

A MULTI PARENTAL CROSS DESIGN APPROACH TOWARDS THE MAPPING OF MAJOR QTLS ASSOCIATED TO RELEVANT FRUIT QUALITY TRAITS IN PEAR

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Pear belongs to the Rosaceae family and together with apple shared a unique set of 17 chromosome, originated as result of a whole genome duplication event. Italy is the second top producer of pear fruits at a world-wide level (after China) and this fruit is highly appreciated by consumers for its specific quality attributes, which are established at the end of the ripening process. Pears are characterized by a climacteric type of ripening, in which the several changes occurring to make the fruit edible and suitable for consumption are regulated by the action of the plant hormone ethylene. Despite many other climacteric fruits (such as apple, peach and tomato), the production of ethylene can be stimulated by cold temperature in a cultivar-dependent fashion, dividing the different cultivars in summer or winter types. Although pear is one of the most important cultivar fruit crop in Italy, the varietal innovation is much more limited compared to other species, especially apple. To support breeding activities oriented to ameliorate fruit quality traits and postharvest performance in pear, a genetic analysis was initiated to target major QTL intervals associated to important pomological traits, ethylene production and the development of serious disorders, such as superficial scald. To this end, two-pear populations linked by a common parental cultivar were employed for the assembling of both family-based and consensus genetic maps. The genotyping was carried out by means of the Affymetrix 70K array, which enabled the generation of high-dense genetic backgrounds. In this work is illustrated the most recent update of this project aimed to the identification of the most valuable molecular markers to be used as routine tool to assist the breeding program oriented to

improve the general quality in new accession of pears.