıkları sebebi ile tercih edilmiyor (yağlı kuyruk).

Çine Çaparı Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi yöresel.

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   et/süt

B. Ek gelir / Ticari / Göçer / Geçimlik

   geçimlik

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   sadece hayvancılık (koyun+keçi)

B. < 20 / 20 – 50 / 50 – 100 / 100+

   50-100

C. Ekstansif / Yarı İntansif / İntansif

   extansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

   aynı

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   birşey yok

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam (2 yetiştirici var. 1'i yaşlı)

8. Bu ırk kaç nesildir yetiştiriliyor?

   atadan, dededen

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   iki kişi var zaten

10. Koyunculuk (ırk) neden terkediliyor?

    düşük verimli ırk. Melezleyip, başka ırklara geçilmiş

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    <1000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    artmıştır

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    hiç

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

sakız, kıvırcık, dağlıç, karya, pırlak

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

2 sürü var. 2005'te başlamış

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

54 hayvan ile. 20-25 koç

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

184 hayvan

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

150-160

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

30 civarı

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

hepsi ilk sürüden

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

ırk özellikleri ve büyüme gelişme

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların

akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

yok

39. Çoban bulma sorunu var mı?

var

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

sayısı çok az. Verimi düşük olduğu için melezleme baskısı var

2.Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

   90 - 95

2. Döl verimi ne kadardır?

   1.1

3. Ortalama kaç yıl döl vermektedir?

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

47.7 / -

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık. 1.2 / 72.8

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   146 gün

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

8. Doğum ağırlığı nedir?

   3.8

9. Sütten kesim ağırlığı nedir?

   20.89

10. Kuzuların ergenliğe ulaşma yaşı nedir?

11. Günlük canlı ağırlık artışı nedir?

    211

12. Yem değerlendime değeri nedir?

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    18 ay

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

    - / -

    19 / 48.8

15. Kuyruk ağırlığı nedir?

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   iyi

2. Irkın otlama yeteneği nasıldır?

   Çok iyi

3. Irkın sürü içgüdüsü nasıldır?

   Çok iyi

4. Irkın sağılabilirliği nasıldır?

   Sağıma elverişli

5. Irkın analık içgüdüsü nasıldır?

   Çok iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   Sakin mizaçlı, idaresi kolay

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   Kanaatkar, hastalıklara ve kötü koşullara dirençli, kuzuların yaşama gücü ve gelişme hızı yüksek

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

11. Yetiştirilen bölgenin özelliği nasıldır?
    a. (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

Ek Bilgi:

87 yılında ingiltereden gelen ırklar öldü. Mera kalitesi düşük, kene var, diken var. öldü gitti. Ankara'da olmamış, Konya'da hiç olmamış, Bandırmaya

gelmiş, safları ölmüş, melezleri kalmış. Yetiştirici deneye deneye bir genotip uydurmuş. O yöreye uygun birşey yapmış. Ne olduğu çok belli değil.

1996 prof. Orhan Karaca tanımlıyor. Koruma altına alınıyor. 2 sürü var. Ç,ine Koçarlı. Toplam 54 baş hayvan var. 1 sürü de üniversitede var. toplamda 200 hayvan var. Irk değil, local genotip diyenler var. 12-20 yıllık bir mazisi var. içerisinde dağlıç kanı olduğunu iddia edenler var. kıvırcık/sakız/dağlıç muhtelif oranlarda karışım.

Adaptasyon yeteneği yüksek. Başka ırkların yaşayamayacağı şartlara uyum sağlamış.

Kültürün içinde koyun hep var. Kültürel değer. Maddi ve manevi değerler iç içe girmiş durumda. Maddi değerler kaybolunca manevi değerler de kayboluyor.

Yün giyilirdi eskiden, artık giyilmiyor. Sayıların azalmasında etken. Halı eskiden çeyizin olmazsa olmazıymış. Yün kazak daha doğal. Koyunun safra kesesi hariç herşeyi değerlendiriliyor. Yapağı para etmiyor. Deri para etmiyor. Yaşam koşulları değişti, koyun yan ürünlerine rağbet azaldı.

Dağlıç Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

   Gıcık- küçük, hareketli, her yere girip çıkabiliyor

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi bölgesel

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   1- yapağı, 2- süt, 3-et

B. Ek gelir / Ticari / Göçer / Geçimlik

   ticari, zor koşullarda yaşayabildiği için. Battaniye, halı ip yapılıyormuş artık para etmiyor. Sütü anca aile için

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   hayvansal+ bitkisel

B. < 20 / 20 – 50 / 50 – 100 / 100+

   50-600 arası, ort. 200

C. Ekstansif / Yarı İntansif / İntansif

   ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi

sebeple?

artık kullanılmıyor, başka yöne çevirmediler

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   melezleme yapılmıyor, çevre köylerden koç katılıyor. Kuyruklu olduğu için pazarı düşük

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   melezleme, koyundan başka bir şey düşünülmüyor, satıp şehre gitmek yok

8. Bu ırk kaç nesildir yetiştiriliyor?

   200+ . Bu bölgede başka hayvan yetişmiyor. Melez kuzu bile yetişmiyor. %30 civarı

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   30%

10. Koyunculuk (ırk) neden terkediliyor?

    çocuklar bu işi yapmıyor

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    1000-10000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    Hızlı azalmıştır. Çiftçi göçü/melezleme

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

çok

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    Dağlıçxivesi, dağlıçxpırlak(dağlıçxpırlak)(çoğunlukla). Kuyruk ucu yukarı olsun, idrar tahriş etmesin diye yapılıyor.

15. Melezlere ne isim verilmekte?

    pırıt, pırlak, kesper, çandır

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    ivesi ama olmamış

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

    4 yetiştirici, 200 baş sürü

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    184 dişi, 16 erkek

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

    200

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

    184 dişi, 16 erkek

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    %60ı yenilendi, hepsi akraba

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

dış görünüşe göre, iri, ırkın özelliklerini gösteren

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    2 tür için

39. Çoban bulma sorunu var mı?

