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The sdh1 mutant alters kernel sugar composition and transcript profiles in addition to its small-kernel phenotype.

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Sorbitol dehydrogenase (SDH) in maize kernels could mediate a centrally-positioned, second-step in metabolism of imported sucrose; that fructose use (fructose + NADH <-> sorbitol + NAD). This is significant because fructose is produced regardless of how sucrose is cleaved (via invertase or sucrose synthase), and sorbitol dehydrogenase provides a potentially advantageous alternative to other paths of fructose use and sensing. To help test hypotheses for the significance of SDH in maize, we identified an sdh1 mutant, as noted earlier, by screening the UniformMu maize population. The sdh1 mutation reduced maximal SDH activity in developing kernels to less than 6% of wild- type levels. The resulting phenotype was a 21% smaller kernel under field conditions (dried-seed weight at maturity, significant to $p<.001$). In the present work, a 3'-UTR profiling strategy was used to generate gene-specific, sequence-based expression profiles for tissues of wild-type and sdh1 kernels. These tissues included pedicel + transfer region, embryo, embryo proximal region, peripheral endosperm, and pericarp. The 454-transcript profiles identified altered expression of genes for specific metabolic pathways between regions within kernels, and between these zones in wild-type and sdh1 mutants. A decrease was observed in the expression of the genes involved in the putative sorbitol pathway. Metabolic analyses also showed that the sdh1 mutation increased sugar levels during development; especially at 25 DAP (near harvest date for many sweet corns). At this stage, hexose levels were more than doubled and sucrose levels were elevated by 16%. The sdh1 mutation may thus have potential value for sweet corn improvement. The 2-fold hexose increases also indicated a central role for sorbitol metabolism in the sugar balance of developing maize kernels. These changes were accompanied by 33% reduction in sorbitol levels, but other paths of sorbitol biosynthesis appear likely in kernels, given the presence of significant residual sorbitol in the sdh1 mutant. In addition, sdh1 decreased mannose levels in the kernel, and levels of arabinose and xylose in the pericarp. The starch content was decreased in the kernel, but no difference was observed in the protein content. These results demonstrate multiple effects of sdh1 mutation in the maize kernel and importance of the sorbitol pathaway in metabolic and physical flux of carbon in developing maize kernels.

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Transcriptional profiling of *Aspergillus flavus* infected maize kernels.

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Maize kernels are susceptible to infection by the opportunistic pathogen *Aspergillus flavus*. Infection results in a reduction of grain quality and contamination of kernels with the highly carcinogenic mycotoxin, aflatoxin. To gain a better understanding of the host response to infection by the fungus, transcription of approximately 9,000 maize genes were monitored during the host-pathogen interaction. RNA was extracted 4 days after infection of kernels at the developmental stages of blister, milk, dough, and dent, and hybridized to custom made Affymetrix GeneChip DNA microarrays. Analysis of these microarrays revealed a complex transcriptional response by maize to infection. Responses included the up regulation of over 1,000 maize genes with a fold change of two or greater. Included in this response was increased expression of genes coding for proteins characteristic of plant defense such as, but not limited to, Pathogenesis-related (PR) proteins, a xylenase inhibitor, and ethylene biosynthetic enzymes. In addition, other transcripts of interest found differentially expressed in the interaction were those associated with the basal endosperm transfer layer, BETL-4 and the cell wall invertase *miniature seed 1*. Additional experiments are being performed using a beta-glucuronidase- expressing *A. flavus* strain, as well as, histological stains to visualize fungal colonization within the kernel. Combined, these data give insight into maize defense mechanisms used against the opportunistic pathogen *A. flavus* and may lead to the development of control strategies for this disease.