

Genomic Mapping, Molecular Marker and Marker Assisted Selection in Rice: A Review

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Abstract. Increased agricultural output is necessary to feed a growing world population, yet crop yield growth rates are currently slowing down. Therefore, qualities related to yield, stability, and sustainability should take center stage in plant breeding initiatives. Durable disease resistance, abiotic stress tolerance, and effective nutrition and water usage are a few of these characteristics. On several rice chromosomes, various resistance genes have been discovered, mapped, and tightly connected DNA markers have been created. The following qualities were chosen as potential molecular marker candidates: fragrance, disease resistance to bacterial, blast, and sheath blights, grain extension while cooking, chalkiness propensity, gelatinization temperature, minor aroma components, and seedling vigor/early establishment. With the help of developments in genetics and genomics, it is now feasible to go into the history of rice domestication and identify the precise genetic processes that were influenced by human selection. Agronomic main effect quantitative trait loci (QTLs) may contribute cumulatively to genetic variation, with hybrids showing stronger effects and comparatively fewer contributions from epistatic effects.

Keywords: allele; gene coding; marker; quantitative traits loci; selection; traits improvement

INTRODUCTION

The largest food crop in the world, rice meets the daily caloric demands of millions of people. Asian rice (*Oryza sativa*) and African rice (*Oryza glaberrima*), which each have distinct domestication histories, are two different varieties of domesticated rice. There are 21 wild rice cousins of domesticated rice in the genus *Oryza* (Vaughan *et al.*, 2003). The *O. sativa*, *O. officinalis*, *O. ridelyi*, and *O. granulata* species complexes are the divisions of the genus. While interspecific crossing is possible within each complex, which all species of the *Oryza* genus have, it is challenging to retrieve fertile offspring from crosses across complexes (Vaughan *et al.*, 2003).

Over a surface area of more than 150 million acres, rice is grown on all continents with the exception of Antarctica, however the majority of rice is produced in Asia. Rice production worldwide expanded thanks to the Green Revolution technology created at the International Rice Research Institute (IRRI) in the 1960s. The output potential of contemporary cultivars has, nevertheless, remained unchanged over the last ten years. To feed the growing global population, it is

essential to enhance rice output in all rice-producing habitats (Khush, 2005).

O. sativa has been the subject of considerable breeding efforts and has become a significant source of food and livelihood for the human population. It is now possible to investigate the history of rice domestication and identify the precise genetic pathways that were affected by human selection thanks to developments in the domains of genetics and genomics. Now that many of the genes causing rice's "domestication syndrome" have been cloned and characterized, it is possible to reconstruct the difficult evolutionary path that rice took to reach its current state (S. McCouch *et al.*, 2010).

A genome map is the relative positions of features that are of interest, or which can serve as reference points for navigation. It pinpoints the location of specific features on the chromosomes of an organism. They are essential tools in identifying genes responsible for diseases or traits, for comparing the genomes of different species, and for complete genome sequencing.

Marker assisted selection or marker aided selection (MAS) is a process whereby a marker (morphological, biochemical or one based on DNA/RNA variation) is used

for indirect selection of a genetic determinant or determinants of a trait of interest.

Therefore the aim of this review is to expand the awareness of marker and their use in shortening rice breeding cycle.

LITERATURE REVIEW

1. Taxonomy, Geographic Origin and Genomic Evolution of Rice

1.1 Taxonomy of rice

Rice is a member of the family Gramineae's tribe Oryzeae and genus *Oryza*. There are 25 identified species in the genus *Oryza*, of which two, *O. sativa* and *O. glaberrima*, are cultivated species and the remaining 23 are wild species (Morishima, 1984; Vaughan, 1994).

Table 1. Rice hierarchical taxonomy

Name	Rice
Kingdom	Plantae
Division	Magnoliophyte
Class	Liliopsida
Order	Poales
Family	Gramineae o Poaceae
Tribe	Oryzeae
Genus	<i>Oryza</i>
Species	<i>Sativa</i>

1.2 Geographic Origin and Domestication

Utilizing genetic diversity, historical and archaeological data, and geographic distribution, the genesis and diversification centers of the two domesticated species *O. sativa* and *O. glaberrima* have been found. The Yangtze and Mekong river basins are thought to be the primary origins of *O. sativa*, whereas the delta of the Niger river in Africa is thought to be the primary origin of *O. glaberrima* (Porteres, 1956; OECD, 1999). Some of the centers of diversity for Asian cultures include the foothills of the Himalayas, Chhattisgarh, the Jeypore Tract of Orissa, northeastern India, northern regions of Myanmar and Thailand, the Yunnan Province of China, etc. The inner delta of the Niger River and a few locations near the coast of Guinea are thought to be

the continent's centers of diversity for *O. glaberrima* species (Chang, 1976; Grant & Oka, 1988). Both *O. sativa* and *O. glaberrima* are thought to have sprung from two distinct ancestors, *O. nivara* and *O. barthii*, and were domesticated in tropical West Africa and South or South-East Asia, respectively. According to several reviews by Chang (1976); Viraktamath (2001) the progenitors of *O. sativa* are thought to be Asian AA genome diploid species, whereas those of *O. glaberrima* are African AA genome diploid species, *O. barthii* and *O. longistaminata*.

