Short Communication

Metabolic indicators in cattle breeding

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Potential associations among glucose tolerance test (GTT) as ability to metabolize glucose, estimated breeding values (EBVs) for milk traits and selected candidate gene polymorphisms were evaluated. German Holstein sires, born in 1993 and between years 1999 and 2003, were analysed. A few significant negative correlations between milk and protein yield and GTT were found in sires born in 1993. Only a few significant correlations were found for protein yield, protein percentage and for fat percentage and yield (sires born in different years). Any linkage of *DGAT1, GH1, GHR, FASN* and *OLR1* to *GTT* was found.

Keywords: milk, glucose, correlation, breeding values

1   Introduction

Energy metabolism plays an important role in production of healthy animals with high performance as the goal of cattle breeding. Energy metabolism is highly affected by insulin. Its function in the organism can be measured using intravenous glucose tolerance test (GTT) (Kneeskern et al., 2016, Deepa et al., 2015).

So far, only a few studies focused on association of GTT results to milk performance (Panicke et al., 2000). Therefore, the aim of this study was to evaluate the relationship between GTT and breeding values for milk performance. Also, we analysed the association among GTT and several candidate genes. For the evaluation, we selected candidate genes with association with milk performance. *DGAT1* is a candidate gene for milk fat (Grisart et al., 2002). Other genes, with potential affect on milk production, are genes for growth hormone (*GH1*) and its receptor (*GHR*) (DiStasio et al., 2005). Other candidate gene associated with milk production is oxidized low-density lipoprotein receptor (*OLR1*) with final effect on the milk composition (Khatib et al., 2006). Finally, fatty acid synthase (*FASN*), which SNP are associated with variations in fatty acid composition, was selected (Morris et al., 2007).

2   Material and methods

In the study, 461 animals were genotyped for *DGAT1* (*K232A* polymorphism), 485 animals for *GH1* (*L127V* polymorphism), 236 animals for *GHR* (a polymorphism at position 257 in exon 10), 184 animals for *FASN* (*A17934G* polymorphism) and 146 animals for *OLR1* (a polymorphism at 8,232 position). DNA was isolated from whole blood or frozen sperm. Genotyping was performed using PCR RFLP methods according to above mentioned studies. The glucose tolerance test (GTT) was performed in 542 sires according to Panicke et al. (2000). Estimation of animal effect for GTT was done using a software packege PEST (Groeneveld, 2006). The results of GTT and the the estimated breeding values (EBVs) were analyzed according to the genotypes.

We performed analyses using the least-squares method, by means of the GLM and MIXED procedures of SAS (SAS 9.3, SAS Institute, Cary, NC, USA). For comparison, contrast between genotypes, the MIXED procedure was used. Following model was developed:

$$Y_{ij} = \mu + gen_i + animal_j + e_{ijk}$$

where

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Y_{ij} is the breeding value of the sire for each trait of milk yield; or the value of GTT indicator; μ is the population mean;

gen = the genotype is fixed effect (i = 1, 2, 3);

animal is the random effect (j = 1 to 542);

e_{ijk} is random residual.

Finally, the phenotypic correlations among GTT and EBVs for milk were calculated by the Pearson correlations.

3   Results and discussion

The most interesting results were found in sires born in year 1993. There were found significant correlations between milk yield estimated breeding value (EBV) and glucose tolerance rest (GTT) and between fat and protein yield and GTT. All corrrelations were negative. In this year of birth, the correlations between EBVs for milk, fat and protein yield and GTT, the correlations ranged from -0.30 to -0.45, when the other correlations except of the mentioned were non-significant.

The analyses discovered low non-significant correlations for sires year of birth between 1998 and 2003. Our results are partially consistent with results of Panicke et al. (2000). They found significant negative correlations between estimated breeding values for milk yield, fat and protein yield and GTT. Their results showed possible use of glucose tolerance test in early testing of sires, but, our study did not confirm it.

We found only small and non-significant differences in GTT according to the genotype of the candidate loci and therefore, the influence of the polymorphisms on the GTT variance was evaluated as not relevant.

4   Conclusions

The GTT is useful tool for studies of the metabolic capacity of cattle. Using of GTT for early breeding value evaluation remains to be solved.

Acknowledgments

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