

Estimation of myostatin gene effect on production traits and fatty acid contents in bovine milk

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The aim of this study was to estimate the genetic parameters of milk, fat, and protein yields, saturated (SFA) and monounsaturated fatty acid (MUFA) contents in bovine milk and to estimate the Myostatin (mh) gene effect on these traits. For this purpose, 51,614 test-day records (24,124, 16,145, and 11,345 for first, second, and third lactation, respectively) of 3,098 dual purpose Belgian Blue cows in 38 herds from the Walloon Region of Belgium were used. Because only 2,301 animals, including 1,082 cows with test-day records, were genotyped for mh, the gene content of non-genotyped animals was predicted from animals with a known genotype using the relationships with these animals. Variance components were estimated using Restricted Maximum Likelihood. A 3-lactations, 5-traits random regression test-day mixed model, based on the official Walloon genetic evaluation model for production traits, was used with an additional fixed regression on mh gene content to estimate allele substitution effects. Daily heritability estimates (average of 3 lactations) were 0.34 for SFA and 0.16 for MUFA and were higher than those for production traits (0.11, 0.10, and 0.09 for milk, fat, and protein yields, respectively). Allele substitution effects (\pm approximate standard-errors) for mh through the three lactations were -0.628 (\pm 0.343), -0.024 (\pm 0.014) and -0.021 (\pm 0.009) kg per day for milk, fat, and protein yields, respectively. Concerning SFA and MUFA contents in milk, the average allele substitution effects were -0.001 (\pm 0.027) and 0.029 (\pm 0.023) g/dl of milk. To conclude, results from this study showed that milk performance traits and milk fatty acid profile are influenced by mh genotypes.