Proceedings of the LXVI SIGA Annual Congress
Bari, 5/8 September, 2023
ISBN: **978-88-944843-4-2**

Poster Communication Abstract – 6.19

DETECTION AND DISTRIBUTION OF TWO DOMINANT ALLELES ASSOCIATED WITH THE SWEET KERNEL PHENOTYPE IN ALMOND CULTIVATED GERMPLASM

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almond, kernel taste, allele mining, Marker-Assisted Selection, breeding

Almond [*Prunus dulcis* Miller (D. A. Webb), syn. *Prunus amygdalus* L.)] is the major tree nut crop worldwide in terms of production and cultivated area. Almond domestication was enabled by the selection of individuals bearing sweet kernels, which do not accumulate high levels of the toxic cyanogenic glucoside amygdalin. Previously, we showed that the Sweet kernel (*Sk*) gene, controlling the kernel taste in almond, encodes a basic helix loop helix (bHLH) transcription factor regulating the amygdalin biosynthetic pathway. In addition, we characterized a dominant allele of this gene, further referred to as *Sk-1*, which originates from a C1036→T missense mutation and confers the sweet kernel phenotype. Here we provide evidence indicating that the allele further referred to as *Sk-2*, originally detected in the cultivar “Atocha” and arising from a T989→G missense mutation, is also dominantly inherited and confers the sweet kernel phenotype in almond cultivated germplasm. The use of single nucleotide polymorphism (SNP) data from genotyping by sequencing (GBS) for population structure and hierarchical clustering analyses indicated that *Sk-2* occurs in a group of related genotypes, including the widespread cultivar “Texas”, descending from the same ancestral population. KASP and dual label functional markers were developed for the accurate and high-throughput

selection of the *Sk-1* and *Sk-2* alleles, and the genotyping of a panel of 134 almond cultivars. Overall, our results provide further insights on the understanding of the almond cultivation history. In addition, molecular marker assays and genotypic data presented in this study are expected to be of major interest for the conduction of almond breeding programs, which often need to select sweet kernel individuals in segregant populations.