Title: Genomics of Winter-hardiness and Yield in Diverse Miscanthus Germplasm

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Project Goals: Develop genomic selection models to improve the efficiency of breeding Miscanthus for adaptation to temperate environments and for biomass yield.

Abstract Text: The current major Miscanthus cultivar, M. ×giganteus 'Illinois', is not sufficiently winter-hardy in the Midwest U.S., which limits its productivity. Because M. ×giganteus is an interspecific hybrid, selecting winter-hardy accessions of its parental species, M. sinensis and M. sacchariflorus, will be essential for breeding new M. ×giganteus cultivars with greater hardiness. Miscanthus is most susceptible to winterkill and damage during the first winter after planting. In this study, M. sinensis and M. sacchariflorus accessions from diverse genetic and geographic backgrounds were evaluated for first-overwintering ability and yield performance. In an initial experiment, 330 half-sib families representing three M. sinensis genetic groups (North, Central, and South Japan; 55, 117, 158 half-sib families respectively) were evaluated in Urbana, IL for first winter overwintering ability in spring 2020 (planted in spring 2019), and yield data were collected in autumn 2020 and are currently being collected for the 2021 season. First-winter overwintering ability was relatively high for the M. sinensis North and Central Japan genetic groups (81% and 82%, respectively) but low for the South Japan group (49%). Substantial variation among families within genetic groups was observed for overwintering ability and yield, which along with sequence data from JGI will facilitate development of genomic selection models for this important trait. In a subsequent experiment planted in spring 2020 at Urbana, IL, we assessed first-winter overwintering ability for diversity panels consisting of 294 M. sacchariflorus accessions and 236 M. sinensis accessions, representing the geographic ranges and all known genetic groups of these species (Clark et al., 2014; Clark et al., 2019). First-year overwintering ability of both species varied among genetic groups, which will allow us to more efficiently target our Miscanthus breeding efforts to different geographic regions in the U.S.

References

1. Clark LV, Brummer JE, Głowacka K, Hall MC, Heo K, Peng J, Yamada T, Yoo JH, Yu CY, Zhao H, Long SP, Sacks EJ. A footprint of past climate change on the diversity and population structure of Miscanthus sinensis. Ann Bot. 2014 Jul;114(1):97-107. doi: 10.1093/aob/mcu084. Epub 2014 Jun 10. PMID: 24918203; PMCID: PMC4071102.

2. Clark LV, Jin X, Petersen KK, Anzoua KG, Bagmet L, Chebukin P, Deuter M, Dzyubenko E, Dzyubenko N, Heo K, Johnson DA, Jørgensen U, Kjeldsen JB, Nagano H, Peng J, Sabitov A, Yamada T, Yoo JH, Yu CY, Long SP, Sacks EJ, Population structure of Miscanthus sacchariflorus reveals two major polyploidization events, tetraploid-mediated unidirectional introgression from diploid M. sinensis, and diversity centred around the Yellow Sea, Annals of Botany, Volume 124, Issue 4, 13 September 2019, Pages 731–748, https://doi.org/10.1093/aob/mcy161

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