

Plant Gene Expression Center
Albany, CA
<http://www.pgec.usda.gov/>

The **Plant Gene Expression Center** contributes to the production of biofuel research through its identification of gene function in plants using molecular biology and genetic tools and its development of recombination tools.

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Feedstock Biomass production. In order to grow large amounts of biomass, plants need to be tolerant of crowding, produce many tillers (in the case of grasses), grow quickly, delay flowering and have large meristems. Research at the PGEC directly impacts these aspects of biomass by gene identification. We have identified the components of the phytochrome pathway that regulate shade avoidance and thus allow plants to successfully compete in crowded growth conditions. We have identified genes that regulate meristem size and thus directly impact the size of stems and number of organs. We have identified genes that regulate number of tillers and regulate flowering time. Homologs of these genes can be identified and their expression can be manipulated in biofuel crops.

Reproduction. In order to create optimal biofuel crops, scientists will need to take advantage of natural diversity as well as transgenes. Perennial grasses identified as potential biofuel crops have reproductive biology features that make them difficult to work with. The Miscanthus intended for biofuel production (Miscanthus X gigantea) is a sterile triploid, derived from a cross of the diploid *M. sinensis* and a tetraploid. Switchgrass (*Panicum virgatum*) and *M. sinensis* are self-incompatible (SI). In addition, grass pollen is short-lived and seed set from manual crosses can be poor or fail altogether. There are additional post-pollination breeding barriers in crosses between tetraploid and octoploid switchgrass, which may relate to endosperm balance number. Understanding the basis of SI and how to manipulate it is necessary to develop biofuel crops. Self incompatibility (SI) has been described in many plant species, and has been studied at the molecular level in the *Solanaceae*, the *Brassicaceae*, and the *Papaveraceae*. In these families there is a multi-allelic single locus, termed the S-locus. Self-incompatibility in grasses is seemingly more complicated, as it is controlled by 2 unlinked genes, S and Z. The SI genes will need to be mapped in biofuel crops so that the alleles can stay variable and not cause problems when selecting for agronomic traits that might be linked to these loci. Furthermore, Self-incompatibility can potentially be used for hybrid breeding schemes, if methods can be devised to establish inbred lines and to temporarily convert self-incompatible lines to self-compatible lines.

Cell walls. Cell walls contain the carbon for future biofuels. Understanding how cell walls are assembled and how they can be degraded is an important goal. We have identified a small family of transcription factors that regulate cellulose synthesis and lignin biosynthesis. Manipulation of these transcription factors in biofuel crops might allow favorable modifications of cell wall composition. We are also using these transcription factors to directly identify the genes involved in cell wall synthesis.