



observed in 2 genotypes (Arpa Pear, Boşkova Pear). The genetic relationship dendrogram between genotypes was constructed according to UPGMA method. In the dendrogram, 6 subgroups were formed. 2 synonyms (genotypes 12-21 and 51-56) and 5 homonymous (genotypes 3-21-43, 31-41, 51-56, 57-58 and 26-38) were identified. In this research genetic relationships between Coruh Valley pear germplasm and some important standard cultivars were determined. It is considered that the obtained data will contribute to the study of next genetic origin studies, advanced breeding studies, protection of genetic diversity in terms of country economy and management of genetic resources.

Keywords: Pear, Coruh Valley, Genetic Diversity, SSR

OS4-3SSR genetic diversity assessment of French walnut (*Juglans* spp.) germplasm collection

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Abstract :

In France, walnut crop is the second largest fruit crop after apple, with 34,000 tons of in-shell walnuts produced in 2014, making France the 10th producer in the world with almost 20,000 hectares devoted. In parallel, the French walnut germplasm collection includes 259 accessions from worldwide thanks to the prospecting work of the late Eric Germain from 1977 to 2007, the former head of breeding program at INRA of Bordeaux. Among them, 220 are accessions of *Juglans regia* with 194 cultivars and 26 intraspecific hybrids, coming from the major growing areas such as North-America, Europe and Asia. The germplasm collection includes also 39 *Juglans* accessions of 16 related species from the two sections *Rhysocaryon* (*J. nigra*, *J. hindsii*, *J. microcarpa*, *J. californica*, *J. major*, *J. mollis*) and *Cardiocaryon* (*J. sieboldiana*, *J. cathayensis*, *J. mandshurica*, *J. cinerea*). In this study, 15 simple sequence repeat (SSR) markers selected from the literature (10 genomic SSRs from *J. nigra* and 5 EST-SSRs from *J. regia*) were used to genotype the 259 accessions. All SSR loci were highly polymorphic with a range from 7 to 33 alleles/locus (mean: 16.2) considering all the accessions, and with a range from 3 to 17 (mean: 8.9) for *J. regia* accessions only. The results indicate a high diversity among the genotypes which could be useful for the new French walnut improvement program. This study permitted to select 200 accessions that will be used for association genetics, using 600K SNP Affymetrix® array, in order to identify the genetic determinism of agronomic traits of interest such as those related to phenology, tree architecture, quality of the fruit and kernel, and susceptibility to different diseases.

Keywords: *Juglans* spp., French germplasm, French walnut improvement program, genetic diversity, SSR.

OS4-4: A Multi-Institutional Project for Breeding Lines/ Cultivars in Cool Climate Vegetables in Turkey

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