



Hormones and Signaling

Elixir Hor. & Sig. 117 (2018) 50032-50037

Elixir
ISSN: 2229-712X

Genetic Diversity in Farm Animals

Marwan Fadhil, Uğur Zülkadir and İbrahim Aytekin

Selçuk University, Faculty of Agriculture, Department of Animal Science, Konya, Turkey.

ARTICLE INFO

Article history:

Received: 22 January 2018;

Received in revised form:
22 March 2018;

Accepted: 2 April 2018;

Keywords

Molecular Markers,
Genetic Diversity,
Conservation Method,
Gene Resources,
Ex-Situ Conservation,
In-Situ Conservation.

ABSTRACT

Recent developments in the molecular biology have provided some specific molecular markers which are generally used to define a specific region of genome. In genetic analyses, three types of markers are used as morphological, protein and DNA markers. After the discovery of polymerase chain reaction (PCR), PCR-based markers have been begun to be more preferred. Studies of genetic characterization have inconsiderable importance in the studies such as determining the level of inter and intra- population genetic diversity, developing protection programs, domestication, and determination of migration routes. In genetic characterization studies, the different biochemical marker systems, alloenzymes, mitochondrial DNA, and Y chromosome specific molecules are used. DNA markers, particularly polymorphic microsatellite markers, constitute the most preferable system in PCR applications. New molecular biology techniques enable analysis of single nucleotide polymorphism to be able to made faster and economically and be used together with microsatellites.

© 2018 Elixir All rights reserved.

INTRODUCTION

Every country in parallel with economic development and population increase, in order to meet the increasing demands; the efforts toward improving the yields of animals are intensified. These efforts, due to the fact that they are mostly appropriate for the conditions specific to country, region, and even locality, are toward the improvement of domestic breeds that are being bred and increasing their yields via crossbreeding them with culture breeds. Moreover in many places, domestic breeds are replaced with high yield culture breeds which cause genetic diversity to decrease. Local genetic resources are the though and abstemious animals, which well adapted to the environmental conditions, where they have been bred for many centuries. They have unique characteristics; even their yields are low; also survive and can reproduce in inadequate environmental conditions. The loss of these breeds also means that the unique qualities they have expire. It is impossible to predict for which of these characteristics in the future will create a need. On the other hand, superior qualities of domestic breeds, not known today, can be used if necessary in case that these resources can survive [1].

Local genetic resources are our original genetic wealth, which survive their life under the positive and negative effects of the environment for many centuries. They adapt the best to the environment. Nowadays, with the improvement studies carried on some certain yield character, while the number of high yielding animals increase, the existence and variation of low yielding genotypes decrease. The ability to meet human needs in a sustainable way depends on genetic diversity among breeds and in breeds and is the most fundamental source for breeders. In recent years, productivity has increased in the sense of economics of production. However, the problems which are shaped by the influence of environment and human factors for centuries will be encountered in the future in terms

of overcoming. Gene pools which are the invaluable and irreplaceable for breeders have contained many important genes. Thus, the increase in intensive production further increases the need to protect indigenous gene resources. There are 7616 domestic animal breeds, recorded in database of Domestic Animal Diversity Information System (DADIS). 6536 of these consist of domestic breed 1080 cross-border breeds. 1491 of these (approx. 20%) are under risk, 691 breeds completely disappeared from the earth. One of the most important genetic resources of poultry is chicken. There are 17.5 billion of chicken on the earth, and 63% of breeds taking place among the poultry species consist of chicken breeds. 1077 of chicken breeds recorded in FAO are domestic breeds and 101 are cross-border breeds. So far, a total of 40 poultry breeds have been extinct. While 419 poultry breeds are under risk, risk condition of 493 breeds is not known [2].

BIOLOGICAL DIVERSITY

Diversity brings the resistance, strength, stability, and liveliness in the system, Biological diversity is an entity consisting of the species, genes, and ecosystems in a region. Biological diversity can be grouped into three main headings as ecosystem diversity, species diversity, and genetic diversity [3].

