ROLE OF FECUNDITY GENES IN PROLIFICACY OF SMALL RUMINANTS

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INTRODUCTION

The aim of every breeder is to get maximum profit possible from the animal he is rearing. This can be achieved by improving the genetic worth of the stock by proper selection methods. For the traits that are to be selected, their relative economic value should be established. Kidding/lambing percentage is the most important factor affecting profitability in small ruminants. Increasing prolificacy offers greater potential for improving reproduction rate and production efficiency. Only way to increase the numerical productivity (no. of kids produced per goat per year) is that those which are closely linked to reproductive parameters. Improvement of reproductive traits in livestock species has become of increasing interest,especially in small ruminants, where small increases in litter size can equal large gains in profit.

PROLIFICACY

Prolificacy is measured as the ability of a female animal to produce large number of young ones in their life span through high ovulation rate and high embryo survival. But, it is difficult to obtain selection improvements in traits associated with reproduction, since kidding/lambing percentage is lowly heritable. Differences among does/ewes in litter size (single, twin, triplet) are largely due to non-genetic factors, such as management and nutrition. Genetic change is permanent but, nutrition and management vary from year to year. Common strategy for increasing prolificacy *via* genetic means is to select ewes that are more likely to produce multiple births and to select rams that are more likely to sire prolific daughters. This can be accomplished through simple selection based on birth type or by selecting for a composite trait, such as weight of young ones weaned. In the absence of any other information, it is best to select males and replacement female lambs/kids that are born as multiples from young females.

FECUNDITY GENES

1. Booroola gene (FecB)

It is a single gene in chromosome 6 in sheep which is the main reason for higher prolificacy of certain breeds. This gene has effects on granulosa cell maturation, oocyte development and its function. The increase in prolificacy is due to autosomal mutation that occurred in this gene which causes increase in ovulation rate and litter

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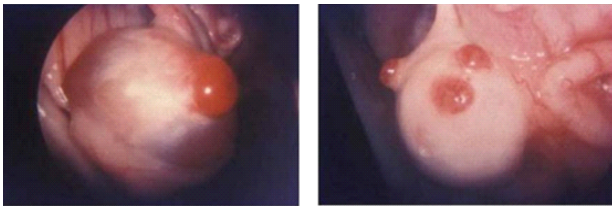

Normal and FecB gene carriers kept at Marshall Building in Edinburgh

size. Term "Booroola" was taken from the name of the ranch in Australia, where the sheep carrying single gene for prolificacy were first discovered. Booroola gene can be transferred to any other breed by crossbreeding. This FecB gene is responsible for the higher prolificacy of Finn sheep, Romanov, Booroola Merino and British Milk Sheep. Up until now, the most numerous breed of sheep containing the FecB gene is Booroola Merino, the breed it was originally discovered in. Feeding maintenance quality hay or pasture is enough for lambing rates of 240-300 percent in heterozygous Booroola ewes.

Ancestor and original source of Booroola Merino sheep FecB gene is the Garole Sheep from the Sunderban (Bengal) area of India. Garole is a small ewe of 12-15 kg, with a mean litter size of 2.3 lambs, adapted to hot, humid, swampy conditions of rice paddies. 10 ewes and 2 rams were originally imported to Australia in 1792, from Calcutta, India. The FecB gene mutation is found in the Garole sheep. Genetic evidence supports the historical records that the prolific Garole sheep, when introduced to Australia, bred with the much larger 35-40 kg Merino sheep. Garole sheep are virtually all homozygous for the FecB gene (BB).

2. GDF9 / FecG gene

Growth differentiation factor 9 (GDF9) is seen in chromosome 5 in sheep and goat. They are expressed in oocytes and play an important role in ovarian folliculogenesis. Single strand conformation polymorphism (SSCP) studies of exon 1 and flanking of GDF9 gene reveals two silent mutations (183A>C and 336C>T) in AA genotype in comparison to BB genotype. Studies show that allele A has correlation with prolificacy in Jining Grey goat. (Chu, 2004).

