

## Inheritance of resistance to rice yellow mottle virus in interspecific and intraspecific rice in Uganda

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### Abstract

*Rice Yellow Mottle Virus sobemovirus* (RYMV) has been noticed as major constraint of both upland and lowland rice. It is highly infectious, variable and several resistance-breaking strains have been identified. The effective control was mainly directed to breeding for resistance. The study aims to understand the mechanism of resistance and number of genes conferring resistance to rice yellow mottle virus (RYMV) in interspecific and intraspecific rice. The Research is being conducted at National Crop Resources Research Institute. Nine genetic materials, 5 susceptible and 4 resistant have been used in full diallel crossing design to generate F1's. Preliminary data showed that the interspecific lines were cross-compatible with genetic materials resistant to RYMV. This indicates that the interspecific lines can simply be used to generate new rice genotypes by introgression or extraction of valuable genes in them. The inheritance of resistance will be determined after a diallel evaluation by inoculating F2's + Parents and scoring for reaction to the virus. Furthermore, this study aims to estimate heritability of resistance to RYMV within advanced generations (F3, F4 & F5). Preliminary data showed that regression of F4 bulk on F3 progeny rows was significant for number of tillers ( $P < 0.05$ ), but was not significant for plant height ( $P > 0.05$ ). Heritability for various traits indicates that selection should be successful for most traits.

Key words: Diallel, gene, heritability, inoculation

### Résumé

*Le virus de panachure jaune de riz sobemovirus* (RYMV) a été remarqué comme la contrainte majeure à la fois pour le riz des montagnes et celui des plaines. Il est très contagieux, et plusieurs souches variables de résistance remarquable ont été identifiées. Le contrôle effectif a été principalement dirigé vers la sélection pour la résistance. L'étude vise à comprendre le mécanisme de résistance et le nombre de gènes conférant une résistance au virus de la panachure jaune du riz (RYMV) dans le riz interspécifique et intraspécifique. La recherche est menée

à l'Institut National de Recherche en Ressources Culturelles. Neuf matériels génétiques, cinq sensibles et 4 résistants, ont été utilisés dans la conception complète de croisement des diallèles pour générer ceux de F1. Les données préliminaires ont montré que les lignées interspécifiques ont été contre-compatibles avec les matériels génétiques résistants au RYMV. Cela indique que les lignées interspécifiques peuvent simplement être utilisées pour générer de nouveaux génotypes de riz par intromission ou par extraction des gènes de valeur en eux. L'hérédité de la résistance sera déterminée après une évaluation diallèle en inoculant Parents + F2 et en marquant la réaction au virus. En outre, cette étude vise à estimer l'héritabilité de la résistance au RYMV au sein des générations avancées (F3, F4 et F5). Les données préliminaires ont montré que la régression de la masse de F4 sur les lignées de descendance de F3 a été significative pour le nombre de tiges ( $P < 0,05$ ), mais n'était pas significative pour la hauteur des plantes ( $P > 0,05$ ). L'héritabilité pour les caractères divers indique que la sélection devrait réussir pour la plupart de caractères.

Mots clés: Diallèle, gène, hérédité, inoculation

## Background

Rice has been of great importance to most people in Sub-Saharan Africa (SSA) (Balasubramanian *et al.*, 2007) where the demand has grown relatively faster than anywhere else in the world, due to the region's rising population and changes in consumer preference. In Uganda, rice production is growing fast and there is an accelerated shift from other cereals such as maize, millet, and sorghum to rice (Lamo *et al.*, 2010). Rice is considered as a crop that provides both food security and income. Despite a continuous increase in rice area under cultivation, yields remain very low, realised actual on farm yield is about  $1.5 \text{ t ha}^{-1}$  for both wetland and upland rice production systems against their respective potentials of 4.5 and 5.5 tones  $\text{ha}^{-1}$ , resulting in a minimum yield gap of 3.0 tones  $\text{ha}^{-1}$  (FAO STAT, 2005). Pests and diseases greatly reduce rice yield and the rice yellow mottle virus (RYMV) represents the major biotic constraints of rice in Uganda.

## Literature Summary

The control of RYMV disease was mainly directed to the use of resistant varieties through conventional breeding since disease control based on crop management techniques and chemical use was inefficient. Different degrees of resistance have been detected in *Oryza sativa* and *Oryza glaberrima*. Deless *et al.*, (2010) identified two resistance genes against

RYMV in *O. glaberrima*. It has been noticed by Mansaray (1994) that resistance to RYMV in *O. sativa*, lowland *indica* rice is controlled by a few major recessive genes while Kumwenda *et al.*, (1995) noted that tolerance to RYMV was primarily an expression of two dominant genes in upland rice. Many and often contradictory results were generated, most probably because of the use of different virus isolates and infection conditions. However, it has been consistently shown that almost all sources of resistance to RYMV belong to *Oryza glaberrima* which originated from Africa.

In Uganda, the rice breeding program has introduced new materials among which some have been identified as the potential sources of resistance for improving susceptible landraces. Ochola and Tusiime (2011) noted WAC 116 and WAC 117. However, the mode of inheritance of resistance to RYMV in those cultivars is not yet adequately understood. It is reported that introgression of resistance into susceptible cultivars requires an understanding of the nature of inheritance and of the gene action controlling resistance (Kornegay *et al.*, 1980; Attere, and Fatokun, 1983).

