

**Name:** Carl-Erik Tornqvist

**Email Address:** [citornqvist@wisc.edu](mailto:citornqvist@wisc.edu)

**Affiliation:** Department of Agronomy and DOE Great Lakes Bioenergy Research Center, University of Wisconsin - Madison, Madison, WI

**Presentation Type:** Poster presentation

**Abstract Title:** Genetic Analysis of Flowering Time in Switchgrass Using a Pseudo-F2 Population from an Upland x Lowland Cross

**Co-authors and affiliations:** Carl-Erik Tornqvist<sup>1,2</sup>, Guillaume Ramstein<sup>1</sup>, Joseph Evans<sup>3,4</sup>, Brienne Vaillancourt<sup>3,4</sup>, Emily Crisovan<sup>3,4</sup>, C. Robin Buell<sup>3,4</sup>, Shawn Kaeppler<sup>1,2</sup>, and Michael Casler<sup>1,2,5</sup>

<sup>1</sup>Department of Agronomy and <sup>2</sup>DOE Great Lakes Bioenergy Research Center, University of Wisconsin – Madison, Madison, WI

<sup>3</sup>Department of Plant Biology and <sup>4</sup>DOE Great Lakes Bioenergy Research Center, Michigan State University, East Lansing, MI

<sup>5</sup>USDA Dairy Forage Research Center, Madison, WI

**Abstract (250 words or less):** Switchgrass is a priority crop for cellulosic biofuel production. Late-flowering lowland varieties have the potential to be more productive than adapted upland varieties in the north, but are susceptible to winter damage. Therefore, it would be desirable to combine the late-flowering lowland trait with the adaptation traits of uplands. The goal of this study is to genetically map flowering time genes in switchgrass. A pseudo-F2 population was generated by crossing two F1 siblings that had been produced by a cross between the lowland variety “Ellsworth” and the upland variety “Summer”. Southern-grown parent plants differ by an average of 10 days in flowering time. Exome-capture sequencing was used to produce single nucleotide polymorphism (SNP) genotypes of the parents and progeny. We will report on construction of the genetic map and provide preliminary information on the phenotypic distribution of flowering time in the population.