

A genome-wide survey of switchgrass genome structure and organization

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Project Goals:

To Elucidate switchgrass Genome Structure and function of Cell Wall-related Enzymes.

The perennial grass, switchgrass (*Panicum virgatum* L.), is a promising bioenergy crop and the target of whole genome sequencing. We constructed two bacterial artificial chromosome (BAC) libraries from the AP13 clone of switchgrass to gain insight into the genome structure and organization, initiate functional and comparative genomic studies, and assist with genome assembly. Together representing 16 haploid genome equivalents of switchgrass, each library comprises 101,376 clones with an average insert size of 144 (Hind III-generated) and 110 kb (BstY I-generated). A total of 330,297 high quality BAC-end sequences (BES) were generated, accounting for 263.2 Mbp (16.4%) of the switchgrass genome. Analysis of the BES identified 279,099 known repetitive elements, >50,000 SSRs and 2,528 novel repeat elements, named switchgrass repetitive elements (SREs). Comparative mapping of 47 full-length BAC sequences and 330K BES revealed high levels of synteny with the grass genomes sorghum, rice, maize and *Brachypodium*. Our data indicate that the overall sequence composition of the switchgrass genome is most similar to that of rice and that the sorghum genome has retained larger microsyntenous regions with switchgrass. The resources generated in this effort will be useful for a broad range of applications.

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