Proceeding

New concepts in plant breeding and genetics

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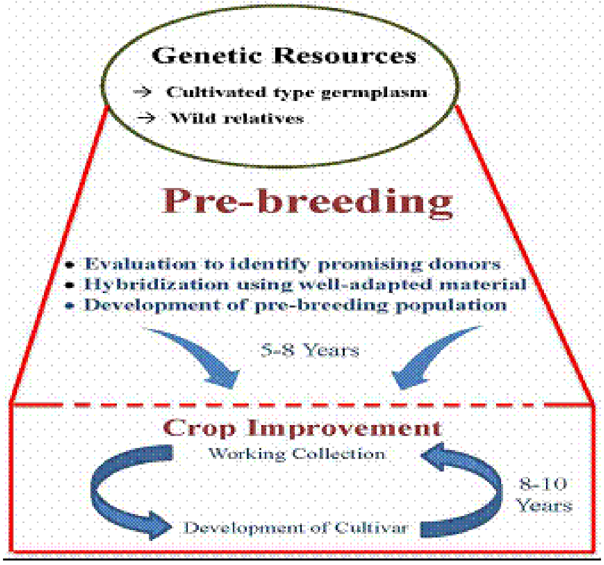
Plant breeding is aimed at developing genetically improved crop cultivars with economic benefits for small-scale and commercial farmers. Plant breeders usually make crosses involving elite varieties and the modern cultivation practices of uniform high yielding varieties (HYVs) had reduced crop genetic diversity and predisposed crop plants to disease and insect pest epidemics. To counter these effects, plant breeder need to make deliberate efforts to diversify the gene pools of their crop to reduce genetic vulnerability. Also it is compulsory for breeder to look beyond the advanced germplasm pool to find desirable genes. The desired genes may reside in unadapted gene pools. But the transfer of genes from unadapted genetic resource often associates with linkage drag and unwanted characters. Hence these exotic germplasm often cannot be used directly in cultivar development. Instead the materials are gradually introduced into the cultivar development programme through crossing and selection for intermediate with new traits, while maintaining a great amount of the adapted traits.



The Global Partnership Initiative for Plant Breeding Capacity Building (GIPB)/FAO and Biodiversity International use the term 'pre-breeding' to describe the various activities of plant breeding research that have to precede the stages involved in cultivar development, testing and release (Biodiversity International and GIPB/FAO, 2008). Further, the Global Crop Diversity Trust defined pre-breeding as 'the art of identifying desired traits, and incorporation of these into modern breeding materials' or the process of the initial introgression of a trait from an undomesticated source (wild) or agronomically inferior source, to a domesticated or adapted genotype is called pre-breeding or germplasm enhancement. Pre-breeding aims to reduce genetic uniformity in crops through the use of a wider pool of genetic material to increase yield, resistance to pests and diseases, and other quality traits. The process varies in complexity and duration, depending on the source, the type of trait, and presence of reproductive barriers. The traditional techniques used are hybridization followed by backcrossing to elite parent, or the use of cyclical population improvement technique. The issue associated with wide crossing are applicable (e.g. infertility, negative linkage drag and incompatibility), requiring techniques such as embryo rescue. The modern tools of molecular genetics and other biotechnological procedure are enabling gene transfer to be made into elite lines without linkage drag.

Despite optimism about continued yield improvement from conventional breeding, new technologies such as biotechnology will be needed to maximize the probability of success. One area of biotechnology, DNA marker technology, derived from research in molecular genetics and genomics, offers great promise for plant breeding. Owing to genetic linkage, DNA markers can be used to detect the presence of allelic variation in the genes underlying these traits. By using DNA markers to assist in plant breeding, efficiency and precision could be greatly increased. The use of DNA markers in plant breeding is called marker-assisted selection (MAS) and is a component of the new discipline of 'molecular breeding'. The fundamental advantages of MAS over conventional phenotypic selection are as follows.

i. It may be simpler than phenotypic screening, which can save time, resources and effort. Classical examples of traits that are difficult and laborious to measure are cereal cyst nematode and root lesion nematode resistance in wheat.

ii. Selection can be carried out at the seedling stage. This may be useful for many traits, but especially for traits that are expressed at later developmental stages. Therefore, undesirable plant genotypes can be quickly eliminated. This may have tremendous benefits in rice breeding because typical rice production practices involve sowing pre-germinated seeds and transplanting seedlings into rice paddies, making it easy to transplant only selected seedlings to the main field.

iii. Single plants can be selected. Using conventional screening methods for many traits, plant families or plots are grown because single-plant selection is unreliable due to environmental factors. With MAS, individual plants can be selected based on their genotype. For most traits, homozygous and heterozygous plants cannot be distinguished by conventional phenotypic screening.

