

Genetic characterization of livestock genetic resources in Türkiye: A Review

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Abstract

The genetic resources of native livestock have adapted to the diverse regions and climatic conditions. Today, many livestock breeds have been lost or are threatened with extinction in Türkiye. Recognizing the value of livestock genetic resources for the sustainability of the livestock system has led to several concrete efforts to characterize the existing genetic variation of native livestock breeds. To fill the gaps in the knowledge of breeds, molecular genetic characterization has been well described in livestock genetic resources. Assessment of the genetic variation of populations is critical for conservation programs and sustainable use of the specific breed. The SNP genotyping-associated gene studies to identify genomic regions under selection practices are important for future research. To understand the biodiversity of livestock genetic resources and to plan conservation and sustainable management, the previous studies and information on the molecular genetic characterizations of native livestock breeds were reviewed in this paper.

INTRODUCTION

Türkiye is one of the centers of domestication (Zeder, 2008) with its various regions, and livestock genetic resources are important for present and future benefits of scientific, cultural, historical, and genetic distinctiveness (Rege and Gibson, 2003; Ruane, 2000). Livestock genetic resources are the main source of income for landless and smallholder farmers. The need to conserve and characterize livestock genetic diversity has been highlighted by the Food and Agriculture Organization (FAO, 1992; 2015). The risk of extinction probability for decision making on conservation and

sustainable use of livestock genetic resources was reported by Yıldırım et al. (2023) in Türkiye. The list of the sequenced genomes of different animals was given in the first World Genetic Resources for Food and Agriculture (FAO, 2015), and this list has been extended throughout the years. The Guidelines for Molecular Characterization (FAO, 2015) gives important information for researchers interested in conducting a molecular characterization study. Phenotypic characterization indicates the genetic diversity of the breeds since unique characteristics can be assumed to have an essential genetic basis, and molecular characterization can confirm this diversity

concerning functional genes and extend it to regions of the genome that are not subject to the forces of selection (Gamaniel and Gwaza, 2017). The conventional phenotypic characterization of breeds is essentially a specification of their genotype. Molecular characterizations or genetic evaluation can therefore be defined as the complementary used to clarify the genetic basis of phenotypes. Microsatellites are ideal tools for gene mapping studies due to their extreme polymorphism (Kemp, 1992). The bottleneck results may serve as a guide for future management practices for livestock genetic resources (Demir, 2024a). mtDNA is a handy tool for investigating genetic diversity in domestic species. It contains highly conserved regions and is maternally inherited; therefore, recombination does not occur in mtDNA (Öner et al., 2013). Understanding breed relationships by calculating genetic distances and comparing specific genes of interest between breeds, or using anonymous polymorphisms to measure many more variables (Kemp, 1992). For example, Demir (2024b) suggested that the Kangal Akkaraman will play an important role in environmental challenges, parasite infections, fat deposition, and water-holding capacity according to SNP genotyping results association study with genomic regions. The techniques described above are potential means of supporting breed characterization.

Genetic characterization studies are important in developing sustainable usage and conservation strategies for native livestock genetic resources. Therefore, the scope of this study was intended to review genetic characterization studies among native cattle, goat, and sheep breed populations in Türkiye.

Materials and Methods

Data were collected from a wide range of peer-reviewed literature. All the data were taken from studies that particularly focused on the molecular characterizations of livestock breeds (cattle, sheep, goats, and Anatolian water buffalo) in Türkiye. Livestock genetic resources and molecular characterization are the main keywords used in the literature. The literature was systematically reviewed in 2024. The

following keyword combinations were used to identify relevant scientific papers published in peer-reviewed journals: livestock genetic resources, molecular characterization, diversity, and indigenous breeds. Only original peer-reviewed studies published in scientific journals were included. Additional searches were conducted using the reference lists of key articles to increase the chance of including as many relevant studies as possible. Selection criteria were based on original publication in peer-reviewed journals, topic, scope, and main outcomes observed.

Genetic characterization studies on livestock genetic resources

Each breed's genomic variation has a unique structure. The emergence of DNA analysis tools in recent decades has significantly increased our ability to characterize variation within and between breeds (Joshi et al., 2012). Molecular characterization studies allow conclusions to be drawn not only about the current genetic structure of a breed population but also about the history of the breed (Gamaniel and Gwaza, 2017). Methods for studying DNA polymorphism can be divided into two broad categories; 1) polymorphism which consists of the techniques that search for polymorphism in a known sequence or genes, and 2) anonymous polymorphism which includes methods that detect arbitrary polymorphisms, i.e. polymorphisms that occur on a purely random basis (Kemp, 1992).

