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Conservation and utilization strategies require fundamental knowledge about levels of genetic diversity, population genetic structure and effective population size, because they are the key elements that determine a species ability to respond to selection, either natural and artificial procedures. Sweet chestnut (*Castanea sativa* Mill.), widely distributed around Europe, is a multipurpose tree species of great economic importance for fruit and timber. Moreover, chestnut contributes to carbon storage, the landscape structure and the biodiversity conservation, that are relevant factors for environment management especially under climate change. Although there is information about chestnut traditional varieties, up to now, there is not complete information on the genetic diversity of natural populations in Spain. In this study, patterns of genetic variation and structure are assessed within and among natural populations of chestnut in Spain. 17 natural populations were evaluated using 7 microsatellite markers and Alleles in Space (AIS) software. This study allowed to describe the level and distribution of the genetic variability in Spanish chestnut populations, showing a high genetic diversity. Moreover, populations displayed a structure that followed a geographical pattern, indicating in a first approach, a separation between populations from West and east of the Iberian Peninsula.

S12.304

Genetic Resources of the *Corylus* L. Genus to Ukraine

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The different cultivars and ornamental forms of the *Corylus* L. genus are being studied to National dendrological park Sofiyivka of the NAS of Ukraine in the course of more than 20 years. *Corylus* L. genus is represented by 14 species, 120 cultivars and 15 ornamental forms. Amongst specimens *Corylus* L. genus only *C. avellana* L. is native plant - another are introduced. The most interesting Ukrainian cultivars to breeding are: Bolhrad's'ka novynka, Borov's'kyi, Dar Pavlenka, Klynovydniy, Koronchatyi, Loziv's'kyi sharovydniy, Pirozhok, Raketnyi, Serebrystyi, Stepovyi 83, Shedevr and Shokoladnyi. The exercisable cultivars introduced are: Futcuramy, Romana, Trapesund at alias. The best ornamental forms of *C. avellana* are: 'Aurea', 'Contorta', 'Fuscorubra', 'Heterophylla' and 'Pendula'. The most interesting forms of *C. colurna* L. are: 'Fastigiata', 'Nadija', and 'Poltawska'. On the basis of the studies of the other species introduced of the *Corylus* L. genus (*C. americana* Mill. (Marsh.), *C. chinensis* Franch., *C. cornuta* Marsh., *C. heterophylla* Fisch., *C. lacera* Wall., *C. mandshurica* Maxim., *C. maxima* Mill., *C. pontica* C. Koch, *C. sieboldiana* Blume, *C. tibetica* Batalin) the prospects of utilization of these species to Ukraine are considered.

S12.305

Agromorphological Characterization of Traditional Spanish Almond (*Prunus dulcis* (Mill) D. A. Webb) Cultivars

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Twenty-six traditional almond cultivars from "Arribes del Duero" in Central-Western Spain were surveyed and characterized agromorphologically. A total of 49 descriptors, mainly defined by the International Plant Genetic Resources Institute and the International Union for the Protection of New Varieties of Plants were used to describe flowers, leaves, fruits, one-year-old shoots and the tree itself over a two consecutive years. This made possible the unequivocal identification of 25 cultivars. A dendrogram gave a clear separation between the cultivars and showed

existing synonymies and homonymies. This work is an important step in the conservation of genetic almond resources in the province of Salamanca (Spain), which show distinctive and interesting agronomical characters such as high productivity, early fruit maturity and great rusticity.

S12.306

Investigation of Diversity among Five Populations of Native Persian Walnut in Golestan Province of Iran Using Quantitative Morphological Traits

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In order to understand diversity among five native populations of Persian walnut (*Juglans regia* L.) tree this research has been conducted. 96 tree samples studied for 32 different morphological traits (according to IPGRI and UPOV descriptors) such as leaf traits include length and wide of leaf, length and wide of leaflet and number of leaflet, nut traits and kernel traits include size (length, wide and thickness), volume, weight and nut index (husk, hull and kernel), thickness of hull, husk weight, percentage of husk moisture and kernel percentage). Variance analysis of traits showed significant differences ($p < 0/01$) among all traits existed, expect of thickness of husk, number, length and wide of leaflet that showed high diversity among native walnut traits in Golestan province. Difference of traits among locations used means comparison and Duncan test. There are positive and significant correlation between husk nut weight on kernel weight ($p < 0/01$) and negative correlation between husk nut weight on kernel percentage ($p < 0/05$). For genetic distance identification and genotypes grouping, used cluster analysis that Put on 6 clusters. These Genotypes was studied based on quantitative data and UPGMA algorithm. Classification of genotype based on molecular data did not match with their Geographical situations and existence high diversity among and between populations. Using principal component analysis for identifying each trait on existence diversity among the genotypes. The first six components constituted the 84% of variances.

S12.307

Brazilian Cashew Germplasm Bank

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The Cashew Germplasm Bank, located in Pacajus, Ceará State, Brazil, holds 621 accessions, the majority of them being from the species *Anacardium occidentale*. The introduction of plants in the bank, the main source of adequate materials for the development of commercial products, started in the 1950's. Nowadays, the main goals of the cashew germplasm bank are the enrichment of genetic variability of the specie, agronomic and morphological characterizations of accessions, supporting of breeding programs, and documentation and conservation. The accessions were characterized by means of morphological, agronomic and molecular descriptors. The genetic variability contained in the collection allowed the development of early dwarf cashew clones, recommended for commercial planting in Northeastern Brazil since the 1980's until today, besides 132 other early dwarf cashew clones and 40 common cashews still under evaluation. These results directly impact the cashew agribusiness. Furthermore, it made possible the expansion of the early dwarf cashew genetic basis by natural and artificial hybridization with regular cashew genotypes from the germplasm bank allowing a significant increase in the weight and size of nut and almond. Interspecies' hybrids of *A. occidentale* × *A. othonianum* e *A. occidentale* × *A. microcarpum* were also obtained with the goal of inserting anthracnose resistance alleles and desired quality traits to table cashew as well, which are under evaluation. The first genetic map of cashew was elaborated using AFLP and SSR, containing a total of 238 markers. This map is the basis for identification of QTL for application in the breeding program in order to reduce cost and time needed for cashew germplasm bank development of superior genotypes. The passport data were submitted to SIBRAGEN data bank and is available to the scientific community and breeding programs.