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**Genetic architecture of flowering-time variation in grasses**

New insights into the genetic control of natural variation in flowering time in *Brachypodium distachyon.*

**The Science**

To explore the genetic architecture of flowering time, we developed a recombinant inbred line population from a cross between two diverse accessions of the grass *Brachypodium distachyon* that have different flowering behavior. We then used a genotyping-by-sequencing approach to identify six quantitative trait locis that control differences in flowering time.

**The Impact**

Increasing biomass yield could improve the economics of biomass as an energy source. By furthering the molecular-level understanding of the flowering regulatory network in the model grass *Brachypodium distachyon*, we are advancing the potential to manipulate flowering time in bioenergy grass crops to increase biomass yield.

**Summary**

The transition to reproductive development is a crucial step in the plant life cycle, and the timing of this transition is an important factor in crop yields. Here, we report new insights into the genetic control of natural variation in flowering time in *Brachypodium distachyon*, a non-domesticated pooid grass closely related to cereals such as wheat and barley. A recombinant inbred line population derived from a cross between the rapid-flowering accession Bd21 and the delayed-flowering accession Bd1-1 were grown in a variety of environmental conditions to enable exploration of the genetic architecture of flowering time. A genotyping-by-sequencing approach was used to develop SNP markers for genetic map construction, and quantitative trait loci (QTLs) that control differences in flowering time were identified. Many of the flowering-time QTLs are detected across a range of photoperiod and vernalization conditions, suggesting that the genetic control of flowering within this population is robust. The two major QTLs identified in undomesticated *B. distachyon* colocalize with *VERNALIZATION1/PHYTOCHROME C* and *VERNALIZATION2*, loci identified as flowering regulators in the domesticated crops wheat and barley. This suggests that variation in flowering time is controlled in part by a set of genes broadly conserved within pooid grasses.

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**Publications**

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