

ABSTRACT

Genome-wide association study for carcass traits, fatty acid composition, chemical composition, sugar, and the effects of related candidate genes in Japanese Black cattle

Nanae Sasago 1, Tsuyoshi Abe 1, Hironori Sakuma 1, Takatoshi Kojima 1, Yoshinobu Uemoto 1

National Livestock Breeding Center, Nishigo, Fukushima, Japan.

We performed a genome-wide association study (GWAS) and candidate gene analysis to: (i) evaluate the effectiveness of the GWAS in our small population by performing GWAS for carcass weight (CW) and fatty acid composition; (ii) detect novel candidate regions affecting non-CW carcass traits, chemical composition and sugar; and (iii) evaluate the association of the candidate genes previously detected in CW and fatty acid composition with other economically important traits. A total of 574 Japanese Black cattle and 40 657 Single nucleotide polymorphisms were used. In addition, candidate gene analyses were performed to evaluate the association of three CW-related genes and two fatty acid-related genes with carcass traits, fatty acid composition, chemical composition and sugar. The significant regions with the candidate genes were detected for CW and fatty acid composition, and these results showed that a significant region would be detectable despite the small sample size. The novel candidate regions were detected on BTA23 for crude protein and on BTA19 for fructose. CW-related genes associated with the rib-eye area and fatty acid composition were identified, and fatty acid-related genes had no relationship with other traits. Moreover, the favorable allele of CW-related genes had an unfavorable effect on fatty acid composition.