    çoban bulunamıyor

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

    yok

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

    79/97

2. Döl verimi ne kadardır?

1.04

3. Ortalama kaç yıl döl vermektedir?

   9 yıl

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   57.06 / 57.06

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık 2.27 / 55 - 60

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   105-120

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   97.06

8. Doğum ağırlığı nedir?

   3.45/3.5

9. Sütten kesim ağırlığı nedir?

   22.7/26.26

10. Ergenliğe ulaşma yaşı nedir?

    225.5

11. Günlük canlı ağırlık artışı nedir?

    241.05

12. Yem değerlendime değeri nedir?

    4.77

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

387 - 547

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

19.28 / 18.58

51.2 / 52

15. Kuyruk ağırlığı nedir?

2.72

16. Et/Kemik/Yağ oranı nedir?

53.28 / 21.26 / 22.65

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

Uzun mesafeleri iyi yürür

2. Irkın otlama yeteneği nasıldır?

çok iyi

3. Irkın sürü içgüdüsü nasıldır?

iyi

4. Irkın sağılabilirliği nasıldır?

iyi

5. Irkın analık içgüdüsü nasıldır?

iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   iyi

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   Elverişsiz bakım ve beslenme koşullarında yaşama gücü yüksektir, çevreye uyma kabiliyeti iyidir

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   göçer olarak yetiştirilir, ağıl+dağ kovukları+ rüzgar almayan yerlerde açık koru + kışın ağılda

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   yazın merada, kışın ağılda, arpa, saman, kuru yonca diğer ırklara göre az harcanır(pırlak, merinos, ivesiye oranla)

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    sadece aşılar yapılır. Pek görünen hastalık yok

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    oldukça dağlık, engebeli arazi, ova yok, kışın çok soğuk ve yağışlı.

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    afyon bölgesinde farklı bölgelerden getirilen ırklardan verim alınamadığını söylediler

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    yok. Halı ipi yapımında dağlıç tercih ediliyormuş

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   yok, farklı bir yapısı yok

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   en önemli özelliği kurban bayramlarında ve düğünlerde gelinlere koö gönderilirken dağlıç seçilir. Boynuz yapısı güzeldir, 900 tl ederi bu kurbanda çok kazanmışlar, denizli ve aydıda gösterişli boynuz

   Ek: 900 TL eder. Bu kurbanda iyi kazanılmış.Denizli ve Aydın'da gösterişli boynuz. Kuyruk ucu yukarı olsun diye melezleme yapılıyor. Amaç idrar tahriş etmesin diye kuyruğu küçültmek.

Gökçeada Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

   imroz

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi yöresel.

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   1.et, 2. süt

B. Ek gelir / Ticari / Göçer / Geçimlik

   ek gelir

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   sadece hayvancılık

B. < 20 / 20 – 50 / 50 – 100 / 100+

   100+

C. Ekstansif / Yarı İntansif / İntansif

   yarı intansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

aslında sütçü ırk ama süt para etmiyor. Artık etçi

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   tarım ilçe müdürlüğü birşeyler yaparsa olur

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam. Melezleme olursa melezlerin hayatta kalması zor

8. Bu ırk kaç nesildir yetiştiriliyor?

   Türklerden önce varmış

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   Yok. Artma var. Kazanç arttı

10. Koyunculuk (ırk) neden terkediliyor?

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    10.000 - 100.000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    Artmıştır

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    az

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

Verimi arttırmak için. Merinos, Sakız, Bafra Koçu

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    yok

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

    2 sürü. 2005 yılında

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    104-16/64-16

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

    200

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

    168 dişi

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

    32 erkek

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    0. 30% akrabalık

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

    dış görünüş.

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

    var. 1 tane. 1993

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    ~50 baş. 4-5 koç

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

    70 tane

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

    63

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

    7

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    0. 50% akrabalık

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

    dış görünüş.

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    yok

39. Çoban bulma sorunu var mı?

    yok. Yarı yabanıl, çobansız otluyor.

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

küçük cüsseli ve yavaş geliştiği için melezlemek isteniliyor.

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

    90

2. Döl verimi ne kadardır?

    1.23

3. Ortalama kaç yıl döl vermektedir?

8 yıl

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   120.39 / 80.77

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Halı tipi 2.24 / 60 - 70

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   3 ay

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   98%

8. Doğum ağırlığı nedir?

   3.75

9. Sütten kesim ağırlığı nedir?

   19.60 - 17.80

10. Kuzuların ergenliğe ulaşma yaşı nedir?

    12 ay

11. Günlük canlı ağırlık artışı nedir?

    190.48 gram

12. Yem değerlendime değeri nedir?

    7.25%

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    337 gün

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

15.44 / 15.06

46.32 / 45.18

15. Kuyruk ağırlığı nedir?

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

    3.06

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   çok iyi

2. Irkın otlama yeteneği nasıldır?

   iyidir

3. Irkın sürü içgüdüsü nasıldır?

   çok iyi

4. Irkın sağılabilirliği nasıldır?

   orta

5. Irkın analık içgüdüsü nasıldır?

   çok iyidir

6. Irkın sevk ve idare kolaylığı nasıldır?

kötü

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   çok soğuğa, çok sıcağa dirençli, kötü meraya dirençli, hastalıklara dirençli, parazitlere dirençli, bulaşıcılara dirençli

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   Çobansız sürü serbest olarak otlar

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   ocak şubat mart temmuz ağustos aylarında takviye yapar. Meranın kuruduğu dönemler

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    son yıllarda. Para bakanlıktan

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    kışın soğuk, yazın sıcak, engebeli, tepelik, dağlık, ova az, çalımsı bitkiler.

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    Yoktur

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    Eti iyidir

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   turistik değeri var.

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   yıllarca burada yaşamışlar, alışmışlar.

Hemşin Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

   Farkli adlari var, morfolojiye bagli. Tokat Krg = Hemsin

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   Yurt ici yoresel. Trabzon, Giresun karayaka; Artvin,Rize ; Erzurum Morkaraman; Ardahan Tuj-Morkaraman

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   Kombine; 1)Et, 2)Sut

B. Ek gelir / Ticari / Göçer / Geçimlik

   Ticari, Yapağısı para ediyor

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   %70 Sadece koyun

B. < 20 / 20 – 50 / 50 – 100 / 100+

   200+ (Bir donum yeri olmadan 1000 bas hayvani olanlar var)

C. Ekstansif / Yarı İntansif / İntansif

   Yari Intansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi

sebeple?

Et amacli, yayla turizminden sonra sut para ediyor. Erzurumda 1 TL, yaylada 4TL

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   Isleyen mekanizma yok

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam

8. Bu ırk kaç nesildir yetiştiriliyor?

   1800'lerden beri. Batum'da kis, Erzurumda yaz

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   Var. 1980-2007 arasinda birakilmis. Agustos 2007den sonra hayvan para etmeye basladi. 2007den sonra artis var. 2008 %100, 2009 %50, 2010 %25

10. Koyunculuk (ırk) neden terkediliyor?

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    54924 anac Artvin, 7300 Ardahan, 6400 Erzurum, ~10000 Rize

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    2007'ye kadar dusus, sonra hizli artis

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

Az

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    Etci irk suffolk, clevrolet, morkaraman karkasi buyutmek icin.

