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Untangling traits, mechanisms, and alleles associated with delayed wilting, canopy temperature, and 13C/12C ratio

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Breeding efforts to improve drought tolerance in soybean by focusing on yield have not been successful because crosses were often restricted to elite lines, essentially reshuffling the same genes, thus limiting genetic diversity and potential progress. In the past 5 years progress has been made in improving drought tolerance by focusing on: (1) utilization of genetic diversity within the soybean germplasm collection and (2) identification of physiological mechanisms that may confer drought tolerance rather than evaluating yield *per se*. Using a panel of 373 diverse, maturity group 4 accessions across multiple field environments, we identified large variation in delayed canopy wilting (CW), canopy temperature (CT), and the isotopic ratio of ^{13}C to ^{12}C ($\delta^{13}C$) as a surrogate measure for water use efficiency. Using data from the 50k SNP chip available at Soybase, we mapped CW, CT, and $\delta^{13}C$ using genome wide association studies (GWAS). GWAS identified 62, 52, and 54 environment-specific SNPs that were significantly ($P \leq 0.0003$) associated with CW, CT, and $\delta^{13}C$, respectively. Loci of CW were coincident with CT loci in 15 chromosomal regions. Using our panel of 373 accessions, we extended our analysis of breeding values for CW, CT, and $\delta^{13}C$ to all 19,000 accessions in the USDA soybean germplasm collection. This analysis found that breeding values for $\delta^{13}C$ were positively correlated with CW ($r = 0.53$) and CT ($r = 0.67$), indicating that genotypes with high WUE tend to have high CW and CT, both of which are unfavorable traits. A positive correlation existed between CW and CT ($r = 0.60$), indicating that genotypes with low CW tend to have cool CT. Specific genotypes were identified with favorable combinations of alleles for all traits, offering an opportunity for moving these favorable physiological traits into high-yielding backgrounds.