

197. Pyramiding genes and alleles for improving energy cane biomass yield

Ray Ming¹, Chifumi Nagai², Qingyi Yu^{3*} (qyu@ag.tamu.edu)

¹University of Illinois at Urbana-Champaign, Urbana, Illinois; ²Hawaii Agriculture Research Center, Kunia, Hawaii; and ³Texas A&M AgriLife Research, Dallas, Texas

<http://www.life.illinois.edu/ming/LabWebPage/Home.html>

Project Goals: Our long term goal is to establish a new paradigm to accelerate energy cane breeding programs and maximize the biomass yield for biofuel production. Our specific objectives are: (1) Phenotyping extreme segregants of the F₂ population for exploring the molecular basis of high biomass yield from transgressive segregation; (2) Mapping genes affecting biomass yield by transcriptome sequencing of the extreme segregants; (3) Identifying differentially expressed genes and alleles through analyses of transcriptomes of extreme segregants from the F₂ population; (4) Developing gene- and allele-specific markers for implementation of marker-assisted selection in energy cane breeding programs. As a C₄ plant, sugarcane/energy cane has been recognized as one of the world's most efficient crops in converting solar energy into chemical energy. Traditional energy cane and sugarcane breeding via interspecific hybridization and backcrossing to *S. officinarum* improved stress tolerance and recovered high sugar and biomass yield. However, this approach reduced the genetic diversity of sugarcane and energy cane breeding materials and limited the potential maximizing biomass yield. We are developing a new paradigm to accelerate energy cane breeding programs and maximize the biomass yield for biofuel production.

An F₂ population with 2616 individuals was created from an interspecific cross between *S. officinarum* LA Purple (2n = 80, x = 10) x *S. robustum* MOL5829 (2n = 80, x = 10). This population showed transgressive segregation with high yielding clones substantially exceeding the biomass yield of both parents. Field trial of the extreme segregants was carried out for three years in Hawaii. Biomass yield of the top 10 F₂ clones ranged from 71.5 to 122.1 MT/ha in 12 months, and the best performing clone showed 338% yield increase compared to its high yield parent LA Purple. The bottom 10 F₂ clones had estimated biomass yield ranging from 3.4 to 8.2 MT/ha in 12 months, and the worst performing clone showed yield decrease to only about 10% of LA Purple yield. It should be noted that sugarcane biomass yield in Hawaii is 30 MT/ha per year, and the potential biomass yield of sugarcane/energy cane is 140 MT/ha per year.

Transcriptome sequencing of the 3rd, 9th, and 15th internodes and the 1st dew lap leaf from the 14 top and 8 low biomass segregants of the F₂ population was carried out in order to map genes or alleles affecting biomass yield in energy cane. Differential gene expression analysis was conducted between the high and low biomass groups. A total of 2,475 genes were up-regulated and 799 genes were down-regulated in high biomass group. GO terms analysis indicated that the differentially expressed genes between the high and low biomass groups were enriched in the cell wall modification, catabolic process, and carbohydrate catabolic process. The genes that encode cell wall and pectin modifying enzymes were up-regulated in the high biomass group.

Twenty percent of the genes in the breakdown pathway of homogalacturonan, one of the major pectin polysaccharides, were up-regulated in the high biomass group. In contrast, no significant difference of the genes involved in pectin polysaccharides biosynthesis was detected between the high and low biomass groups. For the genes in the pathway producing the lignin precursors, genes involved in caffeoyl-CoA synthesis were highly up-regulated, and genes in converting caffeoyl-CoA into downstream products were down-regulated in the high biomass group. Among the 13 genes involved in UDP-D-glucose

synthesis pathway, 4 of them were up-regulated in the high biomass group.

In summary, genes regulating the biosynthesis and breakdown of the cell wall components play essential roles in achieving high biomass yield in energy cane. Increased cell expansion and cell division in high biomass yield energy cane was caused by fast turnover of cell wall components. High biomass yield in energy cane was achieved through promoting primary cell wall production without over-lignification of secondary cell wall.

This research was supported by the DOE Office of Science, Office of Biological and Environmental Research (BER), grant no. DE-SC0010686.