Switchgrass (*Panicum virgatum*) is a perennial, warm-season species native to North America which has evolved into multiple divergent populations that vary in ploidy, morphology, and phenological timing. Its potential uses have expanded in the past few decades to include biofuels. Flowering time is a key life-history trait for biofuel production, as plants cease biomass accumulation upon completion of floral development. Here, we present evidence that photoperiodic sensitivity in switchgrass flowering time varies between genetic subpopulations using a diversity panel grown at seven field sites that cover 17 degrees of latitude in the central United States. We then map the genetic basis of flowering time in this population and in an independent four-way cross created from two highly divergent southern lowland and northern upland populations. We describe eight additive QTLs across these seven field sites with moderate effects on flowering, five of which had overlapping significant associations in the diversity panel. \_sentence about major gene candidates found – prevalence of genes involved in \_\_/expressed in \_\_.

Breeding for photoperiodic sensitivity in plants with earlier greenup dates may allow growers in the northern United States to take advantage of longer growing seasons, as photoperiod-sensitive strains will accumulate more biomass before flowering, contributing to higher biomass yields (cite?). Alternatively, breeding for cultivars with larger cumulative GDD requirements and reduced photoperiod sensitivity could increase the heat requirement needed for switchgrass development and stabilize switchgrass biomass yields at higher levels, which could help offset the negative impacts of climate warming (cite).

Management of switchgrass for biofuels is informed by an understanding of the biology underpinning plant responses to the environment.

Over the course of one season, switchgrass behaves as a determinate plant. It typically produces a single flush of tillers, which all become reproductive after a period of vegetative (leaf) development, and – critically – cease biomass accumulation upon completion of floral development (Van Esbroeck et al 2003). (Parrish and Fike 2005).

Though QTLs detected using the fourway cross are far too coarse to be informative by themselves, combining linkage and association mapping outperforms each method used in isolation.