

Genetic diversity and structure of the Spanish apple genetic resources inferred using SSRs

S. Pereira-Lorenzo^{1*}; *C. Miranda*^{2*}; *P. Errea*³; *E. Dapena*⁴; *M.A. Moreno*⁵; *A.M. Ramos-Cabrer*¹; *J. Urrestarazu*²; *A. Pina*³; *N. Llamero*⁴; *M.B. Diaz-Hernandez*¹; *L.G. Santesteban*²; *M.J. Laquidain*²; *J. Sanzol*³; *Y. Gogorcena*⁵; *V. Urbina*⁶; *J. Dalmases*⁶; *J. B. Royo*²

1 Escola Politécnica Superior, Departamento de Producción Vexetal, Universidad de Santiago de Compostela, Campus de Lugo, 27002 Lugo, Spain

2 Universidad Pública de Navarra, Departamento de Producción Agraria, Campus de Arrosadia, 31006 Pamplona, Spain

3 Unidad de Fruticultura, Centro de Investigación y tecnología Agroalimentaria de Aragón, E-50059, Zaragoza, Spain

4 Servicio Regional de Investigación y Desarrollo de Asturias, 33300, Villaviciosa, Spain

5 Departamento de Pomología, Estación Experimental de Aula Dei CSIC, Apartado 13034, Zaragoza 50080, Spain

6 Departament d'Hortofruticultura, Botànica i Jardineria, Universitat de Lleida, 25198, Lleida, Spain

Keywords: Malus x domestica, germplasm, genetic diversity

A total of 1543 accessions from Spanish collections of *Malus x domestica* Borkh were evaluated with a set of 13 SSRs, including 11 recommended by ECP/GR *Malus/Pyrus* WG, in order to estimate their genetic diversity and to identify the genetic structure and relationships among their accessions, as part of the objectives of the project funded by INIA "Harmonization of the methodology of characterization, assessment of genetic diversity and definition of the core collection of the apple germplasm conserved in Spanish genebanks". 737 genotypes were differentiated, 581 diploids and 156 triploids, among them 78 were international apple cultivars present in our collections used as references. To study population structure and assign individuals to populations based on the SSR genotypes, we used a model-based Bayesian procedure, implemented using the Structure software for diploids and triploids separately. In the 581 diploid genotypes, two reconstructed populations were obtained, one with only Spanish cultivars (42% of genotypes) and a second related to Golden Delicious (with a secondary sub-structure). Analyses performed in the 156 triploid genotypes also revealed two reconstructed populations, one of them clustering exclusively local Spanish genotypes (44%). The Jaccard coefficient allowed clustering by UPGMA diploid and triploid Spanish genotypes from the international and commercial ones. AMOVA analyses showed moderate but significant differentiation among the main groups ($0.08 \leq F_{ST} \leq 0.12$). Our results highlight that Spanish germplasm constitutes a differentiated gene pool with respect to the international and commercial apple cultivars.

Corresponding author:

Santiago Pereira-Lorenzo

santiago.pereira.lorenzo@usc.es

Escola Politécnica Superior, Universidad de Santiago de Compostela, Campus de Lugo, 27002 Lugo, Spain