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    Karayaka, Morkaraman, Tuj olabilir

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

    2005'te bir yetistiriciyle baslandi. 200 bas, 1000'e cikartilacak.

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    184 disi, 16 erkek

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

    350

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

    315

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

    ~35

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    2-3 . %90 akraba. 6 yastan sonra saklanmiyorlar.

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

Dis gorunuse, anne verimine, damizlik deger hesaplamaya gore

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

    Var. 22 ciftcide, 2006dan itibaren

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    300 erkek, 6000 disi

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

    12600

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

~12000

35. Geliştirme sürülerinde kaç baş damızlık koç var?

    ~600

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    %10 ilk suruden

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

    morfoloji/buyume gelisme

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    irk icin yok il bazinda var

39. Çoban bulma sorunu var mı?

    %90 kendisi. Yaz doneminde zaman zaman sorun oluyor

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

Yok

2.Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

2. Döl verimi ne kadardır?

    1.1

3. Ortalama kaç yıl döl vermektedir?

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   110

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   1.7

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

8. Doğum ağırlığı nedir?

   3.4/3.1

9. Sütten kesim ağırlığı nedir?

10. Ergenliğe ulaşma yaşı nedir?

11. Günlük canlı ağırlık artışı nedir?

    215-180

12. Yem değerlendime değeri nedir?

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

18 ay

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

15. Kuyruk ağırlığı nedir?

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   Cok iyi

2. Irkın otlama yeteneği nasıldır?

   Cok iyi, kayalik araziyi keci gibi degerlendiriyor.

3. Irkın sürü içgüdüsü nasıldır?

   Cok iyi

4. Irkın sağılabilirliği nasıldır?

   Orta

5. Irkın analık içgüdüsü nasıldır?

   Cok iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

Cok iyi. 2000-3000 hayvani bir kisi idare edebilir.

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   Cicek hastaligina ve asiri yagislara direncli.

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   Acik agilda, kisin kapali alanda

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   genelde mera, dogum oncesi ve sonrasi ek yemleme

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    ic, dis parazit, koruma hekimligi

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    0-2850 rakim arasi. %30 mera, %50 orman, %20 tarim,engebeli, kayalik, derin vadiler. Sahil iliman, yuksekler soguk. Kisin cok soguk degil, yazin cok sicak degil.

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    Baska hayvan yetismiyor. Yapagi yagmurdan koruyor, yurume yetenegi iyi. (karayaka olur)

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    Henuz yok, ilerde peynir/yogurt

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   Yatik doner. 1) Morkaraman, 2) Hemsim, 3) Tuj

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   %70 koc gelinlik hemsin

Ek: 1986dan sonra Arap piyasası kaybedildi. 2007'de koyun hastalıkları çıktıktan sonra yeniden pazara girdi. Yapağısı ince ırklar bu alanlarda yaşayamıyor. Yavaş yavaş güneye doğru iniyor.

Herik Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

   Herek, Amasya Hereği

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   Yurt içi yöresel

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   Et

B. Ek gelir / Ticari / Göçer / Geçimlik

   Ticari

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   Sadece koyun

B. < 20 / 20 – 50 / 50 – 100 / 100+

   50-100

C. Ekstansif / Yarı İntansif / İntansif

   Ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

Değişmedi

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   Melezleme zaten yapılıyor

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   Hırçın olduğu için ırkı bırakıyor.Bafra koyunu kullanılıyor. (sakızxkarayaka)

8. Bu ırk kaç nesildir yetiştiriliyor?

   50 yaş altı bilmiyor. Yaşlı yetiştiriciler biliyor.

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   Kalmamış, çoğu bırakmış

10. Koyunculuk (ırk) neden terkediliyor?

    para etmiyor

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    <1000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    hızla azalmıştır

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    orta

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    Bafra koyunu -> İkizleme ve iri cusse amacıyla. Merinos -> melez azmanlığı. Karayaka

15. Melezlere ne isim verilmekte?

    özel bir adı yok

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    bilinmiyor

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

    Geçen dönem iki taneydi

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    200 hayvan

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

    200 hayvan

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

    168

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

    32

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

    Dış görünüşe bakarak

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    il bazında var

39. Çoban bulma sorunu var mı?

    var

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

melezlenme(düzensiz/plansız), et fiyatının yeterli olmaması, şehre göç edip fabrikalarda vs. Asgari ücretle çalışılıyor

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

   90%

2. Döl verimi ne kadardır?

   1.1

3. Ortalama kaç yıl döl vermektedir?

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   35-40

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   1.8-2

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

8. Doğum ağırlığı nedir?

   3.3 – 3.5

9. Sütten kesim ağırlığı nedir?

10. Ergenliğe ulaşma yaşı nedir?

11. Günlük canlı ağırlık artışı nedir?

12. Yem değerlendime değeri nedir?

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    18 ay

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

15. Kuyruk ağırlığı nedir?

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   iyi

2. Irkın otlama yeteneği nasıldır?

   iyi

3. Irkın sürü içgüdüsü nasıldır?

   orta

4. Irkın sağılabilirliği nasıldır?

   iyi

5. Irkın analık içgüdüsü nasıldır?

   iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   Orta/zor

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   çok özel bir direnci yok

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   kış-ağıl / yaz-mera

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   yazın mera. Kendisi arazi ekim yapıyorsa arpa/buğday, satın alıyorsa yem

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

   koruyucu tedavi harici veteriner gelmez

11. Yetiştirilen bölgenin özelliği nasıldır?

   (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
   karadeniz/iç anadolu arası iklim. Ankara'dan sıcak. değişken

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

   yoktur

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

   yoktur

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır?

(Turistik vb.)

yok

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   yok

Ek bilgi:

Karayakaxmor(ak)karaman karayakanın hırçınlığını alıyor, yetiştirici terk ediyor. Hotozu var. Karayakadan kısa bacak, hızlı hareket, ince uzun yapağıdan yağmurdan koruma sağlıyor. Geçit bölgesi olduğu için zaten kendisi melez.

İvesi Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir

   arap koyunu (akkaraman kürt koyunu)

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   sınır aşan

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   1. süt, 2. Et (genç kuzular)

B. Ek gelir / Ticari / Göçer / Geçimlik

   Ticari %70-80

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   Sadece koyun

B. < 20 / 20 – 50 / 50 – 100 / 100+

   50-100 dağlık yerde fazla, ovada daha büyük

C. Ekstansif / Yarı İntansif / İntansif

   Ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

Değişmedi(et yönü daha ağır basmaya başladı)

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   gerçek anlamda birlik yok

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam

8. Bu ırk kaç nesildir yetiştiriliyor?

   150 - 160 yıl

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   çok var. Kuraklık döneminde 30-40%

10. Koyunculuk (ırk) neden terkediliyor?

    başka geliri varsa bırakıyor. Genç nesil yapmak istemiyor. Sulu tarım

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    100.000+

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    hızla azalmış

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    hiç

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

akkaraman/karakaş/morkaraman

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

    halk elinde 2005'te

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    6300 baş. 300 koç

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

    12600 baş.

