MARKER ASSISTED SELECTION AND ITS FUTURE USE

Abstract

Marker assisted selection (MAS) is a method used to select the dominant population of the product. MAS depends on the identification of the relationship between genetic markers and linked quantitative trait loci (QTLs). The relationship between markers and QTLs depends on the distance between the marker and the target feature. Once pointers linked to QTLs are defined, they can be used in selection programs. This method of using pointers in selection is called pointer assisted selection.

MAS is useful when quality measurement is difficult and expensive, and features and characteristics are poor. MAS can help increase genetic diversity in breeders and can be used to improve the quality of livestock. Marker assisted selection (MAS) is extensively adopted marker method in breeding.

Keywords: Marker-assisted selection (MAS); BLUP, Quantitative trait loci (QTL); Gene mapping.

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I. INTRODUCTION

Marker assisted selection (MAS) is the process of combining genetic information with phenotypic data to improve selection response compared to traditional techniques. The concept of marker assisted selection (MAS) was proposed as early as 1900, using information about polymorphic regions to aid selection [1]. The process of using genetic markers to indicate the presence of desired genes is called marker selection [2]. Marker assisted selection (MAS) is an indirect selection method in which the interest is selected according to the markers associated with it, not its own characteristics [3]. The aim is to combine all genetic information on markers and QTLs with phenotypic data to improve genetic evaluation and selection.

The advantage of using MAS is that the effect of the gene on production is directly measured by the genetics of the animal and not predicted by the phenotype. The combination of two selection methods, natural selection methods or model selection and molecular genetics methods, facilitates site selection. Multiple predicted QTL effects and multiple positive options facilitate better decision making using MAS in animal treatment.

II. MARKER ASSISTED SELECTION AND QUANTITATIVE TRAIT LOCI

MAS can only increase the value of genes when new QTLs are continuously identified, and the number of genes inserted by MAS decreases rapidly with increasing selection of the same QTL, and the number of new QTLs is also difficult to estimate. . QTL significantly increased MAS when measuring traits such as fertility and carcass. The purpose of MAS is to improve site selection [4]. For the success of QTLs in selection programs, specific polymorphisms responsible for favorable outcomes must be identified [5]. The efficacy of MAS is achieved by combining markers and true QTLs and mutations elsewhere in the genome [6]. Continued progress in genomic mapping and QTL analysis will eventually eliminate the association problem as QTL producing genes and even polymorphic alleles are identified. The genetic makeup of MAS is equal to 10-20% depending on the size of the QTL. When MAS was used in a population, the frequency of suitable QTL alleles increased rapidly during the first generation compared to conventional selection based on BLUP (best linear unbiased estimate). Animals selected for genotyping should be linked to marker loci and QTLs. Using QTL detection data in selection requires the development of selection methods that link molecular data to phenotypic data. The best choice should be to choose the same people as the parents of the next generation.

MAS can be effectively applied to traits controlled by QTLs with large effects and high phenotypic selection rates. However, the use of the MAS requires a unique attachment that can be used as a pet MAS in cattle feed. One problem with the MAS family is that many grandchildren need to have half the family to predict conflict. The selection strategy using cattle training data is generally based on pedigree information [7]. The use of linkage disequilibrium (LD) data to map QTLs is increasing [8].

After the QTLs are well mapped, the next step is to use them to predict breeding outcomes. There are many examples of the use of LD markers for selection in dairy cattle [9]. Using DNA data in populations with LD can improve the accuracy of identifying the correct species.

III. ADVANTAGES OF MARKER ASSISTED SELECTION

Regardless of external factors, gene analysis enables determination of the features that a person will pass on to future generations. Selection based on traits such as disease resistance while phenotypes are not easily quantified. Selection is possible for genetics and mutants. The selection process is faster because the phenotype of an individual can be predicted very early on. For sexual restriction (milk production, egg production), the quality of inheritance is poor or workers are not good for reproductive cost (large litter, fertility) and response quality and genetic increase in normal selection, MAS was better than normal selection. Choice for more profitable and breeding programs [10], physical traits (beef quality), difficult or expensive to measure (line disease resistance), link between milk production and milk protein content [11] as they cannot be measured in breeders, traits expressed at the end of life is controlled by several allele pairs [4] and large genotypes, by interacting with the environment and testing offspring with long generations and long and expensive strides. MAS is used as a tool to shorten progeny through early selection (even before maturity) and selection for traits found in one sex [12].

