

IHC2018-Symposium 1

International Symposium on Tropical and Subtropical Vegetable Production: Tackling Present and Future Global Biotic and Abiotic Stressors

ORAL PRESENTATIONS

Session 1: PGR Management and Utilization; Climate Change

KEY NOTE 1:

Unlocking GeneBanks to Ensure Food and Nutrient Security and Environmental Stability

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Abstract :

Genetic diversity of indigenous minor fruits in Southeast Asia is tremendous but is under a great threat of extinction. This has generated an urgent need to manage the genetic resources and safeguard indigenous traditional knowledge associated with their uses. Most of these species are not only important as food, but also rich in micro-nutrients and antioxidants. Their occurrence in extreme climatic conditions is immensely contributing to environmental sustainability of fragile ecosystems. Therefore, ICAR-National Bureau of Plant Genetic Resources (NBPGR) has taken up extensive programme to collect, characterize and conserve the existing genetic diversity of many of these temperate and tropical fruit species. More than 3000 accessions of underutilized fruit species and their wild relatives have been collected and conserved in the Cryogenebank in the form of seed, embryos and embryonic axes. In some of the species such as *Ziziphus mauritiana*, *Emblica officinalis*, *Aegle marmelos* and *Prunus armeniaca*, few commercial cultivars have been developed and greater emphasis is now being given to adoption of these horticulture crops by farmers. In many of other fruits such as *Buchanania lanzan*, *Carissa congesta*, *Cappris decidua*, *Manilkara hexandra*, *Cordia myxa*, *Grewia asiatica*, *Salvadora oleoides*, *Syzygium cumini* and *Tamarindus indica*, no commercial cultivars are available and propagation is usually undertaken by seeds. Similarly several wild and semi-wild temperate fruits belonging to diverse genera (*Rubus*, *Ribes*, *Prunus*, *Rosa* etc.) have been collected and cryopreserved. These species are being used by local people as minor fruits/vegetables as well as for various medicinal purposes. Opening of the world markets and development of new biotechnological methods of genetic modification in commercial crops would further keep the attention away from these traditional underutilized crops leading to great loss in genetic diversity of these crops. In the present paper management of genetic resource and strategies for repatriation by unlocking the genebanks for several of these minor fruit and vegetable species for food and nutritional security and environmental sustainability would be discussed.

Keywords: Genebank, underutilized fruits, germplasm, cryoconservation



OS1-1: Current Status of Plant Germplasm Management and Utilization in Taiwan

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Abstract :

A National Plant Genetic Resources Center (NPGRC) was established at Taiwan Agricultural Research Institute (TARI) in 1993. The facilities include long-term, medium-term, and short-term storage rooms with different storage conditions in which are suitable for preserving orthodox seeds. The long-term storage room has the capacity of 240,000 accessions in aluminum cans sealed under partial vacuum. Up to September, 2017, the NPGRC has stored totally 91,782 accessions in its long-term and medium-term storage rooms. For the field genebank, the collection and preservation of germplasm including fruit trees, medicinal plants etc., approximately, 4,800 accessions are grown and maintained in several repositories. A total of 1,734 accessions of collecting clonal germplasm are cultured in vitro.

Germplasm distribution remains a major function of the NPGRC. Germplasm materials stored at NPGRC are available to all persons with academic purpose and can be upon application via internet or intranet. The offer of seeds is free of charge and together with relative information included for referring. The varieties distributed from NPGRC and transferred to research institute were approximately 1,200 accessions each year. TARI has engaged in international exchange of crop seeds and seedlings. During the past five years, the average numbers of varieties introducing or collecting from foreign countries were more than 2,000 accessions each year.

In order to modernize genebank operations, promote information exchange and international cooperation on germplasm collection, a computerized information system of NPGRC was completed in 1993. It is well recognized that the establishment of information system of germplasm enables users and breeders to search for needed information and to choose appropriate genetic materials in use on crop improvement program. NPGRC finally aim to become a regional center for tropical and subtropical crop, through international collaboration on collection.

Keywords: Plant germplasm, Seed bank, Seed management

OS1-2: Chestnut genetic resources: a model strategy for the development of local economies in mountain rural areas

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Abstract :

In Italy chestnut (*Castanea sativa* Mill.) is spread across the whole country and is a traditional food still based on cultivars selected centuries ago. In the XX century, most orchards were abandoned due to social changes and the spread of canker blight disease causing a constant decline of the national production, currently below 50.000 t. Yet, in the last decades, there have been policies for the recovery of old orchards and for the planting of new ones.

From a socio-economic point of view, chestnut can play an important role in promoting local identity and social cohesion as well as contributing to landscape; where the cultivation of this species is well established, the rediscovery of traditional local genotypes has the potential to set the bases of initiatives that can be a benefit for the local communities. The evaluation and selection of the cultivars, based on agronomic and quality traits, is essential to give back to the local chestnut growing areas, the uniqueness and specificity typical of the mountain lands.

In this work, we describe our experience on chestnut germplasm characterization aimed at selecting plant material to be used for the development of production chains and the exploitation of new market opportunities in the different growing areas. The final goal of the work was to provide growers with selected plant material able to yield nuts suitable for the fresh market or for processing.

Genetic analyses were carried out on leaves sampled from single grafted trees, found during surveys, using SSR markers. DNA typing allowed to define the identity of trees and to reorganize the genetic resources in several areas of North Italy. Morphological, chemical and sensory analyses were carried out on nuts from single trees in order to assess the quality characteristics of the fruits and define their possible use and exploitation.

Research funded by European Union (MANCHEST QLK5-2001-0029), Regione Piemonte (CIPE 2004), Natural and National Parks, and Mountain Communities

Keywords: *Castanea sativa*, quality, SSR, analysis, cultivar

OS1-3'Current Status of the Tropical Fruits, Musa and Cacao Genetic Resources at the Tropical Agriculture Research Station in Mayaguez, PR'

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Abstract :

The conservation of the broad range of plant genetic diversity, even when limited to agricultural interest, is above the capacity of individuals, private companies, or small groups, although each of these can and does contribute to managing plant germplasm. As one of the clonal repositories of the National Plant Germplasm System (NPGS) and in a long-term effort for the conservation of plant genetic resources under the USDA-ARS National Program 301 (Plant Genetic Resources, Genomics and Genetic Improvement), the Tropical Agriculture Research Station's (TARS) germplasm program in Mayaguez, Puerto Rico,



curates tropical and subtropical fruits germplasm. In addition to a number of tropical and subtropical fruit collections, the program is responsible for the curation of cacao (*Theobroma cacao*), and banana (*Musa* spp.). The project's main responsibilities are to acquire, propagate pathogen-free, maintain, characterize, evaluate and distribute germplasm. Characterization is based on phenotypic traits useful to distinguish accessions as well as morphological traits of horticultural importance. Genetic markers are used for the identification of mislabeling, understanding genetic relationships among accessions, estimating genetic diversity and identifying genetic gaps within the collections. Recent efforts have focused on a collaborative project for the development of SSR markers and SNPs for a number of tropical crop germplasm collections maintained at TARS. All passport, morphological (including voucher images) and molecular data for accessions are publicly available through the Genetic Resources Information System (GRIN-Global) database. Results from recent research conducted on tropical genetic resources at TARS are discussed further.

Keywords: Musa, cacao, germplasm, tropical fruits, Garcinia

OS1-4: The Effects of Global Climate Changes on Awakening and Flowering Times in Fruit Species

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Abstract :

Fruit cultivation is affected by global climate change at a higher rate as it is a multi-year agricultural activity. The purpose of this study is to explain the possible effects global climate change might have on the phenological periods of some horticultural plants. Productivity in fruit species, low flower buds casting and It is expressed by the amount of flowers being high. Together with climate change, flowering time on plants will change. While extreme weather conditions directly affects fruit production and quality, it also has negative effects on the bees that are involved in pollination. Early blooming of fruit trees may increase late frost damage, the quality of early crops will deteriorate and market values will decrease.

