Associations between polymorphisms of the \textit{GFI1B} gene and growth traits of indigenous Chinese goats

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ABSTRACT. This study aimed to investigate polymorphisms of the eighth exon in the \textit{GFI1B} gene among three indigenous Chinese goat breeds (QianBei Ma goats, GuiZhou white goats, and GuiZhou black goats). Furthermore, association analysis was conducted between these polymorphisms and growth traits. Polymerase chain reaction-single strand conformation polymorphism (PCR-SSCP), direct DNA sequencing, and PCR-restricted fragment length polymorphism (RFLP) were applied to detect polymorphism sites, and a general linear model was used to analyze their association with growth traits. We found two consistent single nucleotide polymorphism (SNP) sites in the eighth exon of the \textit{GFI1B} gene among the three breeds: 263 bp G→T and 340 bp G→A. The fixed effects model used to analyze growth traits revealed significant differences in body weight, body length, chest depth, and chest breadth between genotypes CD, CC, and DD (P < 0.01). The 340(G/C) polymorphic sites identified here will provide a basis to further study associations between the \textit{GFI1B} gene and growth
traits, as well as establish a theoretical foundation to develop better feeding and genetic resources of indigenous goats.

**Key words:** GFI1B gene; Indigenous Chinese goats; PCR-SSCP; PCR-RFLP; Growth trait