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Marker Assisted Selection: Biotechnology Tool for Rice Molecular Breeding

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The biotechnology tool of MAS has irreversibly changed the disciplines of conventional rice breeding. Molecular markers are indispensable tools for measuring the diversity of rice varieties and rice breeding. However, MAS is not always advantageous, so careful analysis of the costs, convenience, ease of assay development and automation are important factors to be considered when choosing a technology relative to the conventional breeding programs. This review focuses on possibilities for the application of marker-assisted selection in the genetic improvement of rice breeding.

Rice is a dietary staple food for at least 62.8% of the world population. In Asia it accounts for 29.3%. Global rice consumption is projected to increase from 450 million tons in 2011 to about 490 million tons in 2020 and to about 650 million tons by 2050.The main challenge encountered by scientists involved in rice research and production in the world is to find appropriate solutions for major issues such as the impacts of climate change viz. temperate, water use efficiency and availability of pollution will play a key role in determining food security in large parts of the world. Also the environmental crisis and plant diseases and pests have been the factors that decrease rice production in many countries all around the world. At this time when the world's population is increasing rapidly and the demand for food is high, these problems have threatened food security and people health worldwide. In order to meet these growing problems in future ahead, it is necessary to use rice varieties with higher yield potential, durable resistance to diseases and insects and tolerance to abiotic stresses.

Yield potential of rice can be improved with the help of various strategies; conventional hybridization and selection procedures, ideotype breeding, heterosis breeding, wide hybridization and molecular breeding. There are two strategies in biotechnological application in molecular rice breeding; one is by Marker-Assisted Selection (MAS), also called marker-assisted breeding (MAB) and the other one is by developing the Genetically Modified crops. A genetic marker is any visible character or otherwise assayable phenotype, for which alleles at individual loci segregate in a Mendelian manner. MAS is a technique that does not replace traditional breeding, but can help to make it more efficient. It does not include the transfer of isolated gene sequences such as genetic engineering, but offers tools for targeted selection of the existing plant material for further breeding.

The genetic markers covered include (1) morphological markers (2) biochemical markers (alloenzymes and other protein markers) and (3) molecular markers (based on DNA-DNA hybridization).

DNA-based molecular markers

DNA marker is a small region of DNA sequence showing polymorphism between different individuals. They arise from different classes of DNA mutations such as substitution mutations (point mutations), rearrangements (insertions or deletions) or errors in replication of tandemly repeated DNA. These markers are selectively neutral because they are usually located in non-coding regions of DNA. DNA markers are the most widely used type of marker predominantly due to their abundance. Unlike morphological and biochemical markers, DNA markers are practically unlimited in number and are not affected by environmental factors and/or the developmental stage of the plant.

Properties which desirable for ideal DNA markers include highly polymorphic nature, codominant inheritance (determination of homozygous and heterozygous states of diploid organisms), frequent occurrence in the genome, selective neutral behavior (the DNA sequences of any organism are neutral to environmental conditions or management practices), easy access (availability), easy and fast assay, high reproducibility, and easy exchange of data between laboratories. Also should follow Mendelian inheritance, genetically linked to trait in question and not affected by pleiotropism and epistatic interactions.

There are two basic methods to detect the polymorphism: Southern blotting, a nuclear acid hybridization technique and polymerase chain reaction (PCR) technique. Using PCR and/or molecular hybridization followed by electrophoresis (e.g. Polyacrylamide gel electrophoresis, Agarose gel electrophoresis, Capillary electrophoresis), the variation in DNA samples or polymorphism for a specific region of DNA sequence can be identified based on the product features, such as band size and mobility.

Among the techniques that have been extensively used on plant breeding, are the Restriction Fragment Length Polymorphism (RFLP), Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), Microsatellites Or Simple Sequence Repeat (SSR), Inter Simple Sequence Repeat (ISSR), Expressed Sequence Tag (EST), Cleaved Amplified Polymorphic Sequence (CAPS), Diversity Arrays Technology (DArT), Sequence Characterized Regions (SCARs), Sequence Tag Sites (STSs) and Single Nucleotide Polymorphism (SNP). According to a causal similarity of SNPs with some of these marker systems and fundamental difference with several other marker systems, the molecular markers can also be classified into SNPs (due to sequence variation, e.g. RFLP) and non-SNPs (due to length variation, e.g. SSR) [10]. RFLP is the most widely used hybridization-based molecular marker. The various PCR-based techniques are of two types depending on the primers used for amplification: 1) Arbitrary or semi-arbitrary primed PCR techniques that developed without

prior sequence information (e.g., AP-PCR, DAF, RAPD, AFLP, ISSR). 2) Site targeted PCR techniques that developed from known DNA sequences (e.g., EST, CAPS, SSR, SCAR, STS, SNP).

PCR-based markers are more attractive for MAS, due to the small amount of template required and more efficient handling of large population sizes. AFLP, RAPD and Sequence tagged site (STS) are dominant markers, which limits its application for differentiation of homozygous and heterozygous individuals in segregating progenies. Among the DNA markers, the most widely used markers in major cereal crops are SSRs or microsatellites.