



P309

Analysis of the Genetic Diversity and Structure in a Collection of Pepper (*Capsicum annuum*) Landraces from Spain

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Pepper (*Capsicum* spp.) is one of the most important crops in the family Solanaceae. *Capsicum annuum* is the most widely cultivated species and it represents the main subject of breeding programs. In the majority of growing regions, high-yielding commercial cultivars have replaced traditional landraces. However, these cultivars possess a reduced genetic basis, which make them more susceptible to biotic and abiotic stresses. Therefore, increasing the genetic variability within commercial cultivars appears compulsory. Genetic resources stored at germplasm banks constitute a valuable source of natural variation that could be incorporated into elite varieties. The aim of the present work was to analyze the genetic diversity and structure of a collection of Spanish peppers as well as to investigate their relationship to a group of worldwide accessions. Fifty-two *C. annuum* accessions were selected from the BGHZ (Banco de Germoplasma de Hortícolas de Zaragoza). The collection was genotyped with a set of fifty-five microsatellites markers previously described in the literature. The thirty-three informative loci amplified 151 alleles in the whole collection, with an average of 4.57 alleles per locus. Fifty-two alleles were recorded as rare alleles (those with frequencies <5%) and sixty-seven alleles were considered private alleles (specifically present in only one group). Cluster and STRUCTURE analysis showed a clear differentiation between worldwide and Spanish accessions. Although clear cut-offs could not be established, the pattern of clustering within Spanish accessions seems to be related to fruit shape morphology and organoleptic traits, such as pungency.

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