Molecular Markers and Their Applications in Cattle Genetic Research

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Abstract

Recent developments in the fields of molecular biology and molecular technology involve the use of genetic markers for the improvement of production traits holistically. This takes into consideration most of the factors that may affect the breeding program. In biotechnological language, a molecular marker is a DNA fragment in association with a certain location in the genome and can also be called a genetic marker; the marker is used in identifying partial DNA sequence in an unknown DNA pool. A variety of genetic hybridization based markers have been used widely. The major challenge that faces molecular geneticists is to identify markers for genes that control the phenotypic variation in the target traits. The present review deals with the various molecular markers and the role played by them in: the selection of traits as well as animals for better productivity; disease resistant breeding; conservation and biodiversity; and geographical distribution of cattle breeds.

Introduction

India's livestock sector plays a noteworthy role from the economic point of view, and contributes 28% and 5% of the country's agricultural and total gross domestic product, respectively. India has the world's largest bovine population with 199 million cattle, which is about 14.7% of the world's total cattle population. India is the largest producer of milk, with 121.8 billion kg in 2010-11, of which cattle contribute 45% of the total production, *i.e.*, 54.9 billion kg. However, the average productivity of Indian cows is far less than that of other developed countries. This may be attributable to several reasons, but the major concern of the country is the low productivity of indigenous animals. It is certain that the development of increasingly advanced statistical methods and use of assisted reproductive technologies have helped to maximize selection for genetic gain.

What is a Molecular Marker?

Genetic marker is a broad term for any visible or assayable phenotype or the genetic basis for assessing of the observed phenotypic variability. Genetic markers are classified: based on visually evaluated traits (morphological and productive traits), based on gene product (biochemical markers), and founded on DNA analysis (molecular markers). Molecular marker is a term used to refer to a specific DNA variation between individuals that has been found to be associated with certain characteristics (Yang *et al.,* 2013). These variations include insertions, deletions, translocations, duplications, and point mutations. They have characteristic biological properties that can be detected and measured in any parts of the body such as the blood or tissue at any stage and they are not confounded by environment, pleiotropic, or epistatic effects.

Advantages of using Molecular Markers

Recent developments in biotechnology have made it possible to unravel a large number of genetic polymorphisms at the DNA level. As a result, researchers and scientists have been encouraged to use them as markers in order to evaluate genetic basis for the observed phenotypic variability. The unique genetic properties as well as methodological advantages of molecular markers make them useful and amenable, to a greater extent, for genetic research when compared to other genetic markers. They have a wide range of immediate applications: parentage determination; estimation of genetic distance; twin zygosity determination and freemartinism; sexing of preimplantation embryos and disease carrier identification; and gene mapping as well as marker-assisted selection. Molecular markers can easily be used as reference points in transgenic breeding and to identify the animals having the specific transgenes. Thus, the overall improvement in livestock species is greatly aided by the use of molecular markers.

Application of Molecular Markers in Cattle Genetic Research

Markers in Milk Quality and Production

Conventionally, phenotypic as well as biochemical markers have been used to identify an animal with high genetic merit for economic traits in cattle. These face the main problem that the polymorphic information carried by these markers is meagre and restricted to the coding region of the chromosome. Also, they are sex and age dependent. Nowadays, molecular markers are being identified on a vast variety of genes of economic importance and are widely accepted. Analysis on animal databases shows that around 344 quantitative trait loci (QTL) are associated with milk traits and 71 with mastitis related traits. Association between DNA polymorphism and milk production traits have been studied for a number of genes, including: prolactin; leptin; diacylglycerol acyltransferase (DGAT1); stearoyl-CoA desaturase; bovine leukocytic antigen (BoLA)-DRB3, growth hormone receptor gene, casein α s1 (CSN1S1); ATP-binding cassette, subfamily G, member 2 (ABCG2) gene; protease inhibitor gene; osteopontin gene; proliferator-activated receptor gamma, coactivator (CoA) 1α gene; growth hormone (GH) gene; signal transducer and activator of transcription (STAT)152; oxidized low density lipoprotein receptor 1; cytochrome P450, subfamily XI B, polypeptide 1; fatty acid synthase; caspase recruitment domain-containing protein 15; bovine K-casein gene CSN3, thyroglobulin gene; β-lactoglobulin gene; POU class 1 homeobox 1; STAT5A; and

stearoyl CoA desaturase. There are 14 major milk proteins reported in cattle. These proteins show variability at DNA level perpetuating a protein change chemically, but the allele-specific effects are dependent on genetic background and experimental model (single locus vs. multi locus effects). Some of them such as β-casein and κ-casein have proven valuable in assessing the milk quality and lactation of dairy cattle and are economically significant. Recently, our laboratory reported that polymorphisms of β-casein (CSN2) A1A2 alleles are exist among Ongole (Indian zebu) and Frieswal (Holstein Friesian × Sahiwal crossbred) cattle.