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

    12000

35. Geliştirme sürülerinde kaç baş damızlık koç var?

    600

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

60%-70% akrabalık var.

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

annenin süt verimi, canlı ağırlık

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

yok

39. Çoban bulma sorunu var mı?

çok var. En önemli sorunlardan biri

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

sulama alanı artınca zirai tarıma dönülüyor

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

86.97

2. Döl verimi ne kadardır?

1.14(1,08-1,10)

3. Ortalama kaç yıl döl vermektedir?

5 yaştan büyük tutmuyor, 7-8 yaşına kadar doğurur.

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   172.41 / 69.53

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık, kirli yapağı 2.55 / 61.2

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   105 gün

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

8. Doğum ağırlığı nedir?

9. Sütten kesim ağırlığı nedir?

10. Kuzuların ergenliğe ulaşma yaşı nedir?

    Dişi için 1-1.5 yıl

11. Günlük canlı ağırlık artışı nedir?

12. Yem değerlendime değeri nedir?

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    1-1.5 yıl

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

21.29 / 20.92

49.35 / 48.76

15. Kuyruk ağırlığı nedir?

2.91

16. Et/Kemik/Yağ oranı nedir?

54.08 / 22.11 / 22.67

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

az eğimli ufak taşlı arazide çok iyidir. Uzun yürüyebilirIrkın otlama yeteneği nasıldır?

2. Irkın sürü içgüdüsü nasıldır?

çok iyidir

3. Irkın sağılabilirliği nasıldır?

Iyidir

4. Irkın analık içgüdüsü nasıldır?

Çok iyidir

5. Irkın sevk ve idare kolaylığı nasıldır?

Büyük sürüler halinde idare edilebilirler

6. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

(parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

Sıcağa, soğuğa, yetersiz beslenme koşullarına ve hastalıklara (özellikle kan parazitlerine) dayanıklıdır. Ekstansif koşullara uygundur. Diğer sütçü ırklara gore farklı çevre koşullarına adaptasyon kabiliyeti yüksektir. Kuzular ve burmalar hızlı gelişir

7. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   Göçer system içerisinde yetiştirilir. yazın mera, kışın ahır.

8. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   harcanır. Kışın saman ve arpa

9. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

   hayvan başına 10 lira koruyucu hekimlik

10. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    taşlık arazi

11. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır

    yok

12. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    urfa örgü peyniri, tereyağ

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

yok

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   başlık parası amacı ile tutabilir. Gönül bağı var

Ek: Anaç hayvan mecburiyetten kesiliyor. Her aşiret kendine ait koyun üretmiş. Hatay ivesi Urfa ivesiden farklı, Suriye ivesisi daha etçi. Enstitüde ıslah sürüsü var. 60 baş koç, toplam 300 baş. Genetik kaynak olarak elde bulunması için saflar tutuluyor, melezin ne olacağı belli değil.

Karagül Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi yöresel

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   kombine. Asıl amacı post ama ulaşılamamış

B. Ek gelir / Ticari / Göçer / Geçimlik

   ticari

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   sadece hayvancılık

B. < 20 / 20 – 50 / 50 – 100 / 100+

   100+

C. Ekstansif / Yarı İntansif / İntansif

   ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

asıl kullanım amacına hiç ulaşılamamış.

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   birşey yapmıyor

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam

8. Bu ırk kaç nesildir yetiştiriliyor?

   gençler karagül'ü biliyor

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   Bilemiyoruz

10. Koyunculuk (ırk) neden terkediliyor?

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    <1000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    sabittir

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    orta

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

ivesi ve hemşin katılmış

15. Melezlere ne isim verilmekte?

gıcık

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

akkaraman, ivesi

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

2 yetiştirici 2005 yılında

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

200 hayvan. 32 koç

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

şu anda yok

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

270 civarı

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

30 civarı

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30% değişti. Akrabalık var

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

dış görünüşe göre

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

yok

39. Çoban bulma sorunu var mı?

şu anda yok. Genç nüfus çobanlık yapıyor

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

şu anda 3-5 yetiştirici var. Onlar bırakırsa ırk yok olur. Hayvancılık yapana kız verilmiyor.

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

95%

2. Döl verimi ne kadardır?

1

3. Ortalama kaç yıl döl vermektedir?

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   95%

8. Doğum ağırlığı nedir?

   3.3-3.1

9. Sütten kesim ağırlığı nedir?

10. Ergenliğe ulaşma yaşı nedir?

11. Günlük canlı ağırlık artışı nedir?

12. Yem değerlendime değeri nedir?

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    11-18 ay

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

15. Kuyruk ağırlığı nedir?

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   iyi

2. Irkın otlama yeteneği nasıldır?

   iyi

3. Irkın sürü içgüdüsü nasıldır?

   iyi değil

4. Irkın sağılabilirliği nasıldır?

   aile ihtiyacını karşılayacak kadar

5. Irkın analık içgüdüsü nasıldır?

   iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   orta / zor

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

yaşama gücü yüksek, adaptasyon yüksek

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   kışın ağıl, yazın mera

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   kışın satın alınır

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    herik'e göre daha az

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    yazın sıcak, kışın ankara'dan ılıman, engebeli arazi

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    yok

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    post ve et

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   yok

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

Yok

Ek: 1929'da geliyor. 1939'da bir daha geliyor. 1940'ta adanaya, 1945'de eskişehire, 1956'a lalahan'a geliyor. Sonrasında tokat - turhal - kazova'ya gidiyor. İyiler satıldığı için sürüler geriliyor

Karayaka Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   Yurt içi bölgesel

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   Et

B. Ek gelir / Ticari / Göçer / Geçimlik

   ticari

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   hayvansal + bitkisel

B. < 20 / 20 – 50 / 50 – 100 / 100+

   50-100

C. Ekstansif / Yarı İntansif / İntansif

   ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

eskiden de et+bir miktar süt

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   bir girişim yok

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   melezleme. Bafra koyunu uzun dönemde karayakanın yerini alabilir.

8. Bu ırk kaç nesildir yetiştiriliyor?

   300-400 yıl. Kafkas kökenli olduğu düşünülüyor. Erba/karayaka beldesi

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   10%

10. Koyunculuk (ırk) neden terkediliyor?

    çoban bulamıyor. Yaşlılık. Irkı değiştiren az.