O. sativa, the Asian rice plant, is thought to have been domesticated around 7,000 BC (OECD, 1997). It has spread and evolved into the Indica and Japonica ecological groupings (Grant & Oka, 1988). The domestication of two different wild rice species in China and India led to the autonomous development of the two groups (Second, 1982).

1.3 Genomic Evolution of Rice

According to Vaughan, (1994), the species of the genus *Oryza* can be roughly divided into four complexes: *Sativa*, *Officinalis*, *Ridley*, and *Meyeriana*. The *Sativa* and *Officinalis* complexes have seen the most research of them. The *O. sativa* and *O. glaberrima* cultivars as well as its weedy/wild ancestors, the perennial rhizomatous *O. longistaminata*, *O. barthii* and *O. rufipogon*, *O. nivara* and *O. sativa* f. *spontanea*, make up the *Sativa* complex.

2. Basic features of the rice genome

The rice genome (*Oryza sativa*), which has 12 chromosomes ($2n = 24$), has a total length of 430 Mb, or roughly 1500 cM of genetic material, as determined by the frequency of crossing-over in meiotic genetic recombination (Kurata et al., 1994b; Harushima et al., 1998). This statistic varies by species and depends on genome size; rice has a genome that is relatively small (430 Mb) in comparison to other common cereals. Contrary to genome size, these plants' genetic distances, which range from 1200 to

1500 cM, are quite similar. As a result, their genome sizes vary by a factor of more than eight. recombination occurs in meiosis in each cereal at roughly the same rate even though

Table 2. Species complexes of the genus *Oryza* and their geographical distribution

Species Complex	Chromosome Number	Genome	Geographical Distribution
<i>O. sativa</i> L.	24	AA	Originally South & Southeast Asia
<i>O. nivara</i> Sharma et Shastry	24	AA	South & Southeast Asia
<i>O. rufipogon</i> Griff.	24	AA	South & Southeast Asia, South China
<i>O. meridionalis</i> Ng	24	AA	Tropical Australia
<i>O. glumaepetula</i> Steud.	24	AA	Tropical America
<i>O. glaberrima</i> Steud.	24	AA	Tropical West Africa
<i>O. barthii</i> A. Chev. et Roehr	24	AA	West Africa
<i>O. longistaminata</i> A. Chev. et Roehr.	24	AA	Tropical Africa
<i>O. punctata</i> Kotschy ex Steud.	24	BB	East Africa
<i>O. rhizomatis</i> Vaughan	24	CC	Sri Lanka
<i>O. minuta</i> J.S.Pesl. ex C.B.Presl.	48	BBCC	Philippines, New Guinea
<i>O. malamphuzaensis</i> Krishn. et Chandr.	48	BBCC	Kerala & Tamil Nadu
<i>O. officinalis</i> Wall. ex Watt	24	CC	South & Southeast Asia
<i>O. eichingeri</i> A.Peter	24	CC	East Africa & Sri Lanka
<i>O. latifolia</i> Desv.	48	CCDD	Central & South America
<i>O. alta</i> Swallen	48	CCDD	Central & South America
<i>O. grandiglumis</i> (Doell) Prod.	48	CCDD	South America
<i>O. australiensis</i> Domin.	24	EE	Northern Australia
<i>O. schweinfurthiana</i> Prod.	48	BBCC	Tropical Africa
<i>O. granulata</i> Nees et Arn. ex Watt	24	GG	South & Southeast Asia
<i>O. meyeriana</i> (Zoll. et Mor. ex Steud.) Baill.	24	GG	Southeast Asia
<i>O. longiglumis</i> Jansen	48	HHJJ	Indonesia, New Guinea
<i>O. ridleyi</i> Hook. f.	48	HHJJ	Southeast Asia
<i>O. brachyantha</i> A. Chev. et Roehr.	24	FF	West & Central Africa
<i>O. schlechteri</i> Pilger	48	HHKK	Indonesia, New Guinea

Source: Brar and Khush, 2003

The other portions of the genome are gene-rare sections, each with its own unique size and indicating heterochromatic blocks repressed for recombination. This could be one explanation for the similar amounts of recombinations (Gill et al., 1996). With a lower percentage of repetitive sequences than other cereal genomes, the rice genome is predicted to have generic sections that are similar to those of other cereals. As a result, a highly conserved gene order has been discovered on the chromosomes of rice and other cereal species, indicating that genome synteny exists among Poaceae members (Gale & Devos, 1998; Moore et al., 1995).

