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MOLECULAR AND MORPHO-PHENOLOGICAL CHARACTERIZATION OF A GERMPLASM COLLECTION OF *PRUNUS AVIUM*

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Sweet cherry (*Prunus avium* L.) is an economically important diploid species in the Rosaceae family, with a worldwide production of over 2 million tonnes. Italy is among the top six producers in the world, with a global production of almost 95,000 tonnes, and the second in Europe after Turkey which, with some 600k tonnes, is the leading country(FAOSTAT 2016). In the last years, cherry breeding has been receiving increasing interest due to the concurrent crisis affecting the production of other major fruit tree crops (as is the case in peach). Natural variation present within the species represents a fundamental resource to fuel improvements in the performance of modern varieties. Therefore, the identification and estimation of the genetic diversity of cherry, is the first step towards its exploitation in successful breeding programs. A *Prunus avium* germplasm collection is maintained at the Centre for Plant Germplasm Resources (CPGR) at CREA –OFA in Rome. It consists of about 700 accessions including landraces and varieties of Italian and worldwide origin. Among them, 378 accessions were molecularly characterized with 19 microsatellite markers, mostly developed after the availability of the whole-genome sequence of peach, giving a total of 96 different alleles. A cluster analysis was performed, resulting in the separation of all the accessions with the exception of 36 groups. Morphological data from the fruits were collected as follows: skin color, flesh color, pit adherence, fruit weight, fruit shape, soluble solid content (°Bx), petiole length and pit weight and length. Also, blooming and ripening date were recorded from the plants in the field. All these data are being further analyzed to assess and study the genetic diversity and the structure of the CREA-OFA cherry germplasm collection, in order to efficiently preserve the biodiversity of the species and to exploit its potential in future breeding programs. Results of the analyses will be presented.