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Genomewide association analysis of growth traits in Charolais beef cattle

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ABSTRACT

The objective of this study was to perform a genomewide association study (GWAS) for growth traits in Charolais beef cattle and to identify SNP markers and genes associated with these traits. Our study included 855 animals genotyped using 76,883 SNP from the GeneSeek Genomic Profiler Bovine HD panel. The examined phenotypic data included birth, weaning, and yearling weights as well as pre- and postweaning ADG. After quality control, 68,337 SNP and 823 animals were retained in the analysis. The association analysis was performed using the principal components method via the *egscore* function of the GenABEL version 1.8-0 package in the R environment. Eighteen SNP located in 13 BTA were associated with growth traits ($P < 5 \times 10^{-5}$). The most important genes in these genomic regions were *TRAF6* (*tumor necrosis factor receptor-associated factor 6*), *CDH11* (*cadherin 11, type 2, OB-cadherin*), *KLF7* (*Kruppel-like factor 7*), *MIR181A-1* (*microRNA 181A-1*), and *PRCP* (*prolylcarboxypeptidase [angiotensinase C]*), due to their relationships with perinatal and postnatal survival, bone growth, cell adhesion, regulation of adipogenesis, and appetite. In conclusion, this study is the first to describe a GWAS conducted in beef cattle in Mexico and represents a basis for further and future research. This study detected new QTL associated with growth traits and identified 5 positional and functional candidate genes that are potentially involved in variations of the analyzed traits. Future analyses of these regions could help to identify useful markers for marker-assisted selection and will contribute to the knowledge of the genetic basis of growth in cattle and be a foundation for genomic predictions in Mexican Charolais cattle.

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