EFFECT OF SNP POLYMORPHISMS ON THE BREEDING VALUE OF BEEF IN HUNGARIAN SIMMENTAL CATTLE

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Abstract – The objective of this study was to estimate the effect of SNP polymorphisms on the breeding value of beef (beef merit index). Genotypes were determined by DNA chip technique (Illumina Bovine HD Chip, 777000 SNPs). Data screening and data identification was performed by multi-locus mixed-model. Statistical analyses have been carried out to find association between the individual genotypes and breeding value of beef. Two loci showed considerable association with breeding value ($-\log_{10}P=25.3$ and 22.7) on chromosome 2 and 11, respectively.

Key Words – Hungarian Simmental, SNP, breeding value

I. INTRODUCTION

At present, there is considerable interest in the application of genomic breeding value estimation (BV) to promote rapid and efficient selection in farm animals. In the last few years advances in molecular genetics have enabled the application of MAS (Marker Assisted Selection) in achieving different breeding objectives. Some SNPs (single nucleotide polymorphisms) have been demonstrated to affect intramuscular fat content and meat quality traits in farm animals [1,2]. Genom-wide association study (GWAS) based on typing of 777000 SNPs by DNA chip technique is suitable for the improvement of beef quality and breeding value of beef in different cattle breeds. Correlations among DNA-chip data and breeding value of beef can be highlighted by statistical analysis.

Availability of genomic information on a large number of animals has changed the dairy cattle breeding worldwide. In case of beef cattle and dual purpose cattle GWAS can also change the selection progress, though the effective population number and the accuracy of genomic estimated breeding value is lower compared to dairy cattle.

Contrary to complete genomic breeding value estimation, which –on global scale- is performed only in a few specialized centers, studies regarding several traits (e.g. beef quality and phenotypical breeding value) in case of dual purpose cattle or beef cattle is even locally executable.

Present survey estimates the effect of SNP polymorphisms on breeding value of beef. Relation between breeding value and beef quality will be analyzed as well. This study is part of a comprehensive project which aims the improvement of beef quality in Hungarian Simmental cattle.

II. MATERIALS AND METHODS

60 Hungarian Simmental bulls were selected for this study. Semen samples have been collected from the gene bank of Association of Hungarian Simmental Cattle Breeders and were stored in liquid nitrogen at -196°C until DNA extraction. DNA typing was performed on high-resolution SNP chips developed for cattle (Illumina Bovine HD Chip, 777000 SNPs).

Performance data and breeding parameters of bulls were collected from the database of Association of Hungarian Simmental Cattle Breeders.

For data screening and identification of loci associated with BV genomic relationship matrix and multi-locus mixed-model were used to handle the confounding effects [3]. Statistical analyses were performed by using the SVS

software, which is suitable to fit standard linear models, account for population stratification or environmental interaction [4].

III.   RESULTS AND DISCUSSION

According to the analysis outcome, seven loci have been identified to be associated with breeding value. Among these loci ($-\log_{10}P >5$) two seem to be useful in selection program, which are located on Chromosome 2 and 11, respectively (Figure 1).

Breeding values -collected from database- ranged from 80 to 130. In previous studies, average beef merit index of Hungarian Simmental sires in progeny testing was 103.43 [5]. Allelic pattern of mentioned locus at Chr 2 has changed to homozygous in all animals with breeding value higher than 110. On Chromosome 11 majority of animals with breeding value lower than 102 were homozygous at the indicated locus, as well. The favorable alleles can be found in heterozygous form in the sampled animals; their allele frequencies (0.545 and 0.409) provide straightforward possibility to assist selection by molecular tools.
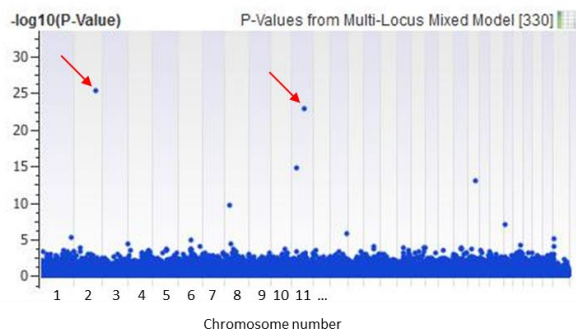

Figure 1. Manhattan plot of SNPs associated with breeding value of beef

Loci marked by arrows display the highest degree of association with the breeding value of beef (beef merit index) in Hungarian Simmental cattle.

IV.   CONCLUSION

Molecular tests can provide facilities for the direct selection among variants. However the benefits of the different alleles depend on economic reasons given in the breeding programs. A possible marker assisted selection (MAS) approach, such as selecting for favorable alleles at reported loci on chromosomes mentioned above, might be performed, if increased weight gain, muscularity and/or higher lean meat production is desirable.

More animals will be included in this investigation in order to discover loci suitable for selection purposes to improve beef quality.

Association of Hungarian Simmental Cattle Breeders has taken measures in the past years to improve quality of beef and to meet demand of consumers with high quality products.

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