

**Developing association mapping in polyploid perennial grasses: I. Switchgrass (*Panicum virgatum*)**

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Switchgrass and Reed canarygrass are perennial forage crops that are being targeted for biofuels. We developed linkage and association mapping populations to learn more about the underlying genomic and phenotypic variation in both of these species. Populations were planted in New York and Wisconsin, where wide variation in numerous traits was observed. Genotyping by sequencing (GBS) was used to identify thousands of single nucleotide polymorphism (SNP) markers in both species, providing unprecedented insight into their genomes. Unlike traditional genotyping methods, GBS is a high-throughput, low-cost way to explore the genetic diversity in populations. Our lab developed a SNP discovery analysis pipeline (UNEAK) for species which lack a reference genome and have complex genomes, and applied it to both switchgrass and reed canarygrass. Statistical models that use these SNPs for quick and accurate identification of genomic regions of interest, as well as favorable lines for use in breeding programs, were explored. The challenges that arose during the development of these models are presented. Implementation of these models in genomic selection and genome-wide association studies has the potential to reduce standard breeding cycles of these perennial grass species from five or more years to one to two years.

This poster focuses on the results of our research on the warm-season grass, switchgrass, and will provide a direct comparison with the results presented in our other poster, which focuses on the cool-season grass, reed canarygrass.