Keywords: fruit, climate changes, flowering time, quality

OS1-5: Determination the effects of ecological differences on volatile compounds in 'Bayramic Beyazi' nectarine variety

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Abstract :

White nectarine fruits, which are registered with the name of ‘Bayramic Beyazi’, are the novel stone fruit genotype grown in Canakkale. The fruits have a favorable and rich flavor for customer acceptance. White nectarines with high quality are the original material for improvement of new stone fruit varieties. The aim of present study was to determine the effect of ecological differences on volatile compounds in ‘Bayramic Beyazi’ white nectarine variety, which is widely grown in Canakkale Province in Turkey. Fruits of ‘Bayramic Beyazi’ white nectarine variety were harvested from 4 different commercial orchards in Bayramic and Ezine locations in Canakkale Province. Volatile component contents of ripe fruits of ‘Bayramic Beyazi’ were extracted by using diethyl ether solvent for liquid–liquid extractions. The amounts and identifications of the volatile compounds of extracted samples determined with a gas chromatography–mass spectrometer. According to the obtained results, a total of 30 volatile compounds were detected in total white nectarine fruits aroma profiles in different regions. Those were 10 esters, 6 C6 compounds, 5 terpenes, 5 aldehydes and 4 lactones. Hexanal, 2-hexanal, γ –decalactone, (Z)-3-hexyl acetate and ethyl acetate were found as important major volatiles in all ‘Bayramic Beyazi’ fruits. Although C6 compounds and lactones were determined higher ratio in Bayramic location; fruits in Ezine location were found to have higher esters, aldehydes and terpenes.

Keywords:Prunus persica, white nectarine, volatiles, flavor, Canakkale

OS1-6: Eco-friendly tomatoes: saving water and nutrient resources?

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Abstract:

Nutrient and water availability as well as sustainable use of resources are of high importance for modern horticulture aiming towards optimal and sustainable food production, particularly in arid and nutrient-poor areas. This also concerns the production of tomato, the world’s favored fruit, for which water and nutrient availability will be restricted due to the effects of climate change and agricultural intensification.

In the EU project TOMRES (www.tomres.eu), 25 partners from 10 countries work together on the optimization of tomato plants coping well under reduced nitrogen, phosphorus and water availability to ensure sustainable resource protection without losing fruit yield and quality. A collection of tomato lines is being screened to select most promising genotypes for detailed analyses. Under optimal and stress conditions, plant performance is being evaluated from vegetative growth to fruit production and from shoot to root zone interactions. Management strategies and decision-making tools will be established to support farmers, inform customers and demonstrate measures for further horticultural science approaches.

In the context of our work package, we screened tomato genotypes at the vegetative growth stage to identify effects of 50% reduced nitrogen, phosphorus and water supply on plant metabolism as well as on biomass accumulation. We found that first effects due to stress application were assessable by thermal detection, showing higher leaf canopy temperatures of



stressed plants and less well performing plants. Differences in leaf compound composition were detected at later developmental stages by spectral evaluation of optical leaf properties. Overall, the selection of promising genotypes as well as more resource-efficient management strategies can effectively contribute to improve sustainability of modern production processes.

OS1-7: Biochemical Components of Snap Bean (*Phaseolus Vulgaris*) Genotypes

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Abstract :

Beans are very important components that have high healthy benefits in daily dietary programmes while the healthy diet habits encouraged by governments all over the world basis. We analysed the extracts of twentyfive snap bean genotypes that include local populations and commercial varieties of *Phaseolus vulgaris* in order to determine their total phenolic content, antioxidant activity (FRAP), total chlorophyll content and sugar components. Total phenolic contents of beans varied between 0.25 and 0.80 mg GAE/g. Antioxidant activities of bean genotypes ranged from 1.70 to 6.30 $\mu\text{mol TE/g}$. Strong positive correlations were found between total phenolic content and antioxidant activity ($r=0.95$). Total chlorophyll content of bean genotypes varied between 21.12 and 77.76 $\mu\text{g/g}$. The sugar content including fructose, glucose and sucrose which contribute taste and flavour of bean genotypes are determined. Sugar composition of bean genotypes as fructose, glucose and sucrose ranged from 0.59-1.66 g/100g, 0.10-1.21 g/100g and 0.14-0.94 g/100g respectively. The analyses showed significant variability observed among snap bean genotypes.

Keywords: Snap bean, total phenolic content, antioxidant activities, chlorophyll content, sugar content, variability.

OS1-8: Germination, storage behaviour and population genetics of wild banana seed

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Abstract :

Bananas are the most important fruit crop in the world with a yearly production of 129 million tons and they are cultivated in more than 120 countries in the humid and semi-humid tropics. Until recent, banana collections existed mainly as field and in vitro collections. In the year 2003 a cryobank was established at the Bioversity International Transit Centre (ITC), Leuven Belgium.



During the last decades there is more and more interest in the CWRs (Crop Wild Relatives). They are considered an increasingly important resource in breeding for improving agricultural production and for maintaining sustainable agro-ecosystems. For wild bananas, *Musa* spp., standardized protocols for the germination and storage of their seeds are not yet available. In this study, we present some first results on the germination and storage behaviour of seed of *Musa acuminata* and *Musa balbisiana*, the wild ancestors of the edible bananas as well as from other crop wild relatives of *Musa*. Greenhouse germination rates are rather low and erratic and never exceeded 10%. This regeneration rate could be improved considerably by applying embryo rescue on in vitro media. The chemical viability test using TTC gave a good estimate on the in vitro regeneration. Subsequently, non-dried (MC between 10.5 and 27.3 %) and dried (MC below 10%) seed was subjected to different storage conditions; room temperature, 5°C, -20°C and -196°C for different time periods. We concluded that when sufficiently dried, *Musa* seed can be stored at -20°C as well as at ultralow temperatures.

Finally, we used 18 microsatellite markers to characterize the genetic diversity in the seeds of different populations of *M. balbisiana* and in accessions from the ITC germplasm collection. We show that these markers can be used to determine genetic variation between and within *M. balbisiana* populations.

Keywords: banana, *Musa*, embryo rescue, population genetics

OS1-9: Interrelationships between agro-morphological parameters on organic tomato (*Solanum lycopersicum* L.)

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Abstract:

Tomato (*Solanum lycopersicum* L.) is one of the important vegetable crops of the world. Evaluation and systematic study of tomato germplasm is of great importance for current and future crop improvement. In this paper, 8 tomato lines, indeterminate types, have been characterized for underlining the morphological traits connected to a high yield and for identifying the genotypes with good performance in yield under abiotic stress. The study has been conducted at Vegetable Research and Development Station Buzau Romania, under the normal testing conditions of 2016-2017 period. The biological material was represented by 8 tomato lines from the germplasm collection of the Physiology, Agro-Chemistry and Organic Crops Laboratory. The biological material has been grown in solarium on the ecological polygon, according to the crop technology in the agro-ecological system which was recommended by the scientific papers. Biometrical and morphological determinations of the plants and fruits have been performed according to the C.P.V.O. protocol, being prepared for measurements the standard papers. This study presents the variability of the main plant and fruits of the selected genotypes. The analysis of variance was represented by 3 repetitions of plants, respectively, fruits. ANOVA has revealed significant differences among the genotypes for all indicators analyzed. In this study, the parameters which have had significant correlations with yield have been the morphological indicators characterized for the stages of



plant anthesis and fruit development. The tomato type characterized with a good performance in yield under abiotic stress of 2016-2017 period has been the indeterminate cherry type analyzed for this study (L30 and L29).

Session 2: Plant Genetic Diversity, Conservation and Use; Crop Wild Relatives and Native Species

KEY NOTE 2:

Development of National Strategies for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture in Some Countries of the Near East and North Africa

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Abstract:

The Near East and North Africa region is the center of origin and domestication for several crops of which many are today considered important for food security and nutrition. A wide diversity of crop genetic resources is available in natural habitats, under cultivation and conserved in the genebanks. The continued availability of, and access to, this diversity are threatened by many factors, with climate change and the inadequate management of the resources being the most critical ones. The diversity of farmer varieties/landraces is eroded by the increasing uniformity of improved cultivars while that of crop wild relatives is eroded by the continuing loss of their natural habitats. Effective strategies are therefore needed for conserving and using these resources sustainably in order to avert this continuing genetic erosion. Within the framework of the FAO Technical Cooperation Project, TCP/SNO/3401, "Optimizing the Use of Plant Genetic Resources for Food and Agriculture for Adaptation to Climate Change" (2013-2015), Egypt, Iran, Jordan and Lebanon developed action plans for the conservation and characterization of plant genetic resources and their utilization in the respective national breeding programs. The major achievement of the project in the four countries has been the development of national strategies for an optimized management of plant genetic resources following a continuum approach, from conservation (in situ and ex situ), pre-breeding and breeding to seed delivery. The ultimate aim is to leverage these resources most effectively in improving the resilience cropping systems and hence the overall food security, nutrition and livelihoods of farming communities. This study reviews the current status of the management plant genetic resources in the Near East and North Africa, presents the major actions projected/planned in the national strategies and shares the lessons learned in developing the strategy documents which are now helpful tools for monitoring progress and reporting on the implementations of the Second Global Plan of Action on Plant Genetic Resources for Food and Agriculture and the Sustainable Development Goals.



