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SNPs analysis in sheep for stabilizing genetic traits and improving fertility

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Abstract: *Prolificity in sheep or the ability to produce more offspring is influenced by several key genes (BMPR-1B, GDF9, NR5A2, DLG1). Genetic selection is a powerful tool in improving lamb survival rates and overall herd productivity. In the present study, we performed SNP analysis on a number of 90 sheep using DNA microarray 50K SNPs in order to identify genetic profiles at the level of the entire genome in the studied animals. The following aspects were identified in the analysis: in the case of the 90 sheep taken into study, a number of 693 SNPs were identified at the exome level with a distribution at the level of the 26 autosomal chromosomes, respectively on the X chromosome and the mitochondrial/Ch. M as follows - 74 SNPs on chromosome 1/Ch.1, 62 SNPs /Ch.2, 62 SNPs /Ch.3, 33 SNPs /Ch.4, 36 SNPs /Ch.5, 28 SNPs /Ch.6, 39 SNPs /Ch.7, 15 SNPs /Ch.8, 18 SNPs /Ch.9, 11 SNPs /Ch.10, 28 SNPs /Ch.11, 20 SNPs /Ch.12, 19 SNPs /Ch.13, 23 SNPs /Ch.14, 42 SNPs /Ch.15, 9 SNPs /Ch.16, 17 SNPs /Ch.17, 21 SNPs /Ch.18, 16 SNPs /Ch.19, 23 SNPs /Ch.20, 12 SNPs /Ch.21, 9 SNPs /Ch.22, 9 SNPs /Ch.23, 18 SNPs /Ch.24, 14 SNPs /Ch.25, 10 SNPs /Ch.26, 24 SNPs /Ch.X and 1 SNP /Ch.M. Based on the analysis, the genotype and allele frequencies of the SNPs were generated in the animals taken into analysis for the fertility trait. In our analysis, we associated twin births with the genotype profile in each animal analyzed, having as references 3 SNPs: SNP2 = AX-124372747, GDF9 gene; SNP = AX-123208711, NR5A2 gene; SNP = AX-124368945, DLG1 gene. For the GDF9 gene the heterozygous genotypic variant is expressed representatively (65%) while for the NR5A2 (89%) and DLG1 (92%) genes it is the homozygous one. In conclusion, based on the SNPs analysis in the studied animals, it was possible to establish the correlation between the 3 SNP/allelic variants and the number of offspring produced at calving.*

• Introduction

Genetic selection is a powerful tool in improving lamb survival rates and overall flock productivity. Here are some key points to consider: maternal phenotypic traits (selecting ewes that exhibit strong maternal instincts, good milk production and ease of calving); lamb survival rates (selecting breeding stock from lines with historically high survival rates); health and resilience - focusing on genetics that promote overall health and disease resistance; selecting traits that support fast, healthy lamb growth. Reproductive efficiency - selecting rams and ewes with high fertility rates and consistent reproductive performance. Implementing these strategies can help improve lamb survival rates and a more successful and sustainable sheep farming operation. In the present study, we performed SNP analysis on a number of 90 sheep using DNA microarray 50K SNPs in order to identify genetic profiles at the level of the entire genome in the studied animals.

• Material and method

We identified and collected phenotypic data from the studied sheep group, a total of 90 sheep belonging to the Țigaie Ruginie breed. Biological samples were also prelevated, blood from the jugular vein in a volume of 6 ml/animal in tubes with EDTA anticoagulant. Furthermore, we performed DNA analysis using the Axiom™ Ovine Genotyping Array (50K)/DNAmicroarray, which can identify up to 50K SNPs (single nucleotide polymorphisms) distributed throughout the genome (both exons and introns).

• Results and discussions

In all 90 animals with reference to the history of phenotypic characters related to prolificacy/products at calving, the following can be noted: the number of twin calvings is increasing in 2021-2024 interval with a higher number of male products; the number of female/male products (in single calvings) is almost equal; for the SNPs analysis of genes, animals with infertile matings or which presented abortion were also taken into analysis, these being, over the analyzed interval, in a number of 5 animals/2021, 9 animals/2022, 7 animals/2023, 8 animals/2024 with infertile matings, respectively 2 animals that presented abortion, more details Fig.1.