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    100.000+

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    azalmıştır. Son 1-2 senede azalma durdu

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    az

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    bafra/merinos/ivesi. Verimi artırmak için

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    yok

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

    2006. 42 yetiştirici

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    6300 hayvan. 300 koç

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

    6819

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

    6493

35. Geliştirme sürülerinde kaç baş damızlık koç var?

326

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

her yıl değişiyor. Hepsi akrabadır

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

5. ay ağırlığı. Yağ ve kas derinliği

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

yok

39. Çoban bulma sorunu var mı?

kesinlikle var

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

ağır tehdit yok. Yöreye uygun verimli ırk girerse olabilir (örn. Bafra/merinos)

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

85.4

2. Döl verimi ne kadardır?

1.1

3. Ortalama kaç yıl döl vermektedir?

   4-5 döl

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   34.9 / 15.9

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık 2 / 65%

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   4 ay civarı

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   90%

8. Doğum ağırlığı nedir?

   3.5 kg

9. Sütten kesim ağırlığı nedir?

   20 kg

10. Kuzuların ergenliğe ulaşma yaşı nedir?

    5-6 ay

11. Günlük canlı ağırlık artışı nedir?

    250-300 gram

12. Yem değerlendime değeri nedir?

    1 kiloya 250 – 260 gram

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    547

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

    18.7 / 18.1

    47.3 / 45.8

15. Kuyruk ağırlığı nedir?

    870 gram

16. Et/Kemik/Yağ oranı nedir?

    63.3 / 18.8 / 15.6

17. Post ağırlığı ne kadardır?

    6.5 kg

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   Çok iyidir

2. Irkın otlama yeteneği nasıldır?

   Çok iyidir

3. Irkın sürü içgüdüsü nasıldır?

   iyidir

4. Irkın sağılabilirliği nasıldır?

   ortadır

5. Irkın analık içgüdüsü nasıldır?

   iyidir

6. Irkın sevk ve idare kolaylığı nasıldır?

   diğer ırklara göre zor

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   Nemli ve soğuk çevre şartlarına oldukça dayanıklıdırlar, ağzı kısa otları yemeye uygun

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   kışın ağıl yazın mera

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   ekonomik gücü yüksek yetiştiriciler hayvan başına 150-200 kilo

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    hayvan başına 10-15 lira

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    sahil - iç kesim farkı var. Engebe var. Ovada sebzeden daha çok para kazanılıyor.

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    hemşin ırkı olabilir.

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    yapağıdan döşek ve halı yapılır.

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   çalışılırsa olabilir.

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   Bölgeye adaptasyonu yüksek. Daha yüksek verimli ırk olursa yetiştirici ona yönelebilir

Ek bilgi:

Koyun kuyruğunun yağını sucuğa koyuyorlar. Koyun etinden sucuk olmuyor. Yemeğe kebaba katılıyor. 21 milyon koyun var diyorlar ama daha az olabilir. TÜİK çiftçi kayıtlarından alıyor ama kayıtlar güncel olmayabilir. Karayakanın et kalitesi iyidir.

Kıvırcık Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

   Tsigaja'nın akrabası olabilir

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   Yurt içi yöresel

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine
   1 et, 2 süt (Edirne peyniri)
B. Ek gelir / Ticari / Göçer / Geçimlik
   geçimlik

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   hayvansal+bitkisel

B. < 20 / 20 – 50 / 50 – 100 / 100+

   50 - 100

C. Ekstansif / Yarı İntansif / İntansif

   ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

   yok

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   yapmıyor, örgütlenme yok

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   yetiştiricide ırk bilinci yavaş yavaş oluşuyor. En iyi verim aldığı hayvanla çalışıyor, melezleme etkili olmayıp sağlık problemi çıkartabiliyor

8. Bu ırk kaç nesildir yetiştiriliyor?

   Genelde atadan dededen

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   Son 10 yılda çok var

10. Koyunculuk (ırk) neden terkediliyor?

    çoban bulunamıyor, yeni nesil devam etmek istemiyor, mera azalıyor

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    10000-100000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    azaldı, ama tagem sayesinde çok hızlı azalma engellendi

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    orta

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta?

Neden yapılmakta?

et için merinos, kuzu için sakız/sakız melezleri

15. Melezlere ne isim verilmekte?

Merinos melezi - depo

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

merinos yapağısı nemli kalıyor, hastalık oluyor

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

1 yetiştirici, 3e çıkacak

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

200 - 16

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

400 baş oldu

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

384

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

16

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

yüksek, serbest aşım uygulanıyor, 1 tanesi sürüden

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

ırkı temsil etme özelliklerine göre

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

20 yıl, 380 civarı

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    50 - 50

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

    380 baş

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

    180 baş

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

    10 baş

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    70%

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

    gelişimleri en iyi, hastalıklara karşı dayanıklı vs olan

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

    bu sene başlatılacak

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    yok. Koyun yetiştiricileri var

39. Çoban bulma sorunu var mı?

    var

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

karacabey merinosu kuzuları daha erken geliştiği için tehdit ediyor

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

    84.2

2. Döl verimi ne kadardır?

    1.2

3. Ortalama kaç yıl döl vermektedir?

6

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   82.5 / 46.4

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık 1.5 / 67.2

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   4 ay

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   95%

8. Doğum ağırlığı nedir?

   2.5-3 / 3-4

9. Sütten kesim ağırlığı nedir?

   30-35

10. Kuzuların ergenliğe ulaşma yaşı nedir?

    303

11. Günlük canlı ağırlık artışı nedir?

    250-300 gr

12. Yem değerlendime değeri nedir?

    6-7 kg / 1 kg

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    547

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

17.8 / 17.2

48.3 / 46.7

15. Kuyruk ağırlığı nedir?

    0.2

16. Et/Kemik/Yağ oranı nedir?

    59.5 / 25.4 / 14.1

17. Post ağırlığı ne kadardır?

    4.3

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   Çok iyidir

2. Irkın otlama yeteneği nasıldır?

   Çok iyidir

3. Irkın sürü içgüdüsü nasıldır?

   Çok iyidir

4. Irkın sağılabilirliği nasıldır?

   iyidir

5. Irkın analık içgüdüsü nasıldır?

   iyidir

6. Irkın sevk ve idare kolaylığı nasıldır?

iyidir

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   Kotü çevre şartlarına ve hastalıklara dayanıklıdır. Uzun mesafeleri yürüyebilme, fakir meralardan istifade etme yeteneğine sahiptir. Sağlam yapılı kanaatkardır.

