MARKER ASSISTED SELECTION IN LIVESTOCK BREEDING: A REVIEW

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ABSTRACT

Conventional breeding strategies in livestock production is time consuming and the effect of conventional breeding scheme in livestock is limited in most cases. This strategies do not take into account all sources of genetic variability efficiently. Also, selection for sex-limited, lowly heritable or late-expressed traits are not only difficult but also very expensive using conventional breeding strategies. However, Marker Assisted Selection (MAS) technique combined all genetic information at markers and Quantitative trait loci (QTL) with the phenotypic records to enhance genetic evaluation and selection. It is an important tool in selection of economic traits in farm animals and hence, it is expected to increase the rate of genetic gain in livestock when relating to traditional breeding programmes.

Key words: Marker assisted selection, Conventional breeding, Quantitative trait loci, Genome wide, DNA based markers

INTRODUCTION

In livestock improvement programmes, most of the traits taken in to account are quantitative traits such as growth rate and milk yield in animals. These traits are affected by several factors such as genetic and environmental factors (Moniruzzaman *et al*., 2014).The main objective in animal breeding is to select an individuals with high breeding values for traits of interest as parents to produce the next generation in a short period of time (Dekkers, 2012). The development of marker assisted selection was, therefore, a major breakthrough. The use of marker genes to indicate the presence of desirable genes is called marker assisted selection (Well *et al*., 1998). Marker- assisted selection is therefore, an indirect selection method where a trait of interest is selected based on a marker linked to it (Ribaut *et al*., 2007). The aim of MAS is to add up all the genetic information and records at markers and QTL level with the phenotypic traits in order to enhance genetic evaluation and selection in farm animals.

The combination of two selection methods, which is the traditional or conventional selection methods with molecular genetics methods is beneficial to selection response. Large number of estimated QTL effects and multiple trait selection could help to make better decisions regarding the application of MAS in the improvement of farm animals (Wakchaure *et al*., 2015). Furthermore, Dekkers (2004) reported that there are three (3) types of MAS; Gene assisted selection (GAS) where the functional mutation and its effects are known, Linkage disequilibrium MAS (LD-MAS) where a marker (marker haplotypes) is in population-wide disequilibrium with QTL and Linkage equilibrium MAS (LE-MAS) where markers are in Hardy-Weinberg equilibrium with the QTL at the population level, but linkage disequilibrium exists within families. A fourth type of MAS is "genome-wide MAS" (GW-MAS), where a denser marker (i.e SNPs) across the genome is used to predict the genetic merit or value of an individual without targeting any individual QTL. Markers have been found for almost all farm animal species, including milk production in dairy cattle (Ansari-Mahyari *et al*., 2008; Lipkin *et al*., 2008), growth and carcass traits of beef cattle (Carr *et al*., 2006), chicken (Lahav *et al*., 2006), and goat (Shen *et al*., 2004). This study was designed to review the significance of marker-assisted selection in livestock breeding programme.

METHODS OF QUANTITATIVE TRAIT LOCI DETECTION IN MAS

There are three important information that are required for detection of QTL in livestock: a) phenotypic information or data collection from a pedigree, b) collection of information on genetic marker, and c) relating this information with both the phenotype and genotype using statistical analysis (Rocha *et al*., 2002). Crucial stages in QTL analysis are not to be overlooked but to ensure that the real effect of QTL and the QTL should be present in the breeding population under study (Spelman and Bovenhuis, 1998). Furthermore, the following are also important in QTL analysis: a) determining the QTL effect on the correlated traits, b) estimating the QTL allele frequencies in the breeding population, c) observing the number of alleles segregating at the QTL locus and d) fine mapping of the QTL. Genome scan and candidate genes are the two approaches that were used to detect QTL in farm animals (George, 1998; Haley, 1999; Anderson, 2001). A well designed genome scan will clearly detect QTL, though it has some limitations. Genome scan methods are expensive and consumed much time as several samples must be genotyped from individuals in order to provide accurate statistical results which has a relatively low mapping resolution of 10-20 cM. The candidate gene approach is basically on either comparison of a suspected orthologous gene in another species or physiological function of a known locus that resemble the phenotype being observed (Haley, 1999; Anderson, 2001). One of important aspect of candidate gene approach is that, it is useful for quickly determining the relationship of a genetic variant with mutation.

