Analysis of the Mitochondrial Genome in Podolian Cattle Breeds

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Abstract

Podolian cattle breeds are represented by: Romanian Grey Steppe, Iskar Grey (Bulgarian Grey), Istrian, Katerini, Ukrainian Grey and Hungarian Grey. The mitochondrial genome in cattle has a length of about 16,338 nucleotides. The majority of taurine mtDNA sequences cluster within macro-haplogroup T, which consists of six sub-haplogroups (T, T1, T2, T3, T4 and T5). Recent developments in DNA sequencing technologies provide new opportunities for the examination of genetic material in extinct or endangered species, providing a new perspective on their evolutionary history. This paper has as main purpose the analysis of the mitochondrial genome in podolian cattle breeds by consulting the most relevant research in the literature.

Keywords: bovine, genetic markers, mtDNA.

1. Introduction

Over the last 15 years, 300 of the 6000 breeds of all Farm animal species identified by the F.A.O. have disappeared It's extinct.
Extinction of different animal breeds is attributable to three factors: genetic erosion due to artificial insemination, strong economic pressure on farmers to concentrate on single traits and unregulated and unrestricted cross-breeding, especially in developing countrie. An example could be Grey Steppe cattle breed, that are facing a drastic decrease in the number of cows at European level, since the 90s [1].
Over the world, the cattle breeds play a key role in human survival and in ensuring food security. However, the genetic resources of this animals are facing an alarming rate of decrease due to economic changes, economic globalization and financial constraints [2].
In the 20th century, the depletion of cattle breeding genetic diversity became an important concern, but conservation efforts were postponed until the Food and Agriculture Organisation (FAO) signaled its interest in this issue as a result of growing knowledge of the loss of breeds suited to different environmental factors, including climatic conditions and various pests or infectious diseases. As a result, the issue of the survival of cattle breeds has begun to develop, including both ex situ and in situ [3]. In 1990, the FAO Council recommended a global initiative for the effective use of animal resources genetic capital. A number of 142 countries have accepted to participate in this global assessment and reporting effort, and submit country reports [4].
The conservation of genetic resources of cattle breeds is important for many reasons, such as: preserve cultural and historical values of a country, the maintenance of genetic diversity to meet the needs of current and future, ensure the

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adaptation to changing environmental conditions, support sustainable for animal production systems for food security, insurance of genetic resources for cross-breeding and development of new genotypes [5].

In the near future, should be prepared a international list with current data of populations indigenous cattle breeds at risk of extinction and those requiring conservation they should be conserved in their native habitats, including conservation programs.

The genetic capital and genetic variability of these breeds are important factors for the development of the global livestock industry, climate change, cultural heritage and biodiversity objectives.

A high number of studies cover one or more of these environmental problems and underline the value of better utilization of genetic capital and enhanced conservation and management strategies for animal genetic resources.

2. Materials and methods

This paper is a review of the most relevant research in the literature in the country and abroad, on molecular markers used in studies of genetic diversity of cattle breeds. For the realization of the paper were consulted a number of 8 bibliographical references in the field, but also information from different international databases.

3. Results and discussion

In the analysis of the Global Databank for Farm Animal Genetic Resources (F.A.O., 2000), cattle breeds are classified into one of four categories, according to risk status (given the population size): critical, critical-maintained, endangered and endangered-maintained.

Table 1. The classification of cattle genetic resource populations in four categories of risk

Risk status	*Total population size*	*No. of breeding males*	*No. of breeding females*
critical	≤ 120	≤5	≤100
critical-maintained	same as "critical" status + conservation programme		
endangered		> 5-20	> 100-1000
	> 80 but < 100		pure-bred females > 80%
	> 1000-1200		pure-bred females < 80%
endangered-maintained	same as "endangered" status+ conservation programme [6]		

The Grey Steppe cattle breed is considered threatened with extinction in Romania, in 2000 being maintained, by Food and Agriculture Organization of the United Nations (F.A.O.), with the risk status “endangered-maintained”. This Romanian endangered cattle breed has a common origin with others European breeds, such as: Maremmana (Italy), Romagnola (Italy), Piemontese (Czech Republic), Mirandesa and Andalusian Grey (Spain), Salers (France), Ukrainian Grey Steppe, Yugoslav Grey Steppe, Bulgarian Grey Steppe (Isker), Turkish Grey Steppe, Hungarian Grey Steppe [7].

An analysis of the risk status of Grey Steppe cattle varieties, showed a different status for individuals spread all over the Europe, ranging from a “critical” rank (Grey Steppe from Bulgaria, Greece and Hungarian Grey cattle) to “endangered-maintained” for Romanian Grey Steppe population [8].

Table 2. Grey Steppe cattle populations size and their risk status according to F.A.O.

