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REVIEW

Rice molecular markers and genetic mapping: Current status and prospects



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Abstract

Dramatic changes in climatic conditions that supplement the biotic and abiotic stresses pose severe threat to the sustainable rice production and have made it a difficult task for rice molecular breeders to enhance production and productivity under these stress factors. The main focus of rice molecular breeders is to understand the fundamentals of molecular pathways involved in complex agronomic traits to increase the yield. The availability of complete rice genome sequence and recent improvements in rice genomics research has made it possible to detect and map accurately a large number of genes by using linkage to DNA markers. Linkage mapping is an effective approach to identify the genetic markers which are co-segregating with target traits within the family. The ideas of genetic diversity, quantitative trait locus (QTL) mapping, and marker-assisted selection (MAS) are evolving into more efficient concepts of linkage disequilibrium (LD) also called association mapping and genomic selection (GS), respectively. The use of cost-effective DNA markers derived from the fine mapped position of the genes for important agronomic traits will provide opportunities for breeders to develop high-yielding, stress-resistant, and better quality rice cultivars. Here we focus on the progress of molecular marker technologies, their application in genetic mapping and evolution of association mapping techniques in rice.

Keywords: genetic mapping, molecular markers, marker assisted selection, *Oryza sativa* L., quantitative trait loci

1. Introduction

The human population of the world is increasing day by day. According to world population data sheet (Population Institute, USA) estimate, the world population will become eight billion in 2024 (Anonymous 2011). At the current rate, about 70% more food will be required to feed about 15 billion

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people by the mid of this century. Rapidly growing population is the major issue in the world, leading to a shortage of food, resulting many challenges to the agricultural community (Borlaug 2000). Biotic stresses such as diseases and insects, and abiotic stresses including drought, salinity, temperature, cold, etc., are the main causes of low yield which lead towards billions of dollar's losses annually in food crops especially cereal group (Borlaug 2000; Kumar et al. 2015).

In cereal group, rice is the staple food source for more than half of the world's population (Hossain 1997; Gupta and Varshney 2005). Rice is an annual plant, belonging to monocot family Poaceae and the genus *Oryza*. The genus *Oryza* consists of two cultivated and 23 wild species. The *Oryza* is also splitted into five complexes named as *Oryza sativa*, *Oryza ridleyi*, *Oryza officinalis*, *Oryza ridelyi*, and unclassified (Jain et al. 2010). Among the cultivated species, *Oryza sativa* (Asian rice) is grown mostly in all rice growing areas of the world while *Oryza glaberrima* (African rice) is only confined to the western tropical Africa. All species of rice have basic chromosome number $n=12$ and classified level is diploid with $2n=24$ and tetraploid with $2n=48$ chromosomes. In this scenario, it is vital to increase the yield of major food crops, including rice, through the development of high yielding varieties with higher resistance to biotic and abiotic stresses.

Rice has great importance around the world due to its nutritional value. It has a special glutelin made protein, having more balanced amino acid compared to other cereals that have prolamine-rich storage proteins. Rice is a good source of thiamin, niacin, riboflavin, phosphorus, magnesium, zinc, and copper. Short-grain of rice is very starchy, cooks soft and sticky while long-grain rice contains less starch. More than 477.5 million tons of rice per year are being consumed by the present world population. Though, the global production of rice is increasing, this increase is not proportional to the demand of increasing human population. The rice production should rise at least 70% in the coming years to fulfill the demand of increasing human population by 2050 (Leegood et al. 2010).

The quality and quantity of rice plants have been improved by conventional plant breeding methods which are well known and still in the practice. The breeding methods in rice can be simplified in three steps: (I) plant breeding based on observed variation in different varieties; (II) plant breeding based on controlled mating by selection of desired characters; and (III) plant breeding based on monitored recombination by selection of specific genes or marker profiles (Brescghello and Coelho 2013). Conventional plant breeding approaches are time-consuming, laborious, and have several other ecological, physiological, and biological constraints.

To overcome the above mentioned problems, researchers are focusing on new modern breeding techniques such as marker assisted breeding, recombinant DNA technology, and 'omics' sciences (genomics, proteomics, metabolomics), to improve the rice plant yield by developing better disease resistance (Wang et al. 2015; Raboin et al. 2016) and grain quality improvement in rice plant (Feng et al. 2016). However, the precision of biotechnological approaches are, mainly genetic engineering and, genetic mapping. These approaches contribute rapidly and significantly in crop improvement by offering a wide array of novel genes and traits identification. Identified gene(s) can be effectively inserted into elite crops to raise yield, nutritional value, and confer resistance to abiotic and biotic stresses (Pandey et al. 2016).

Many outstanding reviews have been published about the different types of molecular markers used in plants and their application in construction of linkage map, genetic mapping, and marker-assisted selection (MAS) techniques (Agarwal et al. 2008). This review thus focuses on: I) recent advances in molecular marker technologies for rice genetics; II) QTLs identification techniques applied in rice germplasm; and III) overview of association mapping evolution in rice.

2. Genetic marker

Markers which designate genetic differences between individuals within a specie or among species are called genetic markers. In the 19th century, the idea of phenotype based genetic markers was introduced by Gregor Mendel (Austria) followed by the genetic linkage theory by T. H. Morgan (Columbia University, USA) by using *Drosophila melanogaster* as an experimental material (William and Michael 1996). Normally, they are not target genes but act as gene tags and are located near to gene controlling the trait of interest. So these markers do not affect the phenotype of the trait of interest. Like genes, these markers also occupy definite genomic locations within chromosomes called loci (Collard et al. 2005). These markers can be classified into various types: I) morphological markers; II) biochemical markers; and III) DNA markers.

2.1. Morphological markers

These are generally characterized by phenotypic traits by means of vision as color, size, shape, etc. (Collard et al. 2005). Due to its limited application, researchers started biochemical markers to detect quantitative trait loci (QTLs) in plants.

2.2. Biochemical markers

Biochemical markers or isozyme markers are enzymes

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