



On the Necessity of Monitoring the Gene Pool of Elk Populations (*Alces Alces L.*) in Elk Farms

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Received: 📅 July 25, 2020

Published: 📅 August 07, 2020

Abstract

The work presents the results of a comparative analysis of the gene pool diversity of a man-made population (herd) of an elk farm and two natural populations from Kostroma and Yaroslavl regions (Russia) using microsatellite loci (3 populations, 169 samples, 9 microsatellite loci). A significant reduction in the diversity of alleles (number of alleles per locus) in the farm elk population compared to the natural populations is found. The need to rehabilitate the gene pool of the elk farm population is shown.

Keywords: Elk farm, population, gene pool rehabilitation

Introduction

No doubt, the production of elk (*Alces alces L.*) milk known for its medicinal properties, as well as of elk milk products for dietetic and medicinal uses is a relevant issue. An elk farm of the Sumarokov National Nature Reserve (Kostroma oblast (region)) with a herd of 40 elk may serve as an example of a unique elk farm. The farm supplies the elk milk to a nearby sanatorium, where it is used to treat patients for gastrointestinal diseases. The Sumarokov elk farm has been specializing in domesticating the elk since 1963. Since then the method for semi-free grazing for elk has been developed, physiological properties and biological indicators have been studied. But the quality of the gene pool has not been monitored. However, the economic effect of an artificial elk population heavily depends on the gene pool quality associated with such practically important properties as fecundity, growth rate and, ultimately, viability and productivity. A 10% reduction in the genetic diversity of a population is known to cause a 25% decrease in fecundity [1].

Therefore, the global problem of preserving genetic resources, including on farms, calls for solutions [2].

Purpose of the Study

The purpose of the study was to analyze the gene pool of the elk population (herd) of the Sumarokov elk farm and develop a strategy to maintain and restore its genetic diversity in order to increase viability and productivity.

This task can be solved with the aid of genourbanology - a new scientific and practical direction of research developed by the authors [3]. Within the framework of genourbanology, the authors formulated the concept that the gene pool diversity should correspond to some natural norm typical of natural (reference) populations adapted to the conditions of a given ecosystem. The authors also worked out the patented "Method for maintaining the viability of populations of animals or plants in urbanized territories",

which can be used to restore the genetic diversity of populations of plants or animals [4]. In accordance with the above concept, a comparative analysis of the gene pool state of the Sumarokov elk farm population with that of two natural elk populations from Kostroma and Yaroslavl regions in order to identify the degree of deviation of genetic parameters of the elk farm population from those of the natural populations.

Materials and Methods

In total, the authors surveyed 169 animals from 3 populations, including 149 samples of muscle tissue (66 and 83 samples were from the natural Kostroma and Yaroslavl populations, taken from 12 and 10 districts respectively) and 20 samples of hair bulbs of the elk farm population. Nine microsatellite loci were used as DNA markers forming one multiplex panel: BL42 (250-274 pairs of nucleotides), BM1225 (224-250 p.n.), BM4513 (115-135 p.n.), BM848 (351-363 p.n.) [5]; Map2C (BOVTAU) (101-111p.n.) [6-8]; NVHRT21 (153-169 p.n.) [6]; RT24 (222-260 p.n.), RT30 (190-214 p.n.), RT9 (108-132 p.n.) [9,10] (the numbers in brackets indicate the range of sizes of DNA fragments). Fragment analysis of PCR products was carried out using the automatic capillary DNA sequencer ABI PRISM 3500 Genetic Analyzer (Applied Biosystems, USA). The fragment size analysis was carried out using the GeneMapper R Software 4.1 (Applied Biosystems, USA). On the basis of the readings of the frequencies of genotypes the authors calculated the frequencies of alleles in the populations as well as intra-population diversity and inter-population differentiation indices using the Pop Gen 1.32 and GenAEx V6.502 software [11-13].

