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Toward Understanding the Sexual Development in the Homothallic Ascomycete *Gibberella zeae*

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Gibberella zeae (anamorph *Fusarium graminearum*) is a filamentous homothallic ascomycete with ubiquitous geographic distribution. This fungus causes serious diseases in cereal crops, such as corn, wheat, barley, and rice [1]. These diseases not only reduce grain yield but also threaten to human and animal health due to contamination of the diseased grain with mycotoxins. Sexual spores (ascospores) of *G. zeae*, which are produced within sexual fruit-bodies called perithecia formed on plant debris, are forcibly discharged from the perithecia and can infect plant spikes via the anther during anthesis in the next spring [2]. Therefore, ascospore production caused by sexual development has been suggested to play important roles in completing the cycle of the plant diseases caused by *G. zeae*. Here, we focus on the *G. zeae* sexual developmental processes genetically controlled by the mating-type locus (*MAT*), a single master regulator for mating. *G. zeae* carries two alternate idiomorphs (alleles, *MAT1-1* and *MAT1-2*) in a single nucleus, only each of which is present in heterothallic species [3, 4]. To massively isolate and characterize genes involved in sexual development from the *G. zeae* genome, we have employed several functional genomics approaches. First, we have generated and characterized a collection of insertional mutants from a representative strain of *G. zeae* using the restriction enzyme-mediated integration (REMI) procedure. Second, we have determined the functions of more than 100 genes using a targeted gene deletion strategy. Those genes were selected based on sequence analyses of REMI mutation genes, their neighbors, and orthologs of previously identified fungal genes, and selected by a small-scale microarray or proteomics analysis using a *MAT1-2*-deleted strain [5, 6]. In this talk, functional characterization of the genes mainly involved in pheromone- or G-protein signaling, mating-type-mediated sexual development pathway, or their related secondary metabolism in *G. zeae* were presented [7].

References

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