Genomic approaches towards an efficient assisted breeding for fruit quality in apple

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Fruit quality is characterized by a set of principal factors which are fundamental for the economic success of a cultivar. The quality components, in the last decades, have been considered by breeders as the major target in the constitution of novel apple accessions distinguished by superior quality features. This goal, however, is still normally achieved by traditional breeding strategies, mainly represented by rounds of cross and selection, making the finding of novel high quality varieties a laborious and expensive activity. The implementation of valuable molecular markers would certainly improve the efficiency of the seedling selection, making this process more precise and cost effective.

In this work, a comprehensive QTL mapping investigation for fruit quality is presented, focusing in particular on the apple fruit texture, to date considered a driver trait for fruit quality. Fruit texture was originally assessed by using a high resolution phenotyping equipment on two type of plant materials: two full-sib progenies and a cultivar collection. As genomic approaches, a QTL mapping investigation was initially chosen to genetically dissect the control of such complex trait, and a candidate gene based association mapping analysis was subsequently employed to fine map and develop the most valuable molecular markers suitable for this purpose. The potentiality of these markers, which were also tested in a breeding program simulation, are here presented and discussed.