**Abstract**

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 eight 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 \_\_.

**Introduction**

*Some disorganized ideas to include*

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).

**Results**

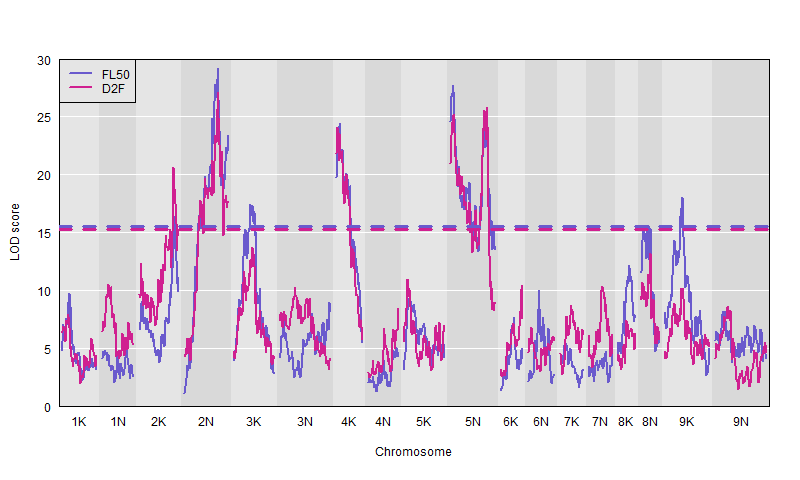
*Diversity panel captures the range of phenological responses across the common gardens*

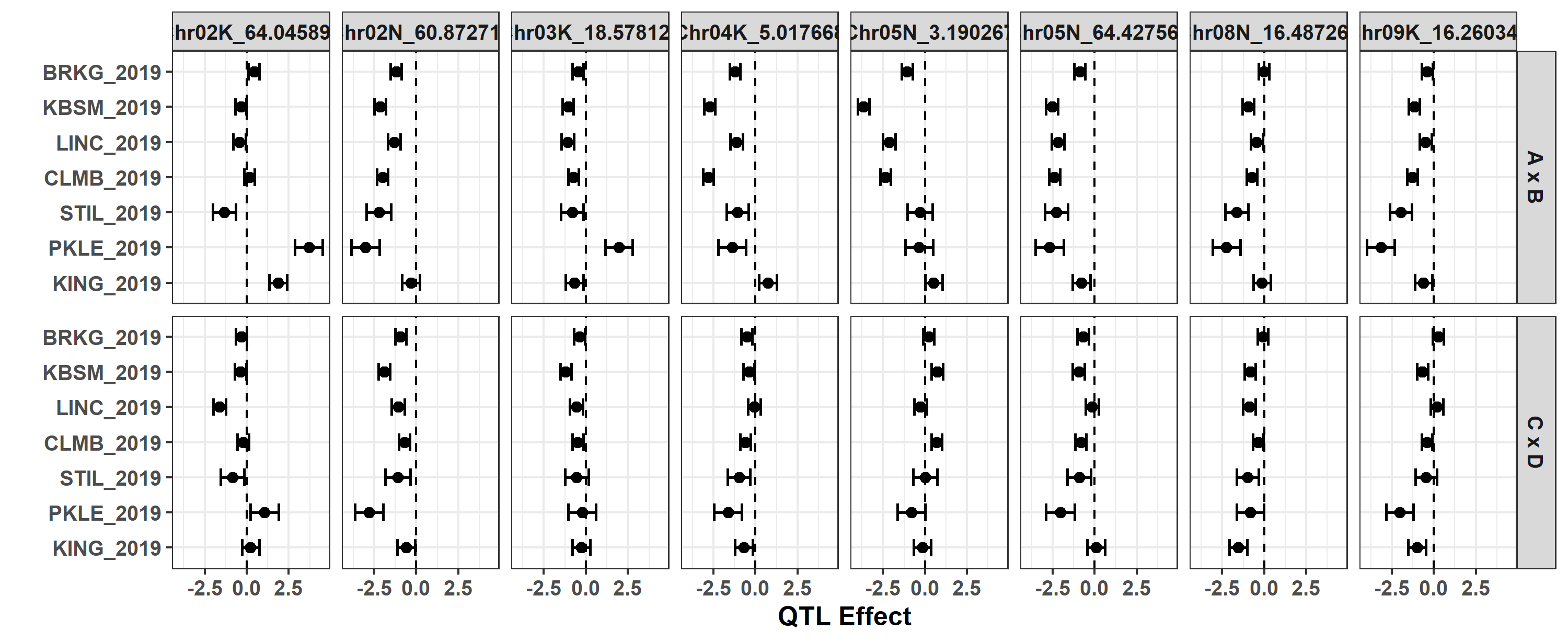
In 2019, we grew and phenotyped a diversity panel of 978 distinct switchgrass genotypes at eight common gardens. These common gardens \_details of latitude and climate range, impressive\_. We scored plant green up and flowering across these locations every three days. We divided these switchgrass genotypes into five categories: tetraploid individuals in the Atlantic, Midwest, and Gulf genetic subpopulations (Lovell et al 202X), admixed tetraploid individuals, and octoploid individuals. We then explored the overall patterns of greenup and flowering within these five categories. We first explored these patterns as a function of cumulative GDD (cite some switchgrass flowering time study, and Li’s study?). Cumulative GDD explained most of the variation in flowering time between sites for most subpopulations, particularly for the Midwest subpopulation (variance components results). The Midwest required the least cumulative GDD before flowering (585 +/- 12 CGDD), and the Gulf required the most before flowering (1238 +/- 378 CGDD), with the other three subpopulations falling in between (708 – 750 +/- 106-123 CGDD). However, cumulative GDD was not sufficient to explain the variation in flowering time in the Gulf subpopulation. Instead, we hypothesized that the Gulf subpopulation also used a photoperiod cue, given the imperfect relationship between GDD, photothermal time, and flowering in the Gulf subpopulation, and the presence of a A screenshot of a cell phone

