Marker Assisted Selection (MAS) in Animal Breeding: A Review

Rajesh Wakchaure[1], Subha Ganguly[2]*, Praveen Kumar Praveen[3], Avinash Kumar[4], Subhash Sharma[5] and Tanvi Mahajan[6]

[1]Department of Animal Genetics and Breeding, Rajasthan, India
[2]Department of Veterinary Microbiology, Rajasthan, India
[3]Department of Veterinary Public Health and Epidemiology, Rajasthan, India
[4]Department of Veterinary Pharmacology and Toxicology, Rajasthan, India
[5]Department of Veterinary Parasitology, Rajasthan, India
[6]Department of Veterinary Anatomy and Histology, Arawali Veterinary College, Rajasthan, India

Abstract

Marker-Assisted Selection (MAS) is a used for indirect selection of superior breeding animals. MAS depend on identifying association between genetic marker and linked Quantitative traits loci (QTL).The association between marker and QTL depend on distance between marker and target traits. As soon as markers linked to QTL have been identified, they can be used in selection programme. This use of marker in selection is called Marker-Assisted Selection. MAS is beneficial when the traits are difficult and expensive to measure and low heritability and recessive traits. MAS facilitate the exploitation of existing genetic diversity in breeding populations and can be used to improve desirable traits in livestock. Marker-Assisted Selection (MAS) is the most widely used application of marker systems in breeding.

Keywords: Marker-assisted selection (MAS); Quantitative trait loci (QTL); Breeding; BLUP

Introduction

The addition of genomic information to phenotypic information to increase the selection response to the traditional method is known as Marker-Assisted Selection (MAS). The concept of Marker Assisted Selection (MAS) utilizing the information of polymorphic loci as an aid to selection was introduced as early as in 1900 [1]. The method where marker genes used to indicate the presence of desirable genes is called as marker assisted selection [2]. Marker assisted selection (MAS) is indirect selection process where a trait of interest is selected not based on the trait itself but on a marker linked to it [3]. The purpose is to combine all genetic information at markers and QTL with the phenotypic information to improve genetic evaluation and selection. The advantage of using MAS is that the effect of genes on production is directly measured on the genetic makeup of the animal and not estimated from the phenotype. The integration of two selection methods, i.e., traditional or conventional selection methods with molecular genetics methods beneficial to the selection response. Multiple estimated QTL effects and multiple trait selection could help to make better decisions regarding the use of MAS in animal improvement.

Marker assisted selection and quantitative trait loci

MAS only can increase the rate of genetic gain when there is a continuous identification of new QTL, The extra genetic gain due to the MAS decreases very quickly with the number of generations of selection for a same QTL also the rate of identification of new QTL is difficult to predict, the gain due to MAS for a certain QTL is higher when the characteristic like fertility and carcass is measured after the selection. The aim of MAS is improving selection response [4]. For a successful implementation of such QTL within selection programs, the identification of specific polymorphisms which are responsible for the observed effect is needed [5]. The effectiveness of MAS by both recombination between the marker and the actual QTL and by mutation elsewhere in the genome [6]. The continued development of genome maps and QTL analysis will eventually remove the recombination problem, as the genes and even the specific polymorphic alleles that generate QTL are identified. Genetic gains from MAS equal to 10-20%,

depending on the size of the QTL. When MAS is used in a population, the frequency of the favorable QTL allele is quickly increased during the first generations compared to conventional selection based on BLUP (Best linear unbiased prediction). Selection of an animal for genotyping should be related to the linkage of marker loci and the QTL. Use of information from the detected QTL in the selection requires developing selection criteria to connect this molecular information with phenotypic information. The optimum selection should identify outstanding individuals as the parents of the next generation. For traits regulated by a QTL with large effects and for which phenotypic selection is expensive, MAS can be efficiently used. However, use of MAS requires linkage disequilibrium which could be used in dairy cattle as MAS within family. One problem of MAS within family is the large number of offspring required from each half-sib family in order to estimate unbiased effects. The selection schemes using marker information for dairy cattle were largely based on information from within families [7]. The use of linkage disequilibrium (LD) information to locate QTL has increased [8]. The next step after fine-mapping of QTL is to use them in prediction of breeding values. There are several examples in dairy cattle with LD markers used for pre-selection of candidates [9]. Using DNA-information in a population with LD can enhance the accuracy of identifying superior animals.