There are five broad areas of marker assisted selection are

a. **Marker-assisted evaluation of breeding material:** Prior to crossing (hybridization) and line development, there are several applications in which DNA marker data may be useful for breeding, such as cultivar identity, assessment of genetic diversity and parent selection, and confirmation of hybrids. Traditionally, these tasks have been done based on visual selection and analyzing data based on morphological characteristics.

b. **Marker-assisted backcrossing:** Backcrossing has been a widely used technique in plant breeding for almost a century. In most cases, the parent used for backcrossing has a large number of desirable attributes but is deficient in only a few characteristics (Allard 1999). The method was first described in 1922 and was widely used between the 1930s and 1960s. The use of DNA markers in backcrossing greatly increases the efficiency of selection. Three general levels of marker-assisted backcrossing (MAB) can be described. In the first level, markers can be used in combination with or to replace screening for the target gene or QTL. This is referred to as 'foreground selection'. This may be particularly useful for traits that have laborious or time-consuming phenotypic screening procedures. It can also be used to select for reproductive-stage traits in the seedling stage, allowing the best plants to be identified for backcrossing. Furthermore, recessive alleles can be selected, which is difficult to do using conventional methods. The second level involves selecting BC progeny with the target gene and recombination events between the target locus and linked flanking markers. This is referred to as 'recombinant selection'. The purpose of recombinant selection is to reduce the size of the donor chromosome segment containing the target locus (i.e. size of the introgression). This is important because the rate of decrease of this donor fragment is slower than for unlinked regions and many undesirable genes that negatively affect crop performance may be linked to the target gene from the donor parent and this is referred to as 'linkage drag'. Third level involves the markers used for selection of recessive parent genome and this is referred to as 'Background selection'.

c. **Marker assisted gene pyramiding:** Pyramiding is the process of combining several genes together into a single genotype. Pyramiding may be possible through conventional breeding but it is usually not easy to identify the plants containing more than one gene. Using conventional phenotypic selection, individual plants must be evaluated for all traits tested. Therefore, it may be very difficult to assess plants from certain population types (e.g. F2) or for traits with destructive bioassays. DNA markers can greatly facilitate selection because DNA marker assays are non-destructive and markers for multiple specific genes can be tested using a single DNA sample without phenotyping.

d. **Early generation marker-assisted selection:** Although markers can be used at any stage during a typical plant breeding programme, MAS is a great advantage in early generations because plants with undesirable gene combinations can be eliminated. This allows breeders to focus attention on a lesser number of high-priority lines in subsequent generations.

e. **Combined marker-assisted selection:** There are several instances when phenotypic screening can be strategically combined with MAS. In the first instance, 'combined MAS' (coined by Moreau et al. 2004) may have advantages over phenotypic screening or MAS alone in order to maximize genetic gain.

Conclusion

Plant breeding has made remarkable progress in crop improvement and it is critical that this continue. It seems clear that current breeding programmes continue to make progress through commonly used breeding approaches. MAS could greatly assist plant breeders in reaching this goal although, to date, the impact on variety development has been minimal. For the potential of MAS to be realized, it is imperative that there should be a greater integration with breeding programmes and those current barriers be well understood and appropriate solutions developed. The exploitation of the advantages of MAS relative to conventional breeding could have a great impact on crop improvement. The high cost of MAS will continue to be a major obstacle for its adoption for some crop species and plant breeding in developing countries in the near future. Specific MAS strategies may need to be tailored to specific crops, traits and available budgets. New marker technology can potentially reduce the cost of MAS considerably. If the effectiveness of the new methods is validated and the equipment can be easily obtained, this should allow MAS to become more widely applicable for crop breeding programmes.

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Conflict of interest

The author declares no conflict of interest.