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Genetic diversity of the Spanish apple genetic resources using SSRs

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Abstract:

The Spanish Program of Plant Genetic Resources integrates, among others, the collections located at Public University of Navarre, Centro de Investigaciones Agrarias de Mabegondo, Cabildos (Tenerife, La Palma and Gran Canaria), University of Lleida, Estación Experimental de Aula Dei-CSIC and CITA of Aragon. Those collections include mainly local cultivars from their respective regions, covering most of the Spanish apple-growing areas. Though some previous studies about the genetic variability of apple genetics resources from Spain were already performed, a complete analysis is needed in order to evaluate the complete diversity of *Malus* spp. in Spain. For doing that, the Spanish Government funded the project “Harmonization of the methodology of characterization, assessment of genetic diversity and definition of the core collection of the apple germplasm conserved in Spanish genebanks”. In total, we have evaluated 1206 accessions using standardized methodologies, with SSR markers and morphological descriptors. SSR fingerprinting was performed with 13 SSR markers. SSR profiles were obtained independently and allele sizes were compared using a common set of cultivars selected as references. Results showed 601 genotypes for 1206 accessions. Most of the genotypes (438) were identified only in one accession. The other 163 genotypes were repeated in two to 81 accessions (involving 767 accessions in total). The harmonization of morphological descriptors will allow us to determine if the accessions with the same genotype are synonymies or closely related individuals. Results of this study highlight the interest of coordinated actions in order to optimize the management of germplasm collections and to evaluate the complete genetic diversity of *Malus* spp. in Spain.

Keywords: apple germplasm, biodiversity, identification, *Malus x domestica* Borkh, SSR markers