SMART BREEDING: FAST TRACKING PLANT BREEDING

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"Plant varieties identified by marker-assisted selection (MAS) are gaining prominence as a publicly acceptable alternative to transgenic crops, such as 'Golden' Rice." (PH 2008). Feeding the world within the carrying capacity of planet earth, improve food security, safety and quality, increase the production, reduce input at the same time, use biomass for biofuels and green chemistry while securing food production is the key challenge to the breeder. So, the need is accelerating the breeding cycle (crossing, evaluation and selection) of a crop. This goal can be achieved by SMART breeding, (**Selection with Markers and Advanced Reproductive Technology breeding**) *i.e.* marker-assisted selection, which is simpler than phenotypic screening, which can save time, resources and effort. MAS is a non-invasive biotechnology alternation to genetic engineering (Stevens, 2008).

How molecular markers server our purpose

Selection can be carried out at the seedling stage of the plant. Single plants can be selected. Shorten the breeding cycle. Selection of drought-tolerant plant without drought—no question of bio-safety and bioethics.

Molecular marker

Defined as DNA sequence with a known location on a chromosome. Qualities of a Suitable molecular marker are: Must be polymorphic, Co-dominant inheritance, Randomly and frequently distributed throughout the genome, Easy and cheap to detect, Easily reproducible. eg. RFLP, RAPD, AFLP, SSR and SNP (Xu et al., 2013).

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Marker assisted selection (MAS)

MAS also called marker-assisted breeding or marker aided selection (MAB) is the indirect selection for the desired plant phenotype based on the banding pattern of linked molecule (DNA) marker.
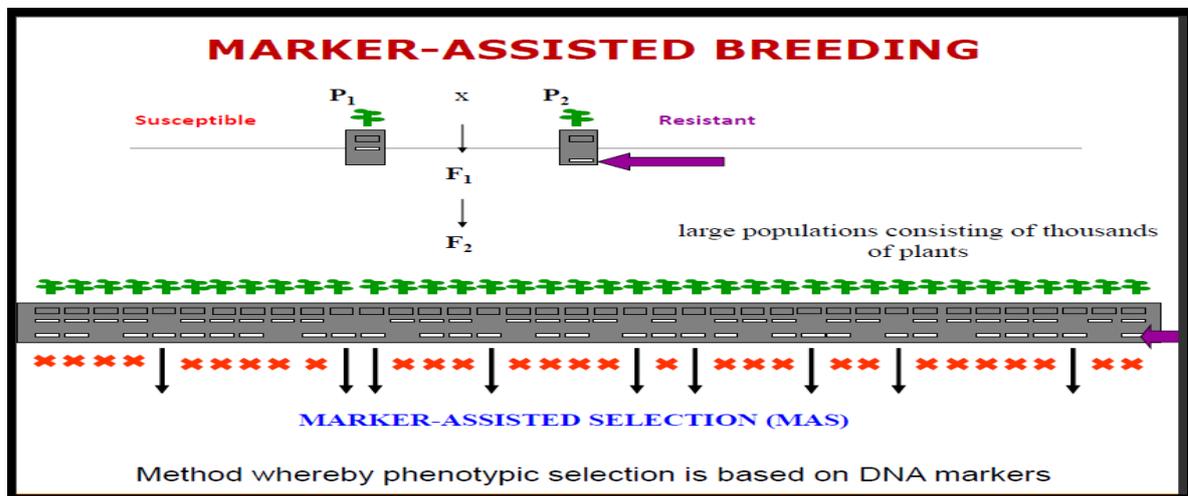
Applications of MAS in plant breeding

1. Marker assisted evaluation of breeding material

2. Marker-assisted backcrossing

3. Marker-assisted pyramiding

4. Early generation marker-assisted selection and

5. Combined marker-assisted selection

1. **Marker-assisted evaluation of breeding material:** Marker genotype data can be used to establish cultivar identity/assessment of 'purity, assessment of genetic diversity and parental selection, the study of heterosis and identification of genomic regions under selection

2. **Marker-assisted backcrossing (MAB):** A backcross program based on the marker is known as MAB. Advantages over conventional backcrossing: minimize linkage drag (Recombinant selection), effective selection of target loci (Forground selection) and accelerated recovery of the recurrent parent (Background selection) (Semagn et al., 2006).

3. **Marker-assisted pyramiding:** It is proposed by Nelson to develop crop varieties with durable resistance to disease by bringing multiple disease resistance oligogenes for specific races of a pathogen. Pyramiding is extremely difficult to achieve using conventional methods.

4. Early generation marker-assisted selection: MAS conducted at F2 or F3 stage. Very useful in self-pollinated crops to fix alleles in their homozygous state as early as possible. It allows breeders to focus attention on a lesser number of high-priority lines in subsequent generations. Linkage between the marker and QTL is not very tight. The disadvantage is the cost of genotyping a larger number of plants.

5. Combined MAS approaches A combination of MAS with phenotypic selection/ screening also known as combined MAS**.** Advantages: to maximize genetic gain (when some QTLs have remained unidentified), especially when large population sizes are used and trait heritability is low, low level of recombination between marker and QTL, to reduce population sizes for traits where marker genotyping is cheaper or easier than phenotypic screening.

'Marker-directed' phenotyping also called **tandem selection**: use when markers are not 100% accurate or when phenotypic screening is more expensive compared to marker genotyping. It saves time and reduce costs and especially for quality traits

Reasons to explain the low impact of marker-assisted selection

Reliability and accuracy of QTL mapping Studies, insufficient linkage between the marker and gene/QTL, limited markers and limited polymorphism of markers in breeding material, 'Application gap' between research laboratories and plant breeding institutes, 'Knowledge gap' among molecular biologists, plant breeders and other disciplines, effects of genetic background, Quantitative trait loci $\times$ environment interaction and high cost of marker-assisted selection.

Conclusion

More than 25 years after the discovery of molecular markers, marker-assisted selection (MAS) has become a routine component of some breeding programmes. Recently, applications of MAS for forward breeding have been shown to increase Significantly the rate of genetic gain when compared with conventional breeding. The cost associated with MAS is still very high. The use of molecular marker in plant breeding programmes is expected to increase with time because of QTL mapping combined with breeding facilities, comparative mapping and high-resolution mapping and genomics.

References

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