

**THE PUBLIC SUNFLOWER ASSOCIATION MAPPING POPULATION**

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**ABSTRACT**

In recent years, major steps have been made toward generating genetic and genomic resources in sunflower; however, the tools for associating phenotype with genotype have remained largely undeveloped. To help fill this gap, we developed a permanent, publicly-available association mapping resource for sunflower. The Sunflower Association Mapping (SAM) population consists of 271 diverse inbred lines and captures nearly 90% of the genotypic diversity in cultivated sunflower. We have grown the SAM population in replicate at three locations and phenotyped it for a number of agronomically important traits including days to flower (DTF) and plant architecture. All individuals within the SAM population were sequenced to a minimum of 8-10x depth with the Illumina platform. Using custom bioinformatics pipelines developed in collaboration with the software company SAP, we extracted 613,011 high confidence SNPs to be employed for genome-wide association study (GWAS) analyses. To identify the alleles associated with phenotypes characterized in the SAM population, we have completed development of a GWAS pipeline which includes imputation, population structure calculation, kinship, mixed linear model, p-values adjustment, meta-analysis across replicates and environments, tests for GxEn, and calculation of variance components and effect sizes at each SNP position. We implemented this custom pipeline on the SAM phenotypic data for DTF and total branching which was previously analyzed using genotypes from a 10K Illumina SNP array. We present details of the SAM population including phenotypic and genetic diversity, results from the newly developed custom GWAS pipeline, and comparisons to previous association results in sunflower employing SNP arrays.

**Key Words** : association mapping, whole genome sequencing, GWAS, flowering time, genetic diversity