

Association Of A Bovine Chromosome 19 Region, 51 Mb, With The Variation Of Oleic Acid In Hanwoo

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ABSTRACT: Carcass samples of 450 Hanwoo steers were collected in the Livestock Research Institute, Ansong, Korea, to detect SNP markers that were significantly associated with oleic acid (C18:1, relative fat %). The bovine Affymetrix 640K beadchip array was used for the SNP genotyping to perform genome-wide association tests. Analyses were performed using the Bayes B model implemented in the Gensel software. Three chromosomal regions, 51Mb of BTA19, 9 Mb of BTA24, and 54Mb of BTA5 were detected for C18:1 with 21.7%, 3.7% and 1.5% of total genetic variance, respectively. At the BTA19 region, a SNP (C/T), AX-21950207 that was located at 51,333kb was detected with 96% posterior probability of inclusion, which was distal to the *FASN* gene location (51,385~51,404 Kb). Additional studies are needed to verify the SNP effect on oleic acid variability between Hanwoo carcasses and to find the causal mutation at the chromosomal region.

Keywords: Hanwoo; Oleic acid; GWAS; SNP

Introduction

Hanwoo, a Korean native cattle, has been selected for high quality of meat as well as growth during the last several decades, so that Hanwoo beef composes great percentage of intramuscular fat, marbling (Jo et al. (2012)). However, due to the increasing concern about health, Korean consumers turned their attention to more nutrient and healthier foods including Hanwoo beef. Due to high throughput genotyping technologies such as the development of the bovine Illumina 770k or Affymetrix 640K SNP chips, genome scans to identify quantitative trait loci or evaluation of genome-based breeding values can be efficiently implemented (Hayes et al. (2013)).

There were several reports, in which chromosomal regions or quantitative trait loci (QTL) were identified for nutritional components in beef cattle (Uemoto et al. (2010); Saatchi et al. (2013)). For Hanwoo, some candidate genes for marbling or fatty acid composition were reported (Lee et al. (2010); Oh et al. (2011)). However, there was no report to find any QTL for fatty acid components through genome scans. In this study, we report the results of genome-wide association study (GWAS) on oleic acid in a sample of Hanwoo steers.

Materials and Methods

Data. Carcass samples of 450 Hanwoo steers with about 30 months of age were collected in the Livestock

Research Institute, Ansong, Korea between Springs of 2012 and 2013. The average carcass weight was 411 ± 51 kg. Tissues of the *longissimus dorsi* muscles at the 14th to 18th vertebrae were collected. Detailed description about sampling procedure and isolation of oleic acid as a fat percentage (C18:1) is in Jayasena et al. (2014). For each steer, the bovine Affymetrix 640K beadchip array was used for the SNP genotyping to perform genome-wide association tests.

Statistical analyses. To perform genome-wide scans to detect chromosomal regions or QTL for oleic acid, Bayes B method was applied using GenSel software vs 4.8 (ISU). Quality control for SNP selection was tested by MAF>0.05, genotyping rate >0.9 and H-W equilibrium test (P>0.001), resulting in 360K available SNPs. Fixed effects of slaughter year-season and a covariate of age of month at slaughter were fitted in the Bayesian model. Estimates of genetic and environmental variances were obtained from a REML method using ASREML program to be used as prior values in the Bayes B method. A fraction of markers (π) with no effects in the Bayesian mixture model was set as 0.997, and 41,000 iterations were done to generate posterior MCMC samples, for which the first 1,000 samples were removed as burn-in, and each of 100th sample were chosen to get the posterior mean and variance for the marker or 1 Mb window effect.

Results and Discussion

Three chromosomal regions, 51Mb of BTA19, 9 Mb of BTA24, and 54Mb of BTA5 were detected for C18:1 with 21.7%, 3.7% and 1.5% of total genetic variance, respectively, (Table 1). At the BTA19 region, a SNP (C/T), AX-21950207 that was located at 51,333kb was detected with 96% posterior probability of inclusion, which was proximal to the *FASN* gene location (51,385~51,404 Kb). In the similar chromosomal region, Uemoto et al. (2010) reported a SNP (ARS-BFGL-NGS-88163) for oleic acid at 52 Mb of BTA19 in Japanese Black cattle. Saatchi et al. (2013) also found a chromosomal region, 51 Mb of BTA19 (rs41923412 ~ rs109147235) that was associated with *cis*-9 18:1 in Angus beef cattle. These results indicate that for the SNPs on BTA19, common effect for oleic acid mechanism exists across cattle breeds, even with different genetic backgrounds. Additional studies are needed to verify the SNP effect on oleic acid variability between Hanwoo carcasses and to find the causal mutation at the chromosomal region.

Table 1. Significant chromosomal regions that were associated with variation of oleic acid (C18:1) in Hanwoo

SNP ^s (AX-)	SNP (AX-)	% ^v var	PPI ^{&}	Position (bp) [*]
28521526	21952187	21.7	0.98	19_51
23657971	23661811	3.74	0.38	24_9
26056910	26060377	1.54	0.20	5_54

^sStarting and ending SNPs at the 1 Mb chromosomal region

^vProportion of genetic variance due to the chromosomal window of 1 Mb

[&]Posterior probability of inclusion rate in the Bayesian B model

^{*}Chromosome number and position (Mb)

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