Country	Romania	Bulgaria	Croatia	Greece	Ukraine	Austria	Germany
Grey Steppe cattle varieties	Sura de stepă	Iskar Grey (Bulgarian Grey)	Istrian	Katerini	Ukrainian Grey	Hungarian Grey Steppe	Hungarian Grey Steppe
Risk status	endangered-maintained	critical	critical-maintained	critical	endangered	critical-maintained	critical
Population data (F.A.O., 2000)	350♀, 12♂	120♀, 5♂	103♀, 7♂	80♀, 5♂	684♀, 13♂	10♀, 4♂	36♀, 5♂

*Global Databank for Farm Animal Genetic Resources (F.A.O., 2000)

In the case of Grey Steppe cattle, the FAO data presented showed a different status for individuals throughout Europe, ranging from a "critical" for Grey Steppe in Bulgaria, Greece, the population of Grey Steppe cattle from Germany and the Hungarian Grey Steppe to the degree of danger for the Romanian population of Grey Steppe (table 2 and figure 1).

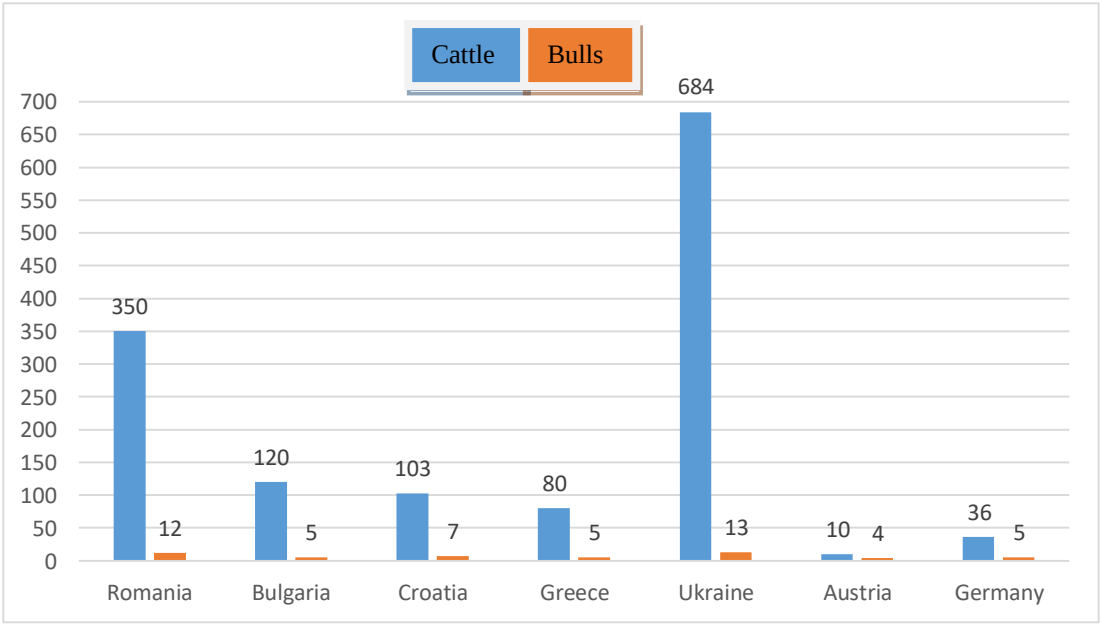

Figure 1. The number of individuals in the Grey Steppe breed, according to F.A.O., 2000

This classification of the populations of Grey Steppe breed was made on the basis of statistical data reported before 2000, but in many cases, approximately the same numerical numbers of individuals belonging to this breed were reported in the case of research published to date. This is not the case for the entire steppe cattle population. An eloquent example is represented by Grey Steppe, the Hungarian variety, whose numerical strength increased after 1970, as a result of a good management of genetic resources, in Hungary, this breed being included in the tourist programs. The subfamily Bovinae belongs to the family Bovidae (genus Bos taurus) which includes a number of 10

subfamilies of the order Artiodactyla. It currently contains more than 140 existing species and about 300 endangered species. Many authors argue that the Bovidae family is monophyletic. Of the 10 subfamilies, currently based on molecular, morphological and fossil signaling studies, the Bovidae family is assumed to comprise 8 distinct subfamilies: Aepyceros, Alcelaphinae, Antilopinae, Bovinae, Caprinae, Cephalophile, Hippotraginae, and Reduncinae. The taxonomic classification of the genus Bos taurus and the subfamily Bovinae can be consulted in figures 1 and 2, which represent phylogenetic trees.