Advantages of marker assisted selection

Analysis of the genes helps in identification of the traits an individual

will pass on to the next generation, regardless of the environmental conditions. Selection based on traits when the phenotype is not easy to evaluate such as for disease resistance genes. Selection is possible for recessive genes and mutants. Faster selection process because an individual's phenotype can be predicted at a very early stage. MAS is profitable than conventional selection for sex-limited traits (milk yield, egg production), low heritability traits or traits that are a poor predictor of breeding value (litter size, fertility) and a corresponding lack of selection response and genetic gain in conventional selection and breeding programs [10], carcass traits as they cannot be measured on breeding animals(meat quality), difficult or expensive to measure (disease resistance), traits that are genetically correlated milk production and protein content of milk [11], traits that are expressed late in life, that are controlled by a few pairs of alleles [4] and large genotype by environment interactions and progeny testing scheme where long generation interval, lengthy and costly step. MAS are used as a tool to reduce generation interval through early selection, even before maturity and to select those traits which are observed in only one sex [12]. MAS could be particularly useful in crossbreeding programmes where, desirable genotypes are introgressed into productive local breeds with overall better breeding values. The disease resistance genes of local breeds are specifically targeted in upgrading programmes with imported stock with higher productivity breeds being crossed to local breeds. Reproduction traits as well as maternal behavior, mothering ability and ewe survival are also good MAS targets as they are sex limited and are only expressed after the first stage of reproduction. Disease resistance traits are generally hard to measure under uniform conditions and would also greatly benefit from MAS. MAS would be expected to have limited benefit for wool production traits because of their high heritability and the ability to measure the traits before the age of first selection. Feed efficiency and maternal efficiency are important determinants of pastoral production systems [13] and genetic improvement would benefit from MAS because of the cost of their measurement. As the reproductive rate is a trait of high economic value and due to the availability of a test for the actual gene mutation, Booroola gene used for MAS and marker-assisted introgression (MAI) programmes [14]. MAS gave an additional gain of 24% when half of the selected candidates were slaughtered to measure phenotypes on carcasses. When the non-selected halves were slaughtered, the marker-phenotype information could be used to select in the next generation, giving 64% additional gain [4]. The use of Marker Assisted Selection (MAS) has the potential if the markers are highly correlated with the desired phenotype to enhance the power of the present-day breeding strategy [15]. Many genetic markers linked with QTL affecting traits of economic importance in livestock, including milk production, conformation and health have been identified and mapped during the past decade [16]. Pongpisantham (1994) found that the inclusion of markers could increase up to 15% the genetic response to selection for growth rate in a population of chickens, compared with selection based on family selection. MAS can increase the reliability of breeding values [17,18].

Limitation of marker-assisted selection

Increased cost involved in sample collection for genotyping and complete genotype information in MAS is a major limitation in a breeding scheme. Genotyping the whole population is also difficult in commercial dairy cattle populations. To decrease genotyping costs by identifying the most informative individuals based on phenotypic information [19], segregation analysis [20] or combining the phenotypic and genotypic information [21], limited number of genes of importance fully characterized and also lack of confidence of users, low

accuracy of QTL detection. In most situations, there is not complete genotype information in the population used in MAS schemes, lack of markers, Selecting on marker information is not fully reliable due to possible overestimation of QTL effects and error in QTL position. A common problem related with QTL estimates is inconsistency, which means that a QTL effect is not expressed similarly in several years or when is used in a different population [22].

Applications of marker-assisted selection

Marker Assisted Selection could be used to detect genes for genetic disorders [23], disease resistance and product quality [24]. The use of Marker Assisted Selection to improve longevity, feather pecking, stress resistance, desired behaviour characteristic of animal [25].

Disease resistance: Large numbers of samples can be screened for the genes conferring resistance to a given disease, distinction between lines that are susceptible and resistant to that disease possible. MAS can enable selection for disease resistance and allows highly accurate selection which is unaffected by environmental factors.

Selection and breeding: The aim of animal breeders is to integrate linked markers for QTL into the breeding program in marker assisted selection (MAS) [26]. MAS can be used either by linking MAS disequilibrium or through gene assisted selection in the livestock breeding industry [9]. Quantitative trait loci (QTL) mapping and genomic research will lead to MAS for precise and efficient selection [27]. MAS allows for selection without the expense of testing progeny. MAS also allows selection to occur among related individuals that do not exhibit the trait (milk production and egg laying in males), and MAS can be used in introgression strategies to select both for the trait to be introgressed and against undesirable traits [28]. MAS is expected to be most useful for highly heritable traits of large effect and such traits are already fixed with near optimal alleles in commercial lines. Ruane and Colleau (1996) found an increase of 6 to 15% from MAS in the selection response for milk production in cattle that used multiple ovulation and embryo transfer (MOET) in the first six generations of selection. The use of the MAS in dairy cattle has economic advantages [29,30]. It is applied with progeny testing and multiple ovulation and embryo transfer (MOET) schemes. Marker-Assisted Selection used for genes with significant effect which are targeted specifically in selection such genes are located at QTL. Knowledge of the genes located at QTL could greatly help in estimating an animal's true genotype. The Information available at QTL adds to accuracy of estimation of breeding value. If genetic effects at QTL are really large such genes could be more specifically exploited in breeding programs. Selection of animals could be based on genetic marker information only. Optimal selection should aim for QTL as well as for polygenes. It should be based on information from markers genotypes combined with information on animal's phenotype. Selection with the help of information at genetic markers is termed as "marker assisted selection" (MAS). Marker-assisted selection (MAS) can increase the rate of genetic response in the range of 5% to 64% in animal breeding populations depending on the trait being selected and marker and quantitative trait loci (QTL) information [31]. Molecular markers are used to identify loci or chromosomal regions that affect single gene traits and also QTLs. By genotyping, accurate detection of specific DNA variations that have been associated with measurable effects on complex traits. By combining phenotypes with genetic markers seems to be a promising approach for improving health and welfare traits in farm animals. MAS is currently been used in commercial livestock breeding. Markers associated with marbling and tenderness in cattle. It is expected that MAS schemes will eventually be more widely implemented [32]. Using marker information in

