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Markers Assisted Selection in Plant Breeding

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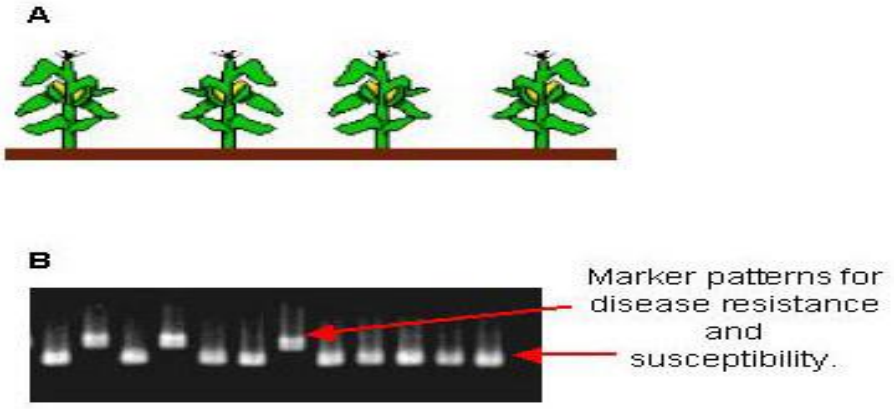
SUMMARY

Marker-assisted selection (MAS) is a method of selecting desirable individuals in a breeding scheme based on DNA molecular marker patterns instead of in addition to their trait values. When used in appropriate situations, it is a tool that can help plant breeders select more efficiently for desirable crop traits. However, MAS is not always advantageous, so careful analysis of the costs and benefits relative to conventional breeding methods is necessary.

INTRODUCTION

Conventional plant breeding is dependent on appropriate environmental conditions in which to identify and select desirable plants. Typically, breeders improve crops by crossing plants with desired traits, such as high yield or disease resistance, and selecting the best offspring over multiple generations of testing. A new variety could take 8 to 10 years to develop. Breeders are very interested in new technologies to speed up this process or make it more efficient. Molecular marker technology offers such a possibility. Marker-assisted selection involves selecting individuals based on their marker pattern (genotype) rather than their observable traits (phenotype) (Fig.1). The term 'marker-assisted selection' has entered the working vocabulary of plant breeders and geneticists.



(**Source:** https://passel2.unl.edu/view/lesson/a7b9c8f0ffa2/2**)**

Fig. 1. A. Conventional selection is based on direct measurement of important traits, such as yield, maturity, or disease resistance.
B. In marker-assisted selection, plants are selected based on molecular marker patterns known to be associated with the traits of interest.

Prerequisites for an efficient marker-assisted selection program Xu (2003) for more details

A. High throughput DNA extraction.

B. Genetic markers.

For efficient MAS, important attributes of markers include:

- Ease of use
- Small amount of DNA required
- Low cost
- Repeatability of results
- High rate of polymorphism
- Occurrence throughout the genome
- Codominance

C. Genetic maps. Linkage maps provide a framework for detecting marker-trait associations and for choosing markers to employ in MAS. Once a marker is found to be associated with a trait in a given population, a

dense molecular marker map in a standard reference population will help identify markers that are closer to, or that flank, the target gene.

D. Knowledge of associations between molecular markers and traits of interest.

The most crucial ingredient for MAS is knowledge of markers that are associated with traits important to a breeding program. This information might come from gene mapping or QTL studies, bulked segregant analysis, classical mutant analysis, or some other means.

E. Data management system. Large numbers of samples are handled in a MAS program, with each sample potentially evaluated for multiple markers. This situation requires an efficient system for labeling, storing, retrieving, and analyzing large data sets, and producing reports useful to the breeder.

Advantages of Molecular Marker Assisted Selection

MAS can theoretically enhance selection efficiency because: It can be performed on seedling material, thus reducing the time required before a plant's genotype is known. In contrast, many important plant traits are observable only when the plant has reached flowering or harvest maturity. Knowing a plant's genotype before flowering can be particularly useful in order to plan the appropriate crosses between selected individuals.

Fig. 2. MAS may be conducted based on DNA collected from young plants, such as the wheat seedlings shown here.

