Effects of Alternate Wetting and Drying Irrigation and Nitrogen Fertilization on Sheath Blight of Rice

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# Abstract

Water and nitrogen management play vital roles in rice production. However, the mismanagement of these two management practices may trigger plant disease epidemics such as sheath blight of rice, caused by *Rhizoctonia solani*, which is favored by wet conditions, high relative humidity, and high nitrogen fertilizer levels. To understand how different combinations of water and nitrogen management affect sheath blight epidemics, we conducted two separate split-plot experiments with two irrigation regimes and differing nitrogen treatments in the dry seasons of 2015 and 2016. Disease scoring was the same in both experiments using a sheath blight assessment scale for field evaluation developed at the International Rice Research Institute to assess the severity on infected sheaths and leaves while sheath blight incidence on tillers were counted per hill. While we were unable to detect any differences in disease in either experiment due to irrigation methods, N rates or the interaction of the two treatments in either season we suggest that further research on this subject is warranted.

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# Materials and Methods

## Experimental design

Two experiments were conducted at the International Rice Research Institute's (IRRI) Ziegler Experiment Station in Los Baños, Calabarzon, Philippines (latitude 14.14˚, longitude 121.27˚) in the 2015 and 2016 dry seasons. For the 2016 season changes were made to optimize the experiment based on findings from the 2015 season. The changes are detailed following.

### 2015 Dry Season

Split plot design with irrigation as the main plot treatment and N rate as the split plot treatment. The main plot size was 12m x 12m (144 sq m), with a sub-plot size of 5m x 5m (25 sq m). Replication size was 12m x 24m (288 sq m) with a buffer of 1m per sub plot for a whole experiment size of 1,152 sq m.

### 2016 Dry Season

The plot design again was a split plot design with irrigation as the main plot treatment and N rate as the split treatment. However, the plot size increased and due to these changes, the sizes of the replicates are not equal as necessitated by the use of a larger area for the experiment. The main plot sizes were: Block 1 (B1) 21m x 20.5m (412.5 sq m) and Block 2 (B2) 20.25m x 21.6m (437.4 sq m). The sub plot sizes were B1 21m x 10.25m (215.25 sq m), B2 20.25m x 10.8m (218.7 sq m). The replication sizes were B1 - 42m x 20.5m (861 sq m) and B2 - 40.5m x 21.6m (874.8 sq m). A buffer 0.5m per sub plot was used and the overall experiment size was 3471.6 sq m.

## Data collection and analysis

Data were analysed using multivariate generalised linear mixed models implemented in the MCMCglmm package (Hadfield 2010) in R (R Core Team 2017).

# Results

# Discussion

# Acknowledgments

# Literature Cited

Hadfield, J. D. 2010. MCMC methods for multi-response generalized linear mixed models: The MCMCglmm R package. Journal of Statistical Software. 33:1–22 Available at: <http://www.jstatsoft.org/v33/i02/>.

R Core Team. 2017. *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. Available at: <https://www.R-project.org/>.