Trends in Molecular Biology of Several Fruit Trees

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Submission: December 18, 2018; **Published:** April 23, 2019

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Abstract

The most relevant trends in the molecular biology of several fruit trees as apple, peach, nectarine and apricots are sumarized in this article. Thus, one of the most important problem is the management of germplasm collections, that is usually due by molecular markers, that could provide valuable information about molecular characterization of cultivars, the expansion of cultivars from centres of origin, identification of synonymies, selection of new cultivars, assessment of genetic diversity/stability after conservation. Other direction of research is identification of molecular markers associated with different traits (Quantitative Trait Loci-QTL) and identification of mechanisms involved in resistance to pathogens (bacteria, viruses, fungi) and different climate conditions (drought, cold) in order to select new valuable cultivars (Molecular marker-Assisted Selection-MAS).

Keywords: Fruit trees; Molecular markers; Genetic diversity; Conservation; Selection

Mini Review

Germplasm of perennial fruit species is conserved by in situ collections of in vitro culture in order to preserve the genetic resources and maintenance of biodiversity [1]. Biodiversity is fundamental for biotechnology and selection of new valuable cultivars and sustainable agriculture. Conservation methods should ensure the stability of plant species or cultivars, thus the periodic evaluation of the genetic composition of the preserved material is needed [2].

Apple (*Malus x domestica Borkh.*) considered the economically most important fruit crop in the temperate zone [3], has a gametophytic self-incompatibility mechanism, which enforces outbreeding and a high level of heterozygosity [4]. Thus, genetic analysis by molecular markers ensure the discrimination of vegetatively propagated apple trees. Several molecular markers were used over years, but microsatellite (SSR) DNA become a popular tool for fingerprinting germplasm collections [5]. SSR markers have been successfully applied for apple tree cultivar identification [6], evaluation of genetic diversity within germplasm collections [7,8] or for parent identification [4,9]. Apple germplasm in USA and Europe was investigated in order to identify a minimal set of markers useful for rapid discrimination of cultivars [10-13]. Molecular markers are also valuable tools for characterization of in vitro plants of fruit trees. Thus, RAPD and ISSR markers were used to prove the genetic fidelity of clonally propagated apple from adventitious buds [14,15].

Another application of molecular markers is connected with the evaluation of apple resistance to fungal pathogen *Venturia inaequalis*, which produces apple scab. 11 apple scab resistance genes are known up to now and several molecular markers linked to these genes are available [16], making the marker-assisted selection an useful tool for breeding programs [17].

Other important fruit crops of temperate climates are apricots, peaches and nectarines. Two centres of domestication of apricot (*Prunus armeniaca L.*) cultivars are known as China and Central Asia-from Tien-shan to Kashmir and the secondary centers of origin is considered the near-Eastern (Iran, the Caucasus and Turkey) and Korezm regions [18]. The European cultivars grown in North America, Australia and South Africa shows the least diversity [19,20]. The discrimination between cultivars is difficult, but nevertheless, the Eastern European cultivars can be clearly distinguished from other cultivars of European origin [21, 22]. Traditional methods based phenotypic descriptions do not provide enough information to trace the expansion of apricot from the centers of origin, or to identify and characterize genotypes during the breeding process. Thus, the molecular markers are also the most suitable tools for such investigation.

In case of peach and nectarine (*Prunus persica* (L.) *Batsch*), despite of a low number of origin cultivars and narrow genetic

base [23], more than thousand new varieties were released around the world [24]. However, the diversity of this crop has been drastically reduced using improved varieties with a common genetic base [25], that has drastically reduced the genetic variability of this crop [23,26-29]. Moreover, peach is a self-compatible species and a high level of inbreeding is found, several cultivars with great breeding value show a low degree of heterozygosity [30]. Thus, a reliable and efficient method of cultivar identification is required. In Spain, the genetic diversity within peaches is also decreasing rapidly, because of the replacement of traditional varieties by introduced ones, mostly from North America [31].

There are many SSR markers for different *Prunus species* [32] as peach and nectarine [30,33,34], apricot [35-38]. SSR markers were also used for identification of hybrids in apricot [39]. It is well known that the selection of markers usually depends on the nature of the germplasm under study and in many cases the existence of a set of markers applied for the identification of germplasm collections was useful but not totally transferable to the others. Another challenge is to find a minimal pannel of molecular markers useful for discrimination of cultivars. Aranzana et al. [25,33] characterized and differentiated over 200 cultivars of peaches and nectarines commonly grown in Spain, using a selected set of 16 microsatellite markers, Bouhadida et al. [40] characterized 94 peaches cultivars also grown in Spain with 15 SSR microsatellite markers and Rojas et al. [41] differentiated 117 cultivars of peaches and nectarine with only 7 SSR markers. Other specific set of SSR markers were valuable for investigation of Asian [42,43] and Tunisian peach germplasm [44,45].

Genetic control of complex traits has been accomplished through quantitative trait loci (QTLs) analysis of biparental populations resulting from crosses between peach and related species [46]. A pedigree-based analysis to map QTLs for a diverse peach breeding pedigree, identified several well-supported QTLs for at least five of the eight traits investigated by Fresnedo-Ramírez et al. [47].

Molecular characterization of fruit trees has multiple application in biotechnology and agriculture as germplasm identification and preservation, genotyping, selection of new valuable cultivars, improvement of quantitative traits.

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