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Identification of functional SNP of FASN related to lipid metabolism in Korean cattle

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In Korea, intramuscular fat (IMF) or marbling in a cross-section of longissimus dorsi muscle area (LM) tissue of cattle is an important component of carcass traits that have an impact on grading of beef quality and determining the meat price. The deposition of fat is mainly determined by lipid metabolism, which indicates the balance between fat deposition and fat removal in the LM. Also, the lipid metabolic gene may contribute to fat deposition. Among these genes, fatty acid synthase (FASN) is a multifunctional enzyme in fatty acid biosynthesis. This complex catalyzes the synthesis of the saturated fatty acids using acetyl-CoA, malonyl CoA and NADPH. FASN is a homodimer of 250 kDa subunits and contains seven catalysis activities and the acyl carrier protein (ACP). Many studies had reported that g.841G, g.16024A, g.16039T and g.17924G SNPs had a significant impact on marbling score in Korean cattle and Japanese black cattle population. These SNPs is a non-synonymous SNP to change amino acid and is in transcription factor binding site and beta-ketoacyl reductase, thioesterase region. The aim of this study was to investigate the relationship between these SNPs of FASN gene and marbling score of *longissimus dorsi* muscular area in Korean cattle. Among these SNPs, the g.841G and g.17924G SNP had a significant impact on marbling score (P<0.001). Therefore, our result suggests that, g.841G and g.17924G SNP will be a causal mutation in fatty acid biosynthesis. But we need further research for validating causal mutation as a site directed mutagenesis.

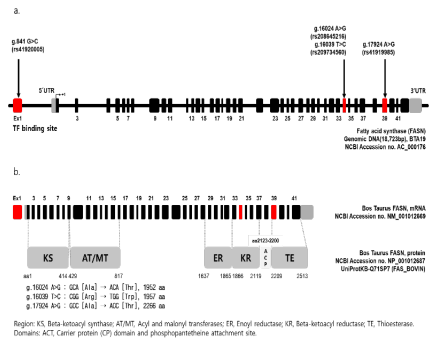

Figure-1: *Diagram of a position of functional SNP within fatty acid synthase in DNA, RNA and protein sequence. (1) Position of functional SNPs in DNA sequence and (2) Position of functional SNPs in RNA and protein sequence.*

Recent Publications

1. Kumar M, et al. (2016) SNP identification in thioesterase domain of fatty acid synthase gene in murrah buffaloes. *J Anim Plant Sci*; 26(6): 1828-1832.
2. Hayakawa K, et al. (2015) The g.841G>C SNP of FASN gene is associated with fatty acid composition in beef cattle. *Anim Sci J*; 86(8): 737-746.
3. Matsumoto H, et al. (2012) Identification of SNPs in the FASN gene and their effect on fatty acid milk composition in Holstein cattle. *Livest Sci*; 144(3): 281-284.
4. Zhang S, et al. (2008) DNA polymorphisms in bovine fatty acid synthase are associated with beef fatty acid composition. *Anim Genet*; 39(1): 62-70.
5. Roy R, et al. (2005) Genomic structure and alternative transcript of bovine fatty acid synthase gene (FASN): Comparative analysis of the FASN gene between monogastric and ruminant. *Cytogenet Genome Res*; 111(1): 65-73.

Biography

Yoonseok Lee has his expertise in evaluation and passion in gene editing and plant synthetic biology for producing high-quality meat.

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