

## Genetic Control of Asexual Sporulation in *Fusarium graminearum*

Hokyung Son<sup>1</sup>, Myung-Gu Kim<sup>1</sup>, Suhn-Kee Chae<sup>2</sup>, and Yin-Won Lee<sup>1</sup>

<sup>1</sup>Department of Agricultural Biotechnology and Centers for Fungal Pathogenesis and Agricultural Biomaterials, Seoul National University, <sup>2</sup> Department of Biochemistry, Paichai University

*Fusarium graminearum* (teleomorph *Gibberella zeae*) is an important plant pathogen that causes head blight of major cereal crops such as wheat, barley, and rice, as well as causing ear and stalk rot on maize worldwide. Plant diseases caused by this fungus lead to severe yield losses and accumulation of harmful mycotoxins in infected cereals [1].

Fungi utilize spore production as a mean to rapidly avoid unfavorable environmental conditions and to amplify their population. Spores are produced sexually and asexually and their production is precisely controlled. Upstream developmental activators consist of *fluffy* genes have been known to orchestrate early induction of conidiogenesis in a model filamentous fungus *Aspergillus nidulans*. To understand the molecular mechanisms underlying conidiogenesis in *F. graminearum*, we characterized functions of the *F. graminearum fluffy* gene homologs [2]. We found that FlbD is conserved regulatory function for conidiogenesis in both *A. nidulans* and *F. graminearum* among five *fluffy* gene homologs. *flbD* deletion abolished conidia and perithecia production, suggesting that *FlbD* have global roles in hyphal differentiation processes in *F. graminearum*.

We further identified and functionally characterized the ortholog of AbaA, which is involved in differentiation from vegetative hyphae to conidia and known to be absent in *F. graminearum* [3]. Deletion of *abaA* did not affect vegetative growth, sexual development, or virulence, but conidium production was completely abolished and thin hyphae grew from abnormally shaped phialides in *abaA* deletion mutants. Overexpression of *abaA* resulted in pleiotropic defects such as impaired sexual and asexual development, retarded conidium germination, and reduced trichothecene production. AbaA localized to the nuclei of phialides and terminal cells of mature conidia. Successful interspecies complementation using *A. nidulans* AbaA and the conserved AbaA-WetA pathway demonstrated that the molecular mechanisms responsible for AbaA activity are conserved in *F. graminearum* as they are in *A. nidulans*.

*F. graminearum* ortholog of *Aspergillus nidulans wetA* has been shown to be involved in conidiogenesis and conidium maturation [4]. Deletion of *F. graminearum wetA* did not alter mycelial growth, sexual development, or virulence, but the *wetA* deletion mutants produced longer conidia with fewer septa, and the conidia were sensitive to acute stresses, such as oxidative stress and heat stress. Furthermore, the survival rate of aged conidia from the *F. graminearum wetA* deletion mutants was reduced. The *wetA* deletion resulted in vigorous generation of single-celled conidia through autophagy-dependent microcycle conidiation, indicating that WetA functions to maintain conidia dormancy by suppressing microcycle conidiation in *F. graminearum*.

In *A. nidulans*, FlbB physically interacts with FlbD and FlbE, and the resulting FlbB/FlbE and FlbB/FlbD complexes induce the expression of *flbD* and *brlA*, respectively. *BrlA* is an activator of the AbaA-WetA pathway. AbaA and WetA are required for phialide formation and conidia maturation, respectively [5]. In *F. graminearum*, the AbaA-WetA pathway is similar to that of *A. nidulans*, except a *brlA* ortholog does not exist. Amongst the *fluffy* genes, only *fgflbD* has a conserved role for regulation of the AbaA-WetA pathway.

### References

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