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Molecular Characterization Of French Local Apple Cultivars Using SSRs



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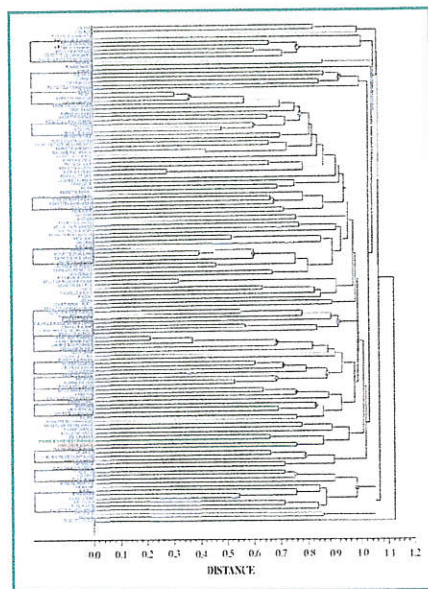
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Conservation of apple genetic resources in France is carried out by many amateur groups, various governmental and non-governmental organizations. A recent survey listed about 20 000 apple accessions planted in 180 different sites.

Passport data, morphological and agronomical descriptors are not informative enough to assess the numerous cases of misidentification and synonyms. Molecular markers have been investigated as a tool to solve these issues. 142 French local cultivars representing various geographic origins have been screened with nine SSR markers, 139 bands have been detected.

Results

■ Structure of the genetic variability



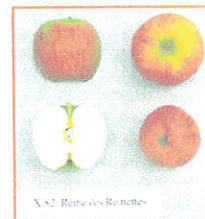
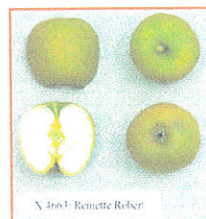
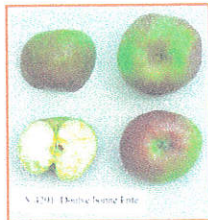
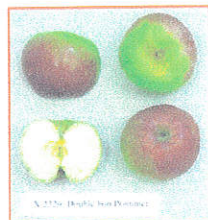
The genetic diversity within the population is very high: 15.3 alleles in average per marker, high proportion of heterozygotes (81%) and a high value of Polymorphic Information Content (PIC=0.8). Factorial and cluster analyses do not show any obvious structure of the genetic variability. The population seems to be constituted by a very heterogeneous pool of cultivars with very few genetic links (Fig. 1). A few groups of genetically related cultivars can be distinguished. Some of them are confirmed by the literature: i.e. the cultivar "Franc Bon Pommier" is assumed to be the common progenitor of the two triploid cultivars "Double Bon Pommier" and "Double Bonne Ente".

The molecular data do not reproduce the grouping in various varietal types which is well known in French local cultivars: Reinette, Calville, Court-Pendu... The geographic origin does not seem to be a structuring factor of the genetic diversity as well.

Fig 1. Cluster analysis on SSR data of 142 French local cultivars generated by UPGMA clustering method based on Jaccard's distances.

■ Variety identification

All nine SSR markers give a very high discrimination level: 122 cultivars can be characterized by a single allelic profile. Seven pairs of cultivars have been proved to be genetically identical; five of them are well known synonyms. The study of the allelic profiles of the four remaining cultivars allow us to detect two misidentified cultivars in the INRA orchard.



We also confirm the origin of some suspected mutants: Reinette Grise du Canada and Reinette Grise du Grand Faye as mutants of Reinette Blanche du Canada; or Reinette Blain and Reinette Robert as mutants of Reine des Reinettes.

Conclusion-Perspectives

■ This study demonstrates the usefulness and the efficiency of SSR markers for varietal identification. The nine SSRs markers will be tested at a larger level to screen the European collection in addition to the passport data and the agronomical descriptors. Nevertheless, some additional analyses would be necessary to test the level of repeatability of such markers before extending their use to the European collection.

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