Analysis of \textit{POU1F1} gene \textit{Ddel} polymorphism in Chinese goats

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ABSTRACT. As a member of the POU-domain family, the POU1F1 is a positive regulator for growth hormone, prolactin and thyroid-stimulating hormone \( \beta \), by binding to target DNA promoters as a dimer in mammals. This study described the polymorphisms at the goat \textit{POU1F1-Ddel} locus and analyzed the distribution of alleles in 15 indigenous Chinese goat breeds. The PCR-RFLP analysis showed a predominance of the \( \text{D}_1\text{D}_1 \) genotype and the \( \text{D}_1 \) allele, with average frequencies of 0.550 and 0.790, respectively, irrespective of goat utility type. The \( \text{D}_1\text{D}_2 \) genotype was the second most frequent, with a mean frequency of 0.371. The distributions of genotypic and allelic frequencies at this locus were found to be significantly different among populations based on a Chi square test \((P < 0.001)\), suggesting that the breed factor significantly affected the molecular genetic character of the \textit{POU1F1} gene. The genetic diversity analysis revealed that Chinese indigenous populations had a wide spectrum of genetic diversity at the goat \textit{POU1F1-Ddel} locus. However, an ANOVA analysis revealed no
significant differences in gene homozygosity, gene heterozygosity, effective allele numbers, or polymorphism information content among meat, dairy, and cashmere utility types ($P > 0.05$). This suggests that the goat utility types had no significant effect on the spectrum of genetic diversity.

**Key words:** Goat; \textit{POU1F1} gene; Polymorphism; PCR-RFLP