

ABSTRACT

MC1R c.310G>- and c.871G > A determine the coat color of Kumamoto sub-breed of Japanese Brown cattle

*Hirokazu Matsumoto, Masatake Kojya, Hiroko Takamuku, Satoshi Kimura, Atsushi Kashimura,
Saki Imai, Kenji Yamauchi, Shuichi Ito*

Coat color is one of the important factors characterizing breeds for domestic animals. Melanocortin 1 receptor (MC1R) is a representative responsible gene for this phenotype. Two single-nucleotide polymorphisms (SNPs) in bovine MC1R gene, c.296T > C and c.310G>-, have been well characterized, but these SNPs are not enough to explain cattle coat color. As far as we know, MC1R genotypes of Kumamoto sub-breed of Japanese Brown cattle have not been analyzed. In the current study, genotyping for c.296T > C and c.310G>- was performed to elucidate the role of MC1R in determining the coat color of this sub-breed. As a result, most animals were e/e genotype, suggesting the coat color of this sub-breed is derived from the e allele of MC1R gene. However, we found six animals with E/e genotype, which coat color would be black theoretically. Subsequently, sequence comparison was performed with these animals to identify other polymorphisms affecting coat color, elucidating that these animals possessed the A allele of c.871G > A commonly. c.871G > A was a non-synonymous mutation in the seventh transmembrane domain, suggesting alteration of the function and/or the structure of MC1R protein. Our data indicated that the A allele of c.871G > A might be a loss-of-function mutation.