Plant Marker-Assisted Breeding and Conventional Breeding: Challenges and Perspectives

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Plant breeding has a long history of development beginning with the artificial domestication of crop species. Modern plant breeding based on the fundamental principles of inheritance has become an important component of agricultural science and technology.It has features of both science and arts. Conventional breeding methodologies have extensively proven successful in development of plant cultivars and germplasm. The most renowned examples include the semi-dwarf high-yielding cultivars of cereals developed during the Green Revolution and the hybrid rice developed in 1970s. However, conventional breeding is still dependent to a considerable extent on subjective evaluation and empirical selection. Scientific breeding needs less subjectiveness and more science, i.e. practical and accurate evaluation, and effective and efficient selection. Molecular marker-assisted breeding (MAB) has brought great challenges, opportunities and prospects for conventional breeding.

Along with progress in molecular biotechnology, various types of molecular markers in crop plants were developed during the 1980s and 1990s [1]. The rapid development of molecular markers (particularly DNA markers) and continuous improvement of molecular assays has led to the birth of a new member in the family of plant breeding – molecular marker-assisted breeding (MAB). The extensive use of molecular markers in various fields of plant science, e.g. germplasm evaluation, genetic mapping, map-based gene discovery, characterization of traits and crop improvement, has demonstrated that molecular technology is a powerful and reliable tool in genetic manipulation of agronomically important traits in crop plants [1,2]. Compared with conventional breeding methods, MAB has significant advantages:

a.   MAB can allow selection for all kinds of traits to be carried out at seedling stage and thus reduce the time required before the phenotype of an individual plant is known. For the traits that are expressed at later developmental stages, undesirable genotypes can be quickly eliminated by marker-assisted selection (MAS). This feature is particularly important and useful for some breeding schemes such as backcrossing and recurrent selection, in which crossing with or between selected individuals is required.

b.   MAB is not affected by environment, thus allowing the selection to be performed under any environmental conditions (e.g. greenhouse and off-season nurseries). This is very helpful for improvement of certain traits that are expressed only when favorable environmental conditions present, e.g. disease/pest resistance and stress tolerance. For low-heritability traits that are easily affected by environments, MAS based on reliable markers tightly linked to the quantitative trait loci (QTLs) for traits of interest can be more effective and efficient than phenotypic selection.

c.   MAB using co-dominance markers (e.g. SSR and SNP) can allow effective selection of recessive alleles of desired traits in the heterozygous status. No selfing or test crossing is needed to detect the traits controlled by recessive alleles, thus saving time and accelerating breeding progress.

d.   For the traits controlled by multiple genes/QTLs, individual genes/QTLs in the same individuals can be identified and selected

simultaneously in MAB, and thus MAB is particularly suitable for gene pyramiding. In traditional phenotypic selection, however, it is problematic to distinguish individual genes/loci because one gene may mask the effect of others.

e.   Genotypic assays based on molecular markers may be faster, cheaper and more accurate than conventional phenotypic assays, depending on the traits and conditions, and thus MAB may have higher effectiveness and efficiency in terms of time, resources and efforts saved.

As such, the research and use of MAB in plants has continued to increase in the public and private sectors, particularly since 2000s [1-3]. In a sense, MAB represents a new direction of future development in plant breeding. However, as a new strategy and methodology of plant breeding, MAB has not been perfect and it has some defects. Marker-assisted selection (MAS) and/or marker-assisted backcrossing (MABC) have been primarily applied to simply-inherited traits, such as monogenic or oligogenic resistance to diseases/pests, although quantitative traits were also involved [4-6]. MAB in plants has not achieved the results as expected previously in terms of extent and success (e.g. release of commercial cultivars). [4] Listed ten reasons for the low impact of MAS and MAB in general. Improvement of economically important agronomic traits like yield and quality that are complicatedly inherited is still a great challenge for MAB, including the newly developed Genome-Wide Selection (GWS) or Genomic Selection (GS) [2,7]. From the viewpoint of a plant breeder, MAB is not universally or necessarily advantageous [2]. The application of molecular technologies to plant breeding is still facing the following drawbacks and/or challenges:

a.   Not all markers are breeder-friendly. This problem may be solved by converting non-breeder-friendly markers to other types of breeder-friendly markers (e.g. RFLP to STS, sequence tagged site, and RAPD to SCAR, sequence characterized amplified region).

b.   Not all markers can be applicable across populations due to lack of marker polymorphism or reliable marker-trait association. Multiple mapping populations are helpful for a better understanding of marker allelic diversity and genetic background effects. In addition, QTL positions and effects also need to be validated and re-estimated by breeders in their own germplasm of interest [8].

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c.   False selection may occur due to recombination between the markers and the genes/QTLs of interest. Use of flanking markers or more markers for the target gene/QTL can help to perform reliable selection.

d.   Inaccurate estimations of QTL locations and effects result in slower progress than expected. The efficiency of QTL detection is attributed to multiple factors, such as algorithms, mapping methods, number of polymorphic markers, and population type and size [9]. Fine mapping with high marker density and in large populations and well-designed phenotyping across multiple environments may provide more accurate estimates of QTL locations and effects.

e.   The methods and schemes of MAB must be easily understandable, acceptable and implementable for plant breeders, unless they are not designed for a large scale use in practical breeding programs.

f.   A large number of breeding programs have not been equipped with adequate facilities and conditions for a large-scale adoption of MAB in practice.

g.   Startup expenses and labor costs are still higher in many cases.

Therefore, as other new methods of plant breeding like transgenic breeding or genetic manipulation do, MAB cannot replace conventional breeding but is and only is a supplementary addition to conventional breeding. High costs and technical or equipment demands of MAB will continue to be a major obstacle for its large-scale use in the near future, especially in the developing countries [4,10]. Therefore, integration of MAB into conventional breeding programs will be an optimistic strategy for crop improvement in the future. It can be expected that the drawbacks of MAB will be gradually overcome, as its theory, technology and application are further developed and improved. This should lead to a wide adoption and use of MAB in practical breeding programs for more crop species and in more countries as well.

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