Altered Transcript Abundances of Aspergillus Flavus and Transgenic Maize
Overexpressing a Bacterial Glutamate Dehydrogenase (GDH) Reduces Aflatoxin
Contamination of Grain

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Aspergillus flavus is a filamentous fungus that causes an ear and kernel rot in maize (Zea mays L.). Ear rots are often associated with the accumulation of aflatoxin in the infected plant. The ability of A. flavus to produce aflatoxin depends on the nature and the composition of the substrate. Transgenic maize lines expressing a bacterial NADPH dependent gcdA (glutamate dehydrogenase) gene showed increased nitrogen metabolism with an overall increase in some amino acids in the ear. Previous studies showed that A. flavus exhibits decreased conidiation and aflatoxin accumulation on GDH+ maize lines. The aim here was to use microarray studies to assess changes in the expression patterns of A. flavus genes on GDH+ maize. Used was artificial inoculation in the field of dough stage maize kernels of inbred ‘P99’ transgenic or non-transgenic with gcdA. The mRNA was isolated after harvest. Increased by more than 2 fold on GDH+ maize were 747 A. flavus transcripts, only 27 decreased. Hydrolyses (EC 3.), kinases (EC 7.) and ABC transporters (non-enzyme) were the major protein families increased. No effect on toxion pathway genes was detected. No maize transcripts were increased by GDH+, though 95 were reduced significantly by two fold. Reduced by GDH transcripts encoding trehalase, branched chain amino acids, primary carbon metabolism and polyphenol synthesis. Metabolites increased by the reduced transcripts in GDH+ maize included cellulose to lignin ratios; non-branched side chain amino acids; and some toxic products of special nitrogen metabolism. Therefore, the gcdA gene was inferred to confer partial resistance to A. flavus by repressing pathways in a way that lead to altered compositions, stronger cell walls and increased defense metabolite concentrations, pathways different from endogenous resistance mechanisms discovered to date. See patents 5,998,700; 6,329,573; and pending.

Reactions in Glutamate Homeostasis

Summary: Plant metabolism was altered in ways that improve NUE, WUE, nutritional value, disease resistance, biofuel characteristics and alternate uses of plants by products. Understanding the molecular basis will help unravel the control of N metabolism and N signaling.