

POLYMORPHISM AND ASSOCIATION OF THE FASN GENE WITH MILK PRODUCTION TRAITS IN CZECH SHEEP POPULATION

Zuzana Sztankoova^{1*}, Jana Rychtarova¹, Marketa Borkova², Alena Svitakova¹, Michal Milerski¹

¹Institute of Animal Science, Pratelstvi 815, 104 00 Prague Uhrineves, Czech Republic

²Dairy Research Institute, Ke Dvoru 12a, 160 00 Prague, Czech Republic

*e-mail: sztankoova@seznam.cz

Abstract

The objective of this study was to identify single nucleotide polymorphism (SNP) of the ovine fatty acid synthase (FASN) gene and to evaluate its effect on milk parameters and fatty acids (FAs) composition in sheep milk. The FASN gene encodes an enzyme catalysing the *de novo* synthesis of FAs in cells and is mainly expressed in adipose tissue. Milk FA profiles play an important role in dairy sheep farming because they have a large effect on cheese characteristics and also because sheep milk may be designated as a source of nutraceuticals inasmuch as it contains higher levels of conjugated linoleic acid than does milk from other ruminants.

Typing SNP within exon 32 of FASN at position g.257C>T was performed using the rapid and efficient TaqMan assay method. The study was performed for 772 sheep kept in the Czech Republic and belonging to the following breeds: East Friesian (529 animals), Lacaune (152 animals), Romanov (51 animals), and Valachian (40 animals). We used 507 animals with 8593 dairy production records to evaluate the effect of genetic polymorphism at the FASN locus on milk parameters. To determine allele frequency, genotype distribution, observed (H_o) and expected (H_e) heterozygosity as well as to verify Hardy-Weinberg equilibrium was used GenAIEx 6.502 analysis. Analysis of variance was carrying out using the MIXED model procedure in SAS software v. 9.4. A two different model equation was chosen for testing performance data depending upon which trait was being evaluated. To determine the effect of genetic polymorphism on milk parameters was used followed model: the fixed effects were genotype, herd-year of performance, days in milk (DIM), DIM*DIM, month of performance, and parity number.

Molecular analysis showed prevalence of the C allele (81.67%) compared to the T allele (18.33%). The dominant genotype was CC (43% - 85%), followed CT (15% - 47%) and TT (0% - 16%) depending on breed and number of animals observed. All four breeds were in Hardy-Weinberg equilibrium ($P < 0.05$) and showed weak heterozygosity at the FASN locus. The SNP g.257C>T within exon 32 of FASN was significantly associated with protein, fat, and lactose percentage. For FA analysis, we used 94 individuals with 112 dairy records. To determine the effect of genetic polymorphism on fatty acids was used followed model: a fixed effect was number of lactation, genotype and year of sample collection. The animal genetic effect was set as the random effect (repeated measurements per sheep). The animal genetic effect was set as the random effect (repeated measurements per sheep). Statistical analysis confirmed association with the minority FA components: valeric acid (C5:0) and pentadecylic acid (C15:0), and a tendency was observed for association with oleic acid (C18:1n9c) and gamma-linoleic acid (C18:3n6) ($P < 0.05$).

In conclusion, the SNP g.257C>T contributes to influence on the medium- and long-chain FAs. FASN is a candidate gene for milk parameters and may be used as a genetic marker for improving milk quality and milk fat content in sheep.

Key words: Sheep, Polymorphism, Milk traits, FASN.