

**Uncovering genetic mechanisms for biological conversion efficiency in
*Brachypodium distachyon***

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Two major potential areas of improvement for plant-derived biofuels are increased biomass accumulation and enhanced conversion efficiency. Large grasses such as miscanthus, sorghum, and switchgrass possess many traits which make them desirable as potential energy crops but additional improvements must be made in order to compete with fossil fuels. In order to better understand important genetic contributors to biomass recalcitrance we characterized a recombinant inbred line population of the model grass species *Brachypodium distachyon* using a *Clostridium phytofermentans* based biological conversion assay to measure plant feedstock conversion to ethanol. Additionally, we measured several quantitative trait loci (QTL) for biomass yield traits including: three QTLs for plant height, one for dry stem weight, and one for number of tillers. One QTL for conversion efficiency was mapped to chromosome two and resulted in a significant 8% increase in ethanol yield. The associated interval is 1027 kb with 139 protein coding genes. Of those genes, 36 contain polymorphisms between the two mapping parents Bd21 and Bd3-1. We refined candidate genes to those having polymorphisms that result in non-synonymous amino acid changes or occur in their promoter sequence and could affect expression. Candidate genes were prioritized based on tissue-specific expression with the best candidates highly abundant in stem; the major source of aboveground biomass in grasses. This approach has allowed us to identify a putative glucosyltransferase (CAZy family GT61) as our top candidate. We have developed and are in the process of characterizing three heterozygous inbred families to further refine the *BIOFUEL1* interval through next-generation sequencing and conversion efficiency testing. Determining the genetic basis for improved conversion efficiency in *B. distachyon* should enable translatable improvements in feedstock quality for energy crops.