

PEACH GENOMICS AND BREEDING APPLICATIONS

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The cultivated peach (*Prunus persica*) is a major temperate fruit crop species with a diploid ($2n=16$) and a compact genome (approx. 220 Mbp) that has been recently sequenced. It originated in China and the variability used in European and American commercial breeding programs is low. Peach germplasm is structured and has a high level of linkage disequilibrium conservation, due mainly to its self-compatible mating system and to a recent bottleneck at the beginning of the modern breeding programs about one century ago. Genetic progress in the last 15 years has been enormous with the development of saturated linkage maps, the widespread use of markers for variability analysis, the mapping of many major genes, cloning of a few of them and the dissection of several quantitative characters of economic interest in their QTL components. The presentation will cover the current use and limitations of markers in commercial plant breeding, the development of new genomic tools, particularly those based on next-generation sequencing technology and the availability of the whole genome sequence of peach and other rosaceous crops, and the progress towards the development of an almond-peach NIL collection, as a tool for fine genetic analysis and a way towards the enrichment of the peach genome with genes coming from related species.