

ABSTRACT

Genome-wide association studies identified variants for taurine concentration in Japanese Black beef

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We performed genome-wide association studies (GWAS) using the BovineSNP50 array to detect significant single nucleotide polymorphisms (SNPs) that may affect the concentration of 22 free amino acids and three peptides in Japanese Black beef cattle. A total of 574 Japanese Black cattle and 40,657 SNPs from the array were used for this study. Genome-wide significant SNPs were detected for β -alanine (three SNPs on chromosomes 22 and 29) and taurine (26 SNPs on chromosome 22). Importantly, the top two SNPs for taurine were highly significant ($p = 6.2 \times 10^{-21}$), and the frequency of the increase-concentration allele (Q) for taurine was found to be 0.73. The Q allele frequency of this population was similar to that of the other unrelated Japanese Black cattle, but different from that of the other breeds. In addition, the significant SNPs were not associated with carcass traits or fatty acid compositions. Interestingly, the top three of the four most significant SNPs for taurine were located near solute carrier family 6, member 6 (*SLC6A6*), which is a membrane transporter for taurine. We also found two associated variants in the 5'-upstream region of *SLC6A6*; however, they were less significantly associated than the SNPs from the BovineSNP50 array.

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