

ABSTRACT

**Novel mutations of the *FASN* gene and their effect on fatty acid composition in Japanese black beef.**

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Eight novel and four known mutations were detected in the coding sequence of the bovine fatty acid synthase (*FASN*) gene of an F2 population from Japanese Black and Limousin cattle. Two mutations, g.16024A>G and g.16039T>C, detected in exon 34, which determine amino acid substitutions of threonine (T) to alanine (A) and tryptophan (W) to arginine (R), were clearly separated in the parental breeds. The haplotypes (TW and AR) segregated in F2 individuals and had a significant effect on the fatty acid composition of backfat, intermuscular fat, and intramuscular fat. The TW haplotype was associated with increasing C18:0 and C18:1 content and the ratio of monounsaturated to saturated fatty acids, and decreasing C14:0, C14:1, C16:0, and C16:1 content. The two mutations were screened in two commercial Japanese Black half-sibling populations and similarly determined the contribution to the fatty acid composition of intramuscular fat. The frequency of the TW haplotype was markedly higher in Japanese Black (0.67) than in Holstein (0.17), Angus (0.02), and Hereford (0.07). We conclude that these mutations may contribute to the characteristic fatty acid composition of Japanese Black beef.

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