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RESEARCH ARTICLE

CONCEPTS OF WHOLE-GENOME SEQUENCING AND SNP MARKERS IN POULTRY BREEDING: A REVIEW

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ABSTRACT

The molecular markers provide unique genetic properties and methodological advantages that make them more useful and amenable for genetic analysis. The possible applications of molecular markers in poultry breeding have been focused with reference to conventional and transgenic breeding strategies. In general, DNA sequencing is the direct approach to reveal such DNA polymorphism. Currently, more potential and less laborious techniques to uncover new types of molecular markers are newly being introduced. Currently, DNA chip technology is usually carried out during (SNPs) Single Nucleotide Polymorphisms investigations.

INTRODUCTION

In India, poultry breeding is based on quantitative genetics which provide methods to maximize the response to selection. Molecular markers can be used for assessing the genetic variations at the DNA level between different populations and individuals; its advantages are being able to find genetic variations quickly and directly. Molecular markers have developed rapidly and they are having more and more informative. Till now, various types of molecular markers have been utilized to evaluate DNA polymorphisms, e.g. RFLPs. Polymerase chain reaction (PCR) can exponentially use to amplify a fragment of DNA in vitro, and since its invention a series of techniques have been emerged in combination with PCR, e.g. PCR—RFLP, AFLP and (SNPs) Single Nucleotide Polymorphisms (Mullis *et al*., 1986).

Whole-Genome Sequencing and Snp Markers

SNPs involve the substitution of one nucleotide for another or the addition or deletion of one or a few nucleotides. SNPs are more stable, Bi-allelic systems, located in coding and non-coding regions. 2 million SNPs identified in cattle. This sort of polymorphism includes single base transitions, transversions, insertions and deletions, and the minor allele frequency should be 1% or greater (Lander, 1996). Of all the SNP mutation types, transitions are the most common (approx. 2/3).

The fundamental principle of SNPs is to hybridize detected DNA fragments with high-density DNA probe arrays (also called SNP chips); the SNP allele is then named according to the hybridization results.

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SNPs are bi-allelic markers, indicating a specific polymorphism in only two alleles of a population. SNPs distribute in both coding and non-coding regions of genomes, they are vital players in the process of population genetic variations and species evolution (Vignal *et al.*, 2002).

A group of associated SNP loci located on a certain region of the chromosome can form one SNP haplotype. SNPs are third generation molecular marker technology coming after RFLPs and SSRs; it has been successfully used to investigate genetic variation among different species and breeds.

SNPs have the following advantages

- They are numerous and widely distributed throughout the entire genome (Primmer *et al.*, 2002).
- High genetic stability, excellent repeatability, and high accuracy.
- Allow for fast, high-throughput genotyping.
- Convenient for effectively distinguishing heterozygote from homozygote alleles because of its co-dominances (Tsuchihashi and Dracopoli, 2005).

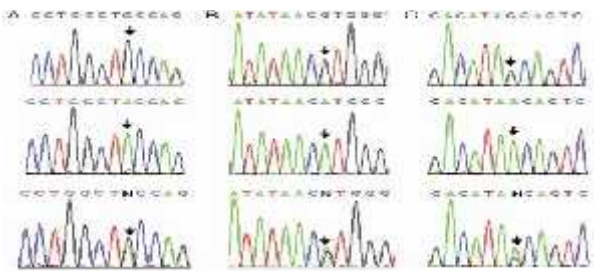

Figure 1 SNP detection by DNA sequencing (Google image)

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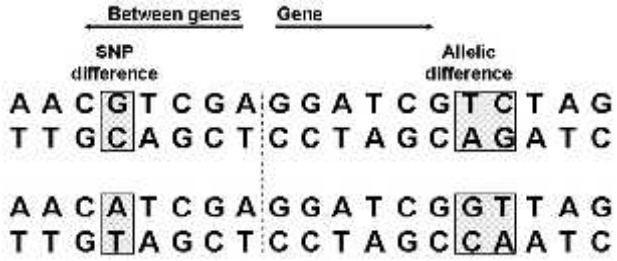

Figure 2 SNP (Google image)

Disadvantage

SNP markers is the low level information obtained compared with that of a highly polymorphic microsatellite, but this can be compensated for by employing a higher numbers of markers (SNP chips) and whole-genome sequencing. With the improvement of sequencing technology, whole-genome/gene sequencing has become available for characterizing genetic diversity among farm poultry's. It is the most straight-forward method and provides more complete information on the genetic variation among different populations because it can detect all the variations within the genome. Currently, the problem with whole-genome sequencing is setting up a high-through data analysis platform to explore useful information for the conservation and utilization of farm poultry's (Stoe cklem, 2005).

CONCLUSIONS

Molecular data eliminate undesirable alleles and increase favourable alleles. It manipulates or create poultry's as desired and needed by the breeders to improve productivity. The genetic improvement of poultry's is a fundamental, incessant and complex process. In current years many methods have been developed and tested.

The genetic polymorphism at the DNA sequence level has provided a large number of markers and revealed potential utility of uses in poultry breeding. The invention of polymerase chain reaction (PCR) in accordance with the constantly increasing DNA sequence data also represents a milestone in this endeavour.

The putting into practice of marker-based information for genetic improvement depends on the choice of an appropriate marker system for a given application. Selection of markers for different applications are influenced by certain factors like the degree of polymorphism (PIC), the automation of the analysis, radioisotopes used, reproducibility of the technique and the cost involved. SNP also successfully used to investigate genetic variation among different species. Presently, the huge development of molecular markers will continue in the near future.

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