Molecular markers in livestock improvement

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Traditional livestock improvement programmes have utilized selection based on genotype, which was inferred from phenotypic information on animals and their relatives. These type of selection resulted in annual genetic gain of only about 1-3% of the mean performance and also have limitations due to sex limited traits (milk yield, litter size), age limited traits (carcass quality, longevity), measuring disease resistance traits etc. Recently several major genes affecting economic performance in farm animals have been identified. Using modern techniques it is now possible to uncover a large number of genetic polymorphism at the DNA sequence level at any age in both sexes.

Genetic Markers

Genetic markers are used for evaluation of the genetic basis for the observed phenotypic variability. Genetic markers can be defined as any stable and inherited variation that can be measured or detected by a suitable method that can be used subsequently to detect the presence of a specific genotype or phenotype other than itself which otherwise nonmeasurable or very difficult to detect.

Several types of genetic markers are identified so for. Morphological (e.g. color pattern or other features), chromosomal (e.g. structural or numerical variation in chromosome) and biochemical (e.g. transferrin, amylase polymorphism) markers show low degree of polymorphism and also influenced by environment significantly. Hence these markers are not very useful as molecular markers. The molecular or DNA markers are revealing variations (polymorphism) at DNA sequence level and are numerous presents throughout the genome.

Molecular/ DNA markers

With the development of recombinant DNA techniques, came several methods for resolving genetic polymorphisms at the DNA sequence level. DNA markers (polymorphism) are directly correlated with their phenotypes. Commonly using methods to detect DNA polymorphism in farm livestock are restriction fragment length polymorphisms (RFLPs), microsatellites, and single nucleotide polymorphisms (SNPs).

Restriction Fragment Length Polymorphisms (RFLPs)

Genomes show changes in nucleotide sequence between species and among individuals within a species. The changes in nucleotide sequence are due to mutations. RFLPs occur as a result of DNA base changes, deletions, insertions of rearrangements that either create, eliminate or translocate restriction endonuclease enzyme (cut the DNA at particular nucleotide sequence specific for each restriction endonuclease) cleavage sites. Such variants are inherited in a Mendelian fashion. If the changes result in the creation or abolition of a restriction endonuclease enzyme recognition site results in two shorter fragments or a long fragment respectively. Using electrophoresis techniques DNA fragments are separated. This is the first technique used for typing DNA polymorphism in farm animals.

Microsatellites

Microsatellites are two to six nucleotide repeats interspersed throughout the genome mainly in non-

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