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Interaction between the Rice Pathogens, *Fusarium graminearum* and *Burkholderia glumae*

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Species belonging to the genus *Fusarium* are widely distributed and cause diseases in many plants. Isolation of fungal strains from air or cereals is necessary for disease forecasting, disease diagnosis, and population genetics [1]. Previously we showed that *Fusarium* species are resistant to toxoflavin produced by the bacterial rice pathogen *Burkholderia glumae* while other fungal genera are sensitive to the toxin, resulting in the development of a selective medium for *Fusarium* species using toxoflavin [2]. In this study, we have tried to elucidate the resistant mechanism of *F. graminearum* against toxoflavin and interaction between the two pathogens in nature.

To test whether *B. glumae* affects the development of *F. graminearum*, the wild-type *F. graminearum* strains were incubated with either the bacterial strain or supernatant of the bacterial culture. Both conditions increased the conidial production five times more than when the fungus was incubated alone. While co-incubation resulted in dramatic increase of conidial production, conidia germination delayed by either the bacterial strain or supernatant. These results suggest that certain factors produced by *B. glumae* induce conidial production and delay conidial germination in *F. graminearum*.

To identify genes related to toxoflavin resistance in *F. graminearum*, we screened the transcriptional factor mutant library previously generated in *F. graminearum* [3] and identified one mutant that is sensitive to toxoflavin. We analyzed transcriptomes of the wild-type strain and the mutant strain under either absence or presence of toxoflavin through RNAseq. Expression level of total genes of 13,820 was measured by reads per kilobase per million mapped reads (RPKM). Under the criteria with more than two-fold changes, 1,440 genes were up-regulated and 1,267 genes were down-regulated in wild-type strain than mutant strain in response to toxoflavin treatment. A comparison of gene expression profiling between the wild type and mutant through gene ontology analysis showed that genes related to metabolic process and oxidation-reduction process were highly enriched in the mutant strain. The data analyses will focus on elucidating the resistance mechanism of *F. graminearum* against toxoflavin and the interaction between the two pathogens in rice. Further evolutionary history will be traced through figuring out the gene function in populations and in other filamentous fungi.

References

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Keywords: *Burkholderia glumae*, conidiation, *Fusarium graminearum*, interaction, toxoflavin