In the genetic maps, this synteny was initially identified between rice and maize (Ahn & Tanksley, 1993) and between rice and wheat (Kurata et al., 1994a). The proof was later elevated to the level of actual maps (Chen et al., 1997; Foote et al., 1997). These findings showed that even on the physical map, the distances between genes and the gene order are mostly the same in the cereal genomes. Because of its small genome, high degree of synteny with other cereal genomes, and significant economic worth, rice has emerged as the principal target for cereal genome study.

3. Molecular Markers in Rice

Comparing morphological markers used in traditional plant breeding with molecular markers for trait selection reveals many advantages. A recent assessment of the use of molecular markers in rice improvement (Mackill, 2007) focused primarily on the use of DNA markers in crop plant improvement in general and placed special emphasis on the use of markers in heterosis breeding. Time savings, consistency, biosafety, efficiency, and more precise selection of complicated features are among the key benefits of molecular markers.

Simple sequence repeat (SSR), restriction fragment length polymorphism (RFLP), expressed sequence tags, sequence tagged sites (STS), and amplified fragment length polymorphism (AFLP) markers are among the molecular markers employed for

trait selection (McCouch et al., 1988; Susan R. McCouch et al., 2002). A number of agronomically significant genes have been extracted from the genome utilizing a map-based cloning technique employing the saturated rice molecular map and genome sequence information (Dai et al., 2007). These include the bacterial blight resistance genes Xa1, Xa5, Xa13, Xa21, Xa26, and Xa27 (Song et al., 1995; Yoshimura et al., 1998; Iyer & McCouch, 2004; Sun et al., 2004; Gu et al., 2005; Chu et al., 2006); the blast resistance genes Pib, Pita, Pi2, Pizt (Xu et al., 2006).

4. Target Traits for Marker Assisted Selection

4.1 Grain Yield and Agronomic Traits

In the past, the creation of semi-dwarf cultivars in the 1960s and 1970s was substantially responsible for the growth in harvest index, which led to the major breakthroughs in boosting rice production (S. Peng et al., 2000). Although some gains in biomass have been noted in more recent cultivars (S. Peng et al., 2000), it has proven to be exceedingly challenging to further increase yields for tropical rice. In general, hybrid rice is thought to be a more promising approach to increasing the yield potential in rice over the existing inbred cultivars. The super hybrid' rice developed in China has recently made some strides in increasing yield potential (Peng et al., 2004). QTLs with a moderate effect on grain filling % were found by (Takai et al., 2005). It was believed that diverse genetic backgrounds could benefit from a QTL for yield potential on chromosome 5, rg5, which represented an allele from the indica cultivar Kasalath examined in the backdrop of japonica Nipponbare (Ishimaru et al., 2005).

Numerous researchers have used the Advance Backcross QTL (ABQTL) method to study rice in order to find QTLs that have a favorable impact on agronomic variables acquired from wild species (Tanksley & Nelson, 1996). Moncada et al. (2001); Septiningsih et al. (2003); Lee et al. (2005);

Tian et al. (2006) developed introgression lines with tiny segments transferred to an elite cultivar using an accession of 'Dongxiang' wild rice (*O. rufipogon*). Generally speaking, the lines with more introgressed wild rice segments did poorly; nevertheless, certain advantageous alleles for grain number on chromosomes 5, 8, and 9 were found. They discovered that the effects in the introgression lines were only weakly predicted by QTL analysis in the BC2F2 generation. Ashikari et al. (2005) identified a cytokinin oxidase with better grain number and yield by map-based cloning. This gene's Null allele (*OsCKX2*) imparted a larger grain number, and they created NILs using an MAB strategy. In order to produce a mutant allele at the *GA20* oxidase gene, this gene was coupled with the main semidwarf gene *Sd1* (Sasaki et al., 2002).

4.2 Heterosis and Hybrid Rice

Although several writers have remarked that it is challenging to detect a correlation between F1 performance and parental genotypes, attempts to identify QTLs controlling heterosis have had some success (Z. K. Li et al., 2001). You et al. (2006) found that main effect QTLs for agronomic variables might contribute cumulatively to genetic variation and that hybrids could show higher effects with relatively less contribution from epistatic effects. On the chromosome, the area closest to the *Sd1* locus appeared to have the most impact. Mei et al. (2005), in two BC and a RIL population using Lemont (*japonica*) and Teqing (*indica*) indicated that the primary genetic basis for heterosis was over dominance from epistatic loci, while Abdelkhalik et al. (2005) suggested it was from the cumulative effects of partially dominant loci. Hua et al. (2003) found little overlap between heterotic effects and trait performance. They found that heterosis could be explained by single-locus effects in combination with dominance by dominance interaction at the two-locus level.

