

GENETIC CHARACTERIZATION OF AN ALMOND GERMPLASM COLLECTION AND VOLATILOME PROFILING OF RAW AND ROASTED KERNELS

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Almond is appreciated for its nutraceutical value and for the aromatic profile of the kernels. In this work, an almond collection composed of 96 Sicilian accessions complemented with 10 widely cultivated cultivars was phenotyped for the production of volatile organic compounds using a proton-transfer time-of-flight mass spectrometer and genotyped using the Illumina Infinium®18K Peach SNP array.

The profiling of the aroma was carried out on fresh and roasted kernels enabling the detection of 150 mass peaks. Sixty-eight, for the most related with sulphur compounds, furan containing compounds, and aldehydes formed by Strecker degradation, significantly increased during roasting, while the concentration of fifty-four mass peaks, for the most belonging to alcohols and terpenes, significantly decreased.

471 robust SNPs were selected and employed for population genetic studies. Structure analysis detected three subpopulations with the Sicilian accessions characterized by a different genetic stratification compared to those collected in Apulia (South Italy) and the International cultivars. The linkage-disequilibrium (LD) decay across the genome was equal to $r^2 = 0.083$. Furthermore, a high level of collinearity ($r^2 = 0.96$) between almond and peach was registered confirming the high synteny between the two genomes.

A preliminary application of a genome-wide association analysis allowed the detection of significant marker-trait associations for 31 fresh and 33 roasted almond mass peaks respectively. An accurate genetic and phenotypic characterization of novel germplasm can represent a valuable tool for the set-up of marker-assisted selection of novel cultivars with enhanced aromatic profile