

**GENOME-WIDE CHARACTERIZATION OF ALMOND DIVERSITY/HOMOZYGOSITY DEFINES STRUCTURE, KINSHIP, INBREEDING AND LINKAGE DISEQUILIBRIUM IN CULTIVATED GERMPLASM AND REVEALS GENETIC ASSOCIATIONS WITH NUT AND SEED WEIGHT**

DELVENTO C.\*, LOTTI C.\*\*, MAZZEO R.\*\*, RICCIARDI F.\*\*, LOSCIALE P.\*,  
GAETA L.\*\*\*, D'AGOSTINO N.\*\*\*\*, TARANTO F.\*\*\*\*\*, SÁNCHEZ-PÉREZ R.\*\*\*\*\*,  
RICCIARDI L.\*, PAVAN S.\*\*\*\*\*

\*) Università degli Studi di Bari

\*\*) Università degli Studi di Foggia

\*\*\*) CREA-AA

\*\*\*\*) Università degli Studi di Napoli

\*\*\*\*\*) IBBR (CNR)

\*\*\*\*\*) CEBAS-CSIC

\*\*\*\*\*) CNR

Recent genome sequencing provides the opportunity to study patterns of DNA variation in almond [*Prunus dulcis* Miller (D.A. Webb)], the main tree nut species worldwide. In this study, we performed genotyping by sequencing (GBS) on a global almond collection. Through the characterization of single nucleotide polymorphisms (SNPs) and runs of homozygosity (ROHs), we defined genetic structure, kinship, inbreeding and linkage disequilibrium (LD) decay in almond cultivated germplasm. In addition, we merged molecular data with four-year phenotypic observations to perform a genome-wide association study (GWAS) and, for the first time in a crop species, homozygosity mapping (HM). This resulted in the identification of genomic associations with nut, shell and seed weight, and the characterization of homozygous regions which possibly originate from human selection for higher nut weight. Overall, this study provides insights on the almond cultivation history and delivers information of major interest for almond genetics and breeding. In a broader perspective, our results encourage the use of ROHs in crop science to estimate inbreeding, choosing parental combinations which minimize the risk of inbreeding depression, and identify genomic footprints of selection for specific traits.