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Genetic basis of fecundity in sheep- a review

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Abstract
Sheep farming is the major income source of the poor and especially of women in developing countries. So, the main aim of any animal breeder is to get maximum profit from sheep farming. This can be achieved by two basic tools i.e. selection and breeding. Sheep production efficiency is mainly conditioned by fertility. Fertility traits typically have low heritability and selection based on phenotype is often inefficient and slow. It is more effective to select breeding animals according to their genotype to improve fertility traits like ovulation rate and litter size in sheep. Number of candidate genes has been identified so far influencing fecundity. Different mutations in the growth differentiation factor 9 (GDF9) and the bone morphogenetic protein 15 (BMP15) genes cause an increase in the ovulation rate in sheep.

Keywords: sheep, fecundity, candidate genes

Introduction
Sheep, is a chief component of rural economy with its multifacet utility for wool, meat, skin and manure particularly in the arid, semi-arid and mountainous areas of the country. It provides a reliable source of income to the shepherds through sale of wool and animals. Sheep farming is of major economic importance, especially for small and marginal farmers because it requires minimum resource (Naqvi, 2013), which is a supplementary advantage of sheep farmimng. Sheep rearing in India is now facing a problem to produce more mutton and wool for growing human population against the reality of shrinking grazing resources, creating a major constraint to further growth of sheep population. The total sheep in the country is 65.06 million numbers in 2012, declined by about 9.07% over census 2007. However, sheep production suffers from major constrain as the majority of sheep breeds in India is having low litter size except the Garole, Kendrapara, and NARI-Suvarna sheep breed (http://www.cswri.res.in/breed_profiles.asp). Increase in litter size i.e. increase in reproductive ability of sheep is a solution to the problem. The prolificacy trait is quantitative in nature and controlled by multiple genes [Miao, 2013] [2]. Improvement of reproductive traits has conventionally been regulated using quantitative genetic methods. Hence, increase in litter size by selection within a breed will be a time-consuming process as the reproductive traits are having low heritability. If the major genes associated with reproduction are identified, they can be introduced in breeding through marker assisted selection and it can infuse superior genotypes rapidly in the breeding population [Dekkers, 2004 Williams 2005] [3, 4]. The number of lambs per ewe is the main factor which contribute maximum to mutton production. Most of the Indian breeds generally single lamb per lambing. The number of offspring obtained per lambing is a good indicator, and it is more important than gain of lambs (Petrovic 2000).

Reproductive traits in sheep and their Importance
Litter size has a major impact on efficiency and profitability in lamb meat production.

Lambing inteval
Genes regulating fecundity in sheep
In sheep, different prolificacy loci have been discovered, namely bone morphogenetic protein receptor type 1B (BMPR1B; or active in-like kinase 6, ALK6), known as *FecB* (Booroola) on chromosome 6 (Souza *et al*., 2001) [5] corresponding to the human chromosome 4q22-23 (Montgomery *et al*., 1993); growth differentiation factor 9 (GDF9), known as *FecG* on chromosome 5 (Hanrahan *et al*., 2004) [7, 12]; and bone morphogenetic protein 15 (BMP15) known as *FecX* on chromosome X (Hanrahan *et al*., 2004; Galloway *et al*., 2000) [7, 12, 8].

BMPR-1B

The protein coded belongs toTGF-ß superfamily. Booroola was the first major fecundity gene, located on ovine chromosome 6 and codes for bone morphogenetic protein 1B receptors in the ovaries. The detected mutation in the Booroola gene is a single nucleotide non-conservative substitution that has an additive effect on ovulation rate (Davis 2005; Pramod *et al*., 2013) [10]. The prolificacy of the Garole breed was due to the *FecB* mutation, which appeared to be a fixed trait in the breed.

BMP15

The BMP15 gene (also known as FecX or GDF9B) codes for the bone morphogenetic protein

15 is an ovary-derived growth factor that is essential for follicular development in sheep

(Hanrahan *et al*., 2004) [7, 12]. The biological functions of BMP15 exhibits by promoting granulosa cell processes included in early follicle growth, while simultaneously acting to confine follicle stimulating hormone (FSH) and causes granulosa cell differentiation. The action of BMP15 is regulated by the binding protein follistatin and it is important to maintain the granulosa cells responsiveness to FSH (Pramod *et al*., 2013) [10]. The mutations in the BMP15 gene increases ovulation rate in heterozygous individuals and decreases in homozygous individuals. (Gemmell and Slate, 2006) [11].

GDF9

The GDF9 gene, also called as FecG, is located on chromosome 5 and codes for oocyte-derived growth differentiation factor 9 and is essential for normal folliculogenesis (Hanrahan *et al*., 2004) [7, 12]. Mutations in the GDF9 gene show similar expression as the BMP15 mutation in the ovaries, however, it increases the ovulation rate in animals even more (Pramod *et al*., 2013) [10].

Woodland Gene

It is otherwise called as **FecX2** gene, located on the X-chromosome, though. It affects ovulation rate is unknown to date (Feary *et al*., 2007) [13]. The mutation may affect ovulation rate by changing the expression patterns of BMP15, BMPR-1B and TGFβR1 in the ovaries. The mutation in the Woodland gene is that it is maternally imprinted which means that it is only ex-pressed in ewes when inherited from their sire (Davis *et al*., 2001). The effect of the mutation is silenced if the ewe inherits it from the dam and will not give an increase in ovulation rate.

Importance of fecundity genes

- Idenifying genes of major effect offers the opportunity to improve production efficiency, product quality and product diversity in livestock industry, through utilizing them in breeding programs.
- Reproductive traits have low heritability, discrete phenotypic expression and are expressed only in sexually mature ewes, leading to the selection of low intensity and long generational intervals.
- Hence, use of an alternative strategy of identification of SNPs of candidate genes related to fecundity and their use as one of the selection criteria seems to be quite promising for improvement of fertility traits.

Conclusion

It is now clear that the increase in prolificacy resulting from mutation in genes is not due to an increase in the circulating FSH concentrations, but rather to an increased sensitivity to FSH mediated by the action of intra-follicular local factors. The identity of these factors is still uncertain, but the results to date are consistent with a major role in modulating proliferative and differentiative responses of both GCs and TCs to gonadotrophic

stimulation, Genomic approach to the fertility traits will improve the accuracy of selection. The increased accuracy will ultimately pave the way for better economics of livestock farming particularly in small ruminants. Numbers of candidate genes affecting fertility have been found in many sheep breeds around the world. So constant genetic profiling of different breeds should be carried out in search for genes showing significant association with fecundity, fertility and prolificacy and their characterization should be done for better understanding of reproduction traits.

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