

## **NADH oxidase *nadA* and its involvement in oxidative stress in *Aspergillus flavus***

Carrie A. Smith

Advisors: Gary A. Payne and Niki Robertson

Department of Genetics

*nadA*, which encodes a predicted NADH oxidase, is adjacent to the aflatoxin (AF) biosynthetic gene cluster in several species of *Aspergillus*. Transcriptional analysis comparing a wild type strain of *A. parasiticus* and a deletion mutant for the pathway regulatory gene *aflR* showed a significant reduction in *nadA* gene expression in the mutant background. Although *nadA* is transcriptionally controlled by AfIR, AF biosynthesis was unaffected in *A. flavus*  $\Delta$ *nadA* strains under several cultural conditions. In contrast, over-expression of *nadA* strongly inhibited AF formation. Although the mechanism of this inhibition is unknown, it may involve a change in the redox status of the cells. Active oxygen species are known to promote AF biosynthesis, and NADH oxidases have been shown to be a source of reactive oxygen species. To examine a possible role of *nadA* in the oxidative status of *A. flavus*, the activity of several antioxidant enzymes were examined in  $\Delta$ *nadA* strains. Peak activity of super oxide dismutase, catalase, and glutathione peroxidase was delayed and lipoperoxide accumulation was altered in the  $\Delta$ *nadA* strains. These data suggest that *nadA* plays a role in the oxidative stress response in *A. flavus*. Investigations are underway to further characterize *nadA* and its role in establishing favorable conditions for producing AF.