Small Ruminant Research 125 (2015) 34–42

Contents lists available at ScienceDirect

Small Ruminant Research

journal homepage: www.elsevier.com/locate/smallrumres

Review

Current status of molecular genetics research of goat fecundity

Sonika Ahlawat*, Rekha Sharma, A. Maitra, M.S. Tantia

National Bureau of Animal Genetic Resources, Karnal 132001, Haryana, India

ARTICLE INFO

Article history:
Received 6 March 2014
Received in revised form 16 January 2015
Accepted 30 January 2015
Available online 11 February 2015

Keywords:
Goats
Fecundity
Candidate genes

ABSTRACT

Reproductive traits are extremely important to the goat industry because moderate increase in litter size can lead to large profit. Traditional selection for improving litter size is difficult due to sex-limited nature and low heritability of the trait (5–10%). In addition, the lack of knowledge on the number of the genes controlling this trait and the possible gene interactions are the other limitations for this trait. Molecular genetics can overcome these limitations offering new opportunities for the improvement of reproductive traits, as it supplies tools to analyze genetic variability directly at the DNA level with the possibility of detecting the individual genes influencing the reproductive capability. For the last decade, molecular genetics has led to the discovery of individual genes or candidate genes with substantial effects on the reproductive trait viz. *BMPR1B*, *GDF9*, *BMP15*, *FSHβ*, *FSHR*, *POU1F1*, *PRLR*, *KiSS-1*, *GPR54*, *GH*, *INH*, *CART*, *GnRH*, *GnRHR*, *LHβ*, *BMP4*, *KITLG*, *MT2*, *CYP21* and *AA-NAT*. Despite the progress made in goat fecundity studies, it's hard to satisfy the actual application because the reproductive traits are complex quantitative traits involving multiple genes, loci and interactions. So it is important to analyze the combined effect of multiple genes or loci on reproductive traits. Little progress has been made on understanding interaction between genes, gene and environment, and genetic effect analysis. Thus the need of the hour is to identify more functional genes, clarify molecular mechanism of action and regulatory network and to resort to more holistic approaches like genomic selection which can tremendously accelerate the goat improvement.

1. Introduction

Goats were among the first farm animals to be domesticated. As indicated by the archaeological evidence, they have been associated with man in a symbiotic relationship for up to 10,000 years (Ensminger and Parker, 1986). Goats disseminated all over the world because of their great adaptability to varying environmental conditions and different nutritional regimes under which they were evolved and subsequently maintained. They have proved to be immensely useful to man due to their productivity, small size, and non-competiveness with him for food (Aziz, 2010). Rearing of goat plays a very important role in the lives of households in developing countries. This is because goats provide the easiest and most readily accessible source of credit available to meet immediate social and financial obligations.

The world goat population is 861.9 million and the largest number of goats is observed in Asia, followed by Africa, representing about 59.7% and 33.8%, summing up to 93.5% out of the total number of the world, respectively (FAOSTAT, 2008). Goat meat is widely consumed in the developing countries. The total amount of goat meat

---

* Corresponding author at: Core Lab, NBAGR, India.
Tel.: +91 9416161369; fax: +91 184 2267654.
E-mail address: sonika.ahlawat@gmail.com (S. Ahlawat).

http://dx.doi.org/10.1016/j.smallrumres.2015.01.027
0921-4488/© 2015 Elsevier B.V. All rights reserved.

produced in 2008 was 4.9 million metric tonnes (MT) and developing countries produced approximately 97% of this amount, reflecting the great importance of goat meat to feed millions of people in these countries (FAOSTAT, 2008). The major part of this amount is not traded as other major meats. It is usually produced and consumed locally among the poor in the developing countries. Hence the potential of goats for sustainable supply of meat for human consumption is unquestioned, and their contribution to improved nutrition of rural people is likely to increase (Aziz, 2010). Goat rearing now faces a dilemma to produce more meat for the growing human population against the reality of shrinking grazing resources, which are creating a major constraint to the further growth of goat population. There is an acute shortage of meat for domestic needs, apart from the huge demand in the international market. The gap between demand and production of meat could be bridged by augmenting the reproductive rate of low-producing goat breeds. In order to decrease the gap of demand and supply, there is dire need to identify genes responsible for more birth per conception and also in life time of the animal.

