

Diversity and genetic structure of European plum in mountainous areas from Northeastern Spain

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Prunus domestica L. is one of the less studied species within the *Prunus* genus, mainly due to its polyploidy and lower economic importance in comparison with other *Prunus* species. As a consequence, there have been few studies for both the evaluation of the diversity and elucidation of the genetic structure in *P. domestica* L. germplasm. Knowing the extent and structure of genetic variation in germplasm collections is an essential step for the conservation and utilization of this biodiversity. In this context, we used codominant markers (SSR) to elucidate the patterns of genetic diversity and structure of *P. domestica* L. germplasm from the Northeastern of the Iberian Peninsula. One hundred and twenty accessions from this major area were analyzed jointly with a set of more than 40 reference cultivars that represents a wide range of diversity in this species. Based on the microsatellite data, a 27% of duplication degree was observed. In addition, a model-based clustering method was applied, after removing the redundant accessions, revealing the existence of four groups with a high percentage of genotypes (71.6%) strongly assigned ($q_i > 0.80$) to these identified groups. In this study, more than 70% of local accessions were located within groups containing nearly no foreign cultivars. This fact may suggest the uniqueness and potential interest of an important fraction of the analyzed local material for conservation purposes and for plum breeding programs. All in all, these results will provide valuable information that will allow to undertake a more rational management of the European plum material preserved in this geographical area.

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