selection schemes indicated that the genetic merit can enhance through increasing the accuracy of genetic evaluation in outbred populations [33], where the accuracy of selection is low when using conventional selection schemes (fertility traits). When the marker is completely linked to a specific QTL, it is possible to detect the best and the worst alleles. These identified markers will be highly useful for the selection plans as well as useful for checking the success of traditional selective breeding programs [34]. In MAS, genetic information of the markers has been used as a criterion of indirect selection for genetic improvement of a quantitative trait. Another benefit of MAS schemes over BLUP was a reduction in the rate of inbreeding, as using additional marker information allows selection of high-ranking animals within families. Progeny testing scheme have high accuracy of selection but generation interval is also high which decreases rate of genetic gain. MAS scheme shorten generation interval considerably but still maintain high accuracy of selection due to use of marker information. Reducing the generation interval to half while maintaining high accuracy of selection, genetic gain would double. In case of carcass traits, where benefits of MAS scheme are up to 65 % higher than those due to conventional selection [4]. If marker-QTL associations have been identified, MAS is used in breeding programmes. Genetic markers can be used in genetic improvement of livestock in breeding programme.

Conclusion

The use genetic markers with the phenotypes in a process called marker-assisted selection. Combined with traditional selection techniques, MAS has become a valuable tool in selecting organisms for desirable traits. MAS is expected to increase genetic gain compared to traditional breeding programs and reduce the cost of progeny testing by early selection of the potential young bulls. The application of MAS in breeding programmes depends on the knowledge of breeders about variable marker information from animal to animal and the different effects on multiple traits and his ability to spend in genotypic information that helps in improve their commercial breeding activities. MAS also provide an apparently possible approach to selection for genetic disease resistance animals. In the future to make MAS effective in large breeding populations, the availability of large-scale genotyping methods and infrastructure that allows the generation of hundreds of thousands of molecular data at a reasonable cost will be necessary.

References

1. Sax K (1923) The association of size differences with seed-coat pattern and pigmentation in Phaseolus vulgaris. Genetics 8: 522-560.

2. Well DN, Misica PM, Tervit HR (1998) Future opportunities in livestock production and biomedicine from advances in animal cloning. Proceedings of New Zealand Society of Animal Production 58: 32-35.

3. Ribaut JM, Ragot M (2007) Marker-assisted selection to improve drought adaptation in maize: the backcross approach, perspectives, limitations, and alternatives. J Exp Bot 58: 351-360.

4. Meuwissen THE, Goddard ME (1996) The use of marker haplotype in animal breeding schemes. Genetic selection Evolution 21: 467-477.

5. Ron M, Weller JI (2007) From QTL to QTN identification in livestock – winning by points rather than knock out: a review. Animal Genetics.

6. Keightley PD, Hill WG (1992) Quantitative genetic variation in body size of mice from new mutations. Genetics 131: 693-700.

7. Spelman RJ, Garrick DJ (1998) Genetic and economic responses for within-family marker-assisted selection in dairy cattle breeding schemes. J Dairy Sci 81: 2942–2950.

8. Uleberg E, Meuwissen THE (2007) Fine mapping of multiple QTL using combined linkage and linkage disequilibrium mapping - A comparison of single QTL and multi QTL methods. Genet Sel Evol 39: 285-299.

9. Dekkers JCM (2004) Commercial application of marker- and gene-assisted selection in livestock- Strategies and lessons. J Anim. Sci 82: 313-328.

10. Hiendleder S, Bauersachs S, Boulesteix A, Blum H, Arnold GJ, et al. (2005) Functional genomics: tools for improving farm animal health and welfare. Rev Sci Tech 24: 355-377.

11. Schwerin M, Brockmann G, Vanselow J, Seyfert HM (1995) Perspectives of molecular genome analysis in livestock improvement. Arch. Tierz. Dummerstorf 38: 2131.

