

The Hunt for the “Silver Bullet”: Reference Genome Development and Comparative Genomics Analysis of Field Isolates of *Aspergillus flavus* for Identification of Aflatoxin Regulators

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Given the known link between aflatoxin contamination and drought stress observed in peanut and other crops and the serious health concerns of aflatoxin contamination, we continue the search for the so called ‘silver bullet’ in order to identify the underlying mechanisms regulating the production of aflatoxin by *Aspergillus flavus* and *A. parasiticus*. We have been using a variety of “omics” approaches in *A. flavus* and oxidative stress interactions including transcriptomics, proteomics, and metabolomics. These studies have revealed a number of mechanisms which may link aflatoxin production in responses to environmental oxidative stress under drought, but the causes of isolate-specific variation in these responses remain still unclear. Comparative genomics is a powerful tool to explore such differences, but is made difficult in the absence of a complete, pseudomolecule-level reference genome which is the case for *A. flavus*. Here, our goal is to develop reference genomes for a high (+++) and a moderate (+) aflatoxin producers of *A. flavus*, and to utilize these as reference genomes in a comparative analysis of field isolates to identify key regulatory mechanisms controlling aflatoxin production under drought stress. The isolates AF13 (+++) and NRRL3357 (+) were sequenced using PacBio technology to a depth of >50X coverage and used as a reference for comparing the genomes of 10 additional isolates, each sequenced to >80X coverage using Illumina technology. The detected polymorphisms between AF13 and NRRL3357 in conjunction with “omics” data obtained from the previous experiments will be used to identify gene families, genomic architecture, and pathways/markers associated with aflatoxin production and other traits relevant to fungal biology and pathogenicity including conidiation, conidial morphology, mating type, vegetative compatibility, and microbial competitiveness. These markers can then be utilized for genomic prediction of these traits in other field isolates to further verify marker-trait associations. These findings will allow for a better understanding of the genetic mechanisms regulating aflatoxin production, the targeted focusing of host resistance research efforts through molecular breeding and genetic engineering, and possibly the “silver bullet” for mitigation of aflatoxin production.