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   Aile / köy / ticari sürüler halinde 20 – 400 baş. Iptidai koşullar

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   erken kuzu kesimi sebebi ile kesif yem tedavisi yapılır. İlk 4 ay

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    koruyucu hekimlik yapılıyor. Hastalıkta veteriner çağrılmıyor

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    karasal denebilir. Yazlar serin, kışlar soğuk, ortalama yağış, engebeli arazi, çok yüksek değil

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    ıstranca, sındırgı. Merinos yapağısı ıslanıyor

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    eti türkiyenin en lezzetli eti. Edirnenin peynirinde kıvırcık sütü var

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   yok

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   Yok

   Ek bilgiler:
   Koyun yetiştiriciliği hastalık, alışkanlık. Babadan, dededen kalma. Şehirleşme ve teknoloji arttıkça ırkın bozulma ihtimali artıyor. Irkı insan deği doğa korumuş.

Morkaraman Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

   kızılkoyun

2. Irkın yayılımı nasıldır?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi yaygın

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   1. et, 2. süt, 3. yapağı

B. Ek gelir / Ticari / Göçer / Geçimlik

   ticari

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

   A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   hayvansal + bitkisel

   B. < 20 / 20 – 50 / 50 – 100 / 100+

   50 - 100

   C. Ekstansif / Yarı İntansif / İntansif

   Ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

eskiden yapağı 1. 2. sıradaydı.

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   genel organizasyon yok

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam. Kontrolsüz melezleme ile kalite artışı. (akkaraman, merinos, tuj)

8. Bu ırk kaç nesildir yetiştiriliyor?

   Uzun zamandır

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   var. 10% civarı

10. Koyunculuk (ırk) neden terkediliyor?

    yer değiştirme, şehirleşme, hastalık

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    100.000+

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    azalmıştır. Son 1-2 senede sabit

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    az

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    akkaraman, merinos, tuj, ivesi

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    78'de merinos gelmiş

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

    2006'da başlamış

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    6592 baş. 284 koç

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

    12600

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

    12000

35. Geliştirme sürülerinde kaç baş damızlık koç var?

    600

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    1%-5% arası aynı koç. 50% akrabalık

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

    morfoloji, üreme, vatandaşın tercihi

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    yok

39. Çoban bulma sorunu var mı?

    var. Pahalı. Mevsimlik. Geçiş döneminde bulmak zor

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

    yok

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

    90.45

2. Döl verimi ne kadardır?

    1.02

3. Ortalama kaç yıl döl vermektedir?

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   59.16 / -

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Halı tipi 1.56 / -

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

8. Doğum ağırlığı nedir?

9. Sütten kesim ağırlığı nedir?

10. Kuzuların ergenliğe ulaşma yaşı nedir? (Erkek / Dişi)

    210 - 240

11. Günlük canlı ağırlık artışı nedir?

12. Yem değerlendime değeri nedir?

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    517 - 547

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

    21.33 / 20.67

    49.09 / 47.05

15. Kuyruk ağırlığı nedir?

    3.17

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

    4.45 – 7.8

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   Çok iyi

2. Irkın otlama yeteneği nasıldır?

   Çok iyi

3. Irkın sürü içgüdüsü nasıldır?

   Çok iyi

4. Irkın sağılabilirliği nasıldır?

   iyi

5. Irkın analık içgüdüsü nasıldır?

   Çok iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   Çok iyi

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   Dayanıklılık, yüksek yaşama gücü, kötü çevre koşullarına adaptasyon yeteneği, yüksek rakımlı ve fakir meraları en iyi şekilde değerlendirir

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   kışın ağıl, ilkbahardan zemheriye kadar dışarıda

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   doğum öncesi ve sonrası 2 ay

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    15-16 lira koruyucu hekimlik

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    hayvan açısından kısa ama elverişli şartlar. Kışın barındırma ıslah edilmeli

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    akkaraman, ivesi, hemşin, norduz yetişebilir.

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    morkaraman sütünden peynir yapılıyor.

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   cağ kebabı

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   gelinlik koç. Kültürel bağ var. Rengi, albenisi, heybetli

   Ek bilgi:

   Türkiye'nin her yerinde ufak tefek bulunabiliyor. Merkeze yakın köylerde gençler bırakma eğiliminde. Hemşinde gençler devam ediyor. Yetiştiricinin tercihi: boynuzlar hilal şeklinde güzel, bacakları orantılı olacak, arkalar kuvvetli, kuyruk düzgün, tarsaldan aşağı sarkmayacak, kızıl renk, büyüme gelişme iyi olacak, yapağısı parlak uzun, vücudu uzun, kafası büyük, aşım isteği yüksek, dişleri beyaz.

Norduz Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir

2. Irkın yayılımı nasıldır?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi yöresel, van ili gürpınar ilçesi

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   1-et, 2-süt, 3-yapağı

B. Ek gelir / Ticari / Göçer / Geçimlik

   geçimlilik, 9.aydaki erkek kuzu gelir kaynağı

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   hayvansal+bitkisel

B. < 20 / 20 – 50 / 50 – 100 / 100+

   20 - 50

C. Ekstansif / Yarı İntansif / İntansif

   ekstansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

   değişmedi, değeri arttı

6. Pazar değerinin artması için çiftçiler ne yapıyor

   klasik alışkanlıklara devam

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam

8. Bu ırk kaç nesildir yetiştiriliyor?

   250 - 300

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   terör sebebi ile bırakan olmuş, %55

10. Koyunculuk (ırk) neden terkediliyor?

    genel olarak göç

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    10000 - 100000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    artmıştır(az)

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    az

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    akkaraman(koç kullanma)

15. Melezlere ne isim verilmekte?

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

    200 baş, 11 yetiştirici(2005)

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    200 baş, 16 koç

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

    200 baş, 16 koç

    aynen devam

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

    184

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

    16

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    1-5 50% akrabalık vardır

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

    Morfoloji, büyümesine, sağlıklı olmasına

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

    şu anda proje başlama aşamasında ön seçim yapıldı.

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

aktif eylemi yok

39. Çoban bulma sorunu var mı?

son dönemlerde var. Maliyeti yüksek

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

yok

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

2. Döl verimi ne kadardır?

1.1

3. Ortalama kaç yıl döl vermektedir?

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   137.2

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   kaşmir

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   75

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   92

8. Doğum ağırlığı nedir?

   4.2

9. Sütten kesim ağırlığı nedir?

   29.89

10. Kuzuların ergenliğe ulaşma yaşı nedir? (Erkek / Dişi)

11. Günlük canlı ağırlık artışı nedir?

    279

12. Yem değerlendime değeri nedir?

    0.176

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    548

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

    10.96 / 10.60

    42.94 / 41.49

15. Kuyruk ağırlığı nedir?

16. Et/Kemik/Yağ oranı nedir?

    46.42 / 38.89 / 10.05

17. Post ağırlığı ne kadardır?

    8.86

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

   oldukça iyi

2. Irkın otlama yeteneği nasıldır?

   iyi

3. Irkın sürü içgüdüsü nasıldır?

   çok iyi

4. Irkın sağılabilirliği nasıldır?

   yerli ırklara göre süt verimi yüksek, sağıma uyumlı

5. Irkın analık içgüdüsü nasıldır?

oldukça iyi

6. Irkın sevk ve idare kolaylığı nasıldır?

   uysal, kolay

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   kene gibi parazitlere dayanıklı. Heliz otu yiyen norduz koyununa kene bulaşmıyor.

