224. Linking genotype and phenotype in a model grass: Building tools for genome-wide- association studies in Brachypodium

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Project Goals: (1) Phenotype a germplasm collection of geographically diverse B. distachyon individuals to determine overall existing diversity for biofuel conversion quality. (2) Assess population structure and genetic diversity in our population using genotype-by-sequencing. (3) Determine the feasibility of using association mapping techniques to find genes of importance in B. distachyon, by assessing genome-wide linkage disequilibrium.

The small, annual grass Brachypodium distachyon, a close relative of wheat and barley, is a powerful model system for cereals and bioenergy grasses. Genome-wide association studies (GWAS) of natural variation can elucidate the genetic basis of complex traits, but have been largely prevented in B. distachyon by the lack of sufficient numbers of well- characterized accessions. Here, we report on genotyping-by-sequencing of 84 B. distachyon, eight B. hybridum, and three B. stacei accessions with diverse geographic origins, including Albania, Armenia, Georgia, Italy, Spain, and Turkey. Over 90,000 high- quality single-nucleotide polymorphisms (SNPs) distributed across the Bd21 reference genome were identified. Our results confirm the hybrid nature of the B. hybridum genome, which appears as a mosaic of B. distachyon-like and B. stacei-like sequences. Analysis of more than 50,000 SNPs for the B. distachyon accessions has revealed three distinct, genetically defined populations. Surprisingly, these genomic profiles are more readily explained by differences in flowering time than by geographic origin. High levels of differentiation in loci associated with floral development support the differences in flowering time between B. distachyon populations. GWAS investigations combining genotypic and phenotypic data also suggest the presence of one or more photoperiodism, circadian clock, and vernalization genes in loci associated with flowering time variation within B. distachyon populations. Our characterization expands the germplasm resources available for Brachypodium and demonstrates the feasibility of GWAS in this model grass.

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