Research Application Summary

Inheritance of bacterial leaf blight resistance in crosses involving interspecific and intraspecific rice genotypes

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Abstract

Bacterial leaf blight (BLB) of rice, caused by *Xanthomonas oryzae* pv. *oryzae* is a destructive disease prevalent in most rice growing countries. It is a serious problem under all managements, but especially in irrigated and high fertilizer input conditions, which are conducive to disease development. The disease causes reductions in crop yields as high as 80% and deterioration of grain quality under severe epidemics. Control of the disease through the use of chemicals is not cost effective or environmentally friendly for resource-constrained farmers. Use of resistant varieties is considered the only viable option. However, this requires prior information concerning the mode of inheritance of the BLB resistance trait. Some studies showed that resistance is a monogenic recessive trait, whereas in other studies it was found to be due to incomplete dominance, with preponderance of additive effect. In Ugandan rice populations, detection of epistatic effects on inheritance of BLB resistance and the resistance of "universally susceptible" IR24 to some local BLB pathotypes provides additional justification to dissect the nature of gene action and the magnitude of G x E in the new sources in order to guide breeding strategies.

Key words: Bacterial leaf blight, inheritance, interspecific, intraspecific, rice

Résumé

La rouille foliaire bactérienne (BLB) de riz, causée par *Xanthomonasoryzaepv. oryzae* est une maladie destructrice répandue dans la plupart des pays rizicoles. Il s'agit d'un problème sérieux dans toutes les gestions, mais surtout dans les conditions d'irrigation et celles d'apport élevé des engrais, qui sont propices au développement des maladies. La BLB entraîne les réductions du rendement des cultures aussi élevé que 80% et la détérioration de la qualité du grain de riz lors de sévères épidémies. La maîtrise de la maladie grâce à l'utilisation de produits chimiques n'est pas rentable ou respectueuse de l'environnement pour les agriculteurs aux ressources limitées. L'utilisation de variétés résistantes est considérée comme la seule option viable. Toutefois, ceci requiert une information préalable concernant le mode de transmission du caractère de résistance à la BLB. Certaines études ont montré que la résistance est un trait récessif monogénique, alors que dans d'autres études, elle a été jugée être due à la dominance incomplète, avec une prépondérance de l'effet additif. Dans les populations ougandaises de riz, la détection des effets d'épistasie sur l'héritage de la résistance à la BLB et la résistance des IR24 «universellement sensibles" à certains pathotypes locaux de la BLB fournit une justification supplémentaire pour disséquer la nature de l'action des gènes et de l'ampleur de G x E dans les nouvelles sources afin d'orienter les stratégies de reproduction.

Mots clés: Rouille foliaire bactérienne, héritage, interspécifique, intraspécifique, riz

Background

Despite the growing importance of rice, both biotic and abiotic factors severely affect its yields in the whole of Africa, particularly in Uganda. Of the biotic constraints, diseases such as rice yellow mottle virus (RYMV) and bacterial leaf blight (BLB) are presently some of the major threats in all rice-growing areas in the country, and in Africa at large. In Uganda, the disease has severely affected the high yielding characteristics and preferred quality traits that were incorporated into local varieties adapted to Uganda's rice-growing environments. These include those widely preferred by most farmers, such as K5 and K85. Yield reductions due to BLB may reach as high as 80% depending on the crop stage at which the infection occurs.

The overall objective of this research is to understand the mode of inheritance and the magnitude of genotype by environment interaction (G x E) for resistance to BLB in Uganda. Knowing these will enable the formation of a breeding strategy for improving rice productivity in East Africa through the development of new rice genotypes that are high-yielding, well-adapted and resistant to BLB. The specific objectives are: to determine the inheritance and gene action conditioning the transmission of bacterial leaf blight resistance to selected rice genotypes, and to determine the magnitude of G x E for resistance to bacterial leaf blight.

Literature Summary

Although much is known about the inheritance of response to BLB in rice in Asia, little is known about resistance to the prevailing local races in Uganda (Onasanya *et al.*, 2010). In a recent study, six different isolates of *X.oryzae* pv.*oryzae*, collected from Eastern Uganda, were used to test for differential virulence on 20 near-isogenic lines having 1-4 resistance genes and on IR24, which has no known gene for resistance. UX00 was identified as a unique isolate (Habarurema, 2011). At least 33 genes for resistance to BLB have been identified and designated in a series from Xa1 to Xa33 (t), etc. (Khush and Angeles, 1999; Xiang *et al*., 2006; Chen *et al*., 2008; Wang *et al*., 2009). Of all these, ten genes have been identified as recessive: xa5, xa8, xa13, xa15, xa19 , xa20, xa24 , xa26b , xa28 (Lee *et al*., 2003) and xa32(t) (Ruan *et al*., 2008). Only xa5 and xa13 have been cloned (Iyer and McCouch, 2004; Chu *et al*., 2006). Olufowote *et al.* (1977) reported that the inheritance is monogenic, either recessive or dominant, depending on whether the segregating population is inoculated at pre- or post-flowering stages, respectively. On the other hand, Tabien (1989) found that the resistance to four Philippine races of *X. oryzae* pv.*oryzae* was due to incomplete dominance, with a preponderance of additive effects.

Study Description

This research is being conducted in both the green house at: a) National Crop Resources Research Institute (NaCRRI, situated at 0º 31’ 47" N and 32º 36’ 9" E. elevation 1133 masl), and in BLB “hot-spot” fields at Namulonge in Wakiso district in central Uganda; b) at Kibimba (0º32’ 14" N and longitude 33º51’ 9"E) in Bugiri district in eastern Uganda; and c) at Olweny (2p 11' 49.3"N and 33p 1' 33.3"E) in Lira district in northern Uganda.

Research Application

To determine the mode of inheritance, four rice genotypes known to be resistant and five susceptible were crossed in a North Carolina (NC) 2 mating design. F_1 hybrid seeds have been obtained and are being planted to produce F_2 populations. The parents, F_1 and F_2 progenies will be evaluated (in Aug-Oct, 2012) for BLB resistance in an alpha-lattice design in the greenhouse, using the most virulent BLB isolate. Twenty diseased samples have been collected from four regions, isolated at the Makerere University laboratory, and preserved at NACRRI for future screening and evaluation of rice germplasm. Based on culture growth, five isolates were selected and evaluated for virulence using local variety K5. The isolate code named UG20-2 obtained from diseased samples from Limoto, Pallisa (Table 1) was the most virulent.

Table 1. Mean BLB disease lesion of the selected five pure isolate on variety K5 (Tester)

Isolate code	Site of collection	Location	Mean disease lesion length (cm)
UG13-1	Doho	N 0p 56' 13.4", E 34p 0' 14.9"	1.2
UG 1-3	Namulonge	N 0p 31’42.6", E 32p 37' 37.2"	1.5
UG 5-1	Lira	N 2p 11' 49.3" E, 33p 1' 33.3"	1.8
UG 20-2	Limoto, Pallisa	N 1p 6' 19.1", E 33p 44' 39.2"	2.1
UG 3-1	Masindi	N 1p 48' 13" ,E 31p 59' 50"	0.7
Mean			1.46
LSD			0.42
F-Test			***
CV (%)			15.4

In the second study, 25 crosses and 5 selected genotypes, with 18 near- isogenic lines (NILs) as differential lines, were evaluated under natural infection. These were planted in April, 2012, in each of the three field environments, in an alpha–lattice design with three replications. All data collected were subjected to analysis of variance (ANOVA), using GenStat software.

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