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Analysis of Polymorphism at *Fecb* Locus in Gaddi Goats of Western Himalayas under Transhumance Production System

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ABSTRACT

In the present study polymorphism of FecB mutation in bone morphogenetic protein receptor- 1 (BMPR1B) locus was analysed by forced PCR-RFLP techniques in 85 of prolificacy in Gaddi goat managed under migratory/transhumance system in western Himalayan state of Himachal Pradesh, India. The screening of samples belonging to animals demonstrated multiple births in different migratory routes did not detect mutation associated with fecundity and all animals studied were wild type homozygote. The findings revealed that prolificacy observed in Gaddi goat is not linked to BMPR1B loci thus, prolificacy in Gaddi goat breed is not due to established ovine fecundity genes. Other factors like genetic mutation at some other locus or manage-mental practices could be responsible for fecundity and other locus must be explored to associate multiple birth in this breed.

Key words: *FecB gene, Gaddi goat, Mutation, Prolificacy*

INTRODUCTION

There is long list of genes affecting ovulation rate which have been discovered since the first breakthrough discovery of *Fec B* (Booroola Fecundity). The list includes 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[2]. Recently these genes have also been screened in prolific Indian sheep populations[14,15]. Many studies[3,9,10,17] carried throughout the world support that Fec B is certainly linked with high prolificacy. On the other hand, exploration of prolific gene in closely related species, goat is limited. Unfortunately, the genetic mechanism of prolificacy in goat is less understood. Researchers throughout the world including India tried to test polymorphism of established fecundity genes in sheep in prolific goat population.

The contribution of the goat husbandry to the livelihoods of people of Himalayas including the state of Himachal Pradesh is well acknowledged. The goats along with the sheep were managed under migratory pastoralism[11].

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Gaddi the distinct tribe of nomadic pastoralist of Himachal Pradesh, Himalayan state of India wearing a characteristic and striking costume is involved in migratory sheep and goat husbandry. Over the last few years' goat farming has gained an edge over sheep farming in the area primarily due to the fact that earlier the wool industry in the state was growing at rapid pace but in the last 10-15 years, it has shown the negative growth and farmers do not get attractive price for wool. The detailed analysis of last four livestock census highlighted that both sheep and goat recorded decline in population over the year but reduction in the sheep is more marked than goat and contrary to sheep, over the last 15 years' goat population has even shown positive growth (2003-2007). The contribution of the goat to total livestock population remains more or less same for the past four livestock, census while sheep has shown clear cut decreasing trend[16]. These facts highlight the importance of goat in hill farming system of Himachal Pradesh. The *Gaddi* breed of goat is the primary goat population and is managed under extensive migratory system with below optimal management conditions. Improving the reproductive trait is of significant importance in these goat populations. The basic objective of this study is to carry out preliminary investigation of prolificacy in *Gaddi* goat managed under migratory/transhumance system and to screen out polymorphism of established fecundity genes of sheep in goat population.

MATERIALS AND METHODS

The study was conducted in five adopted flocks in different migratory route in the Himalayan ranges of the state of Himachal Pradesh, India and the different migratory routes are presented in Fig. 1. The reproductive data recording was done only for goats although the flocks were mixed with sheep and goat. All the animals were tagged and identified and baseline data was generated for reproductive traits were initially recorded. After generation of baseline data these flocks were monitored periodically over five years (2011-2016) to identify animals giving multiple birth. Those animals which recorded the multiple births over the years of monitoring period were subjected to collection of blood samples aseptically from the jugular vein. 85 samples were collected from five adopted flocks from different migratory routes. The genomic DNA was isolated by phenol-chloroform extraction procedure[8].

Forced PCR-RFLP technique was employed as described by various researches[1,4] to detect mutation in *FecB* that was a point mutation deliberately introduced into one of a pair of primers, resulting in PCR products with exact restriction sites in *FecB* carrier goats, otherwise lacking the sites. The primers reported by Hua *et al*[6]., were utilized in the study and were synthesized from IDT Co. Ltd. The primer sequences for forward and reverse primer is CCAGAGGACAATAGCAAA GCAAA and CAAGATGTTTTCATGCCTC ATCAACAGGTC respectively and is optimized for annealing at 60º C. Polymerase Chain Reaction (PCR) was carried adopting modified forced PCR-RFLP method as per Davis *et al*[1]. Point mutation has been introduced by engineered primer R resulting in PCR products with *FecB* mutation containing an *Ava*II restriction site (G/GACC), whereas non carriers lacking this site. The 190bp product was digested by *Ava*II. *FecB* mutation carrying products were digested to yield a160bp fragment, whereas non-carriers remained uncut at 190bp.

