Advances in Molecular Breeding Research of Goat Fecundity

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Abstract: Litter size trait is crucial for the economic benefits of goat industry. But litter size trait which shows low heritability (approximately 0.152) is hard to be improved by traditional breeding technologies. Molecular breeding is the only effective way to alleviate the inefficiency and long cycle length of traditional breeding. This study systematically describes the recent progress in goat fecundity molecular breeding. The necessity of molecular breeding was introduced. The scope, characteristics, achievement, problem and promise of molecular breeding were discussed. The achievements of goat fecundity in the genomic breeding, transgenic breeding and molecular design breeding were stressed. The problem of goat fecundity molecular breeding was discussed. Base on the study, the route, strategy and promise were anticipated.

Key words: Goat, fecundity, molecular breeding, advance, economic benefits, China

INTRODUCTION

The goat number of China is in the second precedence in the world. Goat resource is also very rich in China. There are 43 local varieties, 4 improved varieties and 3 introduced varieties listed in Domestic Animal Genetic Resources in China. The development of goat industry is of great significance to the adjustment of agriculture production structure, the relief of grain contradiction of human beings and domestic animals, the increase of farmers' income and the sustainable development of animal husbandry.

Litter size trait is crucial for the economic benefits of goat industry. But the goat reproduction rate is generally low, the average number of lambs per birth is one to two thus, greatly restrict the production and development of goat farming. On the other hand, there are many species with high performance such as Jining gray goat. How to fully exploit their good quality, promote the basic research level of goat breeding is an extremely urgent task for us.

Gene is an important factor of goat fecundity. But litter size trait which shows low heritability (approximately 0.152) is hard to be improved by traditional breeding technologies. Molecular breeding is the only effective way to alleviate the inefficiency and long cycle length of traditional breeding. Molecular breeding can shorten the time of new improved variety of 8-10 generation to 2-3 generation.

Animal molecular breeding is a new subject which uses genetic theory and technique to improve domestic animal varieties. It is the new theory and method development of conventional animal breeding. Animal molecular breeding mainly covers three aspects; genomic breeding, transgenic breeding and molecular design breeding. Among which genomic breeding is to direct select good trait genes of domestic animals and achieve Marker Assistant Selection (MAS) through DNA markers on the basis of analyzing genome. Transgenic breeding is to import foreign gene to the genome of some animals through gene transfer technology, cultivate new transgenic animal breed (strain), thereby achieve the improvement of important production traits such as growth rate and heredity resistance and location research of target gene of non-conventional traits such as the production of pharmaceutical protein and enzyme for industry and molecular design breeding which achieves good traits of different species to one species. Molecular design breeding is the last development stage of molecular breeding in the long run.

Comparing with traditional breeding, molecular design breeding can not only design and apply for a single gene breeding but also design and optimize the combination of multi genes and the target genes of the whole genome. More and more factors are considered for the effective way to meet the needs of breeding thus can greatly improve the breeding efficiency. The plant and

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animal molecular design breeding was regarded as the foremost priority of technical studies on Essentials of National Medium and Long-Term Science and Technology Plan (2006~2020) promulgated by the state council of China. Therefore, we should grasp the opportunity, fully take advantages of the major achievements of frontier subjects such as Genome Science and Bioinformation, carry out basic theory studies of molecular design and its technical platform building and bring the traditional breeding to the efficient and orientation development.

With the development of modern molecular biology and genome, the research of new breeding technology such as gene location, molecular marker of good traits and transgenic breeding has achieved certain progress thus enhance the selection effect of breeding traits and provide new opportunities for the genetic progress.

