Effects of bovine SMO gene polymorphisms on the body measurement and meat quality traits of Qinchuan cattle

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ABSTRACT. Beef cattle breeding programs focus on improving important economic traits, including growth rates, and meat quantity and quality. Molecular marker-assisted selection based on genetic variation represents a potential method for breeding genetically improved livestock with better economic traits. Smoothened (SMO) protein is a signal transducer that contributes to the regulation of both osteogenesis and adipogenesis through the hedgehog pathway. In this study, we detected polymorphisms in the bovine SMO gene of Qinchuan cattle, and we analyzed their associations with body measurement traits (BMTs) and meat quality traits (MQTs). Using DNA sequencing and polymerase chain reaction-restriction fragment length polymorphism, 3 novel single nucleotide polymorphisms were identified in the SMO gene of 562 cattle: 1 G > C mutation on exon 9 (G21234C) and 2 C > T mutations on exon 11 (C22424T and C22481T). Association analysis showed that polymorphisms on both the G21234C and C22424T loci significantly affected certain BMTs and MQTs (P < 0.05 or P < 0.01),
whereas those on the C22481T locus did not (P > 0.05). Therefore, the SMO gene could be used as a candidate gene to alter BMTs and MQTs in Qinchuan cattle or for marker-assisted selection to breed cattle with superior BMTs and MQTs.

**Key words:** Body measurement traits; Meat quality traits; Qinchuan cattle; Smoothened; Polymorphisms