

## **S8/O3: DIVERSITY ANALYSIS OF *CAPSICUM ANNUUM* GENETIC RESOURCES FROM SPAIN**

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Pepper (*Capsicum spp.*) is one of the most important crops in the family *Solanaceae*. Its production increases every year all around the world due its wide diversity and great attributes for human consumption (high quality in flavor, concentration of vitamins and other antioxidants). *Capsicum annuum* is the most widely cultivated species as a vegetable or spice and it represents the main subject of breeding programs for commercial cultivars.

Nowadays, growers exploit a wide range of cultivars with excellent agronomic performance and highly adaptable to different ecological and cultural conditions. The demand of markets caused that, in the majority of growing regions, such high-yielding cultivars replaced traditional landraces. The main disadvantage of these cultivars obtained under artificial selection in modern plant-breeding programs is their reduced genetic base which makes them more susceptible to the biotic and abiotic stresses inherent to the crop. In order to overcome this limitation, it is compulsory to increase the genetic variability within the commercial cultivars. Genetic resources stored in the germplasm banks constitute an extremely valuable source of natural variation that has been traditionally under-utilized. Knowledge of the genetic diversity in these resources is essential to the identification of accessions for breeding programs and guides the development of efficient conservation programs in situ and in genebanks.

The main goal of the present work was to characterize the genetic diversity in a collection of Spanish peppers and to investigate their relationship to a group of peppers coming from other parts of the world. Fifty *C. annuum* lines were selected from the BGHZ (Banco de Germoplasma de Hortícolas de Zaragoza) and the CIAM (Centro de Investigaciones Agrarias de Mabegondo). Entries were divided into four groups: worldwide accessions, Galician ecotypes, lines with "certificate of origin" (CO) and BGHZ accessions obtained from different geographical regions in Spain. The collection was genotyped with a set of twenty microsatellites markers previously described in the literature. The number of detected alleles ranged from 2 to 10, with an average of 3.85 alleles per locus. Rare alleles (those with frequencies <5%) and private alleles (those present in only one group and absent in the others) were identified in worldwide accessions and lines from the BGHZ. Gene diversity was comparatively higher for the worldwide and BGHZ groups than for the Galician and CO lines. Cluster analysis showed a clear separation between Spanish peppers and lines from other countries. Accessions from Spain grouped together with a similarity of 0.61 but the clustering pattern was moderately a function of geographic origin, since close genetic relationships were sometimes observed between geographically distant accessions.

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