

# Genetic Study of Resistance to Rice Blast in Crosses between Korean and Locally Adapted Rice Genotypes

Zewdu Z<sup>1,2\*</sup>, Edema R<sup>2</sup> and Lamo J<sup>3</sup>

<sup>1</sup>Ethiopian Institute of Agricultural Research, Fogera National Rice Research and Training Center P.O. Box 1937, Bahir Dar, Ethiopia

<sup>2</sup>School of Agricultural Sciences, Makerere University, P.O. Box 7062, Kampala, Uganda

<sup>3</sup>National Crops Resources Research Institute, P. O. Box 7084, Kampala, Uganda

\*Corresponding author: Zewdu Z, Ethiopian Institute of Agricultural Research, Fogera National Rice Research and Training Center, Bahir Dar, Ethiopia, Tel: +251918468882; E-mail: zelalemsafe@gmail.com

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## Abstract

The rice blast (*Magnaporthe grisea*) is a serious constraint to rice production in many rice producing countries including Uganda. Yield losses of up to 100% are attributed to the blast disease in different rice growing regions. In addition to these, the inheritance of resistance to the disease has not yet been studied under Ugandan condition.

Experiment was conducted under controlled conditions by using three resistant and four susceptible elite genotypes as parental lines for population development in half dialled mating design with the aim of providing relevant genetic information as a contribution towards the development of rice varieties with resistance to blast disease. A total of 18 crosses were advanced to F2 level. The F2 segregates and their corresponding parents were evaluated in the screen house against single virulent isolate of rice blast pathogen in 4 by 7 alpha lattice design in three replications.

These results showed that there was significant variation for rice blast resistance among genotypes. Significant general and specific combining abilities were observed, indicating that both additive and non-additive gene effects were important for rice blast resistance, although the additive effect was predominant. A High coefficient of genetic determination in the broad sense (0.99) and narrow sense (0.85), were obtained on a genotype mean basis with a high Baker's ratio of 0.86, indicating primarily additive inheritance among crosses.

The segregation pattern for resistance to rice blast showed single dominant gene in some elite susceptible × resistant crosses, duplicate recessive epistasis in other elite susceptible × resistant crosses and two genes with duplicate dominant epistasis in resistant × resistant crosses. The crosses between susceptible by susceptible genotypes did not show segregation. Overall, resistance was highly heritable, with mainly additive gene action between crosses. Results suggest that simple breeding strategies with selection in early generations would be effective for rice blast resistance.

**Keywords:** Genetics; Segregation; Rice; Blast; Resistance

## Introduction

Development of varieties with improved traits, like resistance to both biotic and abiotic stresses, is very important. Among the biotic stresses, rice blast is the main constraint to rice production. To develop resistant varieties, it is vital to identify the source of resistance, the nature of resistance and the gene action that provides resistance to the disease. Knowledge of these factors helps the breeder to incorporate resistance and to assess whether or not the incorporated resistance is durable and can be expressed in different environments.

The inheritance pattern of resistance from the locally adapted genotypes and the Korean genotypes under Ugandan conditions is not yet known and this should be known for further utilization of these genotypes in resistance breeding. Since the Korean genotypes are new for Ugandan conditions, the inheritance pattern em

population development (Table 1). fYY of them were selected from

## Results

### Gene action determining rice blast resistance

Analysis of variance of F<sub>2</sub> segregating populations evaluated in screen house in season (2016 A) is presented in Table 2. ANOVA revealed significant differences ( $P < 0.001$ ) among genotypes for rice blast severity, resulting from wide genetic variability of genotypes for resistance to rice blast.

Narrow sense heritability of genetic determination was 0.85, indicating that 85% of the variation for resistant to leaf blast among genotypes was due to transmissible genetic variation and 15% was due to environmental variation. Broad sense heritability of genetic determination was 0.97, indicating 97% of the observed inheritance to rice blast resistance is due to genotypes for

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S.E SCA[(P2+p+2)/(p+1)\*(p+2)\* ems/r]1/2=0.08

## References

1. Viana J, Cruz C, Cardoso A (2001) Ycmand analysis of partial diallel crosses. Parents and F2 generations. *Genet Mol Biol* 22: 627-634
2. Allard R (1960) Principles of plant breeding. Wiley, New York, pp: 83-108
3. Herrera RC (1974) Emasculation of rice by vacuum extraction. *Proc Crop Sci Soc Philipp* 5: 12-14
4. Talukder M, Leifert C, Price A (2000) Mapping QTLs for partial resistance to blast in rice T » sn

suggested that the resistant parents involved in the cross might have X] YfYb alleles for resistance. In this study the cross between susceptible by susceptible (S1 × S2, S1 × S3, S1 × S4, S2 × S3, S2 × S4, S2 × S3 and S3 × S4) did not show segregation, but the F2 means were less than either the mid-parent or either susceptible parent. Ig indicates that none of these parents had any resistance genes. YgY crosses suggest presence of recessive genes for susceptibility. Igresult contrasts with the report by Niyongabo et al. [15] that the cross between susceptible by susceptible genotypes showed duplicate dominant epistasis for most of the crosses.

Y cross between susceptible by resistant parents showed that only six crosses of S1 × R7, S2 × R6, S2 × R7, S3 × R6, S4 × R6 and S4 × R7 were confirmed to the 3:1 ratio, suggesting the presence of at least one dominant gene. Ig study coincides with the report by Rahim et al. [16] and Rajashekara et al. [17] that the inheritance of blast resistance gene in F2 populations derived from the cross between susceptible and resistant varieties showed a segregation ratio of 3R:1S, in both the normal and reciprocal crosses. On the other hand, three crosses, (S1 × R5, S2 × R5 and S4 × R5) Hhb[ a 9:7 phenotypic ratios, suggested the involvement of two complementary dominant genes (duplicate recessive epistasis). In contrast, three crosses R5 × R6, R5 × R7 and R6 × R7 ha 15:1 ratio, suggesting the involvement of two independent dominant genes. Igresult is in conformity with those obtained from the F2 populations from cross between genotype Bluebellet and ramatulasi segregating in the ratio of 15: 1 to race IB-1 [18]. In this study, the F2 distribution analysis and the chi-square test suggest the presence of single gene; two complementary dominants and two independent dominant genes are responsible for inheritance of rice blast resistance.

## Conclusion

9 Wj] Ysources of resistance from incorporated genotypes depends on the gene action they contribute and this study showed that three modes of inheritance controlled the genes resistant to rice blast; namely one dominant gene, two complementary dominants and two independent dominant genes. Genotypes SR33859-HB3324-133, SR33859-HB3324-93 and SR33701-HB3330-78 were considered suitable for future resistance breeding, since they have high negative GCA Y Wj] for rice blast resistance. Y inheritance of rice blast resistance is mainly controlled by additive gene Y Wj] although a small contribution of non-additive Y Wj] was found.

## Conf ict of Interest

YfYis no Wb ]Wj]of interest among the authors

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