- **MAS is not affected by environmental conditions.** Some crop production constraints (such as disease, insect pests, temperature and moisture stress) occur sporadically or non-uniformly. Therefore, evaluating resistance to those constraints may not be possible in a given year or location. MAS offers the chance to determine a plant's resistance level independent of environment.
- **When recessive alleles determine the trait of interest**, they cannot be detected through phenotypic evaluation of heterozygous backcross plants, because their presence is masked by the dominant allele. In a traditional backcross program, plants with recessive alleles are identified by progeny evaluation after self-pollination or test crossing to a recessive tester. This time-consuming step can be eliminated in a MAS program, because recessive alleles are identified by linked markers.
- **Similarly, when multiple resistance genes are 'pyramided' (combined) together in the same variety or breeding line**, the presence of each individual gene is difficult to verify phenotypically. The presence of one resistance gene may conceal the effect of additional genes. This problem can be overcome if markers are available for each of the resistance genes.
- **Environmental variation in the field reduces a trait's heritability**

The proportion of phenotypic variation that is due to genetics. In a low **heritability** situation, progress from phenotypic selection will be slow, because so much of the variation for the trait is due to environmental variation, experimental error, or genotype x environment interaction, and will not be passed on to the next generation. If

a reliable marker for a trait is available, MAS can result in greater progress than phenotypic selection in such a situation.

- **MAS may be cheaper and faster than conventional phenotypic assays, depending on the trait.**

Selecting on the basis of a reliable marker would probably be cost-effective. The plant height is cheap and easy to measure, so there may not be an economic advantage in using markers for that trai.

- **A consideration that may affect cost effectiveness of MAS is that multiple markers can be evaluated using the same DNA sample.** Extraction of DNA from plant tissue is one of the bottlenecks of MAS. Once DNA is extracted and purified, it may be used for multiple markers, for the same or different traits, thus reducing the time and cost per marker.

Some Potential Drawbacks of MAS :

MAS is not universally advantageous. Some limitations of the technique are as follows:

- MAS may be more expensive than conventional techniques, especially for startup expenses and labor costs. Recombination between the marker and the gene of interest may occur, leading to false positives. For example, if the marker and the gene of interest are separated by 5 cM and selection is based on the marker pattern, there is an approximately 5% chance of selecting the wrong plant. This is based on the general guideline that across short distances, 1 cM of genetic distance is approximately equal to 1% recombination. The breeder will need to decide the error rate that is acceptable in the MAS program, keeping in mind that errors are also usually involved in phenotypic evaluation.
- To avoid this last problem it may be necessary to use flanking markers on either side of the locus of interest to increase the probability that the desired gene is selected.
- Sometimes markers that were used to detect a locus must be converted to 'breeder-friendly' markers that are more reliable and easier to use.

Examples are:

RFLP markers converted to STS markers

Evaluation of RFLP markers requires several steps and a large quantity of highly purified DNA. **STS** (sequence tagged site) markers can be detected via PCR using primers developed from **RFLP** probe sequences. Thus the same locus can be detected with the two types of marker, but the STS marker is far more efficient.

RAPD markers converted to SCAR markers

Results of RAP Directions may vary from lab to lab, and therefore, may be considered less reliable for MAS. Variable RAPD results are due largely to short (10-base) PCR primers, resulting in low binding specificity. **SCAR** markers are developed by sequencing RAPD bands and designing more specific 18-25 base PCR primers to amplify the same DNA segment more reliably.

Imprecise estimates of QTL locations and effects may result in slower progress than expected.

Many QTLs have large confidence intervals of 20 cM or more or their relative importance in explaining trait inheritance has been over-estimated

Markers developed for MAS in one population may not be transferrable to other populations either due to lack of marker polymorphism or the absence of a marker-trait association.

CONCLUSION

Marker assisted selection is a technology that has already proved its value. Due to the number of QTLs, genes and markers identified the MAS is likely to become more valuable. It is likely to become more valuable as a larger number of genes are identified and their functions and interactions elucidated. Reduced costs and optimized strategies for integrating MAS with phenotypic selection are needed before the technology can reach its full potential.

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