


ORIGINAL ARTICLE

Polymorphisms and association of *GRM1*, *GNAQ* and *HCRTR1* genes with seasonal reproduction and litter size in three sheep breeds

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Abstract

Litter size is one of the important economic traits of livestock. Seasonal oestrus, ovulation and lambing of sheep have severely restricted the development of sheep farming in Xinjiang, China. The purpose of this study was to investigate the polymorphisms and genetic correlation between *GRM1*, *GNAQ* and *HCRTR1* genes and the seasonal reproduction and litter size in three sheep breeds. The DNA mixed pool sequencing and PCR-SSCP methods were used to detect single nucleotide polymorphisms (SNPs) of *GRM1*, *GNAQ* and *HCRTR1* genes in seasonal oestrous (Kazakh and Chinese Merino [Xinjiang Junken type]) and perennial oestrous (Hu) sheep breeds. The association between genetic polymorphism and litter size was also analysed. The results showed that T945C in exon 2 of *GRM1* gene, C589T in exon 2 of *HCRTR1* gene and A191G in exon 2 of *GNAQ* gene were identified by Sanger sequencing, and three genotypes were existed in each SNP site, which all belonged to the synonymous mutation. *GRM1* (CC), *GNAQ* (GA) and *HCRTR1* (TC) were the dominant genotypes of seasonal reproduction and litter size in Kazakh sheep and Chinese Merino sheep, respectively, while, in perennial oestrous Hu sheep populations, the dominant genotypes were *GRM1* (TC), *GNAQ* (GA) and *HCRTR1* (TC), respectively, and association analysis also confirmed the results. The above results implied that *GRM1*, *GNAQ* and *HCRTR1* genes are significantly associated with lambing traits in Kazakh, Chinese Merino and Hu sheep. Among them, the locus of *GRM1* (T945C), *GNAQ* (A191G) and *HCRTR1* (C589T) might be considered as a potential molecular marker, which controls seasonal reproduction and litter size in sheep.

KEYWORDS

GNAQ, *GRM1*, *HCRTR1*, litter size, seasonal reproduction, sheep (*Ovis aries*)