Ecosystem diversity

Entity consisting of livings, which live a certain area and is a continuous interaction to each other, and lifeless environment belonging to, this is referred to ecosystem. All ecosystems, small and large, consist of two main components; living elements (consumers, intermediaries, and producers) and lifeless elements (organic substances, physical conditions, and inorganic substances) [4].

Species diversity

Species means a total of individuals, which show similarity in terms of their basic characters to each other, and which generate efficient offspring. Species diversity expresses the number and density of plant and animal species

and subspecies in a region. However, while species diversity is dealt with, taxonomic diversity should be also considered [4]. Each species has an idiosyncratic common gene pool. Species can only transmit genetic inheritance in gene pool they have for generations by means of their congeners taking place in their taxonomic groups in natural conditions. Originally, between the species close to each other, a gene exchange may rarely occur at a certain measure, because the phenotypic or physiological similarity to each other points out the abundance of their gene sharing. Similarly, if the closer the inbreeding between two individuals, their common genes is the more and the less the degree of inbreeding, their genetic similarity levels are the less [3].

Genetic diversity

Genetic diversity expresses the diversity in species. This diversity is measured by the presence of genes in a certain species, population, sub-species, or breed. In other words, it is a total of the attributes of an individual, determined by the genes. Normally, number of individuals in a species; except for monozygotic twins, each of individuals in species is genetically different from each other more or less. As the inbreeding degree of individuals decrease, genetic differences between them also increase. The distinctions between individuals result from that these individuals have a different allele or a different composition of the same gene for a certain character. Inter-individual genetic diversities result from allelic distinctions. That gene presents in the different frequencies or combinations in the different populations of the same species leads the populations individual belongs to are different from each other and inter-population genetic diversity. For example, that the resistance of the different populations against diseases is different from the other populations arises from that the gene frequency and combination of this population are different. The genes controlling such characteristics are transmitted from generation to generation through parents while this is done, new genetic combinations and new genetic diversities emerge and, thus, the increase of adaptation flexibility of species to the changing environmental conditions is provided. The presence of genetic diversity that is rich and at sufficient level in a species enables new populations to be able to form according to the changing conditions and needs. In the recent years, in measuring genetic diversity, in the light of main principles of population genetics, with assessment of molecular analysis results, genetic diversity can be measured exactly and correctly [3]. In general, two criteria are taken as an expression of genetic diversity. These are polymorphism and heterozygosity degree [5]. Polymorphism is that two or more alleles are present in a population belonging to the same species. In a population, minimum 5% of alleles present in a locus differ [6,7,8-9]. Heterozygosity degree is defined as the percentage or rate of heterozygous genes in population. Each locus of gene holds two transcripts (homozygous) of alleles that are the same as each other or one transcript (homozygous) of two different alleles. For polymorphic gene locus, if two of five individuals are heterozygous, heterozygosity is calculated as $2/5 = 0.4$ or 40% [4].

THE FACTORS OF EMERGENCE OF GENETIC DIVERSITY

The emergence process of genetically different breeds is due to two factors that interact. It is selection pressure made by the people. This pressure is that animals in good conditions in terms of the desired yield attribute are used as the parent of the next generation. What prevailing in the

region, where animal lives, is environmental stress factors. Between animals, in environmental conditions of the region, in which they are bred, there are differences in terms of reproduction, parent, living strength of and young, and their adaptation abilities. These distinctions provide advantage for genotypes that are the most suitable to that environment in reproduction and this also plays important role in shaping the different breeds [2].

IMPORTANCE OF GENETIC DIVERSITY

The species and breeds whose genetic diversity are high have the ability to more successfully adapt to the changing environmental conditions according to the time and place. Species of living that do not have sufficient genetic diversity, not being able to keep step with the different environmental conditions are obliged to disappear. It is possible for species; whose genetic diversity is more, to more easily adapt the changing environmental conditions. That genetic diversity is low in breed makes populations sensitive to unexpected environmental conditions. For the continuity and adaptation of populations, there is a need for genetic diversity. Breeds whose genetic diversity, depending on scientific and technological developments, become more useful in meeting the changing human desires [10].

