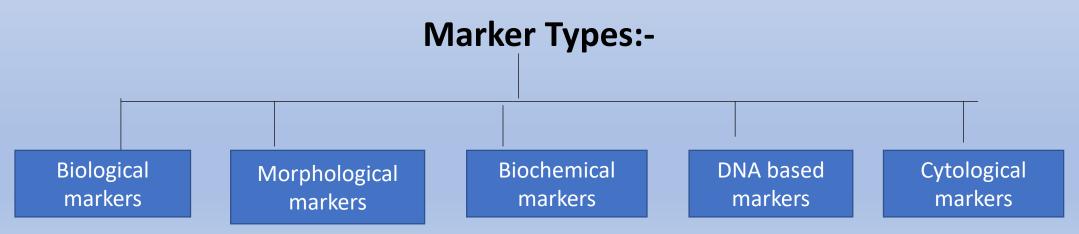


- MAS is a process in which a marker is used for indirect selection of a genetic determinant or determinants of a trait of interest, i.e., abiotic stress tolerance, disease resistance, productivity, and/or quality (Prabhu et al., 2009).
- This method involves selection of plants carrying genomic regions that are involved in the expression of traits of interest through the application of molecular markers.
- The development and availability of an array of molecular markers and dense molecular genetic maps in crop plants has made application of MAS possible for traits governed by major genes and QTLs (Choudhary et al., 2008).
- The success of MAS depends on several factors, including the number of target genes to be transferred and the distance between the flanking markers and the target gene (Perumalsamy et al., 2010).
- MAS is gaining considerable importance as it can improve the efficiency of plant breeding through precise transfer of genomic regions of interest and acceleration of the recovery of the recurrent parent genome (Wijerathna, 2015).

What is Marker Assisted Selection?



 What is Marker Assisted Selection? The addition of genomic information to phenotypic information to increase the selection response to the traditional method is known as Marker-Assisted Selection (MAS).



Important properties of ideal markers for MAS

- Easy recognition of all possible phenotypes (homo- and heterozygotes) from all different alleles.
- Demonstrates measurable differences in expression between trait types or gene of interest alleles, early in the development of the organism.
- Testing for the marker does not have variable success depending on the allele at the marker locus or the allele at the target locus (the gene of interest that determines the trait of interest).
- Low or null interaction among the markers allowing the use of many at the same time in a segregating population
- Abundant in number
- Polymorphic.

Types of Selectable Markers

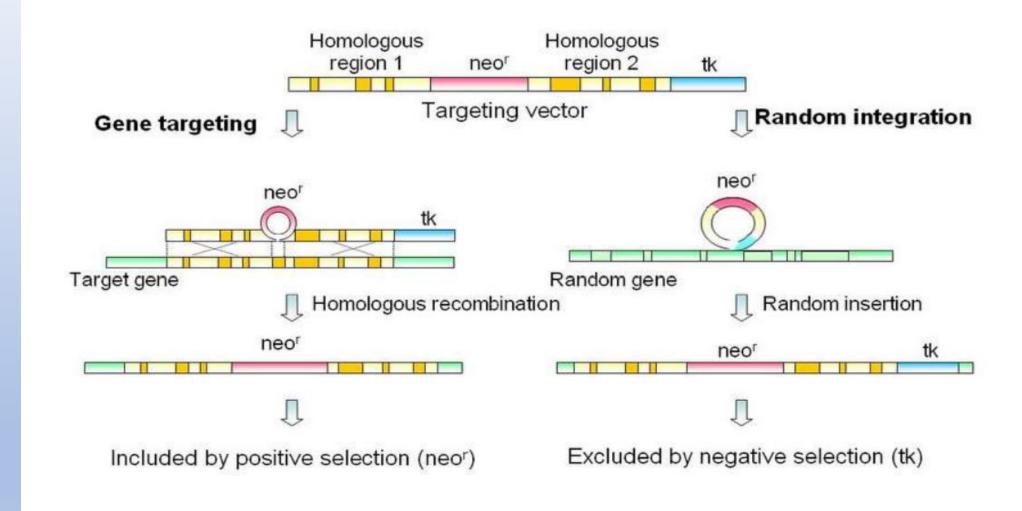
Positive selectable marker

The selectable markers that confers selective advantages to its host organism. An example will be antibiotic resistance, which allows host organism to survive antibiotics selection