The analysis of the allele frequencies at nine microsatellite loci in the three elk populations showed that a number of alleles of the same locus are found only in the population from Kostroma region, while other alleles are found only in the Yaroslavl population. For example, at the BL-42 locus alleles 262, 264, 270 were found only in the Kostroma population, while alleles 266 and 272 were only detected in the population from Yaroslavl region. However, out of 94 alleles found in the natural populations 45 alleles are missing in the elk farm population.

Results and Discussion

The indices of intra-population variability of the elk populations compared by nine microsatellite loci point to a reliably higher variety of alleles (N_A) (one and a half times higher) in the natural populations compared to that observed in the man-made population from the Sumarokov elk farm. For the natural populations from Kostroma and Yaroslavl regions and the elk farm population its values are 9.0, 8.6 and 5.9 respectively. At the same time, the values of average heterozygosity observed (H_o) in the natural and the artificial populations do not differ and are 0.691, 0.605 and 0.606 respectively. The value of the Shannon Index (I) is also higher for the natural populations (in Kostroma – 1.61, in Yaroslavl – 1.595, elk farm – 1.439).

It is shown that the value of the inbreeding coefficient for the Kostroma region population is close to 0 ($F=0.053$). For the elk farm population it is 0.165 and is close to that for the Yaroslavl population ($F=0.167$).

The test on heterogeneity of allelic frequencies detected reliable difference of all the three populations by six loci out of nine. The natural populations from Kostroma and Yaroslavl regions differ reliably by five loci out of nine. The population of the Sumarokov elk farm reliably differs from the natural Kostroma and Yaroslavl populations by the same three loci (BL42, BM1225, RT24). This is shown by the highest values of the differentiation index (F_{st}) found by these loci (0.076, 0.050 and 0.077 - respectively)

Thus, the samples from the elk farm population are found to bear similarities with both natural populations in terms of gene pool, though those similarities occurred by chance solely due to human influence and they don't correspond to the differences found between the two natural populations from Kostroma and Yaroslavl regions. The χ^2 test showed a reliable deviation from the Hardy-Weinberg equilibrium in most cases (by most loci): deviations in the Kostroma population, Yaroslavl population and the population of the elk farm the deviations were found by 6, 8 and 3 loci respectively. The violations are accounted for by both a slight deficiencies of heterozygotes in the Kostroma population (at 4 loci), the Yaroslavl population (at 2 loci) and the elk farm population (at 3 loci) as well as by a slight excess of heterozygotes in these populations (at 5, 6 and 6 loci respectively). However, only isolated significant cases were found when the value of the inbreeding coefficient per locus was different from zero (in 5 out of 27 cases).

Similar values of the gene pool diversity of the Sumarokov farm population were obtained by M.I. Marzanov and his co-authors, who studied samples from 23 elk by six microsatellite loci and the average number of alleles (N_A) varied 1.83-4.29 from locus to locus [13], but no comparisons with the natural populations have been made.

Results

The findings of our study show that the creation of due to absence of genetic control led to changes in the genetic parameters of the elk farm population compared to natural populations and, primarily to a lower allele diversity, a higher inbreeding coefficient and other indicators which resulted in a decrease in the population's adaptive capacity, which, in turn, weakened the viability and productivity of the population. Undoubtedly, the gene pool of the Sumarokov man-made elk farm population, whose allele diversity is significantly lower (1.5 times), needs enrichment (rehabilitation) by introducing genetic material from natural populations. The method developed by the authors has been proposed to increase the viability and productivity of the population of the Sumarokov elk farm [4]. This study was performed under the state assignment. Registration no. AAAA-A16-116042010089-2 "Ecology", "Biosphere Functions

of Natural Ecosystems and Sustainable Nature Management". All applicable international, national and/or institutional principles for animal care and use have been observed.

Conflict of Interest

The authors claim no conflict of interest.

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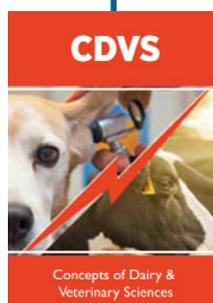


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DOI: [10.32474/CDVS.2020.03.000175](https://doi.org/10.32474/CDVS.2020.03.000175)



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