KEY NOTE 3:

Cryopreservation of *Melia volkensii*

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Abstract :

Melia volkensii is a drought resistant and fast growing tree originating from the East-African savannah that is currently overexploited. Plant tissue culture tools are explored to meet the large demand of plantlets for their mahogany type timber production. Meristems of *Melia volkensii* were cryopreserved and thawed. Radish seeds were sown on Murashige and Skoog basal medium and the roots of the young seedlings were cut in pieces and placed vertically on the same medium. Fresh and cryopreserved *M. volkensii* meristems were grafted on the isolated roots or directly placed on semi-solid medium. The meristems survived, but as expected, there was no vascular connection with the radish roots. Interestingly, the combination cryopreservation + heterografting stimulated endogenous bacteria to grow out. This indicates the failure of cryotherapy to eradicate bacteria. On the contrary, it seems a be a useful technique to detect endogenous latent bacteria.

OS2-1: Vietnamese *Rubus*: crop wild relatives of the raspberries and blackberries

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Abstract :

Vietnam contains a wealth of *Rubus* species diversity. In Fall 2015, and during the year in 2017, wild relatives of cultivated raspberries and blackberries were collected during a Vietnamese-US cooperative expedition in Northern Vietnam. The exploration involved representatives of the Plant Resources Center, Vietnam Academy of Agricultural Sciences, in Hanoi and the U.S. Department of Agriculture, Agricultural Research Service (USDA/ARS) National Clonal Germplasm Repository in Corvallis, Oregon. The exploration was supported through the U.S. National Plant Germplasm System (NPGS) Plant Exploration/Exchange Program. Permissions for collecting were obtained from the Vietnamese Ministry of Agriculture and Rural Development, and the administration of four Vietnamese National Parks. Taxonomic identification and review indicated that about 108 accessions of 33 species of *Rubus* were collected from Northern Vietnam. *Rubus* species were plentiful throughout this region including in Hoang Lien Son National Park on Fansipan Mountain, and in and around Tam Dao, Phja Oac-Phja Den, and Ba Be National Parks. Root samples for propagation and seeds were collected. In October-November after the rainy season, these species simultaneously displayed all stages of phenology from bud break to fruit development. The diversity of the *Rubus* species in the high elevation regions of Vietnam suggests floristic similarities with highland areas in Taiwan, Southern China (Yunnan), and the Himalayas.



This plant material will be established and evaluated for descriptive characters in Vietnamese and U.S. genebanks as further genetic research of these invaluable resources continues.

Keywords: Plant exploration, plant genetic resources, Indochina, Fan Xi Pan, Tam Dao, Phja Oac-Phja Den, Ba Be National Park

OS2-2: Studies on survey, diversity, evaluation and traditional use of wild edibles of Himalaya

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Abstract :

Himalayas are considered as a major hot spot for plant diversity in India. Wild fruit plants play crucial role in livelihood and nutritional security of the local population in hilly regions. These wild resources have tremendous potential to mitigate the challenges of climate change, irrigation water crises and utilization of poor degraded lands since they have the inherent ability to tolerate biotic and abiotic stresses. Various parts of these plants are used in traditional systems of medicines, like Ayurveda and Siddha, etc., for numerous chronic diseases and disorders, the related ethno botanic knowledge of which is now getting eroding day by day.

In this perspective, Defence Research & Development Organisation (DRDO) has done extensive survey and studies, with the aim to identify the potential genotypes, evaluation and conservation of valuable genetic diversity, scientific propagation, cultivation and utilization of these resources to develop, hitherto underutilized, future fruits of Himalayas. Based on the studies, *Pyrus pashia* (Mehal), *Myrica esculenta* (Kaphal), *Rubus ellepticus* (Hisalu), *Berberis aristata* (Kilmora), *Rhododendron arboreum* (Buransh), *Punica granatum* (Darim), *Hippophae* spp (Seabuckthorn), *Ficus palmata* (Bedu), *Cratagus crenulata* (Hawthorn) etc have been identified as potential crops having nutraceutical properties.

Techniques have been standardized for scientific propagation to conserve the diversity and boost the availability of quality planting material for commercial cultivation. Field gene banks have been established in different zones of Himalayan regions to conserve the valuable diversity and support the future breeding programme. Efforts have also been made to develop methods for their commercial cultivation. In order to minimize the wastage of perishable fruits growing in remote hilly regions, value addition technologies have been developed. Initiatives have also been undertaken to patent and commercialize the processing methods where raw materials is available in plenty. Technologies developed have been transferred to private vendors which has created awareness in local population besides generating employment. The need of the hour is to provide policy support in the form of setting up modern nurseries, encouraging commercial plantations through government schemes and setting up vocational training centers for post harvest exploitation.

OS2-3: Genetic Diversity in Pepper (*Capsicum annum* L.) Genetic Resources Collected From The Aegean Region as Revealed by Agromorfological Traits



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Abstract :

In this study morphological characterization was carried out on 61 different pepper populations collected from Aegean Region (Kütahya, Afyon, Uşak, İzmir and Manisa provinces) in 2014, 2015 and 2016, and on 3 different pepper varieties. All populations were characterized in terms of 37 morphological features. Morphological data were analyzed by cluster and principal component analyses. Principal component analysis extracted 14 PC axes containing 79.10% of the total variation. The greater part of variation was accounted for by characters such as fruit shape at pedicel attachment, fruit width, fruit pedicel thickness, nodal anthocyanin, stem length, lamina margin, stem colour, calyx pigmentation and fruit colour at intermediate stage. A wide variation was observed among the populations. As a result of the clustering analysis, 2 main groups and 5 subgroups were formed. There were 2 subgroups in the first main group and 3 subgroups in the second main group and pepper accessions were identified according to this analysis.

OS2-4:Determination of Genetic Biodiversity by Using Morphological Characterization of Some Local Kidney Bean and Fresh Bean Genotypes Grown in Erzincan Province

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Abstract :

In order to determine the genetic diversity of some local fresh and kidney bean genotypes in Erzincan region, the collected 36 bean genotypes were examined for 12 morphological characteristics (fibre status, Finned flower color, Flagicle flower color, status of flaps opening, Style protrusion, apex leaf shape, pod ground color, pod spotting status, pod curvature grade, pod shape, pod peak shape, Seed appear). As a result of correlation analysis, the most significant positive correlation between the flagship color and the aerofil color (0.55**), and again the most significant negative correlation was found between the leaflet shape and the style (-0.70**). Six key components were identified as the result of analysis of the key components. Analysis of these components revealed 71.24% of the total variance among the bean genotypes. The percentage of variance of these key components and the cumulative percentage value are presented respectively 14.86% and 14.85% of the first component, 14.50% and 29.37% of the second component, 11.53% and 40.91% of the third component, 11.19% and 52.11% in the fourth component, 10.04% and 62.15% in the fifth component and 9.08% and 71.24% in the sixth component. For understanding kinship relation between genotypes according to quantitative characteristics and identify heterotic genotypes have been done clustering analysis among genotypes. According to the results of clustering analysis, genotypes were found in 4 groups (80.55% in the first group, 2.77% in the second group, 5.55% in the third group and 11.11% in the fourth group). In terms of clustering analysis, the CVZ 21 and ULU 55 genotypes have the highest genetic distance and therefore,



in the breeding programs to be carried out in the future in order to benefit from the heterosis may be useful in the production of new varieties.