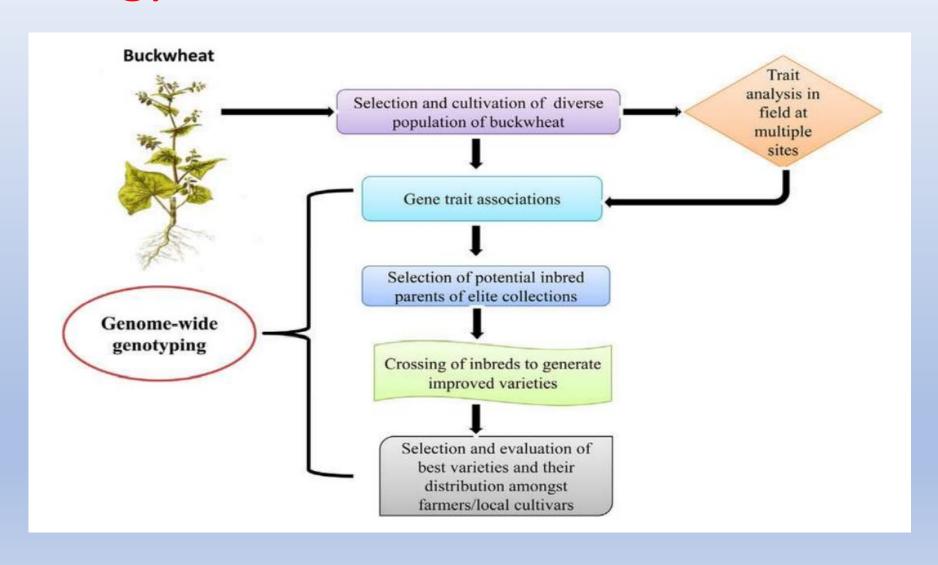
Negative selectable marker

The selectable markers that will eliminate its host organism upon selection. An example would be thymidine kinase, which would make the host sensitive for ganciclovir selection.

Positive-Negative Selection

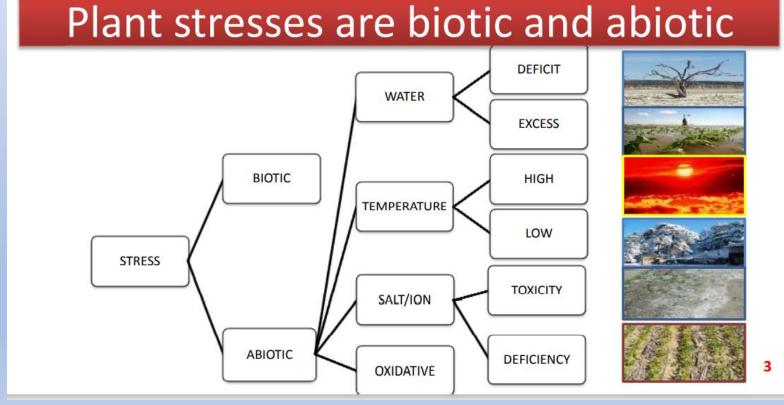


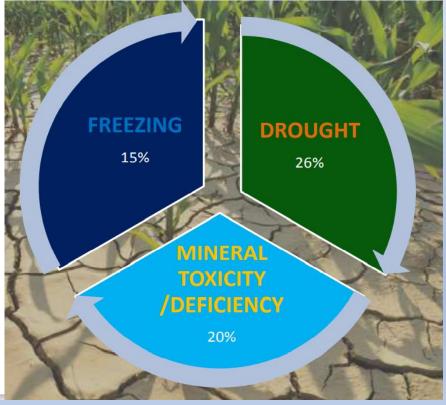
Strategy for Marker Assisted Selection



STRESS:

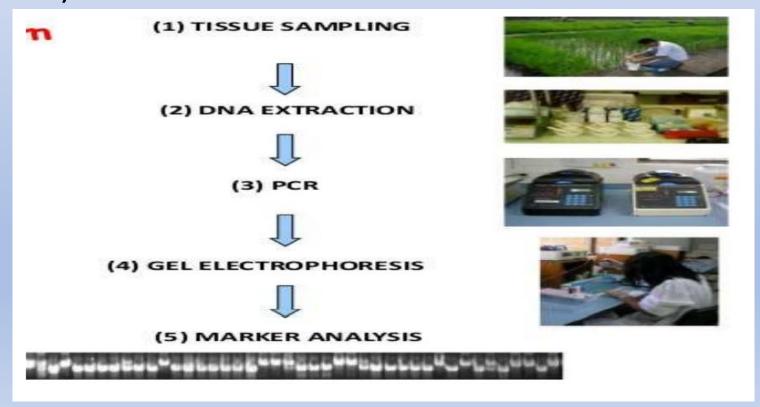
When some factors of the environment interferes with the complete expression of genotypic potential (Singh, B.D). Significant deviation from the ideal conditions, preventing plants from expressing their full genetic potential for growth, development, and reproduction.





Molecular Assisted Selection:

• is an indirect selection process where a trait of interest is selected based on a marker (morphological, biochemical or DNA/RNA variation) linked to a trait of interest.



Case study:-MAS for the Improvement of Stress Resistant Rice



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Insight into MAS: A Molecular Tool for Development of Stress Resistant and Quality of Rice through Gene Stacking

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Rice yield is subjected to severe losses due to adverse effect of a number of stress factors. The most effective method of controlling reduced crop production is utilization of host resistance. Recent technological advances have led to the improvement of DNA based molecular markers closely linked to genes or QTLs in rice chromosome that bestow tolerance to various types of abiotic stresses and resistance to biotic stress factors. Transfer of several genes with potential characteristics into a single genotype is possible through the process of marker assisted selection (MAS), which can quicken the advancement of tolerant/resistant cultivars in the lowest number of generations with the utmost precision through the process of gene pyramiding. Overall, this review presented various types of molecular tools including MAS that can be reasonable and environmental friendly approach for the improvement of abiotic and biotic stress resistant rice with enhanced quality.

Keywords: gene pyramiding, genome mapping, phenotype traits, physiological traits, molecular markers, marker assisted selection, rice

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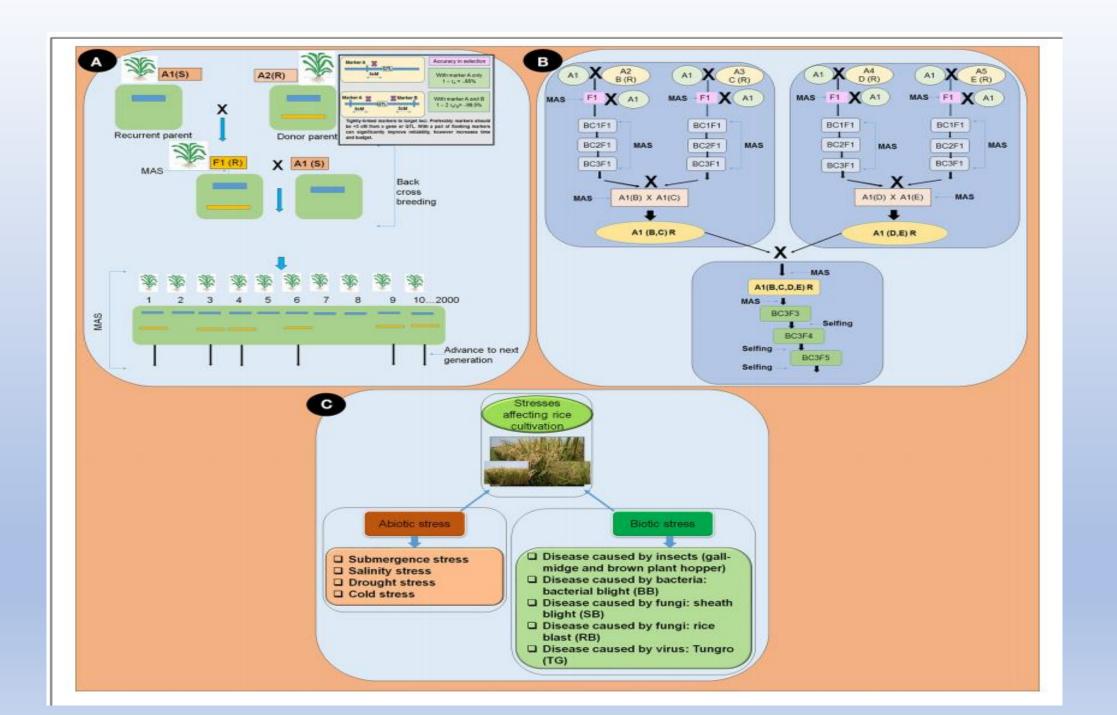
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Marinus J. M. Smulders, Wageningen University and Research, Netherlands Oina-Yona Yana.

