

**REGULATION OF AFLATOXIN
PRODUCTION IN *ASPERGILLUS PARASITICUS***

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Abstract

Several species of the fungal genus *Aspergillus*, including *Aspergillus nidulans*, produce sterigmatocystin (ST) which also serves as the penultimate precursor in the aflatoxin (AF) biosynthetic pathway. Because AF and ST are among the most toxic, carcinogenic, and mutagenic compounds produced in nature, contamination of commercial food crops and feed additives (e.g. cotton seed) by these toxins results in significant health and economic losses. We have found that *flbA* and *fluG*, two genes required for asexual sporulation in *A. nidulans*, are also needed for ST biosynthesis (Hicks *et al.*, unpublished data). In addition, overexpression of *flbA* in submerged culture causes activation of both conidiation and ST production. We have shown that FlbA functions in negatively regulating FadA, the alpha subunit of a heterotrimeric G-protein that functions in stimulating a proliferative growth pathway (Yu *et al.*, 1996). Thus, a common link between sporulation and ST biosynthesis is a requirement for endogenous growth control. We have found that this requirement for growth control in secondary metabolism is conserved in the closely related *A. parasiticus* AF pathway and recently have identified and begun characterizing several putative *A. parasiticus flbA* homologues. Manipulation of this proliferative growth control of AF/ST may be useful in developing antifungals that target genes downstream of *fadA* that function in regulating *afIR*, the regulatory gene of the AF/ST biosynthetic pathway. Alternatively, proliferative growth regulation of ST/AF production may be used to develop defined atoxigenic strains that successfully compete with the more toxigenic strains in field situations.

References

J.-H. Yu, J. Wieser and T. H. Adams. 1996. *EMBO J.* **15**:5184-5190.