PROCESSES CAUSING GENETIC DIVERSITY TO DECREASE

In order to be able to understand very well the relationship between decrease of genetic diversity and disappearance of adaptability, especially in small populations, it is necessary to understand the processes such as genetic bottle neck, random genetic drift and becoming a self, which lead to decrease the genetic diversity.

Genetic drift

Genetic drift expresses random change in gene frequency. In small populations, disappearance probability of alleles is more, because each new generation will only take some part of gene pool of ancestral generation, and this part will not completely reflect gene pool of ancestral generation. This case shows the effect of genetic drift on genetic diversity. Random genetic drift actualizes in case that a population has less individuals along generations. For example, in a population consisting of 10 individuals, after one generation, genetic diversity will survive. After 10 generation, only 60% of genetic diversity will be conserved. In a small population incurring genetic drift along generations, in general, only a single allele in any tissue will survive. Since this gene tissue contains only one allele, it will not be considered as polymorphic. In a small population incurring genetic drift along generations, disappearance probability of genetic diversity is much more than a population exposed to genetic bottle neck, because, following bottle neck, a population can renew itself [5].

Effective population size

It is theoretically the number of individual in the population. In order to better evaluate the effects of genetic bottle neck and random genetic drift, it is necessary for us to make some assumptions. This evaluations accept that organisms are diploid; they sexually reproduce and generations do not overlap; that population size is constant, number of female, equal, and mating, randomly; migration is absent; reproduction successes of all individuals are the same; and that mutation and natural selection do not exist. These acceptations make it possible for us to avoid complexity arisen from the differences between the real population size and effective population size.

In a population of 100 sheep, in which 25 individuals of sample do not reach sexual maturity and 15 individuals are infertile, 60 individuals reproduce. Thus effective population size is 60. In application, this issue is generally complex and population fluctuations include the cases such as not being equal of the number of females and males [5].

DISAPPEARANCE OF GENETIC DIVERSITY

Disappearance of genetic diversity in non-domestic species is generally related to decrease in population size. This case may result from excessive hunting or harvest. In early 1990s, as the reason for depression in population of deep sea water gadoid fish in the coasts of Newfoundland, one of the most productive fishing areas in the world, commercial fishing that excessively hunts is viewed. Also, disappearance of habitat is the major reason for population decrease. In addition, what is under consideration is to isolate populations, squeezed in a narrow region surrounded by the agricultural areas, urban areas, and other areas used by the other areas. This process is termed as population fragmentation. If populations are not in relationship with each other, gene flow disappears, which occurs via migrations and gamete exchange between them and, thus, the most important mechanism that is necessary for genetic variation to form is eliminated. In domesticated species, disappearance of genetic diversity is not generally due to disappearance of life area or dramatic decrease in the number of population. Risk related to disappearance of cattle and maize in the short time is low. The reason for decrease of diversity in domesticated species can be reduced to the changes in agricultural applications and consumer desires. For example, in 1900, while there was different sorts of potatoes more than 100 in USA, today, in this country, in three-fourth of commercial potatoes production, only 9 sorts of it are used. Russet Burbank, as a single type, consists of 43% of total of those planted [11].