Keywords: Phaseolus vulgaris, bean, Erzincan, morphological

OS2-5: Characterization Of Cherry Genotypes From Blacksea Region

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Abstract :

This study was conducted on 20 cherries genotypes collected from Amasya and Giresun, Turkey. Cherry genotypes grafted on mazzard rootstock morphological characterization according to UPOV criteria. In the study, it was aimed to determine phenological, morphological and fruit quality characteristics of these genotypes and to select promising cherry genotypes. In the research, phenological, morphological and fruit quality characteristics such as first blossom, full blossom, harvest date, tree growth habit, leaf width and length (cm), flower shape, fruit weight (g), fruit width, length and height (mm), yield, fruit weight, fruit shape, skin color, soluble solid content (%), titrable acid content (%), flavor and outer appearance of the fruit of 20 cherry genotypes were determined. Cherry genotypes full blooming date 5-10 april, harvest date 3-25 june; fruit weight 2,95-7,58 g, and seed weight 0,16-0,64 g as determined. According to morphological and phenological data genotypes among variation is important.

Keywords: cherry, Giresun, Amasya, genetic source, morphological characterization

OS2-6: Characterization Study in The Local Melon (Cucumis Melo L.) Varieties

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Abstract :

This study has been conducted in order to determine the morphological diversity of the Cucumis melo L. landraces, provided from different regions, in addition to the registered varieties of Aegean Agricultural Research Institute. 43 melon accessions from different cities of Turkey such as Denizli, Muğla, Uşak, Manisa, Çanakkale, İzmir, Van have been collected and studied by using IPGRI and UPOV descriptors. During these studies 10 traits of seed; 3 traits of seedling; 6 traits of plant; 16 traits of leaf; 6 traits of flower and 37 traits of fruit; together with another 8 phenological traits, a total 86 traits have been observed. Morphological and phenological traits showed significant variation among accessions. By applying cluster analysis according to Principal Component Analysis (PCA) and UPGMA to the acquired data,



dendrograms have been formed. Cluster analysis of morphological and phenological characters divided local melon accession into four groups.

Keywords:Melon (*Cucumis melo* L.), morphological characterization, UPOV, IPGRI

OS2-7: Morphologically characterizations of some watermelon genotypes seeds

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Abstract :

Watermelon is a monocious and mostly foreign pollinated vegetable, but its genetic base is quite narrow. This situation causes a challenge about characterization of genotypes or lines. Genetically controlled morphological characters can carry the characterization of genotypes one step further. In watermelon, some seed characters are under genetically control such as grand and over color of testa or patches at hilum. In this study, morphological characterization of 152 watermelon genotypes seeds were performed. 100 seeds from each genotype were examined for seven characters; length, width, length/width ratio, ground color of testa, over color of testa, area of over color in relation to that ground color of testa and patches at hilum. According to principle component analysis of these seven characters were explained 69.17% of cumulative variance with three components (Eigen values>1). Two main and four sub clusters were occurred to hierarchical cluster analysis. Seeds of genotypes are generally separate two main groups phenotypically which are white or yellowish seeds and black and over colored. Withal several extreme phenotypes were observed but they were evaluated with others because there are no relevant character markers. In conclusion length, width and area of over color in relation to that ground color characters had top three effect on explaining to variance between genotypes. Contrary to this length/width ratio had minimum effect on explained total variance.

Keywords:Citrullus lanatus, morphological characterization, seed characterization

OS2-8: Study Concerning the Main Characteristics of Dwarf Bean Seeds in the Environmental Condition of S - E Romania

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Abstract:

Vegetable Research and Development Station (V.R.D.S.) Buzau is one of the main institution from Romania which is preoccupied with conserving biodiversity at vegetable species. Lately, the activity concerning biodiversity conservation have intensified at bean (*Phaseolus vulgaris* L.), thus, the germplasm collection of this species contained over 200 accessions. This paper presents the comparative study of the main characteristics of 40 dwarf bean (*Phaseolus*



vulgaris L. var. nanus) seeds (weight, length, width, thickness, shape in longitudinal section, color and secondary colour distribution) which were cultivated in 2016 in the environmental condition of S – E Romania. Seeds weight (100 seeds mass) varied between 62.12 g (V7) and 19.69 g (V4), having a mean value equal to 38.59 g and a high (28.39%) coefficient of variation. Seeds length varied between 17.68 mm (V7) and 10.13 mm (V40). The coefficient of variation was mean for length (14.18%) and width (14.58%). The highest values concerning seeds width (9.14 mm) and thickness (6.93 mm) was registered at V27, and the lowest values (4.98 mm and 4.23 mm) were registered at V4. More than half of the studied seeds variants presented 1 color (6 – white, 6 – black and 13 with different colors). The secondary color was distributed around hilum (V7 – V9), on half of grain (V10) and on entire grain (V24 – V34). Most variants presented an elliptic shape or kidney – shaped seeds (shape in longitudinal section); only V27 presented circular shape (length/width ratio was 1.3), and V15 and V40 had rectangular seeds. These results dignify a great variability in what it concerns the biological material collected and also justify the works concerning the biodiversity preservation for this species.

OS2-9:Some Flower and Pod characteristics of the Genotypes of Green Beans and Kidney Beans (*Phaseolus vulgaris* L.) Collected from the Erzurum Region

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Abstract :

The objective of the study was to characterize a total of 120 green beans and kidney beans genotypes collected from Erzurum province in terms of morphological characteristics. Local green bean and kidney bean genotypes collected from farmers during the autumn and winter period were sown to observational rows in Atatürk University's application and research area in May of 2016. Data on 15 morphological traits of flower and pod were recorded according to UPOV (2012) protocol. That exhibit the rate at which of the selected characters of flowers (color of standard, color of wing, opening of the wing) and pod (number of fruits in bunch, apparent seed of fruit, shape in cross section the presence of secondary color, secondary color, density of flecks of secondary color, stringiness of ventral suture, degree of curvature, texture of surface, shape of distal part (excluding beak) of genotypes were evaluated using a frequency distribution and percent variation. In the present study, morphological characterization showed a wide variation in terms of some flower and pod characteristics.

Keywords: *Phaseolus vulgaris* L., flower, pod, characterization

OS2-10:A South American forgotten vegetable: *Cyclanthera pedata* (L.) Schrad, a contribution to its agronomic management

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Abstract :

Cyclanthera pedata, was eaten by pre-Columbian cultures in South America. Nevertheless nowadays, this vegetable is not been intensively exploited, in most cases only small orchards or self-supply productions can be seen. In Chile is grown in Arica & Parinacota, Tarapaca and Atacama region only in small farms with little agronomic management. At same time, there is no detailed information about it. Two different trials were done to contribute with cultural improvements of the crop. Optimal range germination temperature was determined between 20-30°C, obtaining the best germination speed at 25°C, similar to other cucurbitaceous species like watermelon, cucumber or melon. On the other hand, under 45% shade net (blue-white stripes), plant density was determined to be best at 2x1 m instead to 2x2 m, either using horizontal wires and hand tutoring strings or using a 15x15 cm vertical plastic net fort self tutoring. In order to evaluate the potential yield, PAR intercepted was measured at two stages. At the beginning of harvest no differences were detected between treatments, whereas, two month after harvest, plants at 2x1 m with plastic net got higher PAR interception than plants at 2x2 m with horizontal wires. In part due to the PAR interception results, number of fruit per ha was higher under 2x1 m, independently of the tutoring system, but keeping the same mean weight per fruit. Considering a period of two month of harvest, planting at 2x1 m is recommended, using plastic net because require less hand labor than horizontal wires.

Keywords:Caigua, tutoring, PAR interception, germination

OS2-11:Evolutionary biogeography of *Pistacia* - from molecules to a global distribution

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Abstract :

The genus *Pistacia* L. (Anacardiaceae) consists of 11 species. Seven species are distributed from the Mediterranean basin to Central Asia (*P. atlantica*, *P. khinjuk*, *P. lentiscus*, *P. palaestina*, *P. terebinthus*, and *P. vera*), two species in Eastern Asia (*P. chinensis* and *P. weinmannifolia*), and two species from the Southwestern United States to Central America (*P. mexicana* and *P. texana*). *Pistacia aethiopica* was defined as a new species in 1980 by J. O. Kokwaro, however, its status has not been evaluated. The global distribution of species of the genus and their genetic relationships in relation to arid and semiarid zones and long-term climate change is in the focus of this work. The presentation will include data based on molecular markers analyses, GIS and remote sensing techniques. We hypothesized that long-term global climate episodes affected differentially the different species, limiting the distribution of those that are more vulnerable to drought and heat and vice versa in relation to the tolerant species. A better understanding of the species distribution related to drought, temperature change tolerance, and nutritional requirements were studied. The availability of an extensive germplasm collection of *Pistacia* from various geographical regions around the globe at the Jacob Blaustein Institutes for Desert Research has made it possible to evaluate their genetic relationships and the evolution of the genus. The adaptation of *Pistacia* trees to harsh desert conditions and their longevity make them ideal candidates for reforestation in arid zones.



