Exploiting Natural Diversity to Identify Alleles and Mechanisms of Cold Adaptation in Switchgrass

Hari Poudel[1], Joseph Dabringer[1], Andrew Hummel[1], Lois Bernhardson[2], Millicent Sanciangco[3], Nathan A. Palmer[2], Gautam Sarath[2,] Michael Casler[1,] C. Robin Buell[3*] (buell@msu.edu)

[1]USDA-ARS U.S. Dairy Forage Research Center, Madison, WI; [2]USDA-ARS Wheat, Sorghum and Forage Research Unit, Lincoln, NE & [3]Michigan State University, East Lansing MI

Project Goals

One of the proposed mechanisms to increase switchgrass biomass is to grow lowland cultivars in more northern latitudes where they have higher yield potential, due in part, to their significantly later flowering time at these latitudes. However, lowland genotypes are not adapted to the colder winter conditions in northern climes and exhibit low survival rates when grown at latitudes outside their adapted range. Many unadapted populations possess a small frequency of individuals that can survive the winter, indicating that, within the collective genetic diversity of the population, alleles are present that confer cold tolerance. If these alleles could be catalogued and converted into molecular markers, they would facilitate accelerated breeding and provide a mechanism to improve the efficiency of breeding switchgrass cultivars with high biomass and cold hardiness. Our hypothesis is that alleles favorable to cold hardiness will be enriched in individuals that survive over-wintering conditions outside their native hardiness zone and that these alleles will be under-represented in individuals within the population that fail to survive over-wintering. Thirty-eight populations of lowland switchgrass have been planted at three locations that provide a span of temperature regimes to assess cold tolerance: DeKalb IL; Madison WI; Arlington WI. Genome-wide association analyses of survivors vs. non-survivors from Winter 2015-16 are in progress. In 2017, we will use allele frequencies determined through bulk segregant exome capture sequencing of Winter 2016-17 survivor and non-survivor pools to identify genes, transcripts, and miRNAs important to cold hardiness in these 38 lowland switchgrass populations. Data from this project will be central to furthering our understanding of cold tolerance in switchgrass and to identify alleles that that can be used in breeding programs to increase switchgrass biomass.