
Symposium 21 (S21): Plant Genetic Resources: The Fabric of Horticulture's Future

Monday · August 12

Location: Metro Toronto Convention Centre, Room 104B

1100–1140

S21–0–1

LOOKING FORWARD TO A BETTER USE OF PLANT GENETIC DIVERSITY

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In spite of the enormous contribution of Plant Genetic Resources to past agricultural development, they have the potential to contribute even more in the future—through the adoption of innovative research strategies for crop improvement and “conservation through use” methodologies that will provide farmers and rural communities with a basis for sustainable and increased production. There are several limitations for the utilization of genetic materials by breeding programs and by traditional farming communities. These are mainly related to the lack of characterization and evaluation data; lack of information on materials existing in both ex-situ and in-situ collections; poor coordination of policies at national level; poor integration of genebanks, users of germplasm and farming communities; difficulty in handling large collections; small range of species addressed in research activities; lack of market incentives and, more recently, the inability for breeding programs to incorporate molecular oriented breeding techniques and functional genomics in their R&D routines in the search for and use of new useful genes. This presentation will explore alternatives on how to approach these limitations, in order to keep genetic resources at the center of global strategies that will meet the needs of present and future sustainable development and food production.

1140–1200

S21–0–2

THE IMPACT OF INTERNATIONAL GENETIC RESOURCES POLICY ON DEVELOPING COUNTRIES: LESSONS AND CHALLENGES FROM THE ANDEAN COMMUNITY

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The Andean region is one of the most biologically diverse areas of the world, and this is particularly true regarding the unparalleled horticultural and agricultural genetic diversity found there. In an effort to comply with the objectives of the Convention on Biological Diversity, the five developing countries of the Andean Community (Bolivia, Colombia, Ecuador, Peru and Venezuela) adopted a Common Regime of Access to Genetic Resources (also known as Decision 391) in 1996. Decision 391 was intended as an instrument to regulate access to genetic resources and help guarantee the conservation, sustainable use and equitable distribution of the benefits derived from those resources. During the five years since its adoption, the implementation of Decision 391 has been problematic for a variety of reasons and, in practice, has had the unforeseen effect of halting all foreign and most domestic access to Andean genetic resources. The sudden lack of access has, in turn, resulted in a reduction in both national and international projects promoting research, conservation, and use of Andean plant genetic resources. Recent experiences in Bolivia and Venezuela are presented and the principle constraints to access and benefit sharing are examined. To address the problems arising from over-restrictive legislation, the Andean countries are now studying ways of streamlining the implementation of Decision 391, particularly in light of the possible ratification of the new International Treaty on Plant Genetic Resources. The goal is to develop a mechanism that facilitates regulated international access and exchange of genetic resources while ensuring that the benefits derived from their conservation and use are equitably shared by all parties.

1200–1220

S21–0–3

SIGNIFICANCE FOR HORTICULTURE OF THE NEW INTERNATIONAL TREATY ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

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After long and complex negotiations, the text of the International Treaty on Plant Genetic Resources for Food and Agriculture was adopted by the member states of the United Nations Food and Agriculture Organization (FAO) on November 3, 2001. This new legally binding international agreement—which will enter into force when ratified by 40 countries—provides a framework to conserve and provide access to plant genetic resources and related knowledge, technologies, and funding. At the heart of the Treaty is a Multilateral System of Access and Benefit-Sharing, which covers some 80 food and forage crops. The Treaty's main provisions are described, particularly as concerns horticultural crops. Special emphasis is placed on what may change for users of horticultural genetic resources when as the Treaty is implemented. Implications for horticultural crops which are not presently included in the Multilateral System are also discussed.

1220–1240

S21–0–4

SHIFTS IN THE USE OF UTILITY PATENTS AND PLANT VARIETY PROTECTION TO PROTECT PLANT INTELLECTUAL PROPERTY IN THE UNITED STATES

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Much of the recent concern regarding transgenic crops in the U.S. has focused on the ownership and control over seeds, particularly through patents and like instruments. However, patented plants need not be transgenic. These concerns are neither particularly recent nor confined to groups opposed to transgenics. Related issues have been expressed by public and seed company breeders regarding the effects of protecting plant intellectual property (IP) on cooperation and the exchange of information and materials among private and public breeding programs, as well as possible implications for germplasm collection, distribution and use in plant improvement. The concerns of each of these groups are very real and based, at least in part, on the perception of increased applications for utility patents for germplasm, cultivars and inbred lines. However, protection of plant intellectual property had been pursued in the US via other strategies before the Supreme Court's 1980 Chakrabarty decision made utility patents possible for life forms, including plants. So the issue is more properly the extent to which there is an increase in protecting plant properties and/or a shift in protection strategies, as well as the extent to which these changes are spread across companies and over crops. One of the factors making assessment of these concerns so difficult is the near absence of data regarding the shifts in the types of property protection strategies being used, and of understanding of the reasons why private firms in particular have chosen to increase the degree of patenting of plants. Our purpose here is to use patent, PVP and related data to document shifts in IP protection use over time within the US. This analysis provides an understanding of how plant protection strategies have and are being used, the implications of their use for future plant improvement, and relevance to current concerns regarding protection of plant IP.

