Management of aflatoxin contamination in groundnut by enhancing host-plant resistance

Liao B[1]*, Lei Y[1], Jiang H[1], Yan L[1], Wan L[1], Huang L[1], Zhou X[1], Luo H[1], Chen Y[1], Wang H[1], Pandey M[2], Sudini H[2], Upadhaya UD[2], Varshney RK[2]

[1]Oil Crops Research Institute of Chinese Academy of Agricultural Sciences (OCRI-CAAS), Wuhan, China
[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: lboshou@hotmail.com

Groundnut (*Arachis hypogaea*) currently ranks first among oilseed crops in China in terms of annual production, average crop and oil yield, and total crop value. Aflatoxin contamination has been a crucial concern for food safety and market competitiveness in groundnut products in most warm regions where heat and drought stresses are generally serious. Genetic enhancement for resistance to aflatoxin has been regarded as the most cost-effective approach to reduce contamination risk in this crop. Based on continuous evaluation of groundnut germplasms, including the core collections from China, ICRISAT and USA, several lines have been identified as resistant to *Aspergillus* infection or aflatoxin production. Recently, more research efforts have been made in identifying materials with shell resistance to *Aspergillus* infection, through cooperation with ICRISAT. Efforts have also been made in identifying and enhancing germplasm lines with diverse resistance components or mechanisms. Several ICRISAT breeding lines have been used in improving aflatoxin resistance of groundnut in Chinese institutions. An elite cultivar developed at OCRI-CAAS, Zhonghua 6, with desirable resistance to aflatoxin production, bacterial wilt and pot rot has been extensively used in central China. Through RNA-seq profiling, it was found that relative higher resveratrol content in Zhonghua 6 was a key mechanism for its reduced aflatoxin production under high infection pressure of *Aspergillus* sp.

Drought stress and aflatoxin contamination: transcriptional responses of *Aspergillus flavus* to oxidative stress are related to stress tolerance and aflatoxin production capability

Fountain JC[1,2], Bajaj P[3], Yang L[1], Pandey MK[3], Nayak SN[3], Kumar V[3], Jayale AS[3], Chitikineni A[3], Lee RD[4], Scully BT[5], Kemerait RC[1], Varshney RK[3,*], Guo B[2,*]

[1]Department of Plant Pathology, University of Georgia, Tifton, GA, USA
[2]USDA-ARS Crop Protection and Management Research Unit, Tifton, GA, USA
[3]International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana, India
[4]Department of Crop and Soil Sciences, University of Georgia, Tifton, GA, USA
[5]USDA-ARS, U.S. Horticultural Research Laboratory, Ft. Pierce, FL, USA
*E-mail: r.k.varshney@cgiar.org, baozhu.guo@ars.usda.gov

Oilseed crops such as maize and peanut are staple food crops which are vital for global food security. The contamination of these crops with carcinogenic aflatoxins during infection by *Aspergillus flavus* under drought stress conditions is a serious threat to the safety of these commodities. In order to better understand the role of aflatoxin production in the biology of this pathogen under environmental stress, a collaborative transcriptome project was undertaken to examine the transcriptional responses of toxigenic and atoxigenic isolates of *A. flavus* to oxidative stress. Selected isolates were cultured in aflatoxin production-conducive and non-conducive media amended with varying levels of H2O2. Isolates which possessed greater tolerance to H2O2 stress and aflatoxin production capability exhibited fewer differentially expressed genes (DEGs) than those which possessed less tolerance and lower aflatoxin production. Primary metabolic mechanisms were also stimulated in response to stress along with antioxidant enzyme-encoding genes. Genes related to fungal development such as aminobenzoate degradation genes and conidiation regulators were also differentially expressed in response to stress. Secondary metabolite biosynthetic processes also formed a large component of the isolate responses to stress including those for aflatoxin, aflatrem, and kojic acid. Co-expression analyses also showed that aflatoxin biosynthetic gene expression along with antioxidant genes were highly correlated with toxigenic isolate biomass under variable stresses. These results along with others in the literature suggest that the production of these secondary metabolites may provide supplemental oxidative stress alleviation. Additional data validation using proteomics, metabolomics and whole genome resequencing (WGRS) approaches will also be discussed.