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Genome-wide association study for body temperature maintenance under the cold stress in Siberian cattle

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Motivation and Aim: There are over 1000 cattle breeds existing worldwide, some of which dwell in local environments characterised by very cold winter temperatures suggesting selection pressure for cold climate tolerance. While being of economic significance, the genetic basis of cold tolerance in cattle is not well understood. Therefore, we performed a genome-wide association study (GWAS) for body temperature maintenance under cold stress in Hereford and Kazakh Whitehead cattle breeds bred in Siberia.

Methods and Algorithms: A total of 183 dams and bulls were used for hourly ear canal temperature measurements for two weeks in February 2017. The area under the curve of body temperature over the period of five coldest days (from –20 to –30 °C) within the two-week interval was considered as the phenotype for each animal. DNA was extracted from blood and genotyped on the GeneSeek Bovine GGP HD150K commercial SNP array. After data filtering in plink: --maf 0.05, --chr1-29, 108298 SNPs were used in association studies. We performed a single SNP GWAS using EMMAX software with sex and breed being taken as covariates. Then the data were phased with fastPhase software, haploblocks were defined in Haploview (D' > 0.8) and the haplotype trend regression (HTR) analysis (R package "gap", function "htr") was performed to test for association between haploblocks and the range of phenotype measurements in the dataset applying the same covariates. In addition, signatures of selections were identified in the whole dataset of 183 individuals using the de-correlated composite of multiple signals (DCMS) framework combining the H1, H12, Tajima's D and nucleotide diversity statistics.

Results: Out of two SNPs found above the suggestive significance threshold (q-value < 0.1) from the EMMAX results, one (BovineHD1500000472) was found within one of two haploblocks reported significant by HTR (q-value < 0.05). The same interval on BTA15: 1.58–2.03 Mbp was reported as a putative signature of selection by DCMS. This interval contains four genes of which two: *MSANTD4* and *GRIA4* are functional candidates for body temperature-related traits.

Conclusion: A genomic interval of 450 Kbp on BTA15 is associated with temperature maintenance in Hereford and Kazakh Whitehead cattle in Siberia under the cold temperature stress. This region contains two relevant functional candidate genes and requires further studies (e. g., resequencing and RNASeq analysis of relevant tissues) to confirm its role and to identify causative variants.

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