1340–1440

S21–P–5

STUDIES ON CONSERVATION OF GENETIC DIVERSITY IN APRICOT IN THE COLD ARID REGIONS OF INDIA

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Apricot (*Prunus armeniaca* L.) is the main fruit crop found growing in the Indian cold arid regions. This fruit has been seen to thrive well even in rocky, sandy and wasteland conditions and can tolerate water stress and temperatures as low as -30°C . Ladakh, which covers the major area under cold arid regions in India and extends from 8,500–12,000 feet above MSL, is a very rich repository of apricot germplasm. However, there is an imminent threat of this highly valuable germplasm becoming extinct due to lack of planned, scientific studies and due to the absence of established propagation techniques. In view of the above, Field Research Laboratory (DRDO), Leh, located at an altitude of 11,500 ft above MSL in the cold arid regions of India, initiated an extensive study on the survey, collection, evaluation, propagation and conservation of this indigenous, valuable genetic diversity in apricot in the region. The findings of the study have highlighted the availability of 64 types of apricot genotypes showing considerable variation in physical parameters viz., fruit shape, size, colour, fruit weight, stone weight, diameters, stone:pulp ratio, chemical parameters like TSS, acidity, pH, sugars, etc. We have come across some very valuable germplasm having TSS as high as 33.2%. Besides this important genotypes for earliness, late maturity, high oil per cent, etc. were also identified. Efforts have also been made to standardize nursery raising techniques and also vegetative methods of propagation in apricot with a view to conserving the genetic variability. Grafting, budding and top working have shown 85–92% success and can be used effectively as propagation methods. Further studies are in progress to initiate methods to conserve these valuable genotypes at different locations in the region for their further evaluation and multiplication of the superior types.

1340–1440

S21–P–6

PHYLOGENY AND BIOGEOGRAPHY OF *CASTANEA* (FAGACEAE) BASED ON NUCLEAR ITS AND CHLOROPLAST NONCODING TRNT-F AND SEQUENCE DATA

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Castanea (Fagaceae), a tertiary disjunct genus which comprises three sections and seven species, is widely distributed in the Northern Hemisphere. The outstanding character of the floristic similarity between Eastern Asia and Eastern North America species and the difference in chestnut blight resistance among species have been of interest to botanists for a century. The genus *Castanea* is thought to have originated on the Asian continent and forced southward during the glacial maximum to refugia and migrated northward after the glacier's retreat. Previous research suggested a complicated history of the genus. Inter-continental species divergence times were estimated at 10–13 million years before present (mybp), but the migration routes after the last glaciation are not clear. In this study, phylogenetic and biogeographic analyses of the seven *Castanea* species were conducted using sequences of the nuclear ITS and chloroplast noncoding trnT-F. The *Castanea* chloroplast genome is conserved among the different species. The American chestnut can be distinguished from the other *Castanea* species by a large deletion in the trnT-trnL intergenic region. Sequence data should highlight routes of postglacial recolonization of species into lands newly released by ice.

1340–1440

S21–P–7

WILD FRUIT TREE GERMLASM OF CHINA

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Wild fruit is the cradle of new cultivated fruit, an important source of resistance genes, as well as an ideal material for organic and special food in the 21st century. China is one of the major centers of origin of fruit trees and has a very rich germplasm of wild fruits. By the end of the 20 century, 73 families, 173 genera, 1076 species, as well as 81 subspecies, varieties, and forms have been found in China, which are distributed horizontally all over the country, especially in south and southwest mountain areas, and vertically up to 4700–5000m. Among the species, 66.33% are concentrated in the families Rosaceae, Actinidiaceae, Saxifragaceae, Fagaceae, Rutaceae, Elaeagnaceae, Moraceae; 60.38% belong to the genera *Rubus*, *Actinidia*, *Cotoneaster*, *Ribes*, *Rosa*, *Elaeagnus*, *Vitis*, *Cerasus*, *Quercus*, *Malus*, *Diospyros*, *Vaccinium*, *Castanopsis*,

