

Use of molecular markers to characterize reference collections of fruit species

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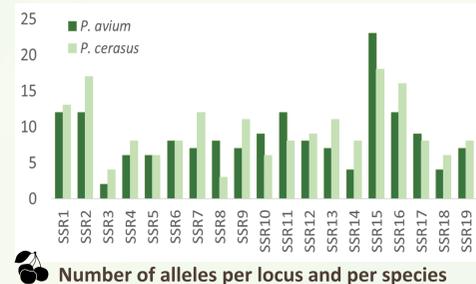
Introduction

The Rosaceae family consists of a wide diversity of species, many of which are of economic importance. The French Group for the study and evaluation of Varieties and Seeds (GEVES) is responsible for DUS (Distinction, Uniformity, Stability) testing of several of these species for variety registration and Plant Breeder's Rights. GEVES developed molecular tools to help to manage reference collections and in support for the sector. Molecular markers such as SSR are valuable and powerful tools for identifying individuals, establishing phylogenetic relationships, managing reference collections.

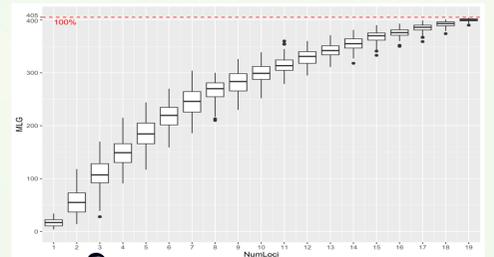
Markers selection

To evaluate, validate and optimize the marker sets, different selection criteria have been applied for each species:

- low % of missing data
- evenly distributed throughout the genome
- quality of the flanked regions
- high level of genetic diversity (number of alleles, polymorphism information content (PIC), heterozygosity)
- discriminating power



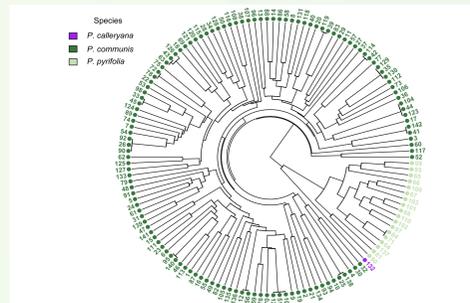
Number of alleles per locus and per species



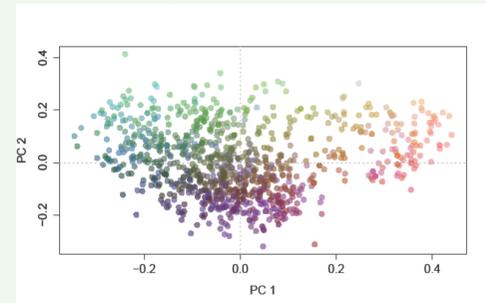
Genotype accumulation curve

Diversity and structure of reference collections

Various methods are routinely used for uncovering population structure and to evaluate the diversity of the collection: model-based approach (STRUCTURE), multivariate analysis (PCA, PCoA), dendrograms generated using UPGMA. Genotypes derived by mutation cannot be distinguished from the original genotype and usually show the same allele profile.



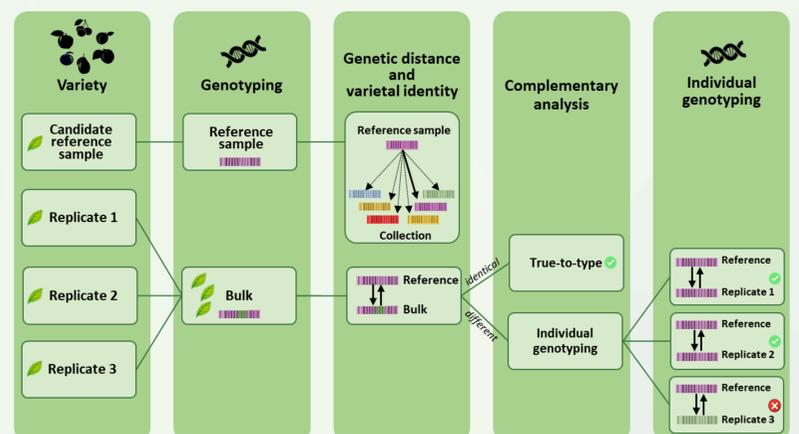
UPGMA dendrogram of 142 pear accessions based on Dice's distance



Principal coordinates analysis of 1001 accessions based on 16 SSR loci

Molecular data in DUS examinations

Several samples are analyzed for each candidate variety: one will be treated as the reference for the variety and the others as replicates and kept as back-up. Replicates will be bulked. Bulk and reference samples for each candidate are genotyped upon reception, and a matrix of pairwise genetic distance is calculated between candidates and references. The matrix is shared with the DUS team. Bulk will be compared to the reference sample; if results are different, each individual plant will be genotyped.



Conclusion

SSR data can help structure reference collections, detect misnamed or duplicated accessions, and complete the phenotypic characterization of tree varieties. Molecular analysis is an effective approach to manage and protect genetic resources of fruit trees. BioGEVES describes all new candidate varieties for registration and for protection for the six species presented here, but other fruit species are also being genotyped e.g., *Malus* and *Prunus* rootstocks.

The main official missions of GEVES are:

- to carry out DUS and VCUS testing for the **registration** of new varieties in the Official Catalogue (national listing)
- to carry out DUS testing for the **legal protection** of varieties (Plant Breeders' Rights)
- to evaluate the quality and varietal identity of seed lots for seed certification for species requiring statutory certification