

## **New Reference Genomes and Comparative Genomics Analyses in *Aspergillus flavus***

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Understanding the biology of *Aspergillus flavus* and the causes of isolate-to-isolate variation in aflatoxin production and pathogenicity-related traits is critical to developing targeted efforts in improving host plant resistance. To facilitate this, we present two chromosome-arm reference genomes for *A. flavus* isolates NRRL3357 and AF13, each with eight chromosomes, lengths of 36.996 and 37.439 Mb, respectively, and updated gene annotations. These two isolates contrast phenotypically with AF13 showing greater levels of aflatoxin production, growth on peanut seed, and oxidative stress tolerance compared to NRRL3357. Comparative analyses between these genomes revealed a large 310kb insertion on Chromosome 1 unique to AF13 containing 60 genes including a novel bZIP transcription factor gene, *atfC*, which may be involved in oxidative stress tolerance and aflatoxin production. Comparisons with previously released or concurrently sequenced genomes of *A. flavus* isolates showed that this 310kb insertion is present completely or partially in few isolates. Using this information, isolate collections are currently in progress for a large-scale *Aspergillus* Re-Sequencing Project. To date, 264 genomes of *Aspergillus* isolates from field soils in Georgia and corn plants in Mississippi have been sequenced with additional isolate collection in progress, particularly from the origin of AF13 in Arizona. These data will be used for genome wide association studies (GWAS) for identifying novel aflatoxin regulators, and shedding light on the origin and evolution of the 310kb insertion. These new reference genomes and additional genomics information represent valuable tools for the aflatoxin and peanut research communities for continuing study in this system.