Genomics-Assisted Improvement of Abiotic Stress Tolerance and Yield in the Biomass Feedstock Crops *Miscanthus* and *Saccharum*

Nicholas LaBonte,[1] Liang Xiao,[1,2] Lindsay V. Clark,[1] Brian Baldwin,[3] Jesse Morrison,[3] Kankshita Swaminathan,[4] and **Erik J. Sacks**[1]* (esacks@illinois.edu)

[1]University of Illinois at Urbana-Champaign; [2]Hunan Agricultural University, Changsha, China; [3]Mississippi State University; [4]HudsonAlpha Institute for Biotechnology

https://cabbi.bio/research/feedstocks-theme/

Project Goals:
- **Develop climate-resilient *Miscanthus* and energycane biomass feedstocks by targeting abiotic stress tolerance traits:**
  - ***Miscanthus* adapted to periodic flooding**
  - ***Miscanthus* that can be cultivated on saline marginal lands**
  - **Improve winter-hardiness and biomass yield of *Miscanthus* for the Midwest**
  - **Improve biomass yield and adaptation of *Miscanthus* for the Mid-South**
  - **Introgress cold-tolerance genes from *Miscanthus* into *Saccharum* to expand the potential area of energycane production in the U.S.**
- **Use genomics to improve breeding efficiency and increase rates of genetic gain:**
  - **Identifying associations between genetic polymorphisms and key traits in *Miscanthus* for use in marker-assisted selection**
  - **Development and implementation of genomic selection in *Miscanthus* to shorten breeding cycles**

Abstract:

Cultivars of bioenergy crops that are tolerant of abiotic stress must be developed in order to utilize marginal lands that do not compete with food production. To address this need, our lab is developing *Miscanthus* and *Saccharum* for high biomass production and improved adaptation to marginal lands. We are building and using genomics tools to greatly improve breeding efficiency of these long-lived perennials. In particular, genomic selection will enable us to identify and cross *Miscanthus* selections within ~1.5 years, whereas under traditional phenotypic selection, a breeding cycle for this crop is ~4 years.

In the Midwest, large areas of croplands are subject to seasonal flooding and experience yield-losses due to standing water. These flood-prone lands are broadly-dispersed in the Midwest, on low edges or depressions ('potholes') within otherwise productive fields. Flood-tolerant *Miscanthus* is an opportunity for farmers to gain income from the currently unprofitable portions of their fields that flood in most years. In an interconnected F1 population (n = 809) of three high-yielding *M. sinensis* crossed to a single high-yielding *M. sacchariflorus* ssp. *lutarioriparius*, we have identified genotypes that grow well after being completely submerged, and quantitative trait loci (QTL) for flooding tolerance will be mapped. A high-density SNP dataset for this population is being generated in cooperation with JGI. *M. sacchariflorus* ssp.

lutarioriparius is indigenous to seasonally flooded edges of lakes and rivers in the Yangtze River watershed, so we expected it to be a good source of submergence-tolerance. We have also conducted preliminary experiments on salinity tolerance in this population and discovered that some of the parents and progeny can survive and grow for more than one month when given highly saline irrigation water (300 mM; i.e. about half the salinity of seawater). QTL mapping for salinity tolerance will be conducted in 2019. Additionally, replicated field trials of this population were established in Illinois and Mississippi during 2018, to assess yield.

Though *M. ×giganteus* 'Illinois' has high yield-potential (~25 T/ha) and the environmental benefits of a long-lived perennial, it is the only genotype of *Miscanthus* for biomass production currently available in the U.S. for farmers to grow, and it is insufficiently winter-hardy to establish reliably every year in the northern Midwest. In addition to winter-hardiness, new *Miscanthus* cultivars must be high-yielding; however, phenotypic evaluation for yield is slow, requiring field evaluations over three years. To address these problems, we have begun to implement genomic selection for yield, and overwintering ability within *M. sinensis* and *M. sacchariflorus* (the parental species of *M. ×giganteus*), and assess the effect of this selection on their 3x *M. ×giganteus* progeny from controlled crosses. To ensure reliable testing of overwintering ability each year, we have begun field-testing at the University of Wisconsin's Spooner Agricultural Research Station (USDA hardiness zone 3b), with cooperation from The Great Lakes Bioenergy Center. In previous DOE-funded studies, we identified seven genetic groups of *M. sinensis* and six genetic groups of *M. sacchariflorus*, and developed initial genomic selection models for each species. In 2018, we initiated seed increases for each genetic group. In 2019, we will grow populations of three genetic groups to test and improve the initial genomic selection models, and conduct population improvement for yield and overwintering ability.

Sugarcane (*Saccharum*) is currently the world's most important bioenergy crop. Sugarcane production in the U.S. is currently limited to a small area of southern Florida, Texas, and Louisiana because this tropical crop is susceptible to damage by cold. However, we expect that cane cultivation for bioenergy feedstocks (energycane) could be expanded substantially northward in the southern U.S. (into hardiness zone 8) by introgressing cold tolerance from temperate *Miscanthus* into the tropical canes. During the current autumn-winter crossing season, we have made >20 crosses between canes and highly cold-tolerant *Miscanthus*, in our greenhouse in Illinois; many of these crosses used *Miscanthus* parents from eastern Russia (hardiness zones 3 and 4). If successful, offspring of these crosses will be backcrossed to sugarcane and used to develop cold-tolerant energycane cultivars with the potential to dramatically expand the landscape of bioenergy feedstocks in the U.S.