© 2015 IJSRST | Volume 1 | Issue 2 | Print ISSN: 2395-6011 | Online ISSN: 2395-602X
Themed Section: Science

Bacterial Blight Resistance in Rice: A Review

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ABSTRACT

Bacterial blight disease, caused by Xanthomonas oryzaepv.oryzae(Xoo), is one of the most serious diseases in rice producing areas. For combating the disease, the most effective and economical measure is exploitation of host plant resistance. To date, more than 38 R genes for BB resistance have been reported. Since the chemical control is not effective, the utilization of resistant varieties carrying resistance genes have been considered to be the most effective way to control the disease .With the development of a wide range of molecular techniques, marker assisted breeding is now used to enhance traditional breeding programs to improve crops. Among various PCR based markers, SSR markers are more popular in rice because they are highly informative, mostly mono locus, co-dominant, easily analyzed and cost effective.Besides disease management, bioagents also stimulate plant growth, even if there is no disease, which results in better yield. Antagonistic potential of different bioagents against bacterial leaf blight of rice has been reported by several workers.
Keywords: : Rice, Bacterial Blight Disease, Resistance Genes, SSR Markers

INTRODUCTION

Rice (Oryza sativa L.) (2n = 24) belonging to the family Poaceae is the staple food for one third of the world's population that occupies almost one-fifth of the total land area covered under cereals (Chakravarthi and Naravaneni, 2006). Bacterial blight (BB), caused byXanthomonas oryzaepv.oryzae (Xoo), is a widely disributed and devastating diseases of both conventional and hybrid rice in south-eastern Asia (Mew, 1987;Nino-Liu et al., 2006). Bacterial blight disease is a systemic disease and can cause severe yield loss up to 50 % depending on growth stage, geographic localization and season (Gnanamanickam et al., 1999; Nino-Liu et al., 2006). In Taiwan, bacterial blight disease often occurs in the second crop season, and its annual incidence area is usually more than 20,000 hectares, accounting for approximately 4 % of the Taiwanese rice production area. Recently, this disease has become more and more serious because of climate change (Hsieh, 2003; Wang et al., 2013). At present, the prevention of bacterial blight includes field management, fertilizer control and resistance breeding. In practice, the cultivation of resistant rice varieties has been proposed to be the most effective strategy to prevent bacterial blight disease (Khush et al., 1989; Shen and Ronald, 2002; Yang et al., 2003). The durable and broad resistance of plants was found to be usually governed by multiple genes or quantitative trait loci (QTLs) (Johnson, 1984). Therefore, the discovery of a resistance gene against Xoois an important area of research leading to breeding programs. With the development of a wide range of molecular techniques, marker assisted breeding is now used to enhance traditional breeding programs to improve crops (Frey et al., 2004). Among various PCR based markers, SSR markers are more popular in rice because they are highly informative, mostly mono locus, co-dominant, easily analyzed and cost effective (Gracia et al., 2004). Simple Sequence Repeats (SSRs) or microsatellites are most suited to routine application in breeding programs. SSRs or microsatellite markers are proved to be ideal for making genetic maps (Islam, 2004; Niones, 2004), assisting selection (Bhuiyan, 2005) and studying genetic diversity in germplasm. Microsatellite marker analysis is promising to identify major gene locus for

BLB resistance that can be helpful for plant breeders to develop new cultivar.

Nucleotide Diversity Analysis of Three Major Bacterial Blight Resistance Genes in Rice

For combating the disease, the most effective and economical measure is exploitation of host plant resistance. To date, more than 38 R genes for BB resistance have been reported (Chen et al., 2008; Kumar et al., 2012). Diversity analysis of these genes in natural population will facilitate identification of allelic variations which can be exploited in resistance breeding programs (Iyer-Pascuzzi et al., 2007). Recent studies conclude that nucleotide changes in the non-coding and regulatory sites of Rgenes also contribute to resistance or susceptibility phenotypes of a disease in addition to nucleotide variations in the coding region (Gu et al., 2005; Romer et al.,2009).

