

Genomics-Assisted Improvement of Biomass Production among *Andropogoneae* Fuelstock Grasses

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Among the wide variety of plant species proposed as potential biofuel feedstocks, four closely related grass species within the *Andropogoneae* tribe (Figure 1) emerge as leading candidates because of their superior efficiencies in photosynthesis, nitrogen economy, and water use. Maize (*Zea mays* L.), sugarcane (*Saccharum* spp.), and *Sorghum* are established and highly productive biomass crops that collectively are cultivated across the global spectrum of agricultural production environments. *Miscanthus* also shows promise as a leading feedstock crop, based on its exceptional biomass yields with minimal production inputs in recent European and U.S. field trials. Each of these grasses also offers complementary advantages in their forms of harvestable carbon, growth cycle and adaptation to diverse climates. A comparative genomics approach to understanding genes that condition phenotypic differences among the closely related *Andropogoneae* genomes is likely to reveal strategies for improving biomass yield and quality in these species. This presentation will present plans and progress to improving biomass production towards this goal, with an emphasis on genetic control of stover biomass in maize and the development of functional genomics resources for *Miscanthus*.