MATERIALS AND METHODS

Genomic breeding has been into the rapid development stage: Since, the analysis of DNA double helix structure in 1953, the research of biologic phenomena and mechanism is going into molecule level. During 1970s-1980s, molecular biology research studies around a single or a small number of genes. In 1985 with the implement of human genome sequence project, high flux and high precision researches emerge, the study of biology has gone into genome era. Low-resolution genetic linkage map of ram genome was reported by Vaiman *et al.* (1996), 223 microsatellites were used to construct a meiotic map covering 2300 cm i.e., >80% of the total estimated length of the goat genome. Schibler *et al.* (1998) achieved 88% genome coverage i.e., 2.737 cm in length and 307 markers were included. But the density of goat genetic linkage map is not high enough, the microsatellite markers used in goat research were from cattle and sheep mostly thus hamper the location of function gene and obstruct the development and utilization of local rare breeds. Analyze the fecundity gene regulatory network can add new signs to the genetic map, speed up breeding progress and improve economic performance.

Searching for major gene and molecular markers controlling the ovulation rate and litter size has been the aim of breeding scientists. Molecular marker of the first generation was based on DNA-DNA cross such as Restriction Fragment Length Polymorphism (RFLP). The second generation was based on PCR such as microsatellite (SSR), Expressed Sequence Tag-Simple Sequence Repeat (EST-SSR), Random Amplified Polymorphic DNA (RAPD), Inter-Simple Sequence Repeat (ISSR), Sequence-Tagged Sites (STS), Amplified restriction Fragment Polymorphism (AFLP) and Mitochondrial DNA (MtDNA). The third generation was based on single nucleotide polymorphism such as Single Nucleotide Polymorphism (SNP) marker selection method.

With the development of DNA molecular genetic markers and the perfection of high precision genetic map, studies of goat fecundity candidate gene have gone in depth. Research scientists from home and abroad have precisely located and cloned a number of new genes, developed a batch of function markers which lays foundation for the development of molecular design breeding.

The most studied candidate genes relating to litter size trait are: Follicle-Stimulating Hormone Beta (*FSHβ*) gene (Liang *et al.*, 2006), Follicle-Stimulating Hormone Receptor (*FSHR*) gene (Ji and Cao, 2007; Tan *et al.*, 2008; Zhu, 2008), Growth Differentiation Factor 9 (*GDF9*) gene (Feng *et al.*, 2010; Wu, 2006; Yan, 2010a), Inhibin-α (*INHA*) gene (Hua *et al.*, 2008; Wang, 2010), Gonadotropin releasing Hormone (*gGH*) gene (Hu *et al.*, 2007), κ-Casein (*CSN3*) gene, αs 2 Casein (*CSN1S2*) gene (Lan, 2005), Prolactin Receptor (*PRLR*) gene (Zhang *et al.*, 2007), Gonadotropin-Releasing Hormone Receptor (*GnRHR*) gene (Han *et al.*, 2009), steroid 21-hydroxylase (*CYP21*) gene (Yan, 2010b), Luteinizing Hormone Beta-subunit (*LHβ*) gene (Sun, 2009), Bone Morphogenetic Protein 4 (*BMP4*) gene (Chu *et al.*, 2010a), the G-Protein-coupled Receptor (*GPR54*) gene (Cao *et al.*, 2011; Feng *et al.*, 2009) and Kisspeptin (*KiSS-1*) gene (Cao *et al.*, 2010) of Kisspeptin/GPR54 signaling which regulate the release of GnRH from hypothalamus. Different from sheep studies, Bone Morphogenetic Protein Receptor type IB (*BMPR-IB*) gene polymorphism sites relating to litter size trait were not found in ten goat breeds (Chu *et al.*, 2010b; Fang, 2010; Hua *et al.*, 2008) and Prolactin (*PRL*) gene has no effect on the prolificacy of Jining Grey goats (Zhao *et al.*, 2007). With regards to Bone Morphogenetic Protein 15 (*BMP15*) gene, different varieties gave opposite conclusion (Chu *et al.*, 2007; Cui *et al.*, 2009; Fang, 2010; Hua *et al.*, 2008). As concerns FSHR, different sites came to different conclusion (Cui *et al.*, 2009; Ji and Cao, 2007; Tan *et al.*, 2008; Zhu, 2008). The litter size trait of goat is a quantitative character controlled by many genes, polymerization effect researches of quality genes were rarely reported (Li *et al.*, 2011; Li, 2009).