GENETIC DIVERSITY AND GENETIC CHARACTERIZATION

In animal production, genetic diversity is composed the basis of improvement programs. Genetic diversity expresses the genetic qualities of living species, adapted to a certain geographic region and commonly grown in the relevant region, breeds belonging to these species, and quality of their relationships with each other in ecosystem, in which they live. Genetic diversity in domestic animals is of two sorts as inbreed and outbreed. Genetic characterizations studies have an important place, in order to identify inbreed and outbreed genetic diversity. In the world and Turkey, in 1980s, while genetic structures of domestic breeds, and their relationships with some yield features are examined by using blood and milk protein polymorphism [12,13], together with the recent developments, microsatellite markers and SNPs have been begun to be used more commonly. In order to identify the origin of breeds and domestication regions, the studies of genetic characterization and archeology have been carried out [14,15,16,17-18]. It is reported that migration routes of European breeds follow two different routes as from North to Central Europe along Danube River and along Mediterranean and that the cattle, sheep, goat, and buffalo was first begun to be domesticated in two different regions of Asia. The oldest one of these centers includes East and Southeast Anatolian Region and it is known that the breeds spread from this region to the earth, especially from Anatolia to Europe [19,20,21,22,23,24-25]. In the studies of genetic characterization, microsatellites are used in the human

[26,27], cattle [28,29], goat [30], sheep [31,32], dog [33], horse [34], monkey [35], pig [36,37], buffalo [38], and the other animal species [39,40]. Biochemical marker systems other than microsatellites were also used in genetic characterization studies [41,42-43]. Although AFLP [44], mtDNA [45,46-47], and Y chromosome [48] specific microsatellites are heavily used, SNP markers have been also begun to be used. In addition, again in genetic characterization studies, other than marker systems, the records of family tree are also utilized. SNPs are simultaneously used in molecular studies of sea products and animal species in much amount [49]. As a result, in marker systems, while many marker systems were used before PCR technology, together with PCR technology, microsatellites have been predominantly begun to be used. In the recent years, the studies on SNP markers have increased, and SNP chips have been begun to be formed [50].

REASONS FOR CONSERVING ANIMAL GENETIC RESOURCES

Before discussing the possibilities and ways of maintaining small populations or so-called rare breeds it is important to make clear why they should be conserved. In Europe, the reasons for conserving genetic variation have been discussed among others by Majjala (1970), Mason (1974), Simon (1984) and Majjala et al. (1984). On the basis of these and other papers, the following list of arguments for conservation can be made:

A. Economic-biological reasons

1. The production conditions for farm animals are changing. This concerns especially feeding, since one has to find new economic feedstuffs, and to utilize various kinds of wastes from agriculture and industry. It may also become topical to return to extensive pastures in case the intensively cultivated areas will be needed for direct production of human food or energy crops. Changes in management of animals may also continue to change (e.g. mechanization, milking frequencies and methods, densities, etc.). Similarly, the housing conditions (regulation of temperature, moisture, light etc.) may change. Changes are possible also in the hygienic conditions of animals (new kinds of disease agents, new vaccines and medicines) and in climatic conditions (temperature, humidity, altitude).
2. The demands for products and services desired from animals may change for many reasons, e.g. with opinions and knowledge concerning wholesome food, with increased standard of living and leisure time or with new fashions in eating and clothing. Changes in international trade and trade blocs influence costs of materials and prices of products. The increased human population may increase the need of quantities, and it is important to combat hunger. The need of compensating exhausted natural reserves of fuels, minerals, etc., with renewable plant and animal materials may become more and more topical. The competition between animal species in production costs and services, as well as that between animals and plants as food producers may affect the usefulness of various kinds of animals. The need of finding new ways of utilizing agricultural plant products in case of surplus problems may also increase.
3. Experiences of crossbreeding in utilizing heterosis and complementarily speak in favor of maintaining the possibility of systematic crossbreeding also in the future.
4. In order to satisfy the rapidly changing needs it is important to make rapid, one-sided progress in some

populations without losing the possibility of starting again in another direction if needed.

5. There is an increasing need of being able to adjust the breeding work to the new bio techniques such as embryo transfer, splitting and sexing, or gene technology.

6. There may appear needs to overcome selection limits and antagonisms.

B. Scientific reasons

1. For the measurement of genetic progress and correlated responses control populations or frozen stocks are very useful.

2. Research in genetics, physiology, biochemistry, immunology, morphology, etc., benefits from maintenance of a large variety of animal materials.

