

A strategy for multiple linkage disequilibrium mapping methods to validate additive QTL

Li Yi*

School of Statistics, Shanxi University of Finance & Economics, Taiyuan, Shanxi,
China

liy3344520@hotmail.com

Jong-Joo Kim

School of Biotechnology, Yeungnam University, Gyeongsan, Gyeongbuk, Korea

kimjj@yumail.ac.kr

Kwan-Suk Kim

Department of Animal Science, Chungbuk National University, Cheongju, Korea

kwanskim@chungbuk.ac.kr

The efficiency of genome-wide association analysis (GWAS) depends on power of detection for quantitative trait loci (QTL) and precision for QTL mapping. In this study, three different strategies for GWAS were applied to detect QTL for carcass quality traits in the Korean cattle, Hanwoo; a linkage disequilibrium single locus regression (LDRM), a combined linkage and linkage disequilibrium analysis (LDVCM) and a BayesC π approach. Phenotypes of 486 steers were collected for carcass weight, backfat thickness, *longissimus dorsi* muscle area, and marbling score, and genotype data were also scored with the Illumina bovine 50k SNP chips for the steers. For the former two methods, threshold values were set FDR <0.01 on chromosome-wise level, while a cut-off such that top 5 variance of 10-SNP windows that were included in the Bayes C π model were determined for the latter model. A total of 12 and 10 QTL were detected by LDRM and LDVCM respectively, and after BayesC π refining four consistent QTL were obtained, which corresponded to QTL regions previously reported. Some well-known candidate genes for the traits of interest were located close to these QTL. Our result suggests the use of combined different LD mapping approaches can provide more reliable chromosome regions to further pinpoint DNA makers or causative genes in these regions.

Key words: QTL, Linkage Disequilibrium, SNP, Hanwoo