

Inheritance of resistance to Brown Spot Disease in upland rice in Uganda

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Abstract

Low yields in rice (*Oryza sativa*) are attributed by many factors including diseases which represent one of the main constraints. The Brown spot disease (caused by *Helminthosporium oryzae*) in most rice growing areas cause's considerable losses which could be averted through development and deployment of resistant varieties. In this study, field trials and screenhouse experiments were conducted at National Crops Resources Research Institute (NaCRRI) – Namulonge, Uganda during 2013/2014 with the objective of identifying new sources of resistance to brown spot disease in rice, establishing the mode of inheritance for resistance to brown spot disease and characterising F₂ progenies of specific crosses for segregating pattern of reaction to brown spot disease. Among the hundred tested rice lines, eighteen lines was rated as highly resistant, fifty two resistant, twenty seven moderately resistant and three lines were susceptible. The results revealed that there was significant variation for brown spot resistance among genotypes tested. The identified resistant lines may be brought forward and involved in rice breeding program for development of brown spot resistant lines.

Key words: *Helminthosporium oryzae*, *Oryza sativa*, sources of resistance

Résumé

Les faibles rendements en riz (*Oryza sativa*) sont attribués par de nombreux facteurs, y compris les maladies qui représentent l'une des principales contraintes. La maladie des tâches brunes (causée par *Helminthosporium oryzae*) dans la plupart des zones de culture du riz, provoque des pertes considérables qui pourraient être évitées par le développement et le déploiement de variétés résistantes. Dans cette étude, des essais sur le terrain et des expériences en serre ont été réalisées à « National Crop Resources Recherche Institut » (NaCRRI) (Institut National de Recherche en Ressources de Cultures (CRRI) de Namulonge, en Ouganda, au cours de 2013/2014, avec l'objectif d'identifier de nouvelles sources de résistance à la maladie des tâches brunes du riz, en établissant le mode de transmission pour la résistance à la maladie des tâches brunes et à la caractérisation des descendance F₂ de croisées spécifiques en vue de séparer de modèle de réaction à la maladie des tâches brunes. Parmi la centaine de lignées de riz testées, dix-huit lignées ont été classées comme très résistantes, cinquante-deux résistants, vingt-sept modérément résistantes et trois lignées étaient résultats vulnérables. Les résultats ont révélé qu'il y avait une variation significative de la résistance des tâches brunes entre les génotypes testés. Les

lignées résistantes identifiées peuvent être présentées et impliqués dans le programme de sélection du riz pour le développement de lignées résistantes aux tâches brunes.

Mots clés: *Helminthosporium oryzae*, *Oryza sativa*, sources de résistance

Background

Rice is the world's most important cereal crop and feeds more than a third of the world population (Khush, 1997). Many development efforts to improve rice production such as development of NERICA varieties have been widely recognized (WARDA, 2001). Despite a continuous increase in rice area under cultivation yields remain very low. The low yield is attributed by many factors including diseases which represent one of the main constraints. Brown spot disease challenges the efforts to enhance the productivity (Norman and Otoo, 2002).

Literature summary

The disease is widespread in all rice growing ecologies. In Uganda, the disease was first reported in 2003 (Biruma *et al.*, 2003) and later 2005 in association with seed transmission (Kawube *et al.*, 2005). Farmers in Uganda subsequently confirmed the disease as the second most important disease of upland rice (Odogola, 2006).

The control of brown spot disease in Uganda is done by spraying chemicals in the field. The intensive rice cultivation practice creates favourable conditions for disease development (Biswas *et al.*, 2011). Chemicals control is known to be environmentally unfriendly, expensive and require expertise that is generally lacking among most resource-poor farmers in Uganda (Kawube *et al.*, 2005). Host resistance would provide a more cost-effective management option for the disease. Disease screening has already been reported by different researchers who have observed higher genetic variation in various genotypes. Yaqoob *et al.* (2011) reported the variation of rice genotypes against brown spot disease. The rice germplasm was categorized from highly resistant to highly susceptible. Mosharraf *et al.* (2004) also reported the reaction of different genotypes to brown spot which ranges from resistant to moderately susceptible.

Study description

In this study, field trials and greenhouse experiments were conducted at National Crops Resources Research Institute (NaCRRI) – Namulonge, Uganda during 2013/2014. A 100 germplasm from Africa rice, IRRI, Tanzania, CIAT, Madagascar, NaCRRI –Namulonge and local ones were screened under rainfed conditions in the field using an alpha lattice design and replicated twice. Plants were artificially inoculated with the disease pathogen and disease scored at 15, 30, 45 and 60 days after inoculation. In the greenhouse, nine parents selected from the screened materials were hybridized in full diallel mating design. The F_1 progenies were advanced to F_2 , and then F_2 's together with parents were evaluated against brown spot disease.

Research application

The results among the 100 screened germplasm, 18 lines were rated as highly resistant, 52 lines resistant, 27 lines moderately resistant; Three lines including the check revealed susceptible response against the disease. In general, there was large variation of germplasm in response to the disease from 30 days of screening onwards (Table 1). The rAUDPC was calculated in order to compare the response of germplasm to brown spot disease (Fig. 1). The results show that host resistant to brown spot disease occurs among genotypes adapted to Ugandan growing conditions. Hence, it is suggested that resistant genotypes evaluated from these studies can be deployed in the future breeding strategies to develop the resistant varieties against brown spot of rice.

Table 1. Summary ANOVA table for brown spot severity at 15, 30, 45 and 60 days of disease scoring.

Source of variation	df	Var. 15days	Var. 30days	Var. 45days	Var. 60days
Total	199				
Entries	99	0.09 ^{ns}	1.09 ^{***}	1.55 ^{***}	1.54 ^{***}
RCB error	99	-	0.46	0.64	-
LSE	72	0.09	-	-	0.915

Var = Variance; df = degree of freedom; *** = very highly significant at $\alpha = 0.001$; ns = statistically not significant

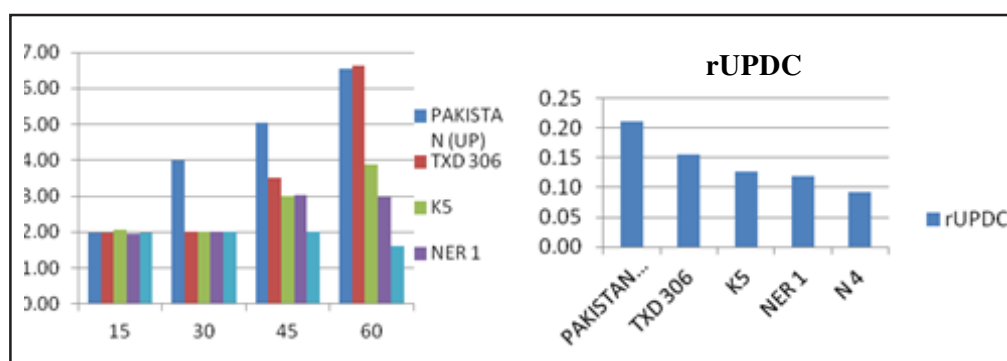


Figure 1. rAUDPC means for resistance to brown spot in few selected parents for crossing.

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Figure 2. Summary procedure in picture for screening in the field and hybridization to generate F₂'s population for brown spot disease inheritance study.

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