Viburnum, *Crataegus*, *Ziziphus* and *Pyrus*. According to the national list of protected plants, 16 species and one variety of wild fruits belong to grade 2, and 23 species and one variety belong to grade 3. Some species (genera) with special excellent characteristics such as *Ziziphus acidojuzuba*, *Vaccinium uliginosum*, *Nitraria schoberi*, *Elaeagnus angustifolia*, *Malus baccata*, *M. sikkimensis*, *Cerasus tomentosa*, *Pyrus betulifolia*, *Poncirus trifoliata*, *Vitis amurensis*, *Actinidia* spp., *Hippophae rhamnoides*, *Rosa roxburghii*, *R. davidii*, *Juglans mandshurica*, *Lonicera standishii*, and *Debregeasia edulis* were introduced in detail. The effects of exploiting wild fruit resources on the development of the 21st century's fruit production were stated on the basis of analyzing the characteristics and present status of wild fruits in China.

1340–1440

S21–P–8

PRESENT DEVELOPMENT AND CHARACTERIZATION OF HORTICULTURAL LANDRACES FOR HUMAN NUTRITION USE FROM THE COMUNIDAD DE MADRID

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The use of ex situ conservation of landraces is important. However, in recent years, in situ conservation has been developed for many crops of landraces in their local areas. Additional research is still needed to test the existing in situ conservation techniques in a genebank context and to develop protocols for other species. In order to recover the landraces in their local areas, it is necessary to verify landrace authenticity. It will be also necessary to prevent the loss of genetic materials, and to obtain characterization data to eliminate fraud. In the Comunidad de Madrid there are a large quantity of landraces with unique products and a social setting that supports the idea of recovering these into a type of crop environment. The project is also a response to the European Union directives of increasing diversification and avoiding production excesses. Six crops have been chosen: garlic "Blanco Fino de Chinchón"; strawberry from "Aranjuez"; tomato "Moruno" from Aranjuez; faba bean from "Tajuña"; beans from "la Sierra de Madrid"; and chick-pea from "Brunete". The main objectives of this work are: preparation of a catalogue of traditional varieties of garlic, strawberry, tomato, beans, chick pea and faba bean from the Comunidad de Madrid; prospecting and collection of all the landraces for human nutrition from the Comunidad de Madrid; landrace conservation both in the field and at a germplasm bank (seed conservation); standardization of the six landraces chosen by morphological and agronomic characterization and by organoleptic evaluation; and initial genetic characterization through molecular markers for strawberry and chickpea.

1340–1440

S21–P–9

PHENOTYPIC AND GENETIC CHARACTERIZATION OF *CUCUMIS* MELO L. LANDRACES COLLECTED IN APULIA (ITALY) AND ALBANIA

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Melon is an important crop in Southern Italy where it is grown in open and covered fields. In the Apulia region, the botanical variety 'Inodorus' is widely cultivated, because of local and ancient traditions. It is harvested in August and stored until the Christmas holiday (winter melon). In addition there are some landraces ('Carosello' and 'Barattieri'), whose fruit are eaten unripe, which are very important in relation both to their high degree of tolerance to salt stress and to their high diffusion on the markets because of good fruit quality. In the present work, data on the main bio-agronomical traits are reported, recorded on accessions and landraces of *Cucumis melo* L. belonging to a collection established by means of exploration work carried out in Apulia and some regions of Albania where it is still possible to safeguard horticultural genetic resources. All the material has also been characterized by means of molecular markers with the aim to describe genetic variation that could be useful in future breeding programs and to discriminate local genotypes that often are indicated

with similar names. The results obtained appear to be of interest for using 'Inodorus' for breeding strategies, particularly for the improvement of earliness, fruit shape, soluble solid content, storage and firmness of fruits. Furthermore, the work has been useful by increasing the knowledge on 'Barattieri' and 'Carosello' that are becoming more and more interesting for people and the national and European markets.

1340–1440

S21–P–10

STUDIES ON NATURAL AND HUMAN INFLUENCED GLOBAL INTROGRESSIONS IN EVOLUTION AND IN SITU CONSERVATION OF ADONIS (SECT. CONSILIGO), GALANTHUS AND TELEKIA SPECIOSA GENETIC RESOURCES

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Difficulties caused by gene-ecological contamination (genetic pollution) for in situ conservation of spontaneous plant genetic resources of horticultural importance on different stages of human influenced plant evolution (domestication in statu nascendi) are analysed. Different types of traditional (non scientific) domestication and breeding are outlined: 1) The *Adonis* case: in sect. *Consiligo* DC. of the genus *Adonis* "domestication-recalcitrant" herbaceous perennial taxa spread in prehistoric times are characteristic. The species complex has a high ornamental value and a potential