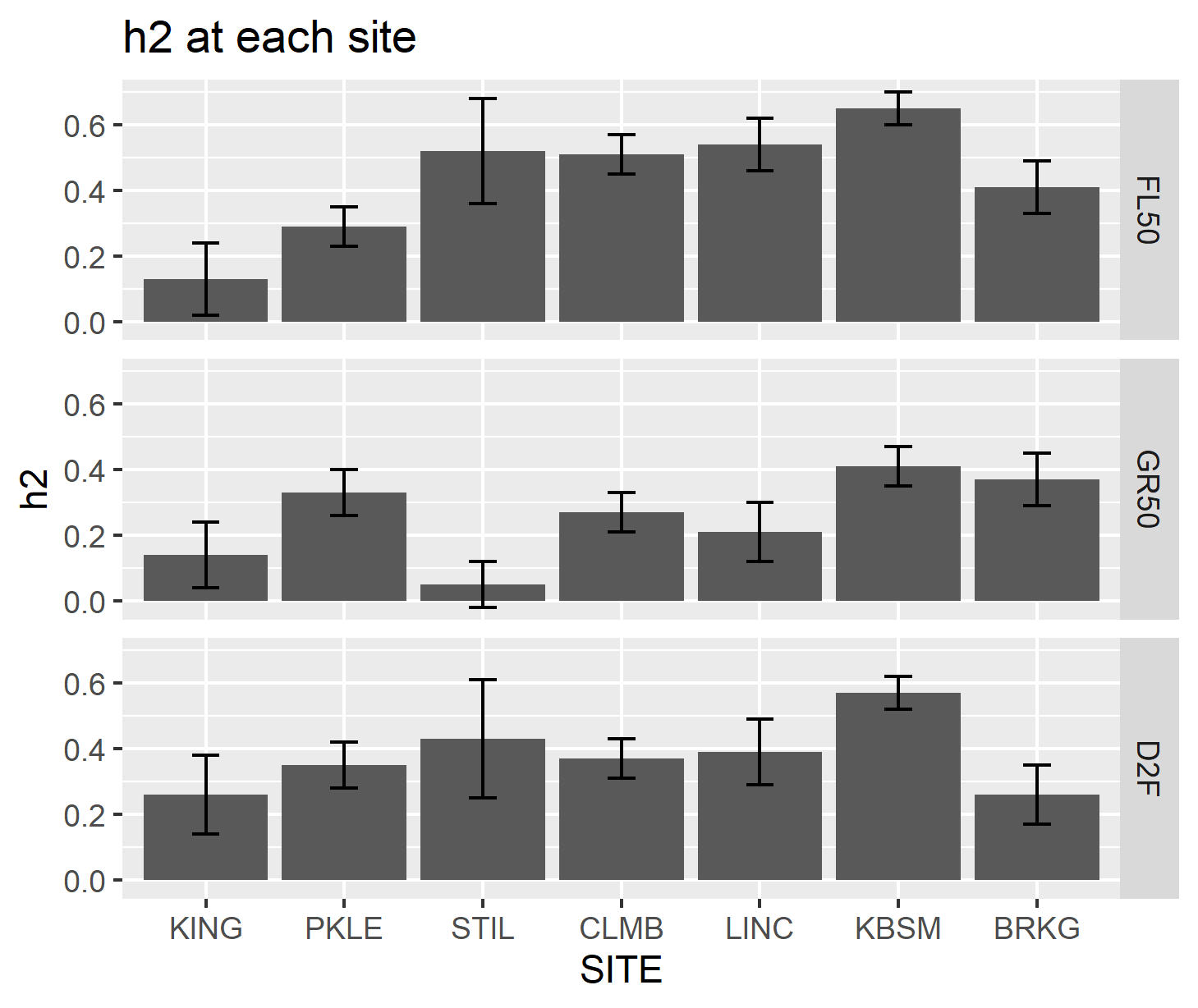
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Description automatically generatedrelationship between latitude of common garden and flowering time based on cumulative GDD.

