

FecB mutation responsible for fecundity in sheep not detected in Indian goats- a short note

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Goats contribute appreciably to the livelihoods of the livestock-keeping households, especially of marginal and low - input farmers, many of whom have scanty resources beyond their small holdings and livestock. In addition, goats are important to the subsistence family food requirements as they provide abundant and regular supply of meat, milk, fur and cashmere. Hence a moderate increase in litter size can lead to larger profit to the rural poor. Improvement of reproduction by traditional selective breeding methods has proved to be difficult due to low heritability and long reproductive cycle. Thus the candidate gene approach provides an alternate tool for early breeding that can accelerate the improvement of goat reproduction (Zhang et al, 2009). Genetic studies on sheep prolificacy across continents have indicated that litter size and ovulation rate are determined by the action of single gene, named fecundity (Fec) genes, with major effects (Davis, 2004). FecB was the first major gene for prolificacy identified in Australian Merino sheep. Single point mutation (A to G substitution) at base 746 (A746G) of the coding region of the BMPRI1B (Bone morphogenetic protein receptor 1B) gene caused an amino acid change (Q249R) that was associated with the hyper prolific phenotype of Booroola ewes (Souza et

al., 2001; Wilson et al., 2001).

This mutation is located in the highly conserved kinase domain of the bone morphogenetic protein receptor 1B, and is characterized by 'precocious' differentiation of ovarian follicles, leading to the production of large numbers of ovulatory follicles that are smaller in diameter than wild-type follicles (Souza et al., 2003). Since the tendency of twinning and triplets is inherited and possibly common in the two small ruminants (sheep and goat), the objective of this study was to screen Indian goats for FecB mutation so as to validate if the same mutation is responsible for prolificacy of goats also.

To explore the genetic variations within BMPRI1B gene, blood samples from a panel of Indian goat breeds were used (Table 1). The panel included six breeds with six samples each based on phenotype (prolificacy), geographical distribution and genetic diversity.

Genomic DNA was isolated and purified from the blood cells using the standard phenol-chloroform-isoamyl alcohol extraction followed by ethanol precipitation as described by Sambrook et al. (2001). Primers were designed for exon 6 with DNA STAR software, Forward Primer-5' GGTCCAGAGGACAATAGCAA-3' and Reverse

Table 1: Indian goat breeds employed in the study

Prolificacy	Breed	Geographical distribution	Twinning percentage % (Acharya, 1982)
High prolificacy	Beetal	Punjab	52.6
	Barbari	Uttar Pradesh	49.3
	Black-Bengal	West Bengal, Bihar, Jharkhand	54
	Malabari	Kerala	42.4
Medium prolificacy	Osmanabadi	Maharashtra	29
Low prolificacy	Ganjam	Orissa	1.6

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Fig 1: Geographical distribution of the goat breeds

Primer-5'-GCCCAAGATGTTTTTCATGC-3'. A total of 50 to 100ng of genomic DNA was amplified by polymerase chain reaction (PCR) in a reaction volume of 25 μ l on i-cycler (BIO-RAD, USA). PCR cocktail consisted of 200 μ M of each dNTPs, 50pM of each primer, 0.5units of Taq DNA polymerase and Taq buffer having 1.5 mM MgCl₂ for each reaction. The PCR reaction cycle was accomplished by denaturation for 1 min at 94°C; 30 cycles of 94°C for 45 sec, 59.8°C for 45 sec, 72°C for 45 sec and final extension at 72°C for 5 min. The amplified region was sequenced using ABI 3100 Automated DNA Sequencer. Multiple sequence alignments were performed with MegAlign program of LASERGENE software to identify polymorphisms in the exon 6 of BMPRI1B gene in indigenous goats.

FecB was the first major gene for prolificacy identified in sheep. The FecB locus is autosomal with codominant expression, which is additive for ovulation rate associated with a mutation (Q249R) in BMPRI1B gene (Souza et al., 2001; Wilson et al., 2001; Davis et al., 2002). The FecB mutation has so far been identified in a number of sheep breeds globally, including the Booroola Merino (Australia), Garole (India), Javanese (Indonesia), Small Tail Han (China), Hu (China), and Kendrapada sheep (India) (Chu et al., 2010). FecB

mutation in these sheep breeds has been utilised in formulating breeding strategies to maximize the benefits of increased prolificacy in these breeds and introgression of this mutation in non-prolific breeds by crossing.

Exon 6 of BMPRI1B gene was amplified and sequenced to screen the FecB mutation in indigenous goats. When compared with *Ovis aries* nucleotide sequence (Accession no. AF312016.1), the results revealed nonexistence of A to G mutation at position 746 of the BMPRI1B gene in all the goats of the six breeds with various levels of prolificacy.

This finding is similar to the results of Hua et al. (2008) who found that the point mutation of BMPRI1B

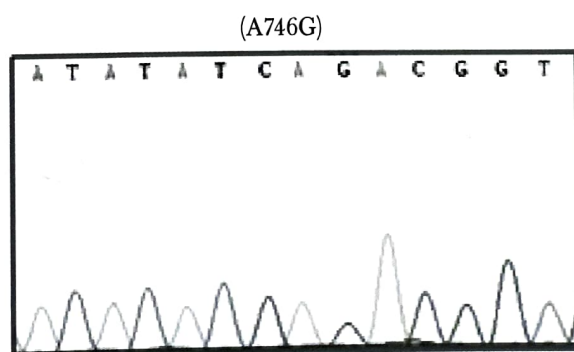


Fig 2: Site of FecB mutation

(FecB) is monomorphic in the prolific goat breeds of China such as Boer, Haimen, Huanghuai, Nubi, Matou. Similarly, a recent study also shows that prolific Chinese goat breeds are monomorphic for this mutation (He et al., 2010). Sheep FecB gene polymorphism was also absent in the Thai multi-breed meat goat population (Supakorn et al., 2010). Chu et al. (2010) reported absence of polymorphism in exon 6 of BMPR1B gene in high prolificacy as well as low prolificacy goat breeds of China. Contrary to all these reports, Polley et al. (2009) discovered that the BMPR1B gene was polymorphic in Black Bengal goats with the predominance of heterozygous genotype AG. However, we could not detect the reported heterozygote genotype (AG) in any of the Black Bengal goats included in our study. Thus, there is a need for a comprehensive screening of this mutation as well as all other mutations responsible for fecundity in sheep in reasonable sized samples (minimum 40-50 from each breed) in other Indian goat breeds with the aim to identify some new variants and association with prolificacy trait in goats. It will be important to find other possible candidate prolificacy genes or markers which can be exploited for increasing the prolificacy of Indian goats in order to achieve optimum progress.

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