112. Genetic and molecular anayses of the regulation of flowering in the temperate grass, Brachypodium distachyon

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Abstract:Proper timing of flowering is essential for reproductive success in plants and is a major determinant of biomass yield. A key adaptation to seasonal variation in temperate climates is the evolution of a vernalization requirement. Vernalization is the process by which competence to flower is achieved only after prolonged exposure to winter cold. A vernalization requirement is found in a range of flowering plant families, yet relatively little is known about the molecular nature of this phenomenon outside the eudicot model Arabidopsis thaliana. We are using the small temperate grass, Brachypodium distachyon as a model to study flowering in the grasses. Here we report the characterization of the vernalization response across diverse Brachypodium accessions, and have begun to assess the genetic basis of the variation in flowering in populations derived from crosses between accessions that vary in their vernalization requirement. There is considerable variation in the vernalization and flowering time responses across the Brachypodium accessions tested, and natural variation studies suggest a few genes with large effects control flowering in Brachypodium. Additionally, we have screened for vernalization-insensitive and rapid- flowering mutants. We have mapped several mutants within our collection using whole genome sequencing followed by the use of the bioinformatics mapping pipeline, CLOUDmap. Several novel flowering time genes have been identified, many of which appear to be negative upstream regulators of the key vernalization gene in grasses, VERNALIZATION1. Relative to the large genomes, long generation times, and domesticated backgrounds of cultivated cereals, Brachypodium offers a powerful opportunity to understand flowering time at a deeper molecular level in grasses.