The Midwest and Gulf subpopulations had the most distinct phenological responses out of all subpopulations across our common gardens. These populations appeared to be flowering in response to two distinct environmental cues –in the Midwest, plants flowered consistently at a similar minimum cumulative GDD, while we hypothesized the presence of a photoperiod cue in the Gulf. To analyze the genes and alleles underlying the phenological responses in our most distinct subpopulations, we used an F2 cross between four individuals, two Midwest and two Gulf individuals. The parents of this cross were DAC, an early flowering Midwest individual, VS16, a late flowering Midwest individual, AP13, an early flowering Gulf individual, and WBC, a late flowering Gulf individual. We made F1 crosses of the two early flowering individuals, AP13xDAC, and the two late flowering individuals, WBCxVS16. We then planted the four parents, the two F1 individuals (AP13xDAC, and VS16xWBC), and XXX F2 individuals at eight field sites, and recorded greenup and flowering date for the 2016-2019 seasons. Though there was a X day gap in flowering between the two F1 crosses, F1 individuals flowered at similar times to the Midwest parents and Midwest subpopulation individuals in general, indicating that the flowering time genetic response to cumulative GDD was dominant to the photoperiod response. At the northern five sites and at Kingsville, F2 individuals had similar greenup and flowering dates as individuals from the Midwest subpopulation. However, F2 individuals at PKLE and TMPL had flowering dates similar to late flowering Midwest individuals to A close up of a map

Description automatically generatedearly- to mid-range flowering Gulf individuals. Thus, at the northern five sites, we expected to find QTL controlling flowering date from the Midwest subpopulation, potentially by affecting the cumulative GDD requirements for the plant before flowering. In contrast, at TMPL and PKLE, there was the potential to isolate some QTL that affected the ability of the plant to flower in response to a photoperiod cue.

We analyzed greenup and flowering in 2019 for seven fourway sites. We anticipated finding QTL at the northern common gardens that distinguished between early and late-flowering Midwestern alleles, while Pickle offered the opportunity to examine some effects of Gulf alleles. There were no significant QTL for greenup. There were eight QTL for flowering date in the fourway cross; the largest QTL were on Chr02N, Chr04K, and Chr05N. All eight QTL exhibited significant GxE between common garden sites. We could estimate allelic effects of alleles from both F1 individuals. In the early flowering alleles, AxB, at PKLE, five of eight lowland alleles delayed flowering date. In the CxD cross at PKLE, four of eight lowland alleles delayed flowering date – four of the same five regions that delayed flowering date in the AxB cross. We therefore hypothesized that these regions: Chr02N, Chr04K, Chr05N, (Chr08N), and Chr09K were important regions affecting flowering in the Gulf subpopulation. At the northern sites, because of the dominance of Midwest phenotypes and alleles that we observed, we compared effects of the Midwest allele from the early and late F1 cross. 28 sites AxB, the early F1, the Midwest allele was accelerating flowering. 16 sites CxD, the late F1, the Midwest allele was accelerating flowering, and 2 sites CxD the upland allele was delaying flowering. All eight QTL affected flowering date for at least one northern site for both the early and late flowering allele sets. Therefore we hypothesized that all eight regions were important regions affecting flowering in the Midwest subpopulation.

In Kingsville, 2 AxB Midwest QTL accelerated flowering, and 2 delayed flowering. In CxD, alleles at four Midwest QTL accelerated flowering. In general, heritability for flowering was lowest at Kingsville in both the diversity panel and the fourway cross, indicating a larger effect of environment on phenotypic variance at this site.

Though QTLs detected using the fourway cross are far too coarse to be informative about gene identity by themselves, combining linkage and association mapping can outperform each method used in isolation (cite Brachi, others?). We therefore conducted GWAS on greenup and flowering date at seven common garden sites for individuals from both the Midwest and Gulf subpopulation. We then analyzed the allelic effects across common garden sites for the top XK SNPs using mash. We then focused on identifying associations in or near the important QTL regions for flowering date from the fourway cross, as well as the population that allele was found within and the effect that that SNP had across sites.

Five of the eight QTL – the four largest QTL, and all five QTL that we hypothesized affected flowering in the Gulf subpopulation – colocalized with one or more of the top 25 mash hits. Discussion of candidate genes, where they are in the QTL interval, what the effects look like in mash, what subpops they are segregating in, for:

* Candidate on Chr02N
* Candidate on Chr04K
* Candidate on Chr05N 4.3 Mb
* Candidate on Chr05N 64.4 Mb
* Candidate on Chr08N
* Possible reasons why we didn’t find candidates in GWAS for other three QTL intervals: false negatives, type of allele shifts we are testing here vs the fourway, other things
* And what are other types of region we can detect with GWAS that we couldn’t detect in our fourway? Particularly differences between Gulf alleles… maybe offer up Gulf specific GWAS/mash here. Or GWAS on any individual that is tetraploid and looks like it’s photoperiod sensitive – including some admixed and Atlantic individuals. As an idea.
* Want to bring back discussion of environmental cues… may be able to lead in to this by talking about which subpopulations are segregating for these things.
* I don’t know how to tie genomic prediction in here. Ideally we’d perhaps have information on which parts of the genome being Midwestern vs Gulf would make you sensitive to photoperiod cues, and which parts affect how much cumulative GDD you need, if you’re not sensitive to photoperiod cues. That would be a nice way to bring this full circle.