



# 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. Smoothed (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