

## Genetic variation and preservation of autochthonous legume landraces grown on saline soils from West part of Romania

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Saline soils in the West part of Romania comprise almost 200.000 ha. We have previously identified this type of soils by analyzing their composition in  $\text{Cl}^-$ ,  $\text{Na}^+$ ,  $\text{Ca}^{++}$ ,  $\text{Mg}^{++}$ ,  $\text{K}^+$ ,  $\text{SO}_4^-$  and precise mapping (Ardelean et al., 2003; 2004). There is a wide variation of salinity resistance in food legumes (Vadez et al., 2007). In order to identify salt-resistance genotypes for breeding programmes, interaction between genotype and environment need to be considered (Flowers et al., 2009). Although there are few salt tolerant species, some genotypes present an acceptable level of adaptability to moderate saline conditions. In legumes, these genotypes are represented especially by local landraces bred over the time by local farmers from areas with saline soils. Many farmers have stopped growing these traditional ecotypes and turned to commercial varieties, which are fast growing and shape enhanced but not necessarily adapted to local environment. Identification of these cultivars represents a priority in breeding programs of vegetables all over the world. We have collected food legume (*Allium sativum*, *Allium ascalonicum*, *Allium cepa*, *Lycopersicon esculentum* Mill and *Phaseolus vulgaris*) landraces from 2 agro-ecological regions known for their salinity from the West Part of Romania in order to assess their phenotypic and genetic variation and to preserve the traditional germplasm. We imposed two criteria for collection: seed saving method by local farmers and no crossing or tweaking for commercial reasons. The distance between each pair of populations ranged from 10 to 50 km. The number of individuals in each population ranged from 10-100. Differences between accessions were observed in the fruit traits. We employed two classes of neutral genetic markers based on polymerase chain reaction (PCR): random amplified polymorphic DNA (RAPD) simple sequence repeat (SSR) markers to assess the genetic diversity. Our preliminary results show a large variation among the genotypes and the need for accurate estimation of allele frequencies. The present study is intended to identify populations to which priority should be given for dynamic conservation of landraces and make a baseline data available for farmers and breeders in this area.

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