The identification of prospective markers for MAS has not been possible due to the rather complex genetic control of yield and heterosis; however, the creation of hybrid rice involves a number of concurrent features that are easily susceptible to MAS. The cytoplasmic male sterility system, which relies on the presence of restoration capacity genes in the male parent, is used by the majority of recently developed hybrids. Due to the fact that they can only be evaluated in mature plants from testcross progeny, these restorative genes are particularly difficult to manage in breeding. The *Rf3* gene has been located on chromosome 1 (Zhang et al., 1997) for the common WA type cytoplasmic male sterility, and a second locus has been located on chromosome 10 (Yao et al., 1997). The *Rf1* gene has been cloned for the Chinsurah Boro II type cms (Yao et al., 1997; Wang et al., 2006), and they discovered that the locus involved two related PPR (pentatricopeptide repeat) genes (*Rf1a* and *Rf1b*). Genetic male sterility genes that are susceptible to temperature and/or photoperiod are a component of the 2-line system of hybrid rice development. The *tms2* gene Lopez et al. (2003), *tms3* gene Lang et al. (1999), *tms4* gene Dong et al. (2000), *tms5* gene Wang et al. (2006), and *tms6* gene Wang et al. (2004); Lee et al. (2005).

A breeding line can be created with one or more of these genes that will be fertile in low temperatures and/or short day lengths for seed maintenance but sterile in high temperatures and long day lengths for producing hybrid seeds. Wide compatibility (WC) is a highly helpful characteristic for giving hybrids from wide crosses typically *indica japonica* crosses spikelet fertility. Although several WC genes have been discovered, the *S5* gene on chromosome 6 has received the most attention (Ikehashi & Araki, 2008). There have been reported candidate genes for this locus (Qiu et al., 2005). Other QTLs have been identified and targeted for MAS in the WC cultivar Dular (Wang et al., 2005). Elongated topmost

internode, a recessive tall allele that may be 152 MACKILL utilized in the female parent to boost panicle effort for hybrid rice development, is another valuable gene for hybrid rice. The *eu1* gene has reportedly been identified as a potential cytochrome P450 gene by a number of groups (Luo et al., 2006; Ma et al., 2006; Zhu et al., 2006).

4.3 Other Agronomic Traits

Numerous agronomic qualities have been identified for breeding programs, including seedling vigor (Kanbar et al., 2006), seed longevity or dormancy Wan et al. (2006); Yamaguchi et al. (2006), and grain shattering (C. Li et al., 2006).

5. Genomic Mapping of Rice Chromosome.

In order to research genome architecture and evolution, physical mapping, and gene cloning, the science of genomics uses both global and local genomes for investigation (Botstein et al., 1980). The study of genomes at the molecular, chromosomal, biochemical, and phenotypic levels is what science is all about (Kartel et al., 1990).

Microsatellite markers are detected in the genome of rice (*Oryza sativa* L.) with a high level of allelic variation in cultivated varieties and distantly related species, according to a review by (Susan R. McCouch et al., 1997). Recently, a map for rice that covers the entire genome and comprises 121 microsatellite sites was released (Chen et al., 1997). With a lower number of SSLP markers produced from microsatellite-containing sequences from Gen Bank (Wu & Tanksley, 1993; Akagi et al., 1996), these simple sequence repeats (SSRs) were primarily poly(GA) motifs recovered from two genomic libraries (Chen et al., 1997; Panaud et al., 1996). Rice's genome is thought to include between 5700 and 10,000 microsatellite sequences with various di-, tri-, and tetra-nucleotide repeat units that might be utilized to create a genetic map using only microsatellite markers (McCouch et al., 1997). Panaud et al. (1995) used hybridization studies to

assess the relative frequencies of 13 distinct di-, tri-, and tetra nucleotide repeats in the rice genome, and numerous markers with GT, AT, TCT, and ATT repeats have been mapped (Wu & Tanksley, 1993; Akagi et al., 1996; Panaud et al., 1996). However, the evaluation of these less common classes of SSR sequences for length variation and genome distribution was constrained by the small number of loci described for each motif.

CONCLUSION

The use of molecular markers in plant breeding has the potential to significantly increase the pace of genetic gain. The only crop for which the complete genome's DNA sequence is known is rice, making it special. The availability of rice's DNA sequence data should make it easier to find molecular markers quickly to help plant improvement. Microsatellite molecular markers, which will continue to be utilized in the molecular marker program, have been the primary class of molecular markers used in plant development efforts in recent years. For a number of rice qualities, microsatellite markers have been created, and they are currently being used for breeding program selection. Several crucial approaches will be used to create microsatellite markers for use in the breeding program for rice. Public websites offer a large number of microsatellites for application in rice. The time between molecular markers and the gene or QTLs associated with the target attributes is crucial to the effectiveness of the MAS approach. In fine mapping, a marker will often be validated.

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