RESULT AND DISCUSSIONS

In the present investigation of genotyping animals of *Gaddi* goat which has recorded multiple birth the study revealed that all the 85 Gaddi goats belonging to different flocks in different migratory routes genotyped were wild type homozygote for BMPR1B. No individuals carried the *Fec*B mutation in BMPR1B locus. This indicated that probably the prolificacy in *Gaddi* goat is independent of these gene loci and some other locus or manage- mental/environmental factors are responsible for observed multiple birth. Similar reports of testing of fecundity genes

and subsequent absence of polymorphism for the loci under evaluation had been documented by Hua *et al*[7]., in different Chinese goat population who had demonstrated multiple kidding. Different studies in Jining Grey goat, Liaoning Cashmere goat, Inner Mongolia Cashmere goat, Beijing native goat (30) supported the same view that there was no polymorphism in BMP15[5]. In Indian goats, prolificacy in case of Raighar goats is also demonstrated not due to the mutation at FecB locus[12]. So far only Black Bengal is the only Indian goat breed which has demonstrated Fec B mutation at BMPR1B gene[13].

A number of other studies had also indicated that *Fec*B and *Fec*X were not the only reason responsible for the high prolificacy. Jining Grey goat, Liaoning Cashmere goat Inner Mongolia Cashmere goat Beijing native goat supported the same view that there was no polymorphism in BMP15[5]. Even many sheep breed which had demonstrated high prolificacy are monomorphic for these loci notably Hu sheep of China[3,17]. These finding suggests that there may be other genes which are associated with caprine fecundity. The prolificacy/multiple birth observed in Gaddi goat breed is not due to established ovine fecundity genes and other locus must be explored to associate multiple birth in this breed.

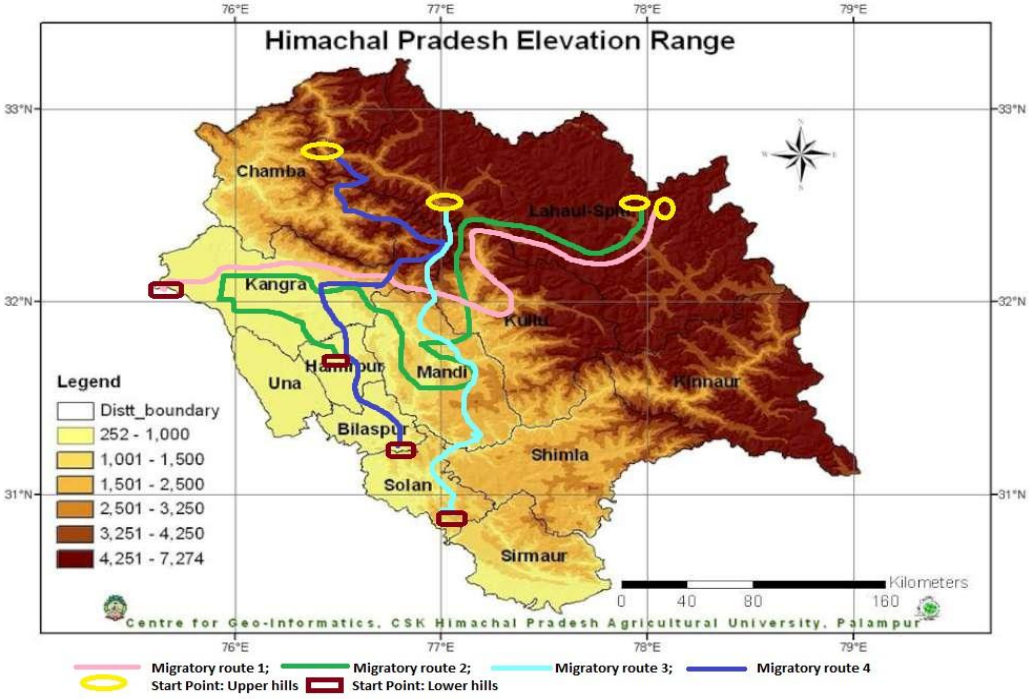

Fig. 1: Map depicted study area and migratory routes of *Gaddi* goat

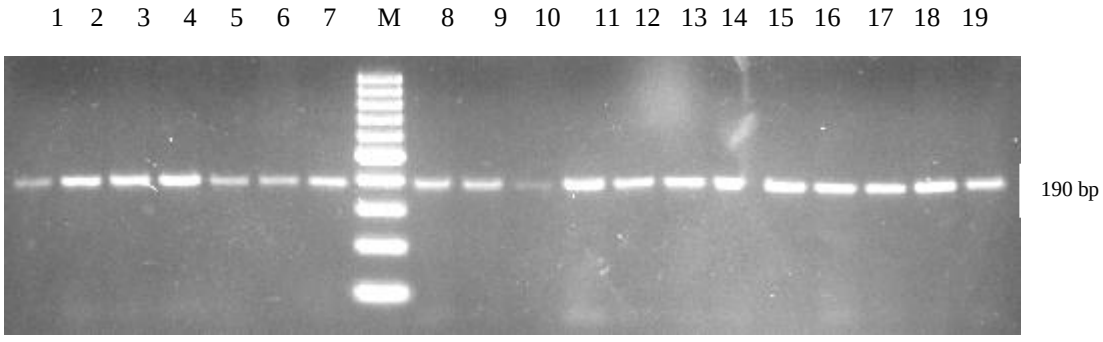

Fig 2: Agarose gel electrophoresis for *FecB l*oci product digested by AvaII of *Gaddi* goat, Lane 1-19 represent uncut product representing *FecB* non carrier M: marker : 50 bp

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