

GWAS to determine the characteristics of metabolism and search for associations in Black Angus cattle

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GWAS is a genome wide association study, which is applying for searching links between genomic variants and phenotypic observations. The main objects for GWAS research are SNPs, related to different illnesses or metabolic characteristics. Data for analysis obtain from DNA-arrays with several alleles of each gene. The main aim of our study was searching of genomic variants, related to economically important features (marbling, or amount of intramuscular fat), for *Black Angus* cows.

Black Angus cattle DNA samples were genotyped using standard Illumina BovineSNP50 v3 DNA BeadChip. For data analysis PLINK 1.9 were used.

SNPs were filtered based on several characteristics: minor allele frequency (>0.05), proportion of missing genotypes (<0.05), Hardy-Weinberg equilibrium ($>10^{-6}$) and proportion of individuals with missing genotypes (<0.1). After filtering 1834 male genotypes and 53218 phenotypes were used for further analysis. Variants with linkage disequilibrium were also pruned.

PCA was used for covariates searching. For selection of the most affective factors we used linear regression as we had quantitative measurements of marbling. Using R script screen plot and Manhattan plot were built.

We identified significant SNPs in 2, 3 and 7 chromosomes of *Bos Taurus* genome. In 2 chromosome 2 SNPs (odds ratio (OR) 23.5 and 25.83) were detected. According to Cattle QTL database those SNPs were related to milk lauric acid content, milk pentadecylic acid content and milk palmitic acid content (locuses id: QTL:172096, QTL:172070, QTL:172071 respectively). In 3 chromosome 3 SNPs (OR 19.85, -19.73 and -19.39) were detected. According to Cattle QTL database those SNPs were related to average daily gain, average daily feed intake and milk fat percentage (locuses id: QTL:20926, QTL: 20989, QTL: 2442 respectively). In 7 chromosome 5 SNPs (OR 22.41, 21.46, 21.07, 22.65 and 20.83) were detected. According to Cattle QTL database those SNPs were related to average daily gain, muscle iron content and saturated fatty acid content (locuses id: QTL: 22785, QTL: 24054, QTL: 19729 respectively). So, we succeed at searching several SNPs related to locuses with economically important features.