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   Yaz ve kış ek yemleme yapılmadan meradan beslenmektedir. Kışın kar yağışı yoğunken saman ve tahıl verilir. Koçlara aşım öncesi sınırlı arpa verilir

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   kışın ağıl, yazın mera, sıcak havalarda karlı meralara gider. İşletmeler ihtiyaçlarını kendileri sağlıyor, besiciler ot satın alıyor

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    yüksek değil, brusella varü hayvan sağlığı konusunda sorun var.

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    yazları sıcak/kurak, kışlar soğuk/kar yağışlı. Zengin çayır, mera ve yaylalar var. Engebeli ve eğimli. Nem yok

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    ekolojik yapı koyunculuğa uygun

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

otlu peynir. Eskiden yün çorap, eldiven yapılırmış

III) Sosyokültürel özellikler

1. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   Van ilinin otlu peyniri koyun ve keçi sütünün karışımı ile yapılır. Ticari bir önemi vardır

2. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   erkek kuzu bekleniyor. Koç katım zamanı tören yapılır. Erkekler güzel elbise giyer, halk oyunu oynanır, erkek çocukları koçların sırtına bindirilir. Koyunculuk yapılacaksa norduz. Norduz daha pahalıdır. Araplar norduz koyunu tercih ediyor. 1 kaburgası fazla. koçlarda heybetli boynuz yapısı var.

Ek bilgiler:

Akkaramandan daha cüsseli. Norduz bölgesinde flora zengin, iklim faktörü ve topoğrafya uygun. Akkaraman varyetesi. Farklılaşmış. Bölgede başka birşey yetiştirmek imkansız. Kendilerine göre seleksiyon var. koyun sürüsünün hareketini arttırmak için keçi kullanılıyor. Koyun keçiyi takip ediyor.

Sakız Koyunu Risk ve Değerleri İçin Örnek Anket

1. Bölüm: Risk Değerlendirilmesi

1. Irkın diğer (yerel) adları varsa nelerdir?

2. Irkın yayılımı nasıldır? Haritada gösterebilir misiniz?

   (yurt içi yöresel / yurt içi bölgesel yurt içi yaygın / sınır aşan)

   yurt içi yöresel (sınır aşan)

3. Irk ne amaçla kullanılıyor?

A. Verim Yönü: Et / Süt / Yapağı / Kombine

   1. et, 2. süt

B. Ek gelir / Ticari / Göçer / Geçimlik

   ek gelir

4. Irkın ağırlıklı işletme büyüklüğü ve yapısı nasıldır?

A. (Sadece koyun / Sadece hayvancılık / Hayvansal + Bitkisel / Diğer)

   diğer. Yan iş olarak farklı meslekleri var

B. < 20 / 20 – 50 / 50 – 100 / 100+

   <20

C. Ekstansif / Yarı İntansif / İntansif

   intansif

5. Kullanma amacı son yıllarda değişti mi? Evetse ne yönde? Hangi sebeple?

geçmişte süt de kullanılıyordu. Şu anda sadece damızlık

6. Pazar değerinin artması için çiftçiler ne yapıyor?

   ırk özelliklerini gösterenler seçiliyor

7. Çiftçinin bu ırk hakkındaki genel düşüncesi ne yöndedir?

   (devam / melezleme/ ırkı değiştirme / koyunculuğu bırakma)

   devam. Eskiden melezleme yapılmış. Artık yapılmıyor.

8. Bu ırk kaç nesildir yetiştiriliyor?

   atadan / dededen

9. Civardaki çiftçilerden bırakan var mı? Yüzde kaç?

   var. Sosyal durum ve meraların azalması. 20%

10. Koyunculuk (ırk) neden terkediliyor?

    genç nesil bırakıyor. Yaşlılar da bırakmak zorunda kalıyor.

11. Irkın toplam sayısı tahminen hangi aralıktadır?

    (< 1,000 / 1,000 – 10,000 / 10,000 – 100,000 / > 100,000)

    <1000

12. Son 5 yılda ırktaki sayısal değişim ne yöndedir?

    (Artmıştır / Sabittir / Azalmıştır / Hızla azalmıştır)

    sabit

13. Yetiştiricinin elindeki ırkı melezleme eğilimi ne kadardır?

    (Hiç / Az / Orta / Çok)

    az

14. Melezleme hangi ırklar arasında yapılmakta? Nerelerde yapılmakta? Neden yapılmakta?

    merinos. Kuzuların canlı ağırlığını arttırmak için.

15. Melezlere ne isim verilmekte?

    kaçari ve provat

16. Daha önceden bu ırkın yaşadığı yere getirilen bildiğiniz ırk var mı?

    melez genotipler. (merinos, kıvırcık, tahirova melezleri)

17. Halk elinde koruma sürüsü var mı? Kaç tane? Kaç yetiştirici ile? Ne zaman başladı?

    4 yetiştiricide 113 baş. 2005 yılında

18. Halk elinde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    113 baş, 8 koç

19. Halk elinde koruma sürülerinde şu anda kaç baş hayvan var?

    250 civarı

20. Halk elinde koruma sürülerinde kaç baş damızlık dişi var?

    230 civarı

21. Halk elinde koruma sürülerinde kaç baş damızlık koç var?

    20 koç

22. Halk elinde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    hemen hemen hepsi yeni. 20-30% akrabalık.

23. Halk elinde koruma sürülerinde koçlar neye göre seçiliyor?

    ikiz döllerde ırk özellikleri en iyi olanlar seçiliyor.

24. Enstitüde koruma sürüsü var mı? Kaç tane? Ne zaman başladı?

    1996da. 1 tane

25. Enstitüde koruma sürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

    70-80 civarı anaç koyun, 15-20 koç

26. Enstitüde koruma sürülerinde şu anda kaç baş hayvan var?

    90 civarı

27. Enstitüde koruma sürülerinde kaç baş damızlık dişi var?

    70-80

28. Enstitüde koruma sürülerinde kaç baş damızlık koç var?

    15-20

29. Enstitüde koruma sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

    hiçbiri. Zaman zaman sürü tamamen yenileniyor

30. Enstitüde koruma sürülerinde koçlar neye göre seçiliyor?

    ikiz döllerde ırk özellikleri en iyi olanlar seçiliyor.