Resistance to Bacterial Blight by Suppressing Auxine Biosynthesis in Rice

IAA, the major form of auxin in rice, is generally believed to play an important role in plant growth and development (Teale et al., 2006; McSteen et al., 2010). However, recent studies demonstrate that IAA acts as a negative regulator in the plant immune response (Yang et al., 2013; Navarro et al., 2006), as exogenous application of IAA or auxin analogs in rice and Arabidopsis sgnificantly promotes disease symptoms. Treatment with IAA and 2,4-dichlorophenoxyacetic acid (2, 4-D; an analog of IAA) in rice resistant to various types of bacterial blight significantly stimulates phytopathogenic Xoo proliferation, resulting in high susceptibility to these compounds (Ding et al., 2008). Similarly, treatment of resistant rice plants with IAA enhances the infectivity of Xanthomonas oryzaepv.oryzicola (Xooc) and Magnaporthe oryzaeto rice (Fu et al., 2011). In addition, exogenous application of 1-naphthalacetic acid (NAA) or 2,4-D on Arabidopsis accelerates the development of disease symptoms during infection by Pseudomonas syringaepv.tomato(Pto) DC3000 or Pseudomonas syringaepv.maculicola (Chen et al., 2007; Wang et al., 2007).

Genetic Analysis and Molecular Mapping of QTLs Associated with Resistance to Bacterial Blight in Rice

The International Rice Research Institute has developed a series of near isogenic lines (NILs) which harbor various Xagenes (IRBB NILs) by using the susceptible cultivar, IR24, as the recurrent parent (Huang et al., 1997). Recently, the molecular markers linking Xa genes in IRBB NILs have been developed using comparative map methods for improving the resistance of commercial cultivars (Kottapalli et al., 2006; Sama et al., 2014). However, climate change has been proposed to affect the microflora of Xoo in the field, life cycle, and even the evolution of the pathogen (Garrett et al., 2006; Coakley et al., 1999). Our previous results also revealed that IRBB lines containingxa5or Xa7showed moderate resistance, while the NILs harboring a singleXa gene were highly susceptible after the inoculation of a Taiwanese local pathogen, suggesting that more Xa genes are necessary to provide resistance (Wang and Wang2009). Recently, a durable and broad-spectrum resistance was reported by transmitting one resistance gene and pyramiding with 2–3 other resistance genes (Li et al., 2001; Perumalsamy et al., 2010).

Screening of Rice Varieties for Bacterial Leaf Blight Resistance by Using SSR Markers

Since the bacterial races vary continually influenced by the artificial and natural selection of genes resistance to bacterial blight, it is critical to explore and identify the new resistant resources to control the changeful races (Xia et al., 2012).Since the chemical control is not effective, the utilization of resistant varieties carrying resistance genes have been considered to be the most effective way to control the disease (Nino-Lui et al., 2006). Several molecular markers viz. RFLP, RAPD, SSRs, ISSRs, AFLP and SNPs are presently available to assess the variability and diversity at molecular level (Joshi et al., 2000). With the development of a wide range of molecular techniques, marker assisted breeding is now used to enhance traditional breeding programs to improve crops (Frey et al., 2004). Among various PCR based markers, SSR markers are more popular in rice because they are highly informative, mostly mono locus, co-dominant, easily analyzed and cost effective (Gracia et al., 2004). Simple Sequence Repeats (SSRs) or microsatellites are most suited to routine application in breeding

programs. SSRs or microsatellite markers are proved to be ideal for making genetic maps (Islam, 2004; Niones, 2004), assisting selection (Bhuiyan, 2005) and studying genetic diversity in germplasm. Microsatellite marker analysis is promising to identify major gene locus for BLB resistance that can be helpful for plant breeders to develop new cultivar.Bangladeshi rice varieties have been developed traditionally by selection, hybridization and back crossing with locally adapted high-yielding lines. The conventional methods of plant selection for BLB resistance are not easy because of the large effects of the environment and the low narrow sense heritability of BLB resistance.

Effect of Bioagent Application Time Against Bacterial Leaf Blight of Rice

Besides disease management, bioagents also stimulate plant growth, even if there is no disease, which results in better yield (Mishra and Sinha, 2000). Antagonistic potential of different bioagents against bacterial leaf blight of rice has been reported by several workers (Manmeet and Thind, 2002; Babu and Thind, 2005; Palaniyandi et al., 2006; Gangwar and Sinha, 2012a,b,c and Gangwar, 2013a,b). Time of application of bioagents may have effect on efficacy of bioagents as these are living entity and need a period of time for upsurge optimum population and establish on host. The level of management of disease depends on time of application of bioagents. Influence of time of application of bioagents in plant disease management was studied by several workers including Sindhan et al. (1997) and Vidhyasekaran et al. (2001). Present study was carried out to test the effect of time of application on efficacy of T. harzianum and P. fluorescens formulations against bacterial leaf blight of rice under field conditions.

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