Satellite research of goat litter size trait was developed quickly, satellite markers related to its high breeding force were: OarAE101 (Song *et al.*, 2008; Zhu, 2008), BM1329 (Lan *et al.*, 2006; Song *et al.*, 2008; Ke *et al.*, 2009; Xu *et al.*, 2007; Zhu, 2008), BMS2508

(Xiang *et al.*, 2006; Song *et al.*, 2008; Zhu, 2008), OarHH55 (Song *et al.*, 2008; Ke *et al.*, 2009; Xu *et al.*, 2007; Zhu, 2008), BM143 (Xu *et al.*, 2007; Zhu, 2008), LSCV043 (Xu *et al.*, 2007; Zhu, 2008), TGLA68 (Xu *et al.*, 2007), ETH225 (Xu *et al.*, 2007), INRA063 (Xu *et al.*, 2007), BM1225 (Xu *et al.*, 2007), MAF0214 (Xu *et al.*, 2007), INRA040 (Xu, 2008), LSCV22 (Xu, 2008) LSCV37I (Xu, 2008), DVGA64 (Xu, 2008), FCB011I (Xu, 2008), NRA129 (Xu, 2008), SRCRSP10 (Xu, 2008), CSSM47 (Xu, 2008), OarHH35 (Xiang *et al.*, 2006) and GC101 (Feng *et al.*, 2006).

RESULTS AND DISCUSSION

The research has provided important there under and necessary condition to enhance the genetic speed and efficiency of goat breeding by molecular Marker Assisted Selection (MAS).

Genomic breeding has made gratifying achievements; in the meantime, thansgenic breeding has also made substantial progress. Transgenic goats were given birth to at home and abroad (Baguisi *et al.*, 1999; Baldassarre *et al.*, 2003; Lan, 2006; Xing *et al.*, 2001). But transgenic technology was mainly used for bioengineering, rarely used for molecular breeding and transgenic technology can only modify a single trait controlled by major gene; it still can not play its advantage on most quantitative traits commanded by many different genes.

Molecular design breeding is at an elementary stage of development: The development of transgenic technology and MAS has provided advantageous conditions for molecular design breeding. The concept of molecular design breeding was first proposed by Belgian scientific research personnel Peleman and van der Voort (2003). At the same time, molecular plant breeding was financed by national 863 project in China. Molecular design breeding has been implemented at home and abroad especially in the plant genetic breeding and has already achieved certain progress in this area.

For example, Quline, a flexible computer simulation software for the quantitative analysis of genetic model and breeding process, QuHybrid, a simulation tool for the analysis of intercross breeding and QuMARS, a simulation tool for the analysis of marker-assisted recurrent selection were developed in China. Molecular design breeding technological system was also founded (Wang and Pfeiffer, 2007; Wang *et al.*, 2003, 2009). As physical conditions of animals are relatively complex than plant, little progress have made in this area. We need to carry out the basic theory research of molecular design and the construction of technical platform to serve for the breeding practice.

Despite people have made huge progress on goat fecundity studies, some genetic and genetic diversity associated with the litter size trait of goat have found but little gene has been localized and it is hard to satisfy the actual application, a lot of research is referred from the relevant reports of sheep and far behind the sheep research. As we know, some functional genes have difference between varieties and need further study and verification. The structure, function and control mechanism of important function genes haven't completely been made clear. Little research has done on interaction between gene and gene, interaction between gene and environment and genetic effect analysis. Excavate more functional genes, clarify its molecular mechanism and regulatory network, simulate and optimize the feasible breeding programme are the aims. Therefore, we need to carry out the molecular design breeding work of goat fecundity.

CONCLUSION

The molecular design breeding work of goat fecundity will deepen the recognition of its molecular mechanism, open up new ideas and theoretical basis for improving its reproduction force and provide effective and efficient technical support for the healthy and sustainable development of goat industry. This research is of great importance to the guidance of animal husbandry production and the sustainable development of livestock breeding.

ACKNOWLEDGEMENTS

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