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Application of Epidemiological Screening Concepts to Identify Rice Genotypes with Quantitative Resistance to Sheath Blight (*Rhizoctonia solani* Kühn)

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INTRODUCTION

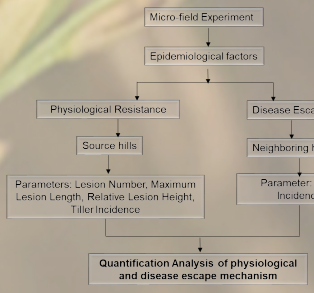
- Rice is the world's second most important cereal crop and the staple food of an estimated 3.5 billion people worldwide.
- Philippines is one of the world's largest rice importer.
- Farmers lose an estimated average of 37% of their rice crop to pests and diseases every year (IRRI).

- Rice sheath blight (ShB), caused by *Rhizoctonia solani* Kühn, is a destructive disease worldwide that causes significant yield loss and quality degradation (Lee and Rush, 1983).
- *R. solani* is known to have a typical quantitative trait controlled by polygenes (Sha and Zhu, 1989) that's why the pathogen is said to be difficult in finding innate immunity among host.
- Willocquet et al., (2011) stated that a detailed and quantitative measurement of the components of physiological resistance and disease escape may provide a relevant basis to quantify mechanisms of resistance and their respective importance to identify potential donors.

OBJECTIVES

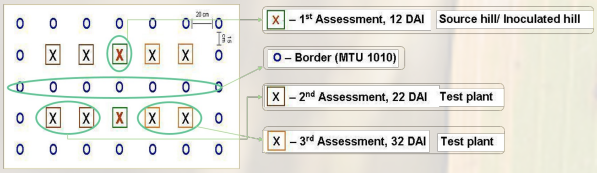
- Hence, the objective of this study was to evaluate potential resistant rice donor varieties through assessment of quantitative effects in both physiological and disease escape mechanism. The findings were therefore for the improvement of rice resistance to sheath blight and provide resources for breeding ShB-resistant varieties.

METHOD



- 16 selected genotypes from previous studies were evaluated to validate its levels of resistance under modified field experiment.
- Seedlings were transplanted to flooded concrete beds filled with soil under semi-controlled conditions.

- Plants at a maximum tillering stage were inoculated at the base of the hill by inserting 5 g of a colonized mixture of *R. solani* and rice grain rice hull.
- The experimental layout considers the epidemiology of the pathogen: physiological resistance which was quantified at 12 dpi targeting only the source hill/inoculated hill whereas disease escape was quantified at 22 and 32 dpi through the neighboring hills.



Schematic diagram of Micro-field experiment

CONCLUSION

▪Phenotypic evaluation revealed that each cultivar has different mechanism shown by their resistant response to each component.

▪The architecture of crop canopy and associated microclimate has strong effects on the mobilization of primary inoculum as well as the spread of the disease.

▪Selected lines were Da Nuo, Gie 57, ShB (6) and ShB (5) from the clusters I, II, and IV designating to be moderately resistant, resistant and highly resistant based on analysis of variance and multivariate analysis.

▪Similarly Da Nuo and Gie 57 were classified as moderately resistant and resistant under semi-field condition, respectively (Oreiro 2016).

RESULTS & DISCUSSION

A. Quantification of physiological and disease escape mechanism for ShB resistance

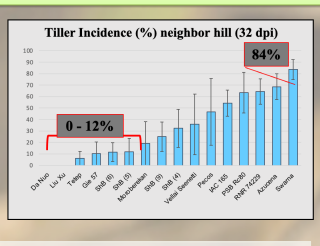
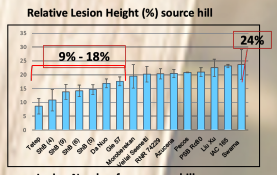


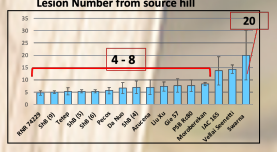
Figure 1. Disease reaction of a susceptible genotype 'swarna'

▪The lines observed in neighboring hills that has low values were intermediate and tall in height which might contributes to disease escape.



▪Lowest RLH are the Da Nuo, Tetep, Gie 57, Shb (6), Shb (4), Shb (5) and Shb (9)

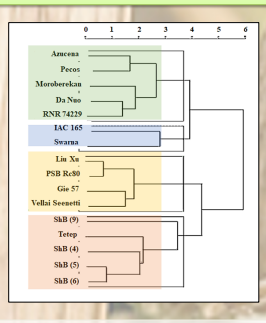
▪ Ahn and Mew (1986), no significant yield reduction was found when RLH was <20%.



▪Lowest number of lesion are the RNR, Da Nuo, Tetep, Pecos, Gie 57, PSB Rc80, Moroberekan, Azucena, Liu Xu, Shb (6), Shb (4), Shb (5) and Shb (9).

▪Yield loss of 46% was possible if sheath blight lesion reached 90% of RLH (Singh et al, 2015).

B. Quantification of physiological and disease escape mechanism for ShB resistance



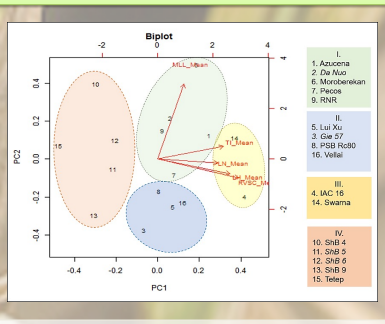


Figure 2. *Multivariate analysis of sheath blight intensification*. (a) Clusters of 16 genotypes were generated according to sheath blight disease variables measured after 12 days inoculation. Color indication: green (cluster I-*moderately resistant*), blue (cluster II-*resistant*), yellow (cluster III-*susceptible*) and pink (cluster IV- *highly resistant*). (b) Principal component analysis (PCA) depicting the relationship of the 5 disease variables with plotted 16 lines grouped into 4 clusters (I, II, III and IV). Variables include MLL_mean; Maximum lesion length, TI_mean; Tiller incidence, LN_mean; Lesion number, LH_mean; Lesion height, and RLH_mean; Relative lesion height. Legend of different colors indicates the 4 clusters and the 16 lines.

Acknowledgements

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