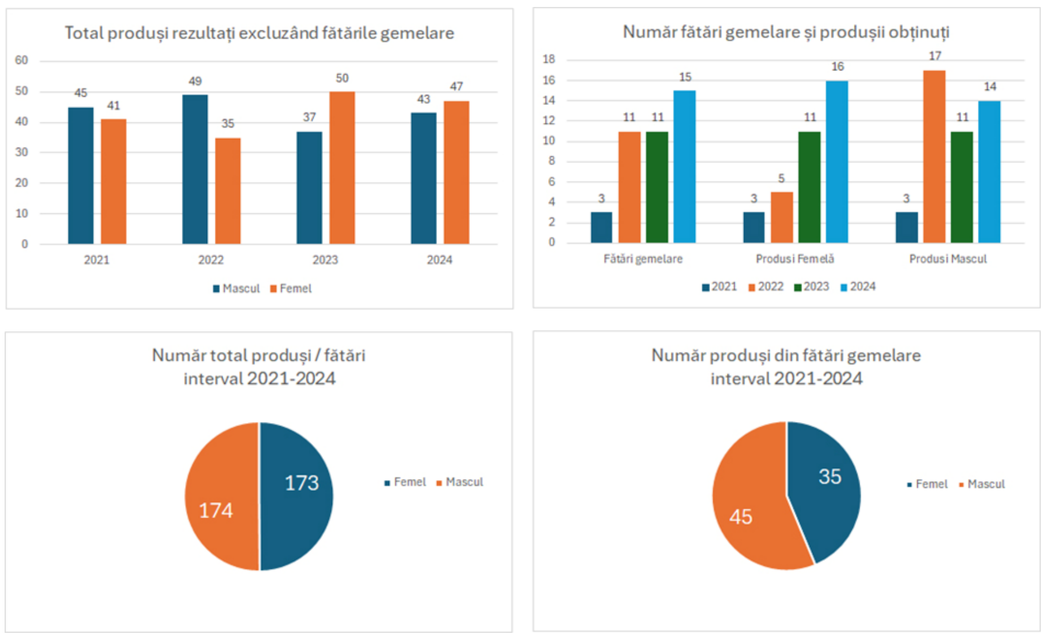

Figure 1. Graphical representation of historical phenotypic data with reference to the number of offspring / distribution by sex at calving (uniparous/twin), for 90 sheep, analysis interval 2021-2024.

A number of 693 SNPs were identified at the exome level with a distribution across the 26 autosomal chromosomes, respectively on the X chromosome and the mitochondrial/Ch chromosome. M as follows: 74 SNPs on chromosome 1/Ch.1, 62 SNPs /Ch.2, 62 SNPs /Ch.3, 33 SNPs /Ch.4, 36 SNPs /Ch.5, 28 SNPs /Ch.6, 39 SNPs /Ch.7, 15 SNPs /Ch.8, 18 SNPs /Ch.9, 11 SNPs /Ch.10, 28 SNPs /Ch.11, 20 SNPs /Ch.12, 19 SNPs /Ch.13, 23 SNPs /Ch.14, 42 SNPs /Ch.15, 9 SNPs /Ch.16, 17 SNPs /Ch.17, 21 SNPs /Ch.18, 16 SNPs /Ch.19, 23 SNPs /Ch.20, 12 SNPs /Ch.21, 9 SNPs /Ch.22, 9 SNPs /Ch.23, 18 SNPs /Ch.24, 14 SNPs /Ch.25, 10 SNPs /Ch.26, 24 SNPs /Ch.X respectively 1 SNP /Ch.M. The genes involved/related to prolificacy for which SNPs were identified are follows: *BMP15* (bone morphogenetic protein), 15*GDF9* (growth differentiation factor 9), *NR5A2*(the nuclear receptor subfamily five group A member 2/ fetoprotein transcription factor) and *DLG1(*discs large MAGUK scaffold protein 1).

• Conclusions

Based on the phenotypic fertility analysis correlated with genomic analysis of the genes involved in reproduction, the selection of favorable animals can be achieved.

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