

# Genome-wide association study of carcass traits in an Angus beef cattle Russian herd using imputed Whole-Genome Sequence data

Baneh H.<sup>1\*</sup>, Grigoreva E.<sup>1</sup>, Nizamutdinov I.<sup>2</sup>, Elatkin N.<sup>2</sup>, Lebedev I.<sup>2</sup>, Gentzbittel L.<sup>1</sup>

<sup>1</sup> *Project Center for Agro Technologies, Skolkovo Institute of Science and Technology, Moscow, Russia*

<sup>2</sup> *Miratorg-genetics LLC, Moscow, Russia*

\* *H.Baneh@skoltech.ru*

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The new genotyping technologies has provided a great opportunity for genomic studies and in particular identifying the genome regions associated with complex traits. Genotype imputation is a cheap and efficient tool to expand genotypes of low-density array to a much higher dense panel, by making use of whole genome sequence information. It appears that denser SNP panels obtained after imputation are more powerful and reliable in deciphering genetic background of the traits, in particular for Genome-wide association studies (GWAS). This study was carried out to optimize a corporate SNP chip array for Angus beef cattle via incorporating new significant SNPs affecting carcass weight (CW), rib-eye area (REA), marbling score (MS) and back fat thickness (FAT). As a first step, the 50K SNP chip genotypes of 338,824 Angus cows belonging to Miratorg Company were imputed to 9,351,538 variants (~173X increase in information), using whole genome sequences of 128 and 47 Angus bulls from the 1,000 genome project and Miratorg Company respectively, as reference population. Results indicated that population-based imputation method is more efficient compared to pedigree-based method and the Beagle software outperforms other programs. As a second step, the high accurately ( $DR2 > 0.8$ ) imputed SNPs ( $n = 6,544,904$ ) of 13,241 bulls having phenotype information were used for association studies. Genome-wide association studies were performed by applying Mixed Linear Model analysis, considering polygenic effect fitted as random part of the model and using a genomic relationship matrix. According to Bonferroni correction adjusted for the number of effective SNPs (threshold =  $3e-7$ ), 1,697 SNPs were found to be associated with CW (842 SNPs), REA (745), MS (340) and FAT (101). Among the signals, those located on BTA6 (for CW) and BTA19 (for MS) were not detected by 50K SNP genotypes. The identified signals were located within either the coding region or regulatory regions (upstream/downstream) of 47 coding protein, miRNA and siRNA genes. In addition, several significant SNPs were found in common between the traits, suggesting the genes with pleiotropic effects or functional polymorphic markers that affect more than one biological pathway. The potential candidate genes for the studied traits play a critical role in some biological process like apoptosis, lipid metabolism, immunity, ion transportations and regulation of translation and transcription. Our findings highlight the power of using imputation to perform GWAS, and provide some valuable information for better understanding of the underlying genetic background of carcass traits in the beef cattle.