3. Many different populations are valuable for research in evolution, ontogeny, behavior, etc.

4. They are also useful as teaching material in animal sciences.

C. Cultural-historical reasons

1. Conserved breeds can be considered to be valuable memorials of nature and culture (living cultural heritage).

2. They can be used as research and teaching material in history and ethnography.

3. There are ethical-moral grounds to take care of the existence of different creations of nature.

METHOD USED IN CONSERVATION OF GENE RESOURCES

In conserving animal genetic resources, basically, two methods are applied.

In-situ conservation method

In this method, animals are kept as breeding herds. In sufficient size of herds consisting of animal breeds, which have or are foreseen to be conserved, are bred with random mating.

Advantages of in-situ conservation

Advantages of the in situ method are:

- The animals are visible, and so pleasing to the eye, and have some cultural value;
- They are a gene bank for future use;
- They are a constant reminder that the needs of posterity must be considered;
- The herd/flock may have some economic advantage (e.g. disease resistance in chickens) which can be exploited and so render the enterprise economically viable [55].

Disadvantages of in-situ conservation

Small population size, leading to inbreeding and random drift. Many models are now available which reduce inbreeding to a minimum, but some scientists argue that random drift over long periods (say hundreds of years; may lead to a population very different in genetic composition from the initial one);

- Gene x environment interactions [55].

Ex-situ conservation method

This method is divided into two within itself as ex-situ in vivo and conservation by frosting. Ex-situ in vivo expresses conserving the breed in lively way in a different environment from its natural environment. The essence of method of conservation by frosting is to conserve by frosting the semen, eggs, or embryos with the appropriate methods. It is possible to conserve genes belonging to the species, breed, or individuals that will be subjected to conservation, frosting blood or other tissues of animal [56].

CONCLUSION

The molecular markers and classical improvement studies of the existing genetic resources should be used together in determination of genetic diversity of these resources, because which of these genetic resources will be needed in the future cannot already be predicted. Most of animal species and breeds played important role in the history of the country, in which they are bred. Domestic breeds, due to the fact that they are the criterion of historical development of animal breeds, have the educational value Domestic gene resources are used as control material in determining the changes provided or occurring in the physiological, genetic, nutrition, production, adaptation, and behavior characteristics of the population developed. In addition, they present service from the aspect of human health, contributing to the studies on the control and treatment of diseases and helping gene(s), responsible for control of many diseases, identify. The changes that maybe occur in environmental conditions and probability of features of domestic animals not known today to adapt these changes make it obligatory to conserve diversity. The genotypes that will be subjected to conservation should be determined based on inventory; the genotypes that are subjected to conservation and conservation studies should be reviewed. Besides ex-situ in vivo conservation, which is currently carried out, the existing studies regarding the methods of ex-situ and in -situ conservation (environment of breeders), should be developed. Enough level of budget should be provided for conservation studies and support should be provided from the funds of international organization.

REFERENCE

1. Ertuğrul M, Akman N, Dellal G, Goncagul T. Animal Gene Resources Conservation and Turkey Animal Genetic Resources. Turkish Agricultural Engineering V. Technical Congress 2000;285-300.
2. Mercan L. Analysis of Genetic Dissimilarity between Native and Commercial Chicken Genotypes by SSR (Simple Sequence Repeats) Method [PhD Thesis]. Samsun, Ondokuz Mayıs University; 2010.
3. Işık K. Biology Diversity [Internet]. [cited 2017] Available from: <http://www.anadolu.edu.tr/aos/kitap/IOLTP/1270/unite02.pdf>
4. Barıtcı İ. Relationships Between Genetic Polymorphism And Yield Properties in Awassi Sheep [PhD Thesis]. Ankara, Ankara University; 2007.
5. Gur H. Biodiversity [Internet]. [cited 2017] Available from: http://www.academia.edu/1739859/biyolojik_cesitlilik
6. Camp PS, Arms K. Exploring Biology. 2th ed. Philadelphia, Saunders College Publishing; 1984. p.587.
7. Becker WM, Deamer DW. The World of the Cell. 2th ed. Redwood City, The Benjamin/Cummings Publishing; 1991. p. 748.
8. Bourdon RM. Understanding animal breeding. London, Prentice-Hall Inc.1997. p. 29-412.
9. Goldstein DB, Schlötter C. Microsatellites. 2th ed. Oxford. 2000. p. 1-22.
10. Fadhil M, Zülkadir U. Molecular Characterization of MSTN Gene in Holstein Friesians and Brown Swiss Cattle Breeds. Selcuk J Agr Food Sci, 2017; 31 (3), 151-153.
11. Öner C. Genetic Concepts. Ankara, Palme Publishing; 2011. p. 500-501.