## Study Description

This study is being conducted at National Crops Resources Research Institute (NaCRRI)-Namulonge (located at 00 32' N of the Equator and 320 37' E). For the first objective of determining the mode of gene action for resistance to RYMV; four rice lines, Gigante, WAC 116, WAC 117, and Naric 1 were used as parents resistant, while five varieties, Nerica 1, Nerica 4, Nerica 6, K5, and K85 were included as parents susceptible to RYMV. The above materials were crossed in a full diallel to generate F1's, and reciprocals. All F1 were advanced to generate F2's. Three susceptible genotypes (SUPA, K5 and K85) were inoculated with 2 different isolates (from Lira & Iganga) and the virulent one (from Iganga) was chosen. The inoculum was maintained on K5 plants. The diallel evaluation (F2's + Parents) has been planted in the nursery in alpha lattice design 25x2 with 2 replications. Inoculation was achieved using the finger-rub technique. Severity of RYMV disease symptoms will be scored on 1-9 scale (IRRI reference). Chi-square test of independence will be used to determine the reciprocal effects. Chi-square goodness-of-fit will be used to test phenotypic ratios to estimate the number of genes and dissect pattern of inheritance. Griffing's method 1 will be used to obtain GCA, SCA, reciprocal effects. For the second objective of estimating heritability of resistance in advanced generations, 29 F3

## Research Application

populations previously generated have been advanced to F5. Eleven F3, F4 and F5 crosses along with their parents (7) have been planted in alpha lattice design 10x4, 3 replications to estimate heritability of resistance in those generations using parent-offspring regression method.

The diallel crossing resulted into 32 successful crosses out of the 36 parental combinations, with 14 having reciprocals, thus making 46 total crosses. All of the interspecific varieties crossed successfully with the resistant rice varieties. This was not the case for intraspecific varieties (Table 2). However, the percentage of seed set was significantly different among interspecific rice x resistant genotype (Table 1). For the crosses with Gigante, the highest percentage of seed set was with Nerica 4 (26%) and the lowest with Nerica 6 (3%). For the crosses with Naric 1, the highest percentage of seed set was found with Nerica 6 (62%), and the lowest with Nerica 1 (16%). For intraspecific varieties, K85 failed to cross with both resistant varieties. In general, this indicates that the interspecific lines can simply be used to generate new rice genotypes by introgression or extraction of valuable genes in them.

The preliminary results for objective 2 where F4 bulks were regressed on F3 progeny; heritability was significant for number

**Table 1. Seed set of crosses between interspecific rice (as female) and resistant rice genotype (as male) parents.**

Interspecific female parent	Resistant male parent	
	Gig	Naric 1
	Seed set (%)	
Ner 6	3	62
Ner 4	26	44
Ner1	18	16

**Table 2. Seed set of crosses between intraspecific rice (as female) and resistant rice genotype to RYMV (as male) parents.**

Interspecific female parent	Resistant male parent	
	Gig	Naric 1
	Seed set (%)	
K5	9	29
K85	0	0

of tillers ( $P < 0.05$ ) with b-value = -0.46, but was not significant for plant height ( $P > 0.05$ ), b-value = -0.15. Heritability for various traits indicates that selection should be successful for most traits.

## References

- Attere, A.F. and Fatokun, C.A. 1983. Reaction of *Oryza glaberrima* accessions to rice yellow mottle virus. *Plant Disease* 67:420 - 421.
- Balasubramanian, V., Sie, M., Hijmans, R. J and Otsuka, K. 2007. Increasing Rice Production In Sub-Saharan Africa: Challenges And Opportunities. International Rice Research Institute (IRRI), Metro Manila, Philippines. Africa Rice Center (WARDA), 01 BP 2031 Cotonou, Benin, West Africa. *Advances in Agronomy* 94:133.
- FAOSTAT, 2005. Rough rice yield (t/ha), by country and geographical region, (1961-2004). FAO, Rome, Italy. <http://www.irri.org/science/ricestat/index.asp>
- Kornegay, J.L., Beute, M.K. and Wynne, J.C. 1980. Inheritance of resistance to *Cercospora arachidicola* and *Cercosporidium personatum* in six Virginia type peanut lines. *Peanut Sc.* 7:4 - 9.
- Kumwenda, A.S., Masajo, T.M., Peat, W.E. and Alluri, K. 1995. The inheritance of tolerance to Rice Yellow Mottle Virus (RYMV) in Rice (*Oryza sativa* L.). Paper presented at the 1st International Symposium on RYMV from 18-22 September, 1995, Mbe, WARDA/ADRAO, Bouake, Cote d'Ivoire.
- Lamo, J., Imanywoha, Bigirwa, G., Walusimbi, M., Kyetere, D., Kikafunda, J. and Kalule, T. 2010. First NERICA rice released in Uganda tops farmers' rankings.
- Mansaray, M.S. 1994. Inheritance of rice yellow mottle virus (Rymv) resistance in African lowland rice (*Oryza sativa* L.) subsp. Indica Ph.D. Thesis, University of Sierra-leone 1993. 290pp.
- Ochola, D. and Tusiime, G. 2011. Pathogenicity of Rice Yellow Mottle Virus and the Potential Sources of Resistance against the Disease in Eastern Uganda. *Asian Journal of Plant Pathology* 5:1-15.