OS2-12: The onset of controlled hybridization, pollination studies and the history of pollinizer application in the commercial fruit tree orchards in Iran

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Abstract :

The effective pollination and use of suitable pollinizer is an important task in the commercial fruit tree orchards. In addition, Iran is a big country with the strength fruit industry in which consists of culture and planting of 2.8 million hectares of wide range of fruit tree species with more than 15 million tones annual production. In addition, Iran has a long history in fruit culture and planting, also well known for some fruit crops and also the centre of origin of many tree species such as pistachio, Persian walnut, apricot, sweet cherry, pomegranate and some other valuable fruit trees. The national and overseas fruit tree breeders always have been interested and benefited from the rich Iran fruit tree germplasm as a good source of working material and suitable gene pool for any related breeding programs. The importance and quality of Iranian fruit tree germplasm always have been confirmed and certified by the national and international fruit tree breeders in any kind of foreign exploration for enriching the working material, establishment of new collection orchards in the framework of any gene reservoir programs. In spite of the long history of fruit culture and the rich of fruit tree germplasm, the onset of documented pollination studies and the history of pollinizer application in the commercial fruit orchards in Iran are short and come back to 1987. Although an initial, but not documented thought for pollination studies has been noticed from 1963 for sweet cherry and a few practical use of pollinizer on apple trees in 1974. The first effective, successful and documented pollination and compatibility studies project had been started in the framework of MSc thesis project at University of Tehran in 1984. The project title was "Compatibility and incompatibility studies of some sweet cherry cultivars in fertilization and fruit set of sweet cherry cv. 'Siah Mashad' and was completed and reported on 1987. The experiment was conducted in the commercial sweet cherry orchard, 20 km west of Tehran during 1985 to 1987. Note that mature sweet cherry trees cv. 'Siah Mashad' on 'Mahlab' rootstock were planted in 5 m between rows and 6 meter within rows with no or very low fruit yield (1 to 2 kg-tree). The output of this effective project leads to the determination of suitable pollinizer for this local important cultivar. In 1988, sweet cherry trees in the mentioned studied orchard top worked and the specific determined pollinizer were grafted on the 10% of the planted trees, resulted the dramatic increase in fruit yield in the following year up to 80 kg-tree . In addition, the other output of this project was increasing the knowledge of pollination studies and pollinizer application in the commercial fruit tree orchards in the country, the onset and continuing pollination studies on the other fruit crops in order to check self compatibilities as well as cross compatibility or incompatibilities in various fruit crop species in the country. In the other hand, the situation of lack of or poor information on pollination studies and use of suitable pollinizers in the orchards with low production was changed during the last three decades from the onset of the sweet cherry MSc thesis project. It has been a dramatic increase of the knowledge of applied pollination and pollinizer use in the orchard after 1987 and based on the continuing pollination studies in the



country, so at the present time any new planting areas in the country, managing with proper pollinizer arrangement and application. The onset, history of fruit trees hybridization and applied pollination studies in various fruit crops that leaded by Pomology Lab at TMU with collaboration with the other universities and research institutes will discuss.

Session 3: Plant Genetic Diversity, Conservation and Use; Crop Wild Relatives and Native Species

OS3-1: Role of U. S. Department of Agriculture's National Genetic Resources Advisory Council (NGRAC) in Providing Strategic Recommendations for Strengthening National Genetic Resources Conservation and Use

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Abstract :

Originally established in 1990 by the Food, Agriculture, Conservation and Trade Act via the U. S. Farm Bill, the National Genetic Resources Advisory Council (NGRAC) is an advisory body to the U. S. Department of Agriculture's Secretary of Agriculture and the Director of the National Genetic Resources Program (NGRP) on the activities, policies, and operation of the NGRP. The main activities of the NGRAC include: provide advice on acquisition, preservation, access, distribution and exchange of genetic resources of life forms important to American agriculture such as plants, forest species, animals, aquatic species, insects, and microbes; make recommendations to ensure that these essential resources are adequately conserved and appropriately accessible in order to address current and future agricultural needs; provide advice on research needs for genetic resources and for coordination of genetic resource plans of several domestic and international organizations; and provide advice on new and innovative approaches to genetic resources conservation. Details of activities undertaken by the NGRAC and their impact on the U. S. National Genetic Resources Program will be discussed.

Keywords: Genetic resources, conservation, advisory council

OS3-2: Effect of different dehydration conditions on osmolyte accumulation, thermal events and survival of vanilla shoo-tips following droplet-vitrification approach

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Abstract :



The impact of different osmodehydration conditions were studied during the cryogenic protocol called droplet-vitrification and by using vanilla (*Vanilla insignis*) shoot-tips as study case. Gas chromatography-mass spectrometry was used to identify the accumulation course of some compatible osmolytes, and Differential Scanning Calorimetry (DSC) to analyse the removal of osmotically active water from the shoot-tips. Survival after each stage of dehydration (preconditioning, loading and PVS exposure) was evaluated by the regeneration of new shoots after 3 months of recovery culture. Vanilla shoot-tips up to 3 mm long were isolated from plantlets propagated in vitro and then, subjected to preconditioning on standard semi-solid MS medium for 7 days, followed by the same medium supplemented with 0.3 M sucrose or trehalose for additional 7 days. After preconditioning, shoot-tips were loaded in solutions containing 0.4 M sucrose or trehalose mixed with 2 M glycerol for 20-30 min, and then exposed to the PVS2 or PVS3 vitrification solutions for 30 min at room temperature. Out of 12 amino acids, 9 carbohydrates and 5 polyols detected in untreated shoots after dissection, proline, sucrose and glycerol varied during all successive dehydration steps, regardless of whether it was not exogenously supplied as in the case of proline. Trehalose was only detected when it was used during preconditioning and/or in loading solution. Osmotically active water was reduced from the initial content 0.80 gg-1 FW up to a maximum of 0.12 gg-1 FW after preconditioning and loading with sucrose followed by the exposure to PVS2; however, the highest survival percentages ranged between 53 and 65% mostly using treatments with trehalose and when freezable water remained around 30% (0.24 gg-1 FW). Melting events were the only thermal event detected after all the dehydration treatments studied. These results might explain why shoot-tips of vanilla do not survive after cryopreservation.

OS3-3:Ex situ conservation of strawberry (*Fragaria* spp.) germplasm in ICAR-NBPGR

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Abstract :

Strawberry, *Fragaria* spp. of family Rosaceae is a potential crop in Indian agriculture. It is a vegetatively propagated perennial crop where good quality fruiting varieties are in demanded by farmers and good quality germplasm is required by breeders for crop improvement purposes. In addition, four species of *Fragaria* occur wild in Indian Himalayan region. Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, India is actively involved in the ex situ conservation of strawberry germplasm. Largely, *Fragaria* germplasm is being maintained in the field genebanks at Regional Station, Bhowali. Since, the field-grown plants are exposed to pest-pathogen and natural vagaries including climate change, in vitro conservation of germplasm was emphasized as a complementary method to the field genebank. The protocols for in vitro conservation were developed for slow growth methods such as at low temperature storage and for normal growth conditions. Cultures were raised from shoot tips and runners from field genebank-grown plants to have true-to-type accessions. As a safety duplicate, about eighty accessions are being maintained in the In Vitro Genebank of ICAR-NBPGR including exotic accessions procured from National Clonal Repository, Corvallis, Oregon, USA. At normal growth conditions ($25\pm 2^{\circ}\text{C}$), the average subculture period ranges from 6-8 months, while at



low temperature (in vitro- shoot tips of *F. vesca*. About 20-30% post-thaw recovery was recorded. The in vitro conserved rooted plants were acclimatized and transferred to field genebank at Bhowali. Tissue Cultured plants were morphologically similar to mother plants.