12. Ceriotti G, Caroli A, Rizzi R, Crimella C. Genetic relationships among taurine (*Bostaurus*) and zebu (*Bosindicus*) populations as revealed by blood groups and blood proteins. *J Anim Breed Genet* 2003; 57–67.
13. Ibeagha-Awemu EM, Erhardt G. Genetic structure and differentiation of 12 African *Bosindicus* and *Bostaurus* cattle breeds, inferred from protein and microsatellite polymorphisms. *J AnimBreed Genet* 2005;12–20.
14. Cañón J, Alexandrino P, Bessa I, Carleos C, Carretero Y, Dunner S, Ferran N, Garcia D, Jordana J, Laloë D, Pereira A, Sanchez A, Moazami-Goudarzi K. Genetic diversity measures of local European beef cattle breeds for conservation purposes. *Genet Sel Evol* 2001; 311–332.
15. Li MH, Adamowicz T, Switonski M, Ammosov I, Ivanova Z, Kiselyova T, Popov R, Kantanen J. Analysis of population differentiation in North Eurasian cattle (*Bos taurus*) using single nucleotide polymorphisms in three genes associated with production traits. *Anim Genet* 2006; 390–392.
16. McKay SD, Schnabel RD, Murdoch BM, Matukumalli LK, Aerts J, Coppieters W, Crews D, Dias Neto E, Gill CA, Gao C, Mannen H, Wang Z, Van Tassell CP, Williams JL, Taylor JF, Moore SS. An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. *BMC Genetics* 2008; 45-50.
17. Kang BT, Kim KS, Min MS, Chae YJ, Kang JW, Yoon J, Choi J, Seong JK, Park HC, An J, Lee MH, Park HM, Lee H. Microsatellite loci analysis for the genetic variability and the parentage test of five dog breeds in South Korea. *Genes Genet Syst* 2009; 245–251.
18. Molae V, Osfoori R, Eskandari Nasab MP, Qanbari S. Genetic relationships among six Iranian indigenous sheep populations based on microsatellite analysis. *Small Rum Res* 2009; 121–124.
19. Loftus RT, MacHugh DE, Bradley DG, Sharp PM, Cunningham P. Evidence for two independent domestications of cattle. *Proc Natl Acad Sci USA* 1994; 2757–2761.
20. Loftus RT, Ertuğrul O, Harba MH, ElBarody AA, MacHugh DE, Park SDE, Bradley DG. A microsatellite survey of cattle from a centre of origin: The Near East. *Mol Ecol* 1999; 2015–2022.
21. Luikart G, Gielly L, Excoffier L, Vigne JD, Bouvet J, Taberlet P. Multiple maternal origins and weak phylogeographic structure in domestic goats. *Proc Natl Acad Sci USA* 2001; 5927–5932.
22. Troy CS, MacHugh DE, Bailey JF, Magee DA, Loftus RT, Cunningham P, Chamberlain AT, Sykes BC, Bradley DG. Genetic evidence for Near-Eastern origins of European cattle. *Nature* 2001; 1088–1091.
23. Hiendleder S, Kaupe B, Wassmuth R, Janke A. Molecular analysis of wild and domestic sheep questions current nomenclature and provides evidence for domestication from two different subspecies. *Proc Biol Sci* 2002; 893–904.
24. Bruford MW, Bradley DG, Luikart G. DNA markers reveal the complexity of livestock domestication. *Nat Rev Genet* 2003; 900–910.
25. Cymbron T, Freeman AR, Isabel Malheiro M, Vigne JD, Bradley DG. Microsatellite diversity suggests different histories for Mediterranean and Northern European cattle populations. *Proc Biol Sci.* 2005; 1837–1843.
26. Bowcock AM, Ruiz-Linares A, Tomfohrde J, Minch E, Kidd JR, Cavalli-Sforza LL. High resolution of human evolutionary trees with polymorphic microsatellites. *Nature* 1994; 455–457.