Disease Resistant Cattle by Marker-Aided Selection/ Breeding

Inadequate animal production significantly contributes to food shortage as well as poverty in the developing nations of the world. It is predicted that demand for animal products will increase by 50% by 2020. Unsustainable disease control measures are a contributory factor for deterioration of the situation that can be checked by breeding for disease resistance. In this regard molecular markers find their importance and the impacts may include a reduction in pathogen or parasite abundance contributing to improved productivity as well as welfare and robustness.

Molecular Markers in Other Diseases

About 200 diseases of cattle, goat, pig, and sheep are thought to be caused by sequence variations in single genes, of which the causal mutations in less than half of them have been elucidated. One of the potential candidate genes that confer innate resistance against various intracellular pathogens is Solute Linked Carrier 11A1 (SLC11A1). It is a transmembrane protein also known as natural resistance associated macrophage protein 1. There exists a significant association of polymorphisms at the 3' untranslated region (UTR) of the SLC11A1 gene with resistance/susceptibility to brucellosis in cattle and buffalo.

Molecular Markers in Conservation and Biodiversity of Cattle Breeds

Thirty well recognized breeds of cattle exist in India along with several other breeds in different states that have not yet been characterized and defined, which reflects the enormous as well as diverse cattle genetic resources of the country. This has become the reason to give much importance to the use of molecular markers. Various fluorescent-labeled microsatellite markers have been used to characterize Kenkatha and Gaolao breeds, indicating a substantial shortfall which is about 21% heterozygous in Gaolao and 22% heterozygous in Kenkatha. There is also little genetic differentiation between the two breeds (approximately 2%). Several microsatellite markers have also been used for conservational studies concerning certain other important cattle breeds (Naqvi, 2007).

Molecular Markers for Selection of Thermo-Tolerant Breeds of Cattle

The selection of thermo-resistant animals is an intelligent way to improve cattle productivity. It is known that zebu breeds are more heat tolerant in comparison to breeds of European origin. Identification and exploitation of *Bos indicus* genotypes to increase thermo-tolerance in cattle will be of great impact in the changing climatic scenario. Olson et al have identified a major gene-designated as the slick hair gene-that is dominant in inheritance and is responsible for producing a very short, sleek hair coat. Cattle inheriting this particular gene are better able to regulate body temperature and have higher milk yields (Deb *et al.,* 2014).

Molecular Markers in Cattle Fertility

Sex-limitedness and low heritability of reproductive traits make phenotype selection more difficult. Also, selection at the molecular level helps in decision-making early in an animal's life, which will substantially reduce the cost of selection programs. Accordingly, there has been considerable interest in mapping and identifying genes involved in the regulation of reproductive traits and in elucidating their expression and polymorphic patterns. Genes that have been found to play an important role in reproduction include: bovine follicle stimulating hormone receptor; luteinizing hormone/ choriogonadotropin receptor; bovine inhibin α; bovine progesterone receptor; and growth differentiation factor 9. These genes are associated with the total number of ova produced and number of transferable embryos in super ovulation. Hence, they can be used as potential markers for super ovulation response.

Conclusion and Future Perspectives

Various molecular markers for improving milk production and their association with disease, and productive and reproductive traits in cattle have proved to be beneficial to the dairy producers and breeders. They can also be used efficiently in breeding and management decisions. The use of various molecular markers in determining the susceptibility to economically important diseases (such as mastitis) along with other diseases caused by a plethora of microbes and parasites proves to be beneficial to check loss of animals and their productivity. Integration of information from all sources along with a search for direct markers and finding their causative sites for the QTL is required. The new era of omics technology provides us with genomic charts as well as genetic variations among individuals and groups that may prove beneficial processing as well as analysis and integration of a large amount of data. Thereby omics technology will provide valuable information regarding the precision of selection of molecular markers in the near future.

References

Deb, R., Sajjanar, B., Singh, U., Kumar, S., Singh, R., Sengar, G., Sharma, A., 2014. Effect of heat stress on the expression profile of Hsp90 among Sahiwal (*Bos indicus*) and Frieswal (*Bos indicus × Bos taurus*) breed of cattle: a comparative study. *Gene* 536, 435-440.

Naqvi, A.N., 2007. Application of molecular genetic technologies in livestock production. *Adv Biol Res* 1, 72-84.

Yang, L., Fu, S., Khan, M.A., Zeng, W., Fu, J., 2013. Molecular cloning and development of RAPD-SCAR markers for *Dimocarpus longan* variety authentication. *Springer Plus* 2, 501.