Microsatellites are randomly distributed in both coding and noncoding regions of the genome. Microsatellites make them ideal tools in gene mapping studies. The opportunities to increase the rate of genetic improvement through the use of molecular information are clear. A joint phenotypic and molecular characterization will enable an overview of the adaptive characteristics of a breed as well as the biological basis for the phenotypes. SNP is one per 1,000 base pairs throughout the genome. For future studies to elucidate genetic variation, the use of SNP arrays and next-generation sequencing technologies is encouraged (Demir et al., 2023, 2024a).

Table 1. Some studies of genetic characterization of native livestock genetic resources in Türkiye. **a;** studies using microsatellites, **b;** genetic diversity studies using mitochondrial DNA, **c;** genetic diversity studies using SNP analyses.

Species	Breed/genotype	References/genotyping method
Cattle	Yerli Güney Sarısı	Demir et al. (2023)c, Öner et al. (2019)a, Doğan and Nizamlioğlu (2023)b,
	Zavot	Demir et al. (2023)c, Doğan and Nizamlioğlu (2023)b,
	Doğu Anadolu Kırmızısı	Demir et al. (2023)c, Öner et al. (2019)a, Doğan and Nizamlioğlu (2023)b,
	Güney Anadolu Kırmızısı	Demir et al. (2023)c, Öner et al. (2019)a, Doğan and Nizamlioğlu (2023)b,
	Yerli Kara	Demir et al. (2023)c, Öner et al. (2019)a, Doğan and Nizamlioğlu (2023)b,
	Bozırk	Demir et al. (2023)c, Öner et al. (2019)a, Doğan and Nizamlioğlu (2023)b,
Sheep	Çine Çaparı	Acar (2010)a,
	Herik	Acar (2010)a,
	Karagül	Acar (2010)a,
	Güney Karaman	Karslı (2024)c, Karslı et al. (2024)c,
	Sakız	Bayraktar (2024)c, Acar (2010)a,
	Dagliç	Acar (2010)a, Acar (2010)a,
	Norduz	Özmen et al. (2020)a, Bayraktar (2024)c, Acar (2010)a,
	Gökçeada	Avanus (2015)a, Acar (2010)a,
	Kıvırcık	Avanus (2015)a, Acar (2010)a,
	Karakaş	Özmen et al. (2020)a, Karslı (2024)c, Karslı et al. (2024)c, Bayraktar (2024)
	Morkaraman	Özmen et al. (2020)a, Karslı (2024)c, Karslı et al. (2024)c, Avanus (2015)a, Acar (2010)a,
	Hemşin	Avanus (2015)a, Acar (2010)a,
	Karayaka	Özmen et al. (2020)a, Avanus (2015)a, Acar (2010)a,
	Kangal Akkaraman	
Akkaraman	Özmen et al. (2020)a, Karslı (2024)c, Demir (2024a)c, Karslı et al. (2024)c, Acar (2010)a,	
İvesi	Özmen et al. (2020)a, Acar (2010)a,	
Goat	Norduz	Ağaoğlu and Ertuğrul (2012)a, Demir (2024b)a, Karslı et al. (2020)a,
	Ankara Tiftik	Bulut et al. (2016)a, Ağaoğlu and Ertuğrul (2012)a,
	Halep	Bulut et al. (2016)a
	Kilis	Bulut et al. (2016)a, Ağaoğlu and Ertuğrul (2012)a,
	Honamlı	Bulut et al. (2016)a, Ağaoğlu and Ertuğrul (2012)a, Demir (2024b)a, Karslı et al. (2020)a,
	Saanen	Bulut et al. (2016)a
	Kıl	Bulut et al. (2016)a, Ağaoğlu and Ertuğrul (2012)a, Demir (2024b)a, Karslı et al. (2020)a, Demiray et al. (2024)a, Cemal et al. (2024)a,

Diversity of livestock genetic resources in Türkiye

In Türkiye, several studies have been carried out on genetic diversity for livestock genetic resources. Assessing the genetic diversity of populations is essential for developing genetic conservation programs and sustainable breeding strategies. This is particularly important for Türkiye because number of the indigenous sheep breeds is decreasing due to nonsystematic crossbreeding (Özmen et al., 2020). The breed survey gives the essential information needed to determine a breed's risk status of a breed. Yıldırım et al. (2023)

reported a preliminary survey at the national level to estimate the size, structure, and geographical distribution of the breed population and to monitor how these change over time.

