

Correlation of Lignin gene expression and biomass quality for biofuel production in Sorghum

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Palavra chave: Keywords: *Sorghum bicolor*; lignin, hidroxycinnamoyl transferase, real time PCR, bioenergy

Plant biomass composition is one of the most important factors regarding bioenergy production. Lignin is a major component of plant cell walls and it can interfere with the process of biomass conversion to cellulosic ethanol. Nevertheless, lignin increases the calorific value of biomass, which is desirable for electricity cogeneration. Sorghum genotypes have a wide variation regarding lignin content and they can provide a quality feedstock for both end purposes. The aim of this work was to evaluate the expression of genes involved in lignin biosynthesis to identify potential gene targets for sorghum breeding. A diversity panel of 100 sorghum genotypes was evaluated for lignin content to identify genotypes showing high biomass production and varying levels of lignin. Acid Detergent Lignin (ADL) 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 showing potential for genetic studies. Sixty genotypes from the analyzed panel, thirty with higher and thirty with lower lignin content were selected for gene expression analysis related to lignin biosynthesis. Lignin gene expression was evaluated by RT-qPCR using SybrGreen in a set of sixteen sorghum genes homologous to previously identified lignin genes in Arabidopsis. Initially, these sixteen genes were analyzed in eight contrasting genotypes, and to identify significant relationships, correlation analysis was applied to the expression and the lignin content data. Only the *HCT1* gene, which codes for a hydroxycinnamoyl transferase, showed a significant correlation ($p < 0.01$; $r = 0.87$) to lignin content. Subsequently, *HCT1* expression analysis was investigated in the 60 previously selected contrasting genotypes. The results determined that *HCT1* showed significant linear relationship ($p < 0.01$, $r^2 = 0.58$) with the lignin content. The enzyme hydroxycinnamoyl transferase (*HCT*) acts at the beginning of lignin and other phenylpropanoid pathways, as reported in previous studies. The present work determines a relationship between *HCT1* gene expression in young plants when lignin genes are highly expressed and high lignin levels at harvest time and therefore gene may be used for future studies on lignin biosynthesis in sorghum, in addition to become a target for marker assisted selection.

Fonte de Financiamento: Financial Support: FAPEMIG and EMBRAPA