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BOOK OF ABSTRACTS

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Mapping the genetic basis of $\Delta^{13}\text{C}$ in almond: Insight into water-use efficiency under water-limited conditions

Jerome Grimplet¹, Dr. Najla Ksouri¹, Dr. Beatriz Bielsa¹, Maria Teresa Espiau¹, Dr. Maria José Rubio-Cabetas¹

¹CITA Aragón, Avenida Montañana 930, 50059 Zaragoza, Spain

Corresponding author: mjrubioc@cita-aragon.es

Water scarcity represents a major constraint to almond cultivation in Mediterranean regions, where enhancing water-use efficiency (WUE) has become a key breeding objective. Carbon isotope discrimination ($\Delta^{13}\text{C}$) provides a robust integrative proxy of WUE; however, the genetic determinants underlying its variation in almond remain largely unexplored. In this study, we conducted a genome-wide association study (GWAS) to dissect the genetic architecture of $\Delta^{13}\text{C}$ and to identify candidate genes contributing to WUE variation. A diverse panel of 144 almond accessions, including wild relatives, landraces, and modern cultivars, was evaluated under field conditions at CITA-Aragón (Spain). Leaf $\Delta^{13}\text{C}$ was determined via isotope ratio mass spectrometry, and genotyping was performed using the Axiom™ 60K almond SNP array. Following stringent quality control and filtering steps, 41,109 high-confidence SNPs were retained and uniquely mapped to the anchored chromosomes of the updated *Prunus dulcis* 'Texas' v3 phase-1 genome assembly. GWAS analysis was performed using BLINK algorithm implemented in GAPIT, which best balanced false-positive control and the detection power. Three genomic regions significantly associated with $\Delta^{13}\text{C}$ were detected on chromosomes 1, 3, and 6 of which two exceeded the Bonferroni-corrected threshold and one met the false discovery rate criterion. The lead locus on chromosome 6 explained 43.9% of phenotypic variance and exhibited an over-dominant allelic effect, suggesting heterozygote advantage. Candidate genes were identified using a dual approach: for SNPs within defined haplotype blocks, gene retrieval was limited to the block boundaries, whereas for isolated SNPs, genes located within ± 100 kb flanking regions were considered. This analysis revealed several biologically relevant candidates, including genes encoding a peroxidase, a plastid-lipid associated protein, and a fructose-bisphosphate aldolase, all implicated in stress-response pathways and potentially influencing stomatal regulation. Overall, this study provides the first genome-wide dissection of $\Delta^{13}\text{C}$ in almond and offers novel insights into the molecular mechanisms governing WUE.