12. Rothschild MF, Ruvinsky A (2007) Marker-Assisted Selection for Aquaculture Species, in Aquaculture Genome Technologies (ed Z. Liu), Blackwell Publishing Ltd, Oxford, UK, ch., 12: 201-216.

13. Ferrell CL, Jenkins TG (1984). Energy utilisation by mature, non-pregnant, non-lactating cows of different types. J. Anim. Sci 58: 234-243.

14. Van der Werf JHJ (2007) Marker Assisted Selection in Sheep and Goats. In: "Marker Assisted Selection (MAS) in Crops, Livestock, Forestry and Fish: Current Status and the Way Forward", FAO Invited Book Chapter 13.

15. Georges M (1998) Perspectives for marker assisted selection in dairy cattle breeding. Proceedings of the European AI Vets 10th meeting, Belgium: 25-29.

16. Van Tassell CP, Ashwell MS, Sonstegard TS (2000) Detection of putative loci affecting milk, health and conformation traits in a US Holstein population using 105 microsatellite markers. J. Dairy Sci 83: 1865–1872.

17. Pongpisantham B (1994) Applying genotype and marker assisted selection for the improvement of quantitative traits in poultry. M.S. Thesis. University of New England: 121.

18. Mackinnon MJ, Georges MAJ (1998) Marker-assisted preselection of young dairy sires prior to progeny testing. Livest. Prod. Sci 54: 229–250.

19. Darvasi A, Soller M (1992) Selective genotyping for determination of linkage between a marker locus and a quantitative trait locus. Theor. Appl. Genet 85: 353-359.

20. Macrossan PE, Kinghorn BP (2003) Cyclic genotyping strategies. I. A comparison of ranking criteria. J. Anim. Breed. Genet 120: 303-311.

21. Mahyari SA, Berg P (2008) Combined use of phenotypic and genotypic information in sampling animals for genotyping in detection of quantitative trait loci. J.Anim. Breed. Genet 125: 100–109.

22. Mayo O, Franklin IR (1998) The place of QTL in the basis of quantitative genetics. I. General considerations. In: Proceedings of the 6th Word Congress on Genetics Applied to Livestock Production, Armidale, NSW 26: 7780.

23. Georges M, Dietz AB, Mishra A, Nielsen D, Sargeant LS, et al. (1993) Microsatellite mapping of the gene causing weaver disease in cattle will allow the study of an associate quantitative trait locus. Proceedings of the National Academy of Sciences of the United States of America 90: 1058-1062.

24. Ashwell MS, Rexroad CE Jr, Miller RH, Van Raden PM, Da Y (1997) Detection of loci affecting milk production and health traits in an elite US Holstein population using microsatellite markers. Animal Genetics 28: 216-222.

25. Neeteson AM, Bagnato A, Merks J, Finocchiaro R, Knol E, et al. (1999) The Reproduction and Selection of Farm Animals. EC - ELSA project report. Farm animal breeding and society: 1-21.

26. Neuner S, Emmerling R, Thaller G, Götz KU (2008) Strategies for estimating genetic parameters in marker-assisted best linear unbiased predictor models in dairy cattle. J Dairy Sci 91: 4344-4354.

27. Liu ZJ, Cordes JF (2004) DNA marker technologies and their applications in aquaculture. Aquaculture 238: 1-37.

28. Hillel J, Schaap T, Haberfeld A, Jeffreys J, Plotsky Y, et al. (1990) DNA fingerprints applied to gene introgression in breeding programs. Genetics 124: 783-789.

29. Ruane J, Colleau JJ (1996) Marker assisted selection for a sex-limited character in a nucleus breeding population. Journal of Dairy Science 79: 1666-1678.

30. Spelman RJ, Garrick DJ (1997) Utilization of marker assisted selection in a commercial dairy cow population. Livest. Prod. Sci 47: 139–147.

31. Hayes B, Goddard ME (2003) Evaluation of MAS in pig enterprises. Livest. Prod. Sci 81: 197-211.

32. Hoeschele I, Meinert TR (1990) Association of genetic defects with yield and type traits: The Weaver Locus Effect on Yield. Journal of Dairy Science 73: 946-952.

33. Villanueva B, Pong-Wong R, Fernández J, Toro MA (2005) Benefits from marker assisted selection under an additive polygenic genetic model. J. Anim. Sci 83: 1747-1775.

34. Liu Z (2001) Gene mapping, marker-assisted selection, gene cloning, genetic engineering and integrated genetic improvement programs at Auburn University, p. 109-118. In: M.V. Gupta and B. O. Acosta (eds.) Fish genetics research in member countries and institutions of the International Network on Genetics in Aquaculture. ICLARM Conf. Proc. 64: 179.