27. Deka R, Jin L, Shriver MD, Yu LM, DeCruz S, Hundrieser J, Bunker CH, Ferrell RE, Chakraborty R. Population genetics of dinucleotide (dC-dA)_n(dG-dT)_n polymorphisms in world populations. *Am J Hum Genet* 1995; 461–474.
28. MacHugh DE, Shriver MD, Loftus RT, Cunningham P, Bradley DG. Microsatellite DNA variation and the evolution, domestication and phylogeography of taurine and zebu cattle (*Bos taurus* and *Bos indicus*). *Genetics* 1997; 1071–1086.
29. Edwards CJ, Gaillard C, Bradley DG, MacHugh DE. Y-specific microsatellite polymorphisms in a range of bovid species. *Anim Genet* 2000; 127–130.
30. Maudet C, Miller C, Bassano B, Breitenmoser-Würsten C, Gauthier D, Obexer-Ruff G, Michallet J, Taberlet P, Luikart G. Microsatellite DNA and recent statistical methods in wildlife conservation management: Applications in Alpine ibex [*Capra ibex*(*ibex*)]. *Mol Ecol* 2002; 421–436.
31. Mukesh M, Sodhi M, Bhatia S. Microsatellite-based diversity analysis and genetic relationships of three Indian sheep breeds. *J Anim Breed Genet* 2006; 258–264.
32. Lawson Handley L-J, Byrne K, Santucci F, Townsend S, Taylor M, Bruford MW, Hewitt GM. Genetic structure of European sheep breeds. *Heredity* 2007; 620–631.
33. Boyko AR, Boyko RH, Boyko CM, Parker HG, Castelhamo M, Corey L, Degenhardt JD, Auton A, Hedimbi M, Kityo R, Ostrander EA, Schoenebeck J, Todhunter RJ, Jones P, Bustamante CD. Complex population structure in African village dogs and its implications for inferring dog domestication history. *Proc Natl Acad Sci USA* 2009; 13903–13908.
34. Luís C, Juras R, Oom MM, Cothran EG. Genetic diversity and relationships of Portuguese and other horse breeds based on protein and microsatellite loci variation. *Anim Genet* 2007; 20–27.
35. Aranguren-Méndez J, Jordana J, Gomez M. Genetic conservation of five endangered Spanish donkey breeds. *J Anim Breed Genet* 2002; 256–263.
36. Behl R, Sheoran N, Behl J, Vijn RK. Genetic analysis of Ankamali pigs of India using microsatellite markers and their comparison with other domesticated Indian pig types. *J Anim Breed Genet* 2006; 131–135.
37. Sollera BP, Paiva SR, Faria DA, Guimarães SEF, Castro STR, Egito AA, Albuquerque MSM, Piovezan U, Bertani GR, Mariante AD. Genetic diversity of Brazilian pig breeds evidenced by microsatellite markers. *Livest Sci* 2009; 8–15.
38. Flamand JRB, Vankan D, Gairhe KP, Duong H, Barker JSF. Genetic identification of wild Asian water Buffalo in Nepal. *Anim Cons* 2003; 265– 270.
39. Cosse M, González S, Maldonado JE. Crossamplification tests of ungulate primers in the endangered Neotropical pampas deer (*Ozotoceros bezoarticus*). *Genet Mol Res* 2007; 1118–1122.
40. Vijn RK, Tandia MS, Mishra B, Kumar ST. Genetic diversity and differentiation of dromedarian camel of India. *Anim Biotechnol* 2007; 81–90.
41. Moazami-Goudarzi K, Laloë D, Furet JP, Grosclaude F. Analysis of genetic relationships between 10 cattle breeds with 17 microsatellites. *Anim Genet.*1997; 338–345.
42. Kantanen J, Olsaker I, Adalsteinsson S, Sandberg K, Eythorsdottir E, Pirhonen K, Holm LE. Temporal changes in genetic variation of north European cattle breeds. *Anim Genet* 1999; 16– 27.
43. Kantanen J, Olsaker I, Holm LE, Lien S, Vilkki J, Brusgaard K, Eythorsdottir E, Danell B, Adalsteinsson S.

