

ABSTRACT

**Identification of mitochondrial DNA substitutions related to meat quality in  
Japanese Black cattle<sup>1,2</sup>**

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Complete sequences of mitochondrial (mt) genomes of eight Japanese Black cattle were determined to investigate the relationships between mt deoxyribonucleic acid (DNA) displacement loop (D-loop) types and other mtDNA regions and to identify the variation in the coding region that may influence the economic traits. The survey of mitochondrial sequences in the encoding region revealed 14 substitutions including six antonymous substitutions and one in 16S ribosomal ribonucleic acid (rRNA). Three methods of polymorphic DNA analyses (polymerase chain reaction [PCR]-restriction fragment length polymorphism [RFLP], mismatch PCR-RFLP, PCR-single-strand conformation polymorphism [SSCP]) were performed on these seven candidate substitutions (base pair [bp] 2,232, 12,158, 12,908, 13,310, 14,122, 14,140, and 14,565) for 202 Japanese Black cattle. The substitution of bp 13,310 was observed in all samples, but not in the reference sequence, indicating that this is a minor substitution or a sequencing mistake in the reference sequence. The substitutions at bp 14,122, 14,140, and 14,565 were observed in only a few samples, suggesting that these were also minor substitutions. The substitutions at bp 2,232 (16S rRNA), 12,158, and 12,908 (reduced nicotinamide adenine dinucleotide-ubiquinone oxidoreductase chain-5) were closely related to mitochondrial D-loop types that have previously been related to differences in the carcass traits of Japanese Black cattle. Evaluation of the effects on six carcass traits with mixed model procedures suggests that the bp 2,232 substitution affects longissimus muscle area and beef marbling score. The substitution at bp 2,232 is a strong candidate for the mitochondrial effect on meat quality.

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