- With the application of MAS, individual plants can be selected based on their genotype during the selection procedure. For most traits, homozygous and heterozygous plants cannot be distinguished by conventional phenotypic screening. MAS can be used to assist selection of parents, increasing the effectiveness of backcross breeding and improving sexlimited traits.
- Sensitivity of rice to salt-stress changes throughout the lifecycle, but the effects are most severe in the seedling and reproductive stages. Several salt resistant rice varieties have been produced by expressing salt responsive genes. QTLs associated with salt tolerant rice varieties can be mapped using microsatellite markers (Singh et al., 2007). Use of molecular breeding techniques have been shown to be the most efficient tools for development of improved varieties tolerable to salt (Mondal et al., 2013). In the salinity-tolerant cultivar NonaBokra, mapping of SKC1 on chromosome1 was a breakthrough that preserved K+ ion homeostasis under salinity conditions.
- Significant improvements have been made in mapping QTLs for drought resistance traits in rice; however, few have been effectively used in marker-assisted breeding (Prince et al., 2015). A number of drought tolerant QTLs for rice have been identified (Huang et al., 2014). DREB transcription factors play a major role in induction of the expression of genes involved in drought stress, and the genes encoding DREB transcription factors exhibit significant enhancement of the response of plants to drought stress (Udvardi et al., 2007).



Selected lists of genotypes improved by MAS; selected abiotic and biotic stress resistance genes/QTLs and linked markers; selected stresses, resistance genes/QTLs, and their donor parents.

Drought	Dreb1	Nagina 22
Submergence	Sub1	FR13A, Swarna sub1, IR64 sub1, FR43B, Kurkurappan and Thavalu
salinity	Saltol	FL496, FL478, FL378, Pokkali, SR26B, Patnai 23, Vytilla 1

- Salinity tolerance at seedling, vegetative, flowering and ripening stages of rice seems to be managed by independent genes (Linh et al. 2012). Saltol is a major QTL and was identified in the salt-tolerant cultivar Pokkali. Its location was found on chromosome 1.
- DREB transcription factors play a major role in induction of the expression of genes involved in drought stress, and the genes encoding DREB transcription factors exhibit significant enhancement of the response of plants to drought stress
- In 2014, Xu and Cai reported that the Ran gene, OsRAN1, is necessary for the development of cold tolerant rice varieties. Pyramiding of cold resistance QTLs using MAS is useful for improvement of new rice cultivars with cold tolerance

conclusion

 Marker-assisted selection is involved in genotype identification, diversity and purity analysis, selection of parent lines, and the study of hybrid vigor. It utilizes DNA-based markers that are directly linked with the targeted gene to help phenotypic evaluation and improvement of breeding efficiency by selecting the target genes within the germplasm, but not genetic engineering, which involves transfer of foreign gene sequences. Marker-assisted selection has been effectively applied for stress resistance development and quality improvement in many important crops.

