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None of polymorphism of ovine fecundity major genes *FecB* and *FecX* was tested in goat

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Abstract

The polymorphism of mutation Q249R in *BMPR-IB* gene (*FecB*) and loci $FecX^{I}$, $FecX^{H}$, $FecX^{G}$, $FecX^{B}$ in *BMP15* gene was analyzed by forced PCR-RFLP method in 550 individuals from 6 flocks or breeds of goats with litter size varied from 1.4 to 2.7 including Boer (209), Haimen (128), second generation of Boer goat crossed with Huanghuai goat (82), Huanghuai (71), Nubi (37) and Matou (23) goat. None of mutations was detected in these goat breeds and their crossbreed. These results suggest that fecundity of goat is not linked to the same loci in *BMPR-IB* and *BMP15* as sheep. Therefore, it is necessary to seek for other genes or loci in order to develop marker assistance selection techniques and study the prolific mechanism of the goat.

Keywords: Goat; *BMPR-IB*; *BMP15*; Mutation; Prolificacy

1. Introduction

Several genes affecting ovulation rate in sheep have been discovered since the first major gene *FecB* (Fecundity Booroola) had been detected in 1980 (Davis, 2005; Davis et al., 2006a). These genes involve in *FecB*, $FecX^{I}$, $FecX^{H}$, $FecX^{B}$ and $FecX^{G}$, which were screened from sheep flocks in Australia, New Zealand, Ireland and the UK (Davis, 2005).

The *FecB* locus is autosomal with codominant expression, which is additive for ovulation rate associated with a mutation (Q249R) in *BMPR-IB* (Bone morphogenetic protein receptor IB) (Souza et al., 2001; Wilson et al., 2001; Mulsant et al., 2001; Davis et al., 2002, 2006a). Studies in many breeds of sheep, Hu, Small Tailed Han (SMH), Chinese Merino (CM), Garole, for example,

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all support the view that *FecB* is responsible for the high prolificacy such as high ovulation rate or litter size (Wang et al., 2003; Liu et al., 2003; Kumar et al., 2006; Guan et al., 2007).

Other loci such as $FecX^I$, $FecX^H$, $FecX^B$ and $FecX^G$ loci are different mutants of *BMP15* (Bone morphogenetic protein 15) gene which is essential for ewe fertility (Galloway et al., 2000; Davis et al., 2001a,b, 2006a; Hanrahan et al., 2004). These mutations have been discovered but each produces the same phenotype (Davis, 2005). The homozygote for the four *BMP15* loci in ewes is infertile whereas the heterozygous individuals have a greater ovulation rate size (Galloway et al., 2002; Liu et al., 2003; Davis, 2004; Hanrahan et al., 2004; Chu et al., 2005).

The incorporation of a major gene for prolificacy into a flock using marker assisted selection (MAS) allows increased selection pressure on other traits leading to increased genetic gain (Davis, 2005). It is supposed that MAS using both *BMPR-IB* and *BMP15* genes is warranted to increase litter size in sheep and will be of considerable economic value to mutton producers. The major gene has the advantage that it can be introduced into any new breed while retaining the new breed's characteristics (Davis, 2005). Introgression of *FecB* allele into the Awassi and Assaf dairy breeds, non-additive genetic effects plays an important role in the milk production with the increasing prolificacy (Gootwine et al., 2001). Introgress *FecB* into Garole sheep by crossing with Malpura is capable of producing good quality semen in a semi-arid tropical climate (Kumar et al., 2007).

Goats contribute largely to the livelihoods of the livestock-keeping households of low- and medium-input farmers, many of whom have few resources beyond their smallholdings and livestock. In addition, goats are important to the subsistence needs as they can provide abundant regular supply of meat, milk, fur and cashmere (Akingbade et al., 2004). The population of goat in the world was approximately 807 millions of which Chinese houses about 25% of the total population by 195 millions (FAOSTAT, 2007). Therefore, it is significant to improve the economic traits of goat such as reproductive trait. Unfortunately, the genetic mechanism of caprine prolificacy remains to be explored. However, the tendency to twinning and triplet is inherited and similar in both sheep and goats. So the objective of this research is to analyze the polymorphisms of genes in goat, which have been confirmed as major genes of fecundity in sheep, so as to find if they are responsible for the prolificacy of goat. It is also of preliminary investigation to enlighten the understanding about different mechanism of prolificacy between sheep and goat.

2. Materials and methods

2.1. Experimental goat flocks and sampling

A total of 550 adult female individuals from 6 breeds (or flocks) of goat were examined in this study, including Boer ($n = 209$), second generation of Boer crossed with Huanghuai goat (BH, $n = 82$), Haimen ($n = 128$), Huanghuai ($n = 71$), Nubi ($n = 37$) and Matou ($n = 23$) goat. The last four are indigenous domesticated goat breeds in China. Boer breed was obtained from Boer Goat Breeding Farm in Hubei province in China. Haimen was the hyper-prolific line collected from farms in Nantong Agricultural Institute and BH goats from Nanjing Jiangpu Ninghua Company both in Jiangsu province. Huanghuai goats were sampled from Xiaoxian Goat Farm in Anhui province. Nubi and Matou goats came from farms in Shiyan city in Hubei province. The average litter sizes of these flocks are 1.42, 1.50, 2.70, 2.38, 2.00, 2.14, respectively, providing a convenient model to study the reproductive differences between prolific and non-prolific goats.

Approximately 10 ml blood was collected aseptically from the jugular vein in EDTA. All samples were taken back to the laboratory under low temperature. The genomic DNA was