31. Geliştirme sürüsü var mı? Kaç tane? Ne zaman başladı?

32. Geliştirme ürüleri kaç baş hayvan ile başladı? Bunların kaçı koç?

33. Geliştirme sürülerinde şu anda kaç baş hayvan var?

34. Geliştirme sürülerinde kaç baş damızlık dişi var?

35. Geliştirme sürülerinde kaç baş damızlık koç var?

36. Geliştirme sürülerindeki koçların kaç tanesi ilk sürüden? Kaçı ilk koçların akrabası?

37. Geliştirme sürülerinde koçlar neye göre seçiliyor?

38. Irk için yetiştiriciler birliği var mı? Birlik iletişim numaraları nedir?

    yok

39. Çoban bulma sorunu var mı?

    var. (fatmagül'ün güttüğü koyunlar sakız)

40. Bu ırka karşı özel bir tehdit var mı?

(yağlı kuyruk / küçük cüsse / düşük döl verimi / hayvancılıkta değişen eğilimler v.b.)

piyasanın yoğun talebi ile üretici en iyi örnekleri elden çıkartıyor. Dar alanda olduğu için salgına zaafı var. Turizmin artması risk

2. Bölüm: Verim, Uyum ve Sosyokültürel Özelliklerin Değerlendirilmesi

I) Verim Özellikleri

1. Doğum oranı nedir?

   70-80

2. Döl verimi ne kadardır?

   2

3. Ortalama kaç yıl döl vermektedir?

   6 yil

4. Süt verimi ortalama kaç kilogramdır? (laktasyon süt verimi vs. sağım dönemi süt verimi)

   163.35 / 58.73

5. Yapağı tipi nedir? Verimi ve randımanı ne kadardır?

   Kaba karışık 1.87 / 50 - 70

6. Kuzuların sütten kesilme yaşı nedir? (Erkek / Dişi)

   90 gün

7. Kuzuların sütten kesilme kadar yaşama gücü nedir?

   80-90

8. Doğum ağırlığı nedir?

   3.4 / 3.6

9. Sütten kesim ağırlığı nedir?

   20/23

10. Kuzuların ergenliğe ulaşma yaşı nedir?

    217

11. Günlük canlı ağırlık artışı nedir?

    186 / 226

12. Yem değerlendime değeri nedir?

    6 kiloya 1 kilo

13. İlk damızlık yaşı nedir? (Erkek / Dişi)

    7-8 ay

14. Karkas ağırlığı ve randımanı nedir? (Sıcak/Soğuk)

    17.32 /

    48.34 / 47.24

15. Kuyruk ağırlığı nedir?

    0.2 - 0.4 kg

16. Et/Kemik/Yağ oranı nedir?

17. Post ağırlığı ne kadardır?

II) Uyum Özellikleri

1. Irkın yürüme yeteneği nasıldır?

    Iyi değildir

2. Irkın otlama yeteneği nasıldır?

    iyidir

3. Irkın sürü içgüdüsü nasıldır?

    büyük sürü yok

4. Irkın sağılabilirliği nasıldır?

    iyidir

5. Irkın analık içgüdüsü nasıldır?

   düşük

6. Irkın sevk ve idare kolaylığı nasıldır?

   hassas bir hayvan. Özel ilgi ister

7. Irka ait özel yetenekler/değerler var mıdır? Varsa nelerdir?

   (parazitlere/hastalıklara/alerjenlere karşı direnç, dudak yapısı, yapağı yapısı vb.)

   en doğurgan ırk. Hızlı gelişir. Adaptasyon kabiliyeti düşük. Narin yapılı

8. Irkın barınma koşulları nedir? (ağıl/mera/göçer vs.)

   kapalı özel koşullarda, aile işletmelerinde

9. Irkın yemlenmesi nasıl olmaktadır? Yıl içerisinde yem için para harcanmakta mıdır?

   hemen hemen yıl boyu ek yem

10. Yıl içerisinde veteriner harcaması ne kadar olmaktadır?

    çok düşük. Koruyucu hekimlik.

11. Yetiştirilen bölgenin özelliği nasıldır?

    (iklim / mera / barınak / arazi / yükselti / kışın sıcaklık / yazın sıcaklık / nem v.b.)
    sıcak iklim, rüzgar, mera çok yok, deniz seviyesi, hafif engebeli

12. Irkın yayılım alanlarında bu ırkın yetiştiriciliğinden başka hiç bir hayvanın yetiştiriciliğinin yapıl(a)madığı alanlar var mıdır?

    yoktur

13. Irka özel ürünler var mıdır? (Norduz sütünün otlu peynir yapımında kullanılması gibi)

    yoktur

IV) Sosyokültürel özellikler

3. Irktan ekonomik özellikleri dışında yararlanma durumu var mıdır? (Turistik vb.)

   damızlık amacı. İzmir için simge. Halkın gönül bağı var.

4. Yöre gelenek, göreneklerinde ırk ne kadar yer tutmaktadır? (Çeyiz, adak vb.)

   ekiden süs hayvanı olarak kullanılırmış. Düğünlerde gelin koçu. Sakız güzellik yarışması var.

   Ciddi bir bağlılık var eskiden beri bakanlarda. Yeni nesil umursamıyor. Yetiştirici hala “eski sakızlar kalmadı” diye yakınıyor.

Ek bilgi:

Vücud yapısı zor şartlara uygun değil.

CURRICULUM VITAE

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EDUCATION

Degree	Institution	Year of Graduation
PhD	METU Department of Biology	2012
MS	METU Department of Biology	2003
BS	METU Department of Biology	1999
High School	TED College, Ankara	1993

WORK EXPERIENCE

Year	Place	Enrollment
2009 – Present	METU CC	System Administrator
2005 – 2008	METU CC	User Support Technician
1998 July	TUBITAK – MAM	Intern Biology Student

FOREIGN LANGUAGES

Advanced English, Basic German

PUBLICATIONS

1. Acan, S. C., Togan, I., 2011. Genetic Diversity of Turkish Sheep Breeds in the Focus of Conservation Research. Poster Presentation. International Symposium on Health Informatics and Bioinformatics (HIBIT'11). Izmir, Turkey.

2. Acan, S. C., Togan I., 2009. Network structure analysis of sixteen food webs. Poster Presentation. International Symposium on Health Informatics and Bioinformatics (HIBIT'09). Ankara, Turkey.