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International Society of Camelid Research and Development
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الجمعية الطبية البيطرية السعودية
Saudi Veterinaray Medical Society

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Camel Research Center

Biodiversity of Dromedary Camels and Hybrids in Kazakhstan

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AIM:

To characterize biodiversity of dromedary camels and hybrids in Kazakhstan by description detailed phenotype and genotype parameters in order to have possibility to compare them with camels in the worldwide.

INTRODUCTION:

Studying the phenotype and genotype of pure breed camels and their hybrids by the latest methods will give an opportunity to develop each "breed standards" and detect genotypes with high productivity qualities.

METHODS:

Seventeen camel farms were visited, located in four different regions of Kazakhstan. In total, 484 female camels of Arvana breed and 98 hybrids (Nar-Maya hybrid (Crossbreed F1) and Kospak hybrid (crossbreed F2)) were described by the phenotype questionnaire including milk parameters data. The software used was XLstat (Addinsoft©, 2022). For the genotyping 347 Arvana camels and 98 hybrids' DNA samples were taken. Genotyping was performed on GeneTitan MC tool and Plate with a wide range of Axiom genome for genotyping camels Axiom myDesign™ Massive plate with 196,000 SNP (Thermo Fisher Scientific).

RESULTS:

The Discriminating Factorial Analysis confirmed the clear separation between the breed based on their body measurements with a total of 95% of well-classed. The main discriminating parameters were in the order: (i) the length of the head, (ii) the neck length, (iii) the neck circumference, (iv) the teat length, and (v) the udder length. Genotyping records results are under the treatment by using different bioinformatical tools. Determination of population structure and phylogenetic tree presented considerable differences between studied populations.

CONCLUSION:

On the basis of expected and current scientific data, it will be possible to develop a "breeding strategy program" for each local camel population as well as to develop a genomic selection domain by designation of specific SNP markers for the native camel populations.

KEYWORDS

Dromedary camels, hybrids, phenotype, genotype, biodiversity

CITATION

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