Genetic diversity and population structure of 20 North European cattle breeds. *J Hered* 2000; 446–457.

44. Negrini R, Nijman IJ, Milanesi E, MoazamiGoudarzi K, Williams JL, Erhardt G, Dunner S, Rodellar C, Valentini A, Bradley DG, Olsaker I, Kantanen J, Ajmone-Marsan P, Lenstra JA, European Cattle Genetic Diversity Consortium. Differentiation of European cattle by AFLP fingerprinting. *Anim Genet* 2007; 60–66.

45. Bradley DG, MacHugh DE, Cunningham P, Loftus RT. Mitochondrial diversity and the origins of African and European cattle. *Proc Natl Acad Sci USA* 1996; 5131–5135.

46. Finnilä S, Lehtonen MS, Majamaa K. Phylogenetic Network for European mtDNA. *Am J Hum Genet* 2001; 1475–1484.

47. Mannen H, Kohno M, Nagata Y, Tsuji S, Bradley DG, Yeo JS, Nyamsamba D, Zagdsuren Y, Yokohama M, Nomura K, Amano T. Independent mitochondrial origin and historical genetic differentiation in North Eastern Asian cattle. *Mol Phylogenet Evol* 2004; 539–544.

48. Cai X, Chen H, Wang S, Xue K, Lei C. Polymorphisms of two Y chromosome microsatellites in Chinese cattle. *Genet Sel Evol* 2006; 525–534.

49. Muir WM, Wong GKS, Zhang Y, Wang J, Groenen MAM, Crooijmans RPMA, Megens HJ, Zhang H, Okimoto R, Vereijken A, Jungerius A, Albers GAA, Lawley CT, Delany ME, MacEachern S, Cheng HH. Genome-wide assessment of worldwide chicken SNP genetic diversity

indicates significant absence of rare alleles in commercial breeds. *Proc Natl Acad Sci USA* 2008; 17312-17317.

50. Özşensoy Y, Kurar E. Marker Systems and Their Use in Genetic Characterization Studies. *Journal of Cell and Molecular Biology* 2012; 11-19.

51. Maijala K. Need and methods of gene conservation in animal breeding. *Ann. Génét. Sel. Anim* 1970; 403-415.

52. Mason IL. The conservation of animal genetic resources: Introduction. 1th ed. Madrid, Congr. Genet. appl. Livest. Prod; 1974. p. 13-21.

53. Simon DL (1984). Conservation of animal genetic resources - reviewing the problem. *Livest. Prod. Sci* 1984; 23-35.

54. Maijala K, Cherekaev AV, Devillard JM, Reklewski Z, Rognoni G, Simon DL, Steane DE (1984). Conservation of animal genetic resources in Europe. *Prod. Sci* 1984; 3-22.

55. Newton TH. Principles for preservation of endangered species and breeds in the tropics. *FAO Animal Production and Health Paper* (FAO). 1987.

56. Binbaş P. Detection of Genetic Diversity in Çine Çaparı Sheep by RAPD Technique [Master Thesis]. Ankara, Ankara University; 2006.