Successful reproduction is the outcome of complex interactions of genes and environment to transfer the genetic 'blueprint' to the next generation. One goal of reproductive biology is to understand the key events that regulate the development and function of the reproductive axis (Montgomery, 2000). Primates and many ruminants typically release a single oocyte at each cycle whereas species such as mice and pigs have consistently high ovulation rates. In mammals the ovulation rate and the litter size is a result of well-regulated interactions of endocrine and paracrine mediators. How precisely the litter size is controlled remains a critical and important question in reproductive biology (Polley et al., 2009). Information about genes and their protein products, variation in genes that lead to significant physiological differences (or phenotypes), and the interaction of genes and the environment is required to achieve this understanding (Montgomery, 2000).

"Fecundity" means the ability to produce live offspring, and "fertility" means the actual production of live offspring. So fecundity refers to the potential production, and fertility to actual production, of live offspring. Improvement of reproductive traits in livestock species has become of increasing interest, especially in sheep and goats, where small increase in litter size can equal large gains in profit (Ghaffari et al., 2009; Di et al., 2011). Traditional selection for improving litter size is difficult due to the sex-limited nature and low heritability of the trait (5–10%). In addition, the lack of knowledge on the number of the genes controlling this trait and the possible gene interactions are the other limitations for this trait. Molecular genetics can overcome these limitations offering new opportunities to the improvement of reproductive traits, as it supplies tools to analyze genetic variability directly at the DNA level with the possibility of detecting the individual genes influencing the reproductive capability. The identification of polymorphism and DNA markers associated with reproductive traits can lead to genetic improvement through the implementation of marker assisted selection (MAS) by the breeder to increase litter size and reproduction efficiency (Caballero and Toro, 2002).

For the last decade, molecular genetics has led to the discovery of individual genes or candidate genes with substantial effects on the traits of economic importance. The candidate gene approach, employed in identifying the polymorphisms in genes likely to cause phenotypic variation based on physiological and biochemical evidence, could accelerate the improvement of goat reproductive traits. Recently, the development of next generation sequencing (NGS) allowed *de novo* sequencing of the goat genome, which paved the way for creation of International Goat Genome Consortium (IGGC, www.goatgenome.org) in 2010, whose aims were to consolidate research efforts at the international level. The goat genome reference sequence has been published (Dong et al., 2013) and is available to the scientific community through a web interface and mirror (http://goat.kiz.ac.cn/GGD/). These approaches have proven to be valuable tools to delineate genes and mutations implicated in goat fecundity. In recent years, a number of candidate genes for prolificacy (*BMPR1B*, *GDF9*, *BMP15*, *FSH*β, *FSHR*, *POU1F1*, *PRLR*, *KiSS-1*, *GPR54*, *GH*, *INH*, *CART*, *GnRH*, *GnRHR*, *LH*β, *BMP4*, *KITLG*, *MT2*, *CYP21* and *AA-NAT*) have been identified which might contribute towards molecular breeding to enhance productivity of goat. Hence, the aim of this article is to review the published candidate genes which have influence on fecundity in goats.

2. Bone morphogenetic protein receptor 1B (*BMPR1B*)

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 *BMPR1B* gene (Souza et al., 2001; Wilson et al., 2001; Davis et al., 2002). The *FecB* mutation is present in Booroola Merino (Australia), Garole (India), Javanese (Indonesia), Small Tail Han (China), Hu (China), and Kendrapada sheep (India) (Chu et al., 2010a). Artificial insemination and embryo transfer programmes have been used to successfully introgress the Booroola into other breeds in several countries, and these artificial breeding technologies have been particularly useful while only small numbers of progeny tested individuals have been available (Davis, 2004). Many researchers have reported absence of *FecB* mutation in high prolificacy as well as low prolificacy Chinese, Thai and Indian goat breeds (Hua et al., 2008; Supakorn and Pralomkarn, 2010; Chu et al., 2010a; Ahlawat et al., 2013). Contrary to these reports, *BMPR1B* gene was found to be polymorphic in Black Bengal goats with the predominance of heterozygous genotype AG (Polley et al., 2009). Ahlawat et al. (2014) reported two novel SNPs T(−242)C and G(−623)A in the promoter region of *BMPR1B* gene in a panel of nine Indian goat breeds but no association with prolificacy trait was reported.

3. Growth differentiation factor 9 (*GDF9*)

It plays a critical role as a growth and differentiation factor during early folliculogenesis in female reproduction