Lignin Gene Expression and Biomass Quality Analyses of a Bioenergy Sorghum Panel

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Industrial production of lignocellulosic biofuels is challenged by the interfering effect of cell wall lignin in the biomass conversion process. Sorghum has the potential to become an important biomass crop for bioenergy production due to its high yield and tolerance to abiotic stresses. To identify sorghum accessions showing lower lignin levels and high biomass, a genetically diverse sorghum panel comprising 100 accessions was screened for lignin content and biomass yield traits. Lignin content varied from 2 to 11.8% on the basis of total dry matter and averaged 5.7%. Substantial phenotypic variation was observed among the accessions for all evaluated traits showing potential for genetic studies. To better understand lignin synthesis in sorghum, we have identified sorghum homologs of twenty key genes potentially involved in the lignin biosynthesis pathway, and used Real-Time PCR to study their expression. Initially, sixty accessions selected from the panel based on lignin levels were grown under controlled conditions and the stems were collected for gene expression analysis. Differential expression among accessions was observed for most genes and some appear to be co-regulated. However, when regression analysis was performed to identify correlation between lignin content and gene expression levels only one gene from the HCT family showed a positive and significant correlation (r 0.76, R^2 0.58, $p<0.01$). We are now in the process of identifying SNPs in the HCT gene from all genotypes of the panel in order to develop and validate SNP-specific markers to accelerate the efforts of biomass sorghum breeding programs.

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