POLYMORPHISM AT BTN1A1, SCD AND LPL AND ITS ASSOCIATION ON MILK PARAMETERS IN CZECH WHITE SHORTHAIRED GOAT BREED

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Abstract

Increasing productivity, improving milk composition, and boosting milk yield are of great economic importance for the dairy industry. Goat milk is appealing for its nutritional aspects, healthy properties, and functional food effects. Milk traits can be modified extensively by both environmental and genetic factors. The aim of this study was to investigate variation at the BTN1A1, SCD, and LPL loci and to investigate the effects of genetic variants of BTN1A1 (exon 4), SCD (exon 3 and intron 3), and LPL (signal peptide and intron 1) genes on goat milk traits in White Shorthaired goats kept in the Czech Republic.

Typing of *BTN1A1* was performed by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) and of loci *SCD* and *LPL* by primer extension analysis (PEA). In the analysis, we used 363, 350, and 156 animals with 6196, 5635, and 1175 performance records for the *SCD*, *BTN1A1*, and *LPL* genes, respectively. A mixed model with repeatability was used to estimate the impact of polymorphism in *BTN1A1*, *SCD*, and *LPL* genes on milk production traits (milk yield, fat and protein percentage). The fixed effects were genotype, herd-year-season of performance, age* age, month of performance, and parity number, depending upon which trait was being evaluated. The random effect was the animal (repeated measurements per goat).

Molecular analysis confirmed that the most prevalent genotype at the *BTN1A1* locus was GG (77.43%), followed by AG (20.57%) and AA (2.00%). Occurring most frequently at the *SCD* locus was genotype combination AAAACCGGGG (56.75%), followed by AGAACTGGAG (16.80%) and AGAGCCAGAG (11.29%). At the *LPL* locus, the most prevalent genotype combination was GGGACCCC (30.77%), followed by GGGGCCCC (19.23%) and GGGGCTCC (14.74%).

Association analysis confirmed an effect of genetic polymorphism at the *BTN1A1* locus on milk yield (kg) and protein content (%). Loci *SCD* and *LPL* were associated with milk yield (kg), protein content, and fat content (%). We conclude that the analysed loci may serve in breeding as candidate genes for improving goat milk's qualitative and quantitative traits (NAZV QJ1310107).

Key words: *Goat, Polymorphism, Milk traits, BTN1A1, SCD, LPL.*