Steps involved in MAS

The first step is the validation of molecular markers which entails extraction of DNA from test individuals to find out whether there is one-to-one relationship with marker and the trait of interest. Secondly, it involves the extraction of DNA from breeding population at an early stage of growth and apply MAS. Selection of the individuals based on the presence of desired molecular markers for the trait concerned. From markers to MAS, the next step is that, putative genes that have an effect on the traits of interest can be detected by testing the associations between the marker variants and any trait of interest. The success of MAS depends on the relationship between the markers and the genes of interest. Dekkers (2004) observed three kinds of relationship: (i) the molecular marker is located within the gene of interest which is called gene-assisted selection (GAS). This is the most favourable situation in MAS. However, it is difficult to find these markers. (ii) The marker is in linkage disequilibrium (LD) with gene of interest throughout the whole population. LD is the tendency of certain combinations of alleles (e.g. M1 and Q1) to be inherited together. Selection using these markers is referred to as LD-MAS. (iii) The marker is in linkage equilibrium (LE) with gene of interest throughout the whole population, selection using these markers is called LE-MAS and this is the most difficult situation for applying MAS.

Markers are categorized into; Morphological markers, Cytological markers, Biochemical markers and Molecular markers (Microsatellites, Restriction fragment length polymorphism, Random amplified of polymorphic DNA, Amplified fragment length polymorphism, and single nucleotide polymorphisms).

Table 1: Some traits of livestock and their associated markers

Species	Traits	Markers	Reference
Cattle	Carcass traits	*SDC V293A* *FASN*	Kawaguchi *et al.* (2020)
	Fat content in milk	*DGAT1*	
Sheep	Laptin	*LEP*	Erhardt and Weimann (2007)
	Spider lamb syndrome	*DQA2*	
Chicken	Complex vertebral malformation	*SLC35A3*	
	Egg production	GRB14 GALNT1	*Lieu et al.* (2011)

Application of Marker Assisted Selection in Farm Animals

Marker assisted selection could be used to identify genes for mutation (Georges *et al*., 1993), disease resistance and product quality (Ashwell *et al*., 1997). MAS is also used in the improvement of growth such as improving performance in laying chickens and carcass composition in pigs as well as control of milk fat in dairy cattle.

Merits of Marker- Assisted Selection

MAS offered some advantages which include (i) MAS aid in identification of traits at early stages of growth in an individual that will be passed from one generation to the next generation, irrespective of the environmental conditions or factors. (ii) MAS is an important tool in selection particularly for sex-limited traits such as milk yield and egg production. (iii) Low heritable traits or traits that are poor predictor of breeding value such as litter size and fertility, benefits from marker assisted selection. (iv) Trait that are difficult or expensive to measure such as disease resistance traits, or those that are genetically correlated e.g. milk production and protein content can be detected using MAS.

Demerits of Marker-Assisted Selection

(i) Cost involved in sample collection for genotyping and complete genotype information of an animal is high. (ii) Requirement of technical skill. (iii) Low accuracy in quantitative trait loci detection (iv) DNA markers are not affected by environment but traits may be affected by the environment and show genotype- environment interaction. (v) DNA marker has to be validated for each breeding population (Moniruzzaman *et al*., 2015).

CONCLUSION

Marker assisted selection plays a significant role in livestock breeding programmes, as the rate of genetic improvement achieved through it may be substantial. Combined MAS with conventional selection methods, it has therefore, become a valuable tool in the selection of farm animals for identification of economically important traits which is expected to increase genetic gain.

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