3. BMP15 / FecX gene

Bone morphogenetic protein 15 (BMP15) is an X linked gene seen in sheep and goat. BMP15 gene is essential for oocyte and follicular development. Higher prolificacy of Inverdale, Lacaune, Belclare, Small Tailed Han ewes and Jining Grey goats is due to this gene. Single strand

conformation polymorphism (SSCP) studies show SNPs in exon 1 and exon 2. Two point mutations (G963A and G1050C) are found in AB genotype in comparison to AA genotype (Vacca, 2010).

4. POU1F1 gene

POU domain, class 1, transcription factor 1 (POU1F1) is otherwise known as Pit1 and GH factor 1. It is seen in chromosome 3 in sheep. POU1F1 is an important transcription factor for Growth Hormone. Single strand conformation polymorphism studies reveals six mutations - C256T in exon 3, C53T and T123G in intron, G682T, T723G and C837T in exon (Feng, 2012).

5. Estrogen Receptor gene

Estrogen receptor gene in sheep has two regions - ESR1 in chromosome 6 and ESR2 in chromosome 14. Single strand conformation polymorphism studies show SNP of exon 1 of Estrogen Receptor (ESR) gene. AC→G mutation was noticed at the 363bp of exon 1 in BB genotype on comparison to AA genotype. Marked assisted selection (MAS) of animals with estrogen receptor gene polymorphisms can be done to increase litter size and thus increase in economic value to mutton producers (Xiao-Dan, 2005).

6. Prolactin receptor gene

Prolactin receptor gene is seen in chromosome 5 of sheep. This gene mainly interacts with prolactin and thus increases prolificacy. Single strand conformation polymorphism studies of exon 10 of prolactin receptor gene reveals two mutations (186G→A and 220T→C) in AB genotype in comparison to AA genotype. (Zhang, 2007).

7. FSH receptor gene

FSH receptor gene is seen in Chromosome 2 in sheep. It affects the follicular growth and hence plays an important role in prolificacy. Variations in aminoacid sequence of receptor protein are due to point mutations. Single strand conformation polymorphism studies shows that polymorphisms at codon 307 and 680 influence responsiveness to FSH and affects prolificacy (Tisdall, 1995).

8. KiSS-1 gene

Kisspeptin (KiSS-1) gene is important for proper GnRH function and thus affects prolificacy. It is seen in chromosome 1 in sheep. Single strand conformation polymorphism studies reveals that polymorphism of intron 2 results in two SNPs T2643C and 8bp base deletions (2677AGTT CCCC) giving rise to four different genotypes CC, TT, TG and TC (Hou, 2011).

9. INH gene

INH gene (Inhibin gene) is essential for normal oocyte and follicular maturation and affects prolificacy. Inhibin genes - INHA and INHβA are found in chromosome 2 in sheep. Single strand conformation polymorphism studies reveal a C865T silent mutation in exon of INHA gene (Yuanqing He, 2010).

CONCLUSION

Genetic improvement of reproductive

traits has traditionally been restricted to use of quantitative genetic methods but gain has been limited when using these methods. Recent improvement in molecular genetics provided that the major genes associated with reproduction can be utilized in breeding through marker-assisted selection (MAS). Reproductive traits are often suggested as prime targets for marker-assisted selection for their low heritability and the fact that the trait can be measured only in one sex.

The fecundity genes has posed the unique and exciting opportunity to add a high level of prolificacy to sheep and goat, that fit the environment well, without having to add undesirable traits of other breed. These genes have proved to be trackable and persistent, after its introduction to a breed. Fecundity traits offer a new option that can allow certain breeds producing lambs/kids to obtain a high level of prolificacy by genetic introgression of desired allele of the fecundity gene. The presence of fecundity genes, Booroola and Inverdale has been proved as a cause for high prolificacy for Malabari goats also. So, by using genetic molecular markers we can detect the mutations which results in high prolificacy in certain breeds (Davis, 2004). Breeders can select males from these breeds to incorporate into crossbreeding and can attain high level prolificacy. Speed and efficacy of selection is expected to increase by the use of these molecular markers in selection.

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