More than 30 sheep breeds were defined as breed or "type" of breed in Türkiye (Yıldırım et al., 2023). Among them, Akkaraman has the largest population among the sheep breeds. Karakas, Kangal, and Savak that the types of Akkaraman breed were assessed for genetic structure and relationship with Morkaraman, Awassi, and Norduz breed using 29 microsatellite loci by Özmen et al., (2020). Kiraz et al. (2021) analyzed the mtDNA polymorphism,

mtDNA haplotypes, haplogroups (lineages), and phylogenetic relationships among haplotypes in Akkaraman and İvesi sheep from the Şanlıurfa region based on mitochondrial Cyt b gene sequence data. Akkaraman types (Karakaş, Kangal, and Şavak) were distinguished from each other and Savak-Akkaraman and Awassi sheep populations distinctly separated from all other sheep populations (Özmen et al., 2020). The studies concentrated on the main sheep breeds and their types revealed notable results. The Karayaka, Kıvırcık, and İvesi sheep breeds have recorded the comprehensive genetic diversity of Türkiye's native sheep breeds (Togan et al., 2011). Karslı (2024) according to SNP analyses reported that HO values were higher than He values, and negative FIS values varied between -0.034 to -0.060 across Akkaraman, Morkaraman, Karakaş, and Güney Karakaş breed populations (n = 80). Karslı et al. (2024) reported a SNP genotype ROH analysis results indicated that Güney Karaman affected different selection practices or experienced different adaptation processes occurring in raised climatic conditions compared to the Akkaraman breed. Genetic distance results, using the WIDDE database (SNP genotype), showed the most significant variation between the Cyprus fat tailed populations and Sakız sheep, and genetic similarity between Chios and Sakız breeds (Bayraktar, 2024). Genetic variability of Kıvırcık, İmroz, Karayaka, Hemşin, Mor Karaman, and Karakul determined using the RFLP method that all breeds except Kıvırcık and Hemşin were found in Hardy-Weinberg equilibrium (Avanus, 2015). Genetic diversity in thirteen Turkish sheep breeds (Sakız, Karagül, Hemşin, Çine Çaparı, Norduz, Herik, Akkaraman, Dağlıç, Gökçeada, İvesi, Karayaka, Kıvırcık, and Morkaraman) were studied using 20 microsatellite loci by Acar (2010). It was revealed that Dağlıç, Karayaka, and Morkaraman breeds are highly admixed but Kıvırcık, Akkaraman and İvesi are relatively distinct (Acar, 2010).

Bulut et al. (2016) reported higher genetic diversity among Turkish goat populations with 11 microsatellites. Demir (2024b) reported a lack of recent genetic bottlenecks and maintained effective population sizes over the generations for Kıl, Honamlı and Norduz goats. Demir (2024b) suggested no migration from the Kıl and Honamlı populations to the Norduz breed, probably due to its geographic isolation. Similar

distinctive results were reported by Karslı et al. (2024) using 20 microsatellites for Norduz goats between Honamlı and Kıl goat breeds. A study from 10 regions using 20 microsatellite markers reported sufficient levels of polymorphism for the genetic variability of the Hair goat population (Demiray et al., 2024). The inbreeding coefficient was estimated for Norduz, Angora, Kıl, and Honamlı goat breeds by microsatellite markers (Gül et al., 2020; Karslı et al., 2020). Mitochondrial DNA is used as a molecular marker in studies such as identifying populations, and determining the origins of populations (Kiraz et al., 2013). Kul (2010) investigated the mtDNA diversity and genetic relationships among Ankara, Honamlı, Kilis, Kıl, and Norduz goats, which are the most commonly bred native goat breeds in Türkiye. In these breeds, three different haplogroups A, D, and G were identified.

Several studies revealed an extremely high level of genetic diversity among and within cattle breeds. Özsensoy et al. (2010) found the highest Fis value (as 0.066) for Yerli Güney Sarısı breed. Öner et al. (2019) estimated Fis value as 0.059 and 0.064 for Güney Anadolu Kırmızısı and Yerli Kara breeds, respectively. A higher genetic variation was observed in native Turkish cattle with an average of 0.380 observed heterozygosity (Demir et al., 2023). The highest genetic distance (0.064) was detected between Yerli Güney Sarısı and Brown Swiss (Demir et al., 2023). Öner et al. (2019) reported Yerli Güney Sarısı, Güney Anadolu Kırmızısı, and Yerli Kara breeds were closely related using 22 microsatellite markers.

CONCLUSION

In this review, molecular characterization of genetic diversity in livestock genetic resources was summarized. A combination of phenotypic and molecular characterization will provide an overview of the adaptive features of a breed, as well as the biological basis for the recorded traits. Molecular characterization can be useful in assessing the potential of a breed for genetic improvement. Breed characterization studies must take into account the role that molecular biology may play now or in the future. The use of SNP arrays and next generation sequencing technologies is encouraged for future studies to elucidate genetic variation. Finding and applying

markers useful for breed characterization is now a straightforward task.

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