Introgression of Novel Disease Resistance Genes from *Miscanthus* into Energycane

Alexander E. Lipka[1], Marcus O. Olatoye[1], Nicholas R. LaBonte,[1] Jack C. Comstock[2], Sushma Sood[3], Vanessa S. Gordon[3], Per McCord[3], Keiji Motomura[4], Ken-Taro Sekine[4], Toshihiko Yamada[5], and **Erik J. Sacks**[1*] (esacks@illinois.edu)

[1]University of Illinois, Urbana, IL; [2]Department of Plant Pathology, University of Florida, Gainsville, FL ; [3]USDA-ARS Sugarcane Field Station, Canal Point, FL; [4]University of the Ryukyus, Okinawa, Japan; [5]Hokkaido University, Sapporo, Japan

Project Goals: Our long-term goal is to improve energycane productivity and sustainability by providing resistance to key diseases with novel genes from *Miscanthus*.

1) **In miscane BC_1 populations (sugarcane x (sugarcane x *Miscanthus*)), identify molecular markers associated with novel genes from *Miscanthus* that confer resistance to at least two out of four of the following economically important diseases of sugarcane: ratoon stunt, yellow leaf, orange rust, and smut.**
2) **Compare effectiveness of different molecular marker analysis methods for selecting disease resistance alleles in miscane backcross populations. In particular, compare the pseudo-testcross QTL mapping strategy with genomic selection.**
3) **Screen germplasm collections of *M. sinensis* and *M. sacchariflorus* for resistance to ratoon stunt, yellow leaf, orange rust, and smut to confirm that *Miscanthus* is uniformly immune to these diseases as prior data suggest or to quantify genetic variation for resistance if not all accessions are resistant.**

Sugarcane is among the world's leading bioenergy crops. Modern sugarcane cultivars are derived from a relatively small set of founder genotypes, which has contributed to cultivar susceptibility to diseases. Modern sugarcane cultivars originated in the late 1800's when cultivars of *Saccharum officinarum* with high sugar yield potential but disease-susceptibility were crossed with the undomesticated, non-sugar producing but disease-resistant *S. spontaneum*, then backcrossed to *S. officinarum* to recover sugar yield. Recent efforts to improve sugarcane for disease resistance, pest resistance, and abiotic stress tolerance have continued to rely primarily on introgressions from *S. spontaneum*. Similarly, energycanes (sugarcanes bred specifically for energy) are also bred from modern sugarcane cultivars and *S. spontaneum*.

Yet, diseases are the primary constraints to cane productivity in commercial fields. Sugarcane is a perennial crop but a planting's commercial productivity in the U.S. is typically limited to 3-5 years because disease pressure reduces yield and decreases stand via plant death each year. Moreover, the utility of a successful cane cultivar for commercial production is typically ended by the emergence of a virulent strain of a common pathogen, resulting in reduced yields. Though many diseases affect sugarcane, the following four are of especially great concern (Rice, 2007): 1) ratoon stunt (bacterium *Leifsonia xyli* subsp. *xyli*.); 2) sugarcane yellow leaf (virus, Sugar Cane Yellow Leaf Virus (SCYLV); 3) orange rust (fungus *Puccinia kuehnii*); and, 4) smut (fungus *Sporisorium scitamineum*). Arguably, *Miscanthus* would be a better source of genes for improving sugarcane than *S. spontaneum* because the former is highly resistant to diseases and pests, is more broadly adapted to diverse environments, and is more genetically distant from *S. officinarum* (thus providing more novel alleles). Previously, we have obtained more than a dozen F_1 hybrids between sugarcane and *Miscanthus*.

We conducted disease screenings on miscane F_1 progeny, and core collections of *M. sinensis* and *M. sacchariflorus*. For the most part, our hypotheses of ubiquitous resistance in *Miscanthus* were confirmed. For smut, all of the 66 *Miscanthus* genotypes tested were fully resistant, and for orange rust all but one of the *Miscanthus* genotypes tested were fully resistant. For ratoon stunt disease, only two *Miscanthus* genotypes were susceptible and these were much less susceptible that the sugarcane positive control. Response of *Miscanthus* to SCYLV was more variable than for the other diseases tested, with 14/31 *M. sacchariflorus* and 24/35 *M. sinensis* fully resistant, but the remainder were partially to fully susceptible. Of six miscane genotypes tested, one was fully resistant to all four diseases, six were fully resistant to orange rust and smut, four were resistant to ratoon stunt, and three were resistant to SCYLV.

Backcross progeny (BC_1F_1) were obtained for two populations (n = 210 and n = 30) and planted in the field at Canal Point, FL in spring of 2018. In 2019, the BC_1F_1 progeny will be phenotyped for disease-resistance and genotyped. Both QTL selection and genomic selection will be conducted on the BC_1F_1 and the relative effectiveness of these methods compared by evaluating BC_2F_1 progeny of the selected BC_1F_1s crossed to a susceptible cane. To increase the size of the smaller population, we have made additional crosses in the greenhouse to obtain more BC_1F_1 seed, and we are also self-pollinating the BC_1F_1s in the field.

To predict the relative efficiencies of QTL selection and genomic selection under different genetic architectures, we conducted simulation studies in F_1 and subsequent BC_1 populations, using marker data and linkage maps from previous studies of *Miscanthus* and sugarcane. For traits with four or fewer QTLs, we observed that the performance of QTL selection was comparable and sometimes superior to genomic selection. In contrast, as the number of simulated QTL increased, all four GS models that were evaluated outperformed QTL selection. Thus, we expect genomic selection to be preferable to QTL selection for introgressing genetic sources of horizontal disease resistance from *Miscanthus* to energycane, whereas QTL selection remains a suitable option for introgressing vertical disease resistance.

Because disease susceptibility is a major limitation for cane production, cultivar durability, and sustainability, the introgression of resistance genes from *Miscanthus* is expected to increase the economic and environmental benefits of energycane while reducing costs and risks. Such benefits should promote further investment by industry in energycane.

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