Keywords:In vitro conservation, cryopreservation, virus indexing, post-thaw recovery, exotic and wild species, field genebank, cryotherapy

OS3-4:Genome evolution and genetic diversity of grapes

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Abstract :

Botanical diversity of grapes culture, reflected in the classification and taxonomy of varieties and forms of the Vitaceae family of Vines, reflects the process of natural evolution, natural and artificial selection. Scientists in the various countries in the XVIII—XX centuries carried out a grandiose work that made it possible to differentiate representatives of the Vitaceae family in botanical taxons. The conducted researches established that all this botanical variety of the Vitaceae family was formed in different centers of origin of the grapes culture on the planet. Depending on the abiotic conditions in the centers of origin of culture, a genome was formed in the forms of individual botanical taxons, in particular within genera and species differentiated in resistance to abiotic stress factors. Biotic conditions in these same centers of origin formed the genome in the forms of the same individual botanical taxons, within the genera and types of grapes as a host plant, differentiated by resistance to biotic stress factors and the pathogen gene in the process of conjugate evolution. In the end result, samples of grapes were formed in each separate center of origin of the culture, differentiating not only according to botanical characteristics, but also on a set of biological characteristics, in particular, resistance to biotic and abiotic stress factors of the biosphere.

Speciation, specifically the formation of the species *Vitis vinifera* L., is directly related to the existence of wild forest grapes, belonging to the relics of Eurasia. The studies established a significant difference, including morphological, morphometric features and molecular genetic markers, between forms of wild forest grapes from various regions of Eurasia. Consequently, it may be considered necessary to continue these studies in order to isolate in the centers of origin of the culture of the grapes individual foci or sub centers of origin.

OS3-5:Genetic variation and in vitro regeneration of wild pear *Pyrus elaeagnifolia* genotypes collected from different part of Turkey

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Abstract :



Pyrus elaeagrifolia Pall. (Ahlat) is one of 22 *Pyrus* species and spreads in Southeast Europe, Russia and Turkey. The trees are medium-sized, rounded crowned, often branched and thorny. The fruit is small, round and very smooth. This species has been described as a rootstock that is well-suited to arid climatic conditions, deep rooted, completely xerophyte-like and can be used in pear farming. Among the *P. elaeagrifolia* types, there are differences in fruit weight and shape, resistance to abiotic stress conditions and vegetative growth potentials. In this study, in vitro propagation efficiency and genetic variation of 40 *Pyrus elaeagrifolia* genotypes were determined. To determine multiplication efficiency MS media (9.0 μ M BA (benzyladenine), 0.5 μ M IAA (indole-3-acetic acid), 0.3 μ M gibberillic acid (GA3), were used. Twenty genotypes out of 40 genotypes showed in vitro shoot formation at rates ranging from 3.3% to 16.6% and genotype N37 numbered from Nevsehir with maximum shoot formation of 16.6% and genotype KM53 from Kahramanmaraş were obtained. Molecular analyzes performed using 13 ISSR primers. According to dendrogram genetic similarities between the genotypes ranged from 0.75 to 0.98. The most distant genotype was AN64, while the closest genotypes were N40 and N41. All of genotypes were distinguished. Our results showed that there were moderately high level of variation among the genotypes. This results may offer new insight for breeding and conservation strategies of wild pear.

Keywords: genetic diversity, in vitro, wild pear

OS3-6: Induced polyploidy alters *Plectranthus esculentus* plant morphology and response to environment

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Abstract :

Due to the negative impact of biotic and abiotic stressors on sustainable crop production, it is critical that endangered germplasm is not only conserved but that technology is used to harness and improve these genetic resources. With an ever increasing global population, particularly in the context of the unpredictability of climate change, declining food and nutrition security urgently needs to be addressed. *Plectranthus esculentus* (wild potato), is a tuberous crop indigenous to South Africa and is considered a 'lost crop'. It is listed as data deficient on the Red List of South African plants as there is insufficient information to determine conservation status. Although *P. esculentus* was cultivated widely in the past, the plant appears to be exceptionally rare in its natural habitat and therefore its natural distribution and the extent of its range are not well understood. This root crop is an excellent food source and can survive suboptimal soil conditions, thriving under moderate rainfall. It is affected by root knot nematodes which have a negative impact on tuber yield. Artificial induction of polyploidy in vitro resulted in the development of tetraploid *P. esculentus* plants with altered morphological characteristics. The impact of polyploidy on the morphological and physiological status, compared with the diploid progenitors, as well as potential for further genetic characterisation and subsequent impacts on this species as well as others, will be discussed.



Keywords: climate change, chromosome doubling, orphan crop, wild potato

OS3-7:Diversity, Uses and Conservation Strategies for the Brassica oleracea complex species in Europe

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Abstract :

The Brassica genus represents the most complex one of the Brassicaceae family and is an important source of vegetables, condiments and both edible and industrial oils. The Brassica oleracea complex represents the primary gene pool of Brassica genus C genome ($n=9$) which is involved in the domestication processes of several vegetable crops, such as broccoli, cabbage, cauliflower, kale, kohlrabi etc. Over the time, growers have managed the disruptive selection-based evolution of the several B. oleracea crops and many researchers are tracing their domestication processes and their relationships in order to diversify, improve and innovate agricultural systems and products. In the Mediterranean area, Italy owns the largest diversity of B. oleracea landraces, grown in home gardens and in peri-urban vegetable farms of the Southern regions like in Sicily where, broccoli, cauliflower, kale and kohlrabi showed different potentially useful traits for the innovation of relevant production chains, and have been bio-morphologically, biochemically and genetically characterized to this purpose. Over the last century Brassica wild relatives ($n=9$) have been widely used in breeding programmes to improve resistance/tolerance to biotic and/or abiotic stresses in various crops. Recently, high antioxidant properties were found in some Sicilian broccoli landraces, of which have been used in breeding programmes allowing to obtain new cultivars with high levels of glucosinolates. The activities carried out at Di3A led to identify several interesting sites of B. oleracea complex species for their ex situ, in situ and on farm conservation. The large variation observed among the analyzed accessions confirmed the importance of the Sicilian gene pool of B. oleracea complex species ($n=9$), endorsing the need to promote their protection by the establishment of genetic reserves.

Keywords: Germplasm, innovation, vegetables, domestication, in situ conservation

OS3-8:Fruit quality assessment and oil extraction of some mature wild trees of Persea schiedeana Nees grown in Mexico

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Abstract :

Persea schiedeana Nees is an underutilized and very little known species whose fruit is consumed in Mesoamerica where it grows wild. This study was carried out to evaluate: 1) the variability of fruit characteristics of different accessions; 2) the effects of centrifugation and microwave treatment on extracting oil from the fruit and on its qualitative characteristics; 3)



the nutraceutical characteristics of the fruit and seeds of different accessions. The results showed a large variability in fruit size and oil/dry matter contents among the different accessions. There was a significant relationship between the dry matter and oil contents in the pulp. The combined use of centrifugation and microwave treatments gave high oil extraction yields (67-68%). The oils had good fatty acid composition and antioxidant capacity. The results gave an initial picture about the total phenol contents and antioxidant capacities in the seeds and in the different parts of the fruit.

Keywords: antioxidants, centrifugation, Lauraceae, microwaves, oleic acid, *Persea schiedeana* Nees, total phenols.