MAS is particularly useful in crossbreeding programs where desired genotypes are incorporated into high yielding cultivars with improved overall yield. Disease resistant genes in native cultivars are a particular target of an amplification program that crosses many foreign crops with many local cultivars. Along with parenting behavior, maternal ability, and survival, reproduction are also good MAS targets because they limit sex and only show after the first stage of reproduction. Antibiotic resistance, which is often difficult to measure in non-invasive conditions, may also benefit from MAS. Because of the high heritability of MAS and its ability to measure quality before first selection, the utility of MAS on wool products should be limited.

Nutritional quality and maternal performance are important determinants of animal production [13] and genetic improvement will benefit from MAS because of its cost-effectiveness. The Booroola gene is used in MAS and related intervention programs (MAI) because its breeding value is of good economic value and genetic variation can be detected [14].

IV. LIMITATION OF MARKER-ASSISTED SELECTION

Breeding operations are severely constrained by the growing expense of sample collection for genotyping and the processing of genotype data in MAS. The dairy sector has difficulties when trying to genotype entire herds. By finding the most frequent individuals based on phenotypic data [15], exclusion analysis [16], or combining phenotypic and genotypic data [17], genotyping costs can be reduced. However, because there aren't many reliable users and few key markers for the gene, QTL detection is inaccurate. In general, the population employed in MAS studies lacks complete genotyping data, lacks markers, and selection of marker data is unreliable due to the possibility of overestimating QTL effects and using the wrong QTL locations. A common problem with QTL estimation is heterogeneity, meaning that QTL effects are not expressed uniformly over years or when using different populations [18].

V. APPLICATIONS OF MARKER-ASSISTED SELECTION

Selective marker services can be used to identify genetic diseases [19], disease resistance and quality [20]. Use marker assisted selection to improve lifespan, feather pecking, depression, and desired behavior in animals [21].

Disease Resistance: Many models can detect genes affected by certain diseases, allowing to differentiate between disease-susceptible and resistant strains. MAS allows selection for immunity and allows selection to be independent of the medium.

Selection and breeding: The goal of animal breeding is to integrate QTL-linked markers into breeding programs using marker selection assistance (MAS) [22].

By combining MAS deficiency or by genetic selection, MAS can be exploited in farm animals [9]. Precision and effectiveness in MAS selection will be achieved by genomic research and quantitative trait loci (QTL) mapping [23].

MAS enables selection without the cost of evaluating offspring. In the case of milk production and egg laying in males, MAS also permits selection to take place among related individuals who do not display the trait. MAS can therefore be utilized in introgression techniques to select both for the desired trait and against unwanted characteristics [24]. High heritability characteristics with big effects that are already fixed with nearly optimum alleles in commercial lines are predicted to benefit the most from MAS. The selection response for milk production in cattle that used multiple ovulation and embryo transfer (MOET) in the first six generations of selection was found to increase 6 to 15% from MAS. There are financial benefits to using the MAS in dairy cattle. [25,26].

VI. CONCLUSION

Marker-assisted selection is the use of genetic markers in conjunction with phenotypes. When used in conjunction with conventional selection methods, MAS has emerged as a crucial tool for selecting desired features in organisms. Through the early selection of young bulls, MAS is anticipated to increase genetic quality in comparison to conventional breeding programmes and lower the cost of progeny testing. Breeders' understanding of the genetic variety and variability of animals and their capacity to use genotype data to enhance their small enterprises are prerequisites for the application of MAS in breeding programmes. Animals can be chosen for their genetic resistance using MAS as well.

In the future, for MAS to be useful in large breeding populations, the infrastructure must exist for large-scale genotyping methods and generating hundreds of thousands of molecular data at an affordable price.

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