

Adoption Of Molecular Markers For Analysis Of Genetic Diversity In Fruit Tree

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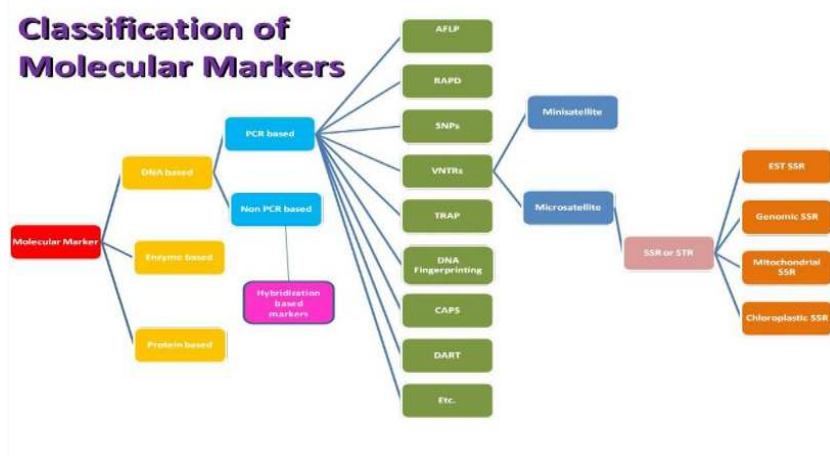
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Critical advances in the application of molecular tools to analyze genetic diversity in annual and perennial crops have taken place in the last two decades. Although in most cases the new technologies are first developed in annual crops, some particularities of most fruit crops, such as their perennial nature, long generation time, large individual size, or vegetative propagation, make the advantages of

determine the ability of populations and crops as a whole to adapt to environmental changes. This is becoming increasingly important in the current scenario of global climatic change where conserving genomic pools that will allow the development of

resilient cultivars to a wide range of biotic and abiotic stresses is an increasing necessity. In this sense, it is important to keep in mind that conservation of



using these new approaches even more relevant in these species. In this work, the information available on the different strategies used to analyze genetic diversity in temperate and tropical fruit tree species using molecular approaches is reviewed.

Conservation and sustainable management of crop genetic resource diversity is the key for guaranteeing food security for future generations since this will

plant genetic resources worldwide has been concentrated on a small group of species. Thus, from about 7,000 plant species that have been indeed used by humans, Moreover, in order to be effective in the long term, this conservation effort should also include crop wild relatives that can be source of interesting genes (Ford-Lloyd et al. 2011). Of the 30 most important crops in terms of production worldwide,

only five can be considered as fruit crops (bananas, oranges, grapes, apples, and mangoes) (Faostat 2014) although perennial crops account for about one-eighth of the world cultivated area. However, there are hundreds of neglected and underutilized fruit crops that are important in specific local markets. Common characteristics of most fruit crops compared to domesticated annual crops are their perennial nature, long generation cycles, and long juvenile periods that often limit breeding programs and hinder genetic conservation efforts. Additionally, most fruit crops are highly heterozygous and usually propagated vegetatively favouring the cultivation of a few clones of selected cultivars. As a result, often the genetic diversity found in most of the commercially cultivated fruit tree crops is low. However, while most annual crops have been domesticated over a long period of time, only very few woody perennial tree species can be considered as truly domesticated. Consequently, most are separated by few generations from their wild relatives which can become interesting sources of additional genes.

Genetic Diversity In Fruit Tree Crops Due To Molecular Markers

Traditionally, genotype identification and diversity studies in cultivated plant species including fruit trees have been carried out through morphological markers and phenotypic trait characterization. However, this is a slow and expensive process that limits the number of genotypes that can be studied as well as the accuracy of the observations. Some of those observations, like those related to phenological characters, need to be analyzed late in development, and some can affect other morphological characters or agronomical traits

due to pleiotropic gene action (Le Corre and Kremer 2003). Although these observations can still be very useful tools to match phenotype with genotype and a good phenotyping is ultimately needed to link molecular markers with traits of interest, genotype characterization and genetic diversity studies in plants require research strategies that complement phenotypic characterization and estimation of diversity such as molecular techniques. During the last two decades, fast and important advances in the methods used to study nucleic acids in both animals and plants have taken place resulting in the continuous development of different types of genetic markers.

Molecular Markers And It's Types Used In Genetic Diversity Analyses In Fruit Trees

Molecular markers can be biochemical or based on DNA sequences. Biochemical markers involve the separation of proteins (allozymes and isozymes) into specific banding patterns by electrophoresis. They are codominant, and their main disadvantage is that the number of available enzymes is limited and, thus, their power to analyze diversity is reduced. Valuable information for diversity studies in fruit trees shown in some recent works in apple, hazelnut (Leinemann et al. 2013) in general terms, be classified into dominant (such as RAPDs or AFLPs) or codominant (such as RFLPs, microsatellites, or SNPs) markers depending on whether heterozygous and homozygous genotypes can be distinguished.

Advancement For Use Of Different DNA-Based Markers For Diversity Analyses In Fruit And Nut Crops

Although genetic diversity studies in annual crops clearly outnumber those in woody perennial crops, a

great number of studies have been published on the application of molecular markers to study genetic diversity in temperate and tropical fruit tree crops. Thus, a basic search in the ISI web of knowledge for the seven most common types of markers (AFLP, ISSR, RAPD, SSR, RFLP, SNP + EST, and NGS), with the keyword “diversity”, and 32 important genera of temperate and tropical tree fruit crops (Actinidia, Anacardium, Annona, Averrhoa, Carica, Carya, Castanea, Citrus, Cocos, Cydonia, Dimocarpus, Diospyros, Eryobotria, Ficus, Juglans, Litchi, Malus, Mangifera, Musa, Olea, Passiflora, Persea, Phoenix, Pistacia, Prunus, Psidium and Vitis

Interpretation Of The Results Obtained: Parameters And Software Tools

The variances or polymorphisms shown by the different molecular markers can be analyzed with a range of different diversity parameters based (i) on the number of variants (number of percentage of polymorphic loci or allelic richness, i.e., mean number of alleles per locus) or (ii) on the frequencies of the alleles obtained (effective population size, expected and observed heterozygosities, or fixation index). Genetic diversity between different (sub) populations/collections is based on significant differences in allele frequencies among the different groups that can be estimated with F-statistics, Rst, Gst, or AMOVA, among others. In addition, graphic representation of genetic distances and cluster analyses are usually performed to visualize relationships among the different genotypes studied.

References

Landscape Genetics

A step forward would be the application of landscape genetics, an approach that combines landscape ecology and population genetics to provide information about microevolutionary processes, such as gene flow and genetic drift and selection. (**Manel and Holderegger 2013**). The main goal of this new approach is to combine the high resolution obtained from molecular information with spatial data and a variety of statistical methods to evaluate the role that landscape variables play in shaping genetic diversity and population structure.

Conclusions

Conservation and sustainable use of genetic diversity in fruit tree crops is a global commitment for present and future generations. Locating neutral genetic diversity could be a starting point for selecting material for both conservation and agronomic assessment/breeding programs. On the other hand, it is necessary to keep in mind that the huge amount of molecular data that are becoming available will still need phenotypic studies. A paradigm shift that is already taking place is that, in many cases, appropriate phenotyping rather than genotyping is becoming the main limiting factor. Association between nucleotide sequences and functional traits will be needed for agronomic, genetic mapping, functional diversity, breeding, or evolutionary studies this would be applicable to both wild and cultivated fruit trees.

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