

High through-put analysis of genes involved in sexual development in *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 many cereal crops. These diseases not only reduce grain yield but also threaten to human and animal health due to contamination of the diseased grain with mycotoxins. Ascospores (sexual spores) of *G. zeae*, which are produced in perithecia formed on plant debris and wind-disseminated, can infect plant spikes via the anther during anthesis. 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*. To understand the molecular basis of sexual reproduction in *G. zeae*, we have employed several functional genomics approaches. First, we focused on the *G. zeae* genes homologous to those mainly involved in pheromone- or G-protein signaling, mating-type-mediated sexual development pathway, or their related secondary metabolism in model fungi. Second, 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. Third, we have determined the functions of more than 100 genes using a targeted gene deletion strategy, which were selected based on sequence analyses of REMI mutation genes, their neighbors, and by a small-scale microarray or proteomics analysis.