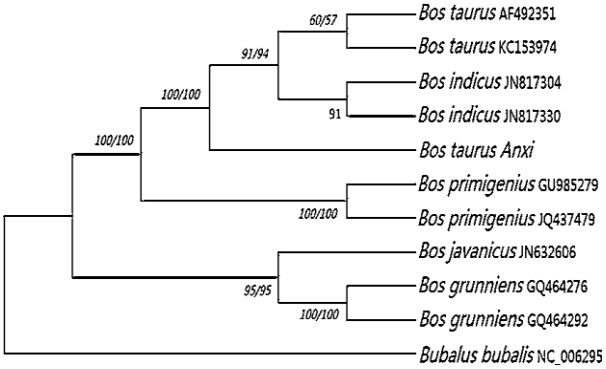

Figure 2. Systematics of the genus Bos Taurus

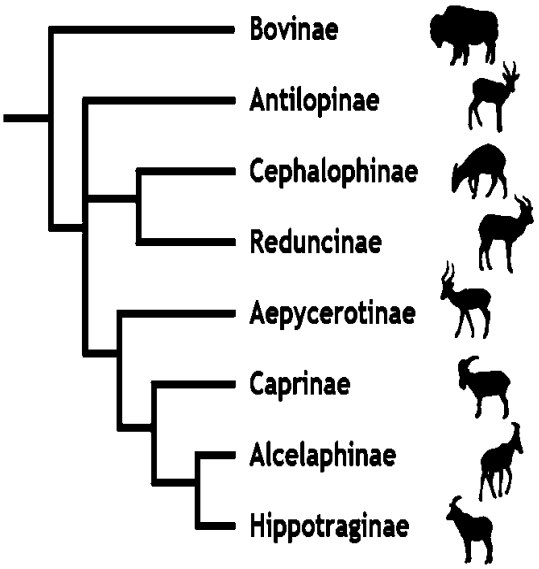

Figure 3. Systematics of the family Bovidae (taxonomic classification of the subfamily Bovinae)

In the Bovinae species, the mitochondrial genome is approximately 16,340 base pairs long (figures 3 and 4).

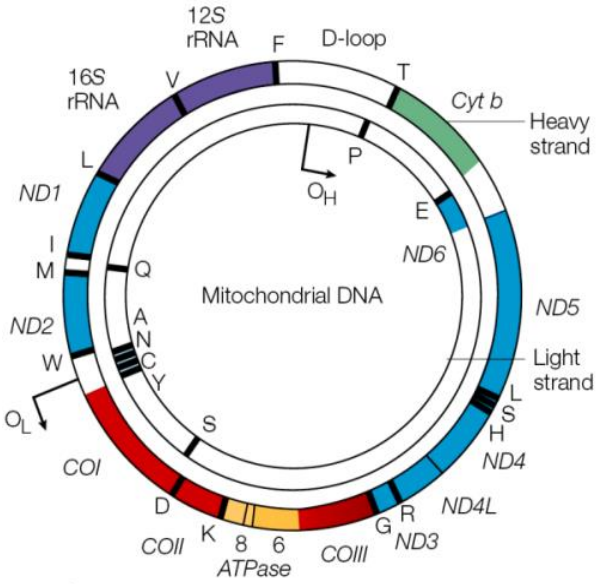

Figure 4. The map of the mitochondrial genome of mammals

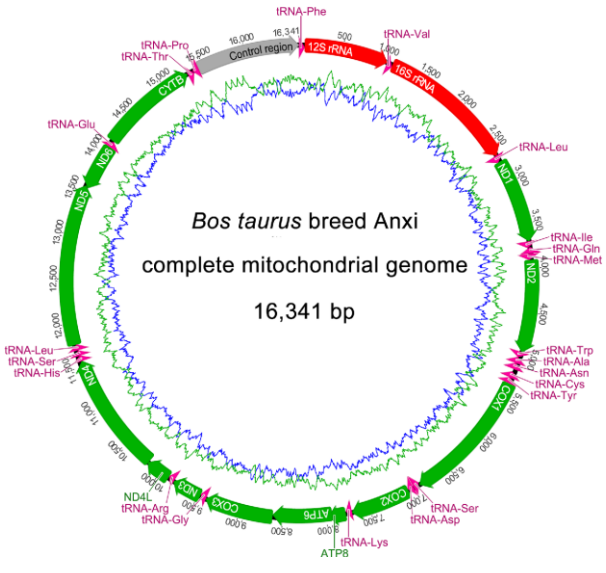

Figure 5. The gene map of the mitochondrial genome for Anxi cattle (Bos taurus)

The origin of podolian cattle breeds as well as the main phenotypic characteristics have been analyzed over time by many researchers in the field and the data are presented by publishing scientific papers. At the same time, special attention was paid to the characterization of these endangered indigenous cattle breeds in terms of genetic markers associated with milk or meat production as well as the application of molecular techniques in genetic conservation programs.

The Grey Steppe cattle breed is endangered since 2000, when the Food and Agriculture Organization of the United Nations (FAO) reporting this issue of national interest. FAO reports draw attention to the numerical decline of different species, currently various races being classified taking into account the number of individuals existing in each race as well as the female / male ratio. A priority at country level is the inclusion of these breeds in active genetic conservation programs either on livestock farms or under the auspices of research institutions, taking into account the severity of the risk status: extinct breeds, critical breeds, breeds endangered, endangered breeds, endangered breeds without risk of extinction.

4. Conclusions

Traditional methods of conserving the genetic diversity of endangered cattle breeds are no longer sufficient at present. A more modern approach, such as genome-wide association studies, should be incorporated into selection plans.

The validation of molecular analysis methods will allow the use of genetic information in genetic conservation programs both nationally and internationally.

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