OS3-9: *Chrysanthemum repens*, a rare new species of the Genus *Chrysanthemum* L. from China

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Abstract :

In the collection of wild species of *Chrysanthemum* L. in the coastal area of Yantai, Shandong Province, a wildly distributed creeping species was found, which was classified as a genus of *chrysanthemum* L. with white or brown membranous margins on the phyllaries. Because of its morphological characteristics are extremely specific, so called a rare new species of the genus *Chrysanthemum* L. from China -- *Chrysanthemum repens* M. Sun et J. T.Chen, sp. nov. It appears most closely related to *Chrysanthemum indicum* L., but its characteristics are quite different from *Chrysanthemum indicum* L.. 1) plants are not common upright, but creeping, low, height less than 10cm, and large crown; 2) inflorescence types are different: Single flower blooms on the top of lateral branchlets, or 2 to 4 flowers bloom on leaf axils the top of lateral branchlets. Flowering branches forming large loose panicles; 3). The size of the flowers are obviously different: flower large: 2.5 ~ 3.0 (~ 3.5) cm in diameter; 4) There is a clear difference in leaf morphology: thick leafy, nearly Leathery, veins raised on both surfaces; Main branch leaves, larger, length 4 ~ 6cm, width 3.4 ~ 4.5cm; lateral flowering branchlet leaves, smaller, length 1.5 ~ 2.0cm, width 0.6 ~ 1.0cm; 5) Chromosome ploidy and ordinary *Chrysanthemum* are different: *Chrysanthemum indicum* L. is diploid, but its chromosome number is $4n = 36$. For creeping growth, multi-branched, covering the ground ability, drought resistance, wide adaptability, and the large amount of flowers, this rare germplasm resource will play a huge role in the breeding of creeping ornamental *Chrysanthemum*. After 4 years of observation, introduction and cultivation experiments, the results show that the morphological characteristics of this species is stable, and the species has important scientific significance in the theory of its origin, deformation and horticultural breeding.

Keywords: China; Coast; Morphological specificity; Compositae; *Chrysanthemum* L.; New Species



OS3-10:Genetic Diversity in Tomato (*Solanum lycopersicum* L.) Genetic Resources Collected From The Aegean Region as Revealed by Agromorfological Traits

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Abstract :

In this study morphological characterization was carried out on 55 different tomato populations collected from Aegean Region (Kütahya, Afyon, Uşak, İzmir and Manisa provinces) in 2014, 2015 and 2016, and on 3 different tomato varieties. All populations were characterized in terms of 20 morphological features. Morphological data were analyzed by cluster and principal component analyses. Principal component analysis extracted 6 PC axes containing 79.59% of the total variation. The greater part of variation was accounted for by characters such as fruit shoulder shape, width of pedicel scar, shape of pistil scar, ribbing at calyx end, number of locules, intensity of greenback (green shoulder), exterior colour of mature fruit, flesh colour of perikarp, fruit length, fruit weight, plant growth type, presence of green (shoulder) trips on the fruit and blossom end shape. A wide variation was observed among the populations. As a result of the clustering analysis, 2 main groups and 6 subgroups were formed. There were 2 subgroups in the first main group and 4 subgroups in the second main group and tomato accessions were identified according to this analysis.

Keywords:Tomato (*Solanum lycopersicum* L.), agromorphological characterization, landraces.

OS3-11:Morphological evaluation and oil quality aspects of Jordanian olive cultivars

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Abstract :

This study was carried out to evaluate the morphological characteristics and oil chemical quality aspects of Jordanian traditional olive cultivars. Olive groves were selected in four different traditional olive regions in Jordan including Irbid, Ajloun, Jerash and Salt. The selected cultivars were: Nabali Baladi, Rumi, Souri and Nabali Muhassan. A standard protocol for morphological characterization and oil chemical composition of olive cultivars were followed. Oil was extracted from weighted fruits of individual trees using an olive mill suitable for small quantities and was used for the chemical and organoleptic evaluation. Results showed significant differences between olive cultivars from different locations in fruit morphological measurements and in fruit and oil content. All oil samples obtained from the traditional cultivars were of high quality and classified as extra virgin olive oil. Data showed significantly high content of total polyphenols in 'Nabali Baladi' and 'Rumi' olive oil compared to other cultivars. Vitamin E content was significantly the highest in olive oil from



Souri and Rumi cultivars. Results of fatty acids composition showed significant differences between cultivars in the main fatty acids, i.e. stearic acid, linoleic acid and linoleic acid. However, no significant differences were observed in oleic acid content between all cultivars. Significant differences were found between the same cultivars from different locations like Souri for linoleic acid, linolenic acid and behenic acid; Rumi for linoleic acid; Nabali Muhassan for linoleic acid. Olive oil organoleptic evaluation showed higher positive attributes for Nabali Baladi, Souri and Rumi cultivars compared to Nabali Muhassan cultivar.

OS3-12:Evaluation of Morphological and Molecular Diversity in Wild and Cultivated Pomegranate Germplasm of Pakistan

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Abstract :

Pomegranate (*Punica granatum* L.), is an important fruit for its nutritional, medicinal and pharmaceutical properties, still it is a minor fruit in most parts of the world for its restricted growth and various production and fruit quality issues including germplasm conservation. Objective of this study was to characterize pomegranate germplasm and to evaluate genetic diversity for pomegranate repository and breeding program. In this manuscript, 20 qualitative and 16 quantitative fruit characters of 53 wild and 62 domesticated pomegranate accessions (collected from 14 different regions) were studied. Moreover, molecular diversity was also evaluated in amplification with simple sequence repeat (SSR) markers. There was high level of diversity for fruit and aril (weight, shape, color and size), aril taste, seed hardness and wood portion index (WPI) with 92.4% of diversity covered in first five Principle components (PCs). Principle Component Analysis (PCA) of quantitative data declared domesticated accessions as more diverse than wild with 83.8 and 86.6% variability explained in first 6 PCs, respectively. Wild and domesticated accessions were clustered in separate classes with 33.7 and 66.3% variability within and between regions, respectively regardless of their growing regions. Some domesticated accessions of Bahawalpur, D.G. Khan and Chakwal grouped with wild accessions with 18.3% variability for morphological traits and declared as semi wild in nature. Polymorphic information content (PIC) values proved broad genetic base of collected pomegranate accessions, however, wild accessions showed more diverse genetic makeup in DNA based studies. Most of the studied morphological traits are important for breeders and pomegranate growers which could be explored in expanding harvest window and supply chain of quality pomegranate fruits to address malnutrition issues in the world.

Session 4: Genomic Resources, Characterisation and Conservation; Safe Movement of Germplasm

OS4-1:Determination of Genetic Variation Among Melon Genotypes Grown in Aegean Region by Morphologic and Molecular Markers

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Abstract :

Turkey, one of the secondary centers of the melon, has lots of local melon varieties. Many of them have not been produced commercially, although there is considerable variation in fruit size and shape, taste, brix and storability, and disease resistance which are important for breeding programme. In this research some local melon varieties and commercial varieties were evaluated based on morphologic and molecular markers to establish an overview of the genetic relationship among them.

Thirty eight melon genotypes collected from various parts of Turkey by Turkish Gene Bank and American Gene Bank, were characterized by using morphologic-agronomic characters and molecular markers to investigate genetic variation among them. 29 morphologic and agronomic characteristics such as leaf shape and color, fruit shape and weight, flesh color and firmness, brix, some features of plants according UPOV criteria and 56 polymorphic ISSR markers were used to define genetic similarity among the melon genotypes by using Principal Component Analysis (PCA) and cluster analysis using the UPGMA in NTSYS-pc (2.2j) programme.

The genetic similarity coefficient among melon genotypes based on morphologic and agronomic characters was lower compared to that based on molecular markers. This data indicated that although there is a wide morphological variation among the melon genotypes, the genetic distance among these genotypes, essentially is not far in basis of DNA markers.

Keywords: melon genotype, genetic diversity, morphologic marker, ISSR marker

OS4-2: Molecular Characterization of Coruh Valley Pears by SSR

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Abstract :

In this research it was aimed to characterize genetic relationship between 65 Coruh Valley pear genotypes and standart cultivars at molecular level. Pear genotypes were selected from Coruh Valley biodiversity between 2011-2012 years within the scope of the project "Investigation of Fruit Genetic Resources in Eastern Anatolian Region" which started in 1994 year. These genotypes preserved in the collection parcel in Erzincan Horticultural Research Station. Some international pear cultivars (Santa Maria, Coscia B PLMO, Williams and Kieffer) and Turkish local pear cultivars (Mustafabey, Limon, Ankara and Deveci) were used as reference cultivars. SSR method was used for molecular chracterization. SSR markers NH0021a, NH0027a, BGT23b, NH004A, KA4B and KA14 which were derived from pear genome and CH02d11, CH02b10, CH02f06 which were derived from apple genome were used because of their high polymorphism and defining properties. For 74 pear genotypes (including standard cultivars) used in the study, the average expected heterozygosity value was found 0,552, the average observed heterozygosity value was found 0,425 and the mean Shannon Information Index value was calculated as 0,892. CH02f06 loci was the most identifying loci (PIC:0,557, Shannon Information Index:1,073, F_{IS}:0,047). Triple alleles were



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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Abstract :

The main aim of the project is to develop open pollinated and hybrid lines/cultivars in cool climate vegetables widely produced in Turkey, including onion, carrot, lettuce, spinach, red cabbage and broccoli. The project is going to be carried out in five public universities and five Institutes of Ministry of Food, Agriculture and Livestock, therefore will pioneer large breeding project for other agriculturally important crops in Turkey.

Collection of gene pools for vegetables is going to be the starting point for the vegetables that are missing it, such as broccoli, followed by the characterization of the gene pools by morphological and molecular methods. The ultimate outcome is to generate cultivars with early bolting resistance, more suitable to market demands or, at least for onion, spinach and lettuce, more tolerant to common diseases/abiotic stresses affecting the yield. Development of molecular markers is one of the main goals of the project. In addition, development of domestic male sterile and maintainer lines, restorer lines, and thereafter hybrid cultivars are to be developed.

The outcomes of the project is to develop hybrid cultivars in cool climate vegetable in Turkey having a very limited number of domestic hybrid cultivars, which ultimately will reduce Turkey's foreign dependency in imported vegetable seed.

Keywords: Gene pool, breeding cool climate vegetables, hybrid cultivar development

OS4-5: Germplasm Genetic diversity and relationship analysis of *Pyrus. ussuriensis* in China based on chloroplast DNA

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Abstract :

Eight pairs of chloroplast DNA (cpDNA) universal primers selected from 34 pairs were used to assess the genetic diversity of 41 *P. ussuriensis* pear accessions (29 Ussurian cultivars and 12 wild Ussurian accessions) preserved in the National Repository of Pear Germplasm Resources in Xingcheng, China, among them 4 cpDNA fragments amplified showed genetic diversity. Six parsimony informative sites and 11 insertion-deletion (INDEL) fragments were obtained from combined cpDNA sequences (5309bp-5535bp). Two trnL-trnF-413 haplotypes, three trnS-psbC haplotypes, two accD-psaI haplotypes and three rps16-trnQ haplotypes were identified among the individuals, respectively. Seven haplotypes were identified based on the combined fragments. Values of nucleotide diversity (P_i), average number of nucleotide differences (k) and haplotype diversity (H_d) were 0.00042, 2.22195 and 0.7659, respectively. No statistical significance was detected in the four non-coding regions in Tajima's D test. A



length of 229bp INDEL fragment was observed in one of the hypervariable regions accD-psaI. Meanwhile, one parsimony informative site was found in this 229bp insertion fragment. No 141bp length deletion fragment was found in another hypervariable region rps16-trnQ. The haplotype number of 29 Ussurian pear cultivars was 5 and that of 12 wild Ussurian accessions was also 5. The values of P_i , k and H_d of 29 cultivars were 0.00042, 2.20197 and 0.6453, respectively. And those of 12 accessions were 0.00039, 2.04545 and 0.833, respectively. This demonstrated that compared to wild Ussurian accessions, Ussurian pear cultivars in Northern China exhibited a nearly same range of genetic diversity and haplotypes in cpDNA. The results of Tajima's D test indicated that D values of cultivars and wild accessions were both positive. H_6 and H_7 were the haplotypes only belonging to wild accessions. The Median-Joining network analysis showed H_2 and H_6 had a close relationship with each other, and so did H_1 and H_7 .

Keywords: pear; germplasm resource; chloroplast DNA; Genetic diversity; Relationship

OS4-6: DArTseq SNP based Assessment of Genetic Diversity in IITA Cassava Collection

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Abstract :

Cassava is an important staple food crop for millions of people in Africa and South America. IITA Genetic Resources Center (GRC) holds an international collection of 3398 cassava germplasms maintained in both the field and in vitro. Plant genetic resources, especially landraces and wild relatives are key elements for developing high yielding, nutritional and climate-resilient cassava varieties for future food security, in the context of climate change. Knowledge of both genetic diversity and the genotype population structure using high-throughput SNP fingerprinting can speed up understanding and utilization of cassava genetic diversity for crop improvement. As a first step, a set from of 280 accessions of the core collection from IITA cassava international collection, originated from 19 African countries, with 24 wild relatives and 15 breeding lines were used to discover a total of 31K single nucleotide polymorphism (SNP) using DArTseq (Diversity Array Technology) platform. Results from neighbor-joining cluster analysis, principal component analysis and population structure analysis were consistence and suggested $K = 7$ population groups in diverse IITA core collection. The phylogenetic relationship generally shows correspondence of accessions with their origin information and also all the wild relatives were clustered together, showing greater diversity than landraces and breeding lines. Secondly, another set of 3000 cassava accessions from IITA collection is under progress for DArTseq SNP genotyping for similar analysis. Genetic information about African cassava landraces, core collection set and its wild relatives can be effectively utilized to define trait based subsets, in line with preferred traits targeted in next generation cassava varietal improvement for African smallholder farmers.

Keywords: Cassava, Germplasm, Core Collection, Genetic Diversity, SNP



OS4-7: Papaya mealybug infestation in Nigeria: Incidence, spread, abundance and damage estimate on pawpaw

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Abstract :

The papaya mealybug, *Paracoccus marginatus* Williams and Granada de Willink, is a small hemipteran insect recently introduced in Nigeria that attacks several genera of host plants, including economically important tropical fruits, vegetables and ornamentals. An intensive survey was conducted in 2014 and 2015 to assess its spread, abundance and damage levels on pawpaw in orchards and homestead trees. The survey covered 23 states of Nigeria distributed in various agro-ecological zones which included Swamp forest, Rainforest, Forest-Savannah transition, Southern Guinea Savannah, Northern Guinea savannah and Sudan savannah. Sites for sampling were earmarked at 20km intervals. Five pawpaw plants were selected at random per site for observations on the infestation levels and damage of leaves and fruits. Other plants in the vicinity of pawpaw were also sampled. Presence of natural enemies were investigated. Infestation/damage were scored 1-4 corresponding to 0 - >50 infestation/damage of leaves/fruits. A total of 116 sites were surveyed. Papaya mealybug attacked the leaves and fruits of pawpaw. Twenty two (22) alternative hosts were also attacked. The percentage of infested plants in 2014 and 2015 ranged between 0 - 57% and 29 - 70% respectively. Rated population levels on leaves and fruits of pawpaw ranged between 0 - 2 and 0 - 4 in 2014 and 2015. Similarly in both years, damage severity ranged between 0 - 3 and 0 - 4 in the visited sites. Infestation increased in the survey of 2015 compared to the survey of 2014; thus showing the need for immediate intervention. The consequences of rapid spread of papaya mealybug on horticultural plants and the presence of natural enemies were discussed.

OS4-8: Genetic Diversity of Bean (*Phaseolus vulgaris* L.) Germplasm collected from Erzincan Province in Turkey Using iPBS Markers

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Abstract :

Common bean is a widely distributed crop in worldwide as well as Turkey. It is the most important edible food legume in the world representing 50% of grain legumes for direct human consumption. Characterization of germplasm using molecular marker techniques provides quantitative estimates of genetic diversity and the information, which is essential for a rational utilization of germplasm in breeding programs. In this study, inter-primer binding site retrotransposon (iPBS) marker system was applied to evaluate the genetic diversity of seventy-five common bean (*Phaseolus vulgaris* L.) genotypes collected from Erzincan province of Turkey. Eighty-three iPBS primers were used and 26 out of 83 primers gave



sufficient polymorphic data. A total of 972 polymorphic bands were produced by 26 iPBS primers among 75 bean (*phaseolus vulgaris* L.) genotypes, the number of alleles per primer ranged from 13 for iPBS 2077 and 69 for iPBS 2385, with an average of 37.38 allele/marker. Polymorphic information content ranged from 0.194 from iPBS 2077 to 0.422 from iPBS 2386 with an average of 0.326 per primer. The genetic similarity between accessions was calculated using the software NTSYS-pc. Maximum genetic distances were between ≠ Genotype 16 and ≠ Genotype 18 (0.60). Cluster analysis using Neighbour joining method divided 75 bean genotypes into 3 groups. The genetic diversity information generated from this study can be used for planning future dry bean breeding programs.

Keywords: Bayesian clustering, Bean and iPBS

