Research Application Summary

Inheritance of resistance to rice yellow mottle virus disease in selected rice cultivars in Uganda

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Abstract

Rice yellow mottle sobemovirus (RYMV) has been identified as the most destructive viral disease in lowland and upland rice. In this study, the mode of inheritance of resistance to a prevalent RYMV strain in Uganda was determined for five resistant lines (upland NERICAs 8, 11, 12, 13 and Gigante (an *O. sativa* lowland variety). These resistant lines were crossed with four susceptible lines (lowland NERICAs 4, 6, 10 and IR64 (an *O. sativa* lowland variety)) in a full diallel mating design. Segregating F_2 progeny were planted in both field and screenhouse in an α-lattice design, and inoculated by standard mechanical procedures. GCA effects were significant ($P \leq 0.001$), and were larger than SCA effects. Both the field and screenhouse experiments strongly expressed genotype differences. GCA, SCA and reciprocal effects were significant ($P \leq 0.001$) in both experiments. The narrow sense coefficient of genetic determination based on genotype means was relatively high in both screenhouse (76%) and field (84%) experiments. These results suggest that additive gene effects were more important than non-additive effects, and that selecting as early as F_2 or F_3 generations can be effective. However, reciprocal effects showing a consistent tendency of F_2 progeny to reflect the resistance level of the female parent indicates the need for careful choice of male and female parents in hybridization programs to achieve RYMV resistance in the offspring.

Key words: Area under disease progress curve (AUDPC), General Combining Ability (GCA), Coefficient of experimental variance (C.V), Specific Combining Ability (SCA), rice

Résumé

Rice yellow mottle sobemovirus (RYMV) a été identifié comme la maladie virale la plus destructive du riz de plaine et de montagne. Dans cette étude, le mode de la transmission de la résistance à la contrainte de RYMV en Ouganda a été déterminé pour cinq lignées résistantes (NERICAs de montagne 8, 11, 12, 13 et Gigante, une variété de plaine) croisées avec quatre lignées sensibles (NERICAs de plaine 4, 6, 10 et et une variété de plaine *O. sativa* IR64) dans une complëte conception joignante de diallële. La progéniture F_2 de séparation a été examinée en utilisant des procédures mécaniques standard d'inoculation dans le champ et d'observation avec des expériences conçues comme trellis-α. Les effets du GCA étaient significatifs ($P \leq 0.001$) et hauts par rapport aux effets du SCA. L'expérience sur le terrain était plus favorable pour exprimer la performance du génotype comme démontré par un coefficient de variance experimentale C.V. bas et une erreur expérimentale. SCA et les effets réciproques étaient significatifs ($P<0.001$) dans l'expérience sur le terrain. L'héritabilité étroite était significative ($P <0.001$) dans des expériences d'observation (76%) et sur terrain (84%). Ces résultats suggèrent que les effets additifs de gène aient été plus importants et un sélectionneur puisse accomplir le progrès par le choix dans la génération F_2 ou F_3. Les effets réciproques significatifs suggèrent le besoin pour des choix appropriés des parents mâle et femelle dans des programmes d'hybridation pour la résistance de RYMV impliquant ces cultivars.

Mots clés: Region sous une courbe d'evolution de la maladie(AUDPC), Capacite de combinaison generale (GCA), Coefficient de variance experimentale (C.V), capacite de combinaison Specifique (SCA), riz

Background

Breeding for genetic resistance to RYMV has been identified as an effective strategy for sustainable rice production, since chemical treatments and cultural practices are likely to be of limited use (Fomba, 1988). Paul *et al*. (2003) suggested that the mechanism of resistance to RYMV may differ, depending on the parental sources. Mansaray (1994) reported that in *O. sativa* lowland *indica* rice, resistance to RYMV is controlled by a few major recessive genes, while Kumwenda (1988) concluded that in upland rice tolerance to RYMV was primarily an expression of two dominant genes.

RYMV is known to be highly variable, and several strains have been identified that have broken through resistance to it (Traore *et al.,* 2006). One strategy for improving the durability of resistance to RYMV is to pyramid genes for both complete and partial resistance. Tsunematsu *et al.* (2000) postulated that developing new differential lines for each country may be necessary, and suggested identifying differential lines possessing genes for complete resistance against the country's local isolates. Thus, partial resistance can be measured in lines that lack those genes, or be identified by exposing the lines to isolates that overcome that major-gene resistance (Tsunematsu *et al.*, 2000).

In Uganda this effort is still a challenge because appropriate resistant genotypes have not yet been identified or characterised. Although the rice breeding program has introduced new materials, a better understanding of the mode of gene action to the prevailing RYMV strains is required to effectively use the new germplasm in breeding for resistance to RYMV. This is especially important, given the narrow genetic base of the available germplasm in Uganda.

Literature Summary

Control of RYMV by conventional breeding for resistance was initiated in 1978 by the International Institute of Tropical Agriculture (IITA) in Nigeria, and in the mid-1980's by the National Centre for Agricultural Research (NCAR) in Cote d'Ivoire, and the West African Rice Development Association (WARDA) in Cote d'Ivoire (Kouassi *et al.*, 2005). Several lines from *Oryza sativa* or *Oryza glaberrima* have been used to diversify the sources of resistance. The recessive, monogenic high resistance found in Gigante and Tog5681 can be used more easily than polygenic partial resistance. However, since the genes for high resistance are frequently overcome by pathogens (Fraser, 1990), additional sources of resistance with different genetic determinants should be incorporated to increase the stability and durability of the resistance (Fargette *et al.*, 2002).

Study Description

This study was conducted in the field at the National Crops Resources Research Institute (NaCRRI)and in a screenhouse nearby at Makerere University Agricultural Research Institute, Kabanyolo (MUARIK), 19 km north of Kampala. Mean daily temperatures there are 28.5^{0}C maximum, and 13.0^{0}C minimum.

Experiments in both environments were laid out in an α-lattice design, the soil was fertilised with NPK (1:1:1) one week prior to planting, and sequentially every two weeks after planting. Due to the limited number of seedlings in some crosses, evaluations were made for 8 parental lines (excluding Gigante, which had very few successful crosses) and the resulting 40 F_2 populations (26 parental combinations and 14 reciprocals). In the field, there were two replicates with 20 plants per plot in 25 cm rows with 20 cm between plants, while in the screenhouse, there were six replicates with 3 plants per pot, 10 cm apart. At 14 days post-emergence, when most plants had achieved a 3-leaf stage, inoculation was achieved by rubbing the leaves of the test plants from the leaf-base to the tip with fingers moistened with prepared inoculum. Inoculation was repeated a week later to avoid any escapes. Standard procedures of disease scoring were followed one week after the initial inoculation and subsequently for the next three weeks.

Research Application

Significant ($P \leq 0.001$) variances for crosses, GCA, SCA and reciprocal effects in F_2 populations were observed for screenhouse and field analysis (Table 1). Generally, GCA effects were very high relative to the SCA effects in both screenhouse and field experiments, as indicated by Baker's ratio (Table 1). Reciprocal effects were significant, and F_2 populations consistently reflected the resistance level of the female parent, suggesting that resistance involved an interaction between nuclear genes and cytoplasmic genes.

Table 1. ANOVA for AUDPC mean squares of RYMV severity.

Source	Screenhouse			Field		
	d.f	Ms	Fcal	d.f	Ms	Fcal
Rep	5	2.57	1.87^{ns}	1	31.98	43.97^{***}
Rep.Block	12	1.28	0.93^{ns}	2	1.37	1.89^{ns}
Entry	47	28.50	20.71^{***}	47	21.62	29.73^{***}
GCA	7	120.77	87.76^{***}	7	103.47	142.29^{***}
SCA	26	11.18	8.12^{***}	26	6.48	8.91^{***}
Reciprocal	14	15.01	10.91^{***}	14	9.99	13.74^{***}
Error	223	1.38		45	0.73	
Mean AUDPC		14.70			15.60	
% C.V		19.60			7.80	
Baker's ratio ($2\sigma^2_{gca}/ 2\sigma^2_{gca}+ \sigma^2_{sca}$)		0.75			0.82	
Narrow sense coefficient of genetic determination ($2\sigma^2_{gca}/ 2\sigma^2_{gca}+ \sigma^2_{sca}+ \sigma^2_{e}{}'$)		0.71			0.79	

*** Significant at $P < 0.001$; ^{ns} Not significant at $P<0.05$. AUDPC = Area under disease progress curve.

[1] Mean squares were derived from the analysis of entry means, while the coefficient of experimental variation was calculated based on analysis of individual plot data.

[2] Baker's ratio was estimated based on variance components.

Mid-parent-offspring (F_2) regression was significant ($P \leq 0.001$) in both the screenhouse and field experiments, with a regression coefficient "*b*" of 0.53 and 0.58 respectively (Table 2). This, according to Falconer (1989) and Simmonds (1981), is a direct estimate of the narrow sense heritability (h^2). F_2 data indicated

Table 2. ANOVA for mid-parent regression on F_2 offspring for RYMV resistance.

Source	d.f	Mean squares	
		Screenhouse	Field
Regression	1	483.70^{***}	506.40^{***}
Residual	38	10.80	9.40
"*b*"		0.53	0.58

*** Significant at $P \leq 0.001$.

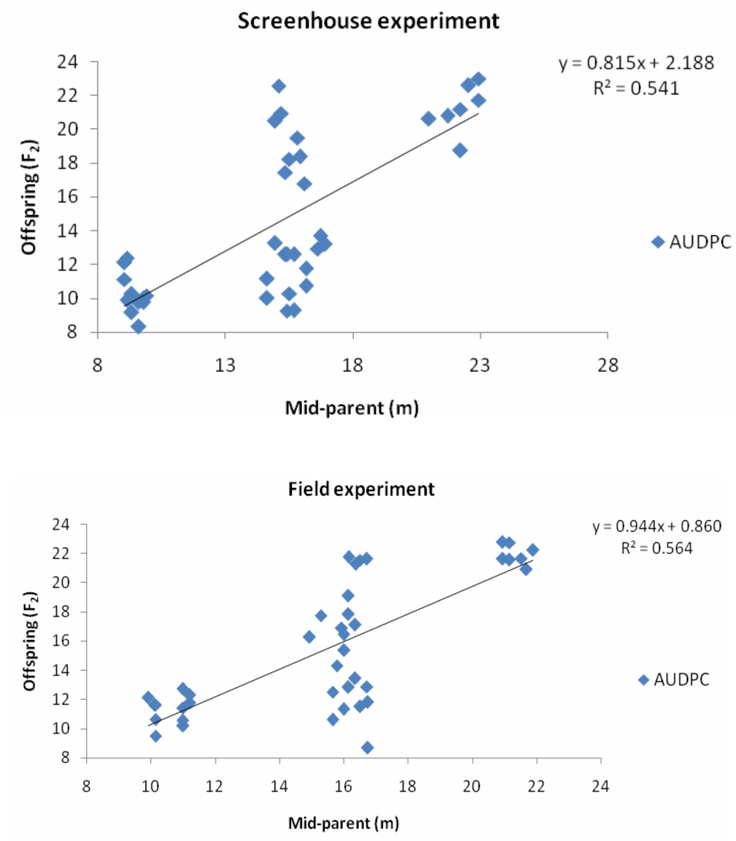

Figure 1. Regression of F_2 offspring AUDPC values onto their mid-parent values for RYMV score.

that 54% and 56% (in screenhouse and field experiments respectively) of the total variation in the mean AUDPC scores of F_2 population was accounted for by the mid-parent scores (Fig. 1).

Recommendation

The results of this study support earlier work by Paul *et al.* (2003), which showed that additive gene effects were more important than non-additive effects for the inheritance of resistance to RYMV, and these GCA effects can be exploited in developing materials resistant to RYMV. Reciprocal effects reflecting the resistance level of the female parent show the need for careful selection of male and female parents in hybridization programs for RYMV resistance. With adequate disease pressure, field experiments, especially in RYMV hot spot areas, can provide good results when evaluating lines for RYMV resistance. However, this should be carried out with caution so as not to introduce a new strain into an area without that strain. Additional sources of resistance with different genetic determinants need to be identified and exploited in breeding for resistance to RYMV.

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