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Poster Communication Abstract – 1.16

SNP MOLECULAR DIVERSITY AND GWAS IN SWEET CHERRY GERMPLASM

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Sweet cherry *(Prunus avium* L.) is a diploid species (2n = 2x = 16) belonging to the Rosaceae family, believed to have originated around the Caspian and Black Sea regions. Cherry trees expanded through Europe during Roman times and are currently widely cultivated in temperate areas.

Many sweet cherry landraces can still be found in rural areas in Italy, along with modern and improved varieties, which have been selected for some important traits such as fruit size, shape, and firmness, self-compatibility, etc.. The availability of the sweet cherry genome sequence (Shirasawa et al. 2017; Pinosio et al. 2020) allows the mapping of thousands of SNPs (Single Nucleotide Polymorphisms) obtained by the GBS (Genotyping-by-Sequencing) technology. As part of a project funded by the Basilicata Region, BioDruBa (Biodiversità delle Drupacee della Basilicata), sweet cherry local varieties maintained in the ALSIA (Rotonda, PZ) field collection, have been genotyped using GBS technology together with other known varieties from the University of Bari collection.

The SNP markers obtained from sequencing were used to assess genetic diversity and relationships among genotypes. Population structure, principal component, and phylogenetic analysis showed that most of the local varieties from Basilicata are genetically closer to some traditional varieties from the Campania Region, suggesting a common genetic origin. The other genotypes showed groupings generally referable to common genealogical origins and/or to the sharing of morpho-agronomic traits.

In order to associate SNPs with highly inherited phenotypic traits, a GWAS (Genome Wide Association Study) analysis was performed. The results showed the association of some SNP markers with agronomically important traits (e.g. self-compatibility). For the sweet cherry varieties whose genome sequence is available in NCBI and for which we possess phenotypic data, the genomic sequence of candidate genes was retrieved, aligned to the reference genome, and polymorphisms characterized.

Pinosio et al. 2020. Plant J. 103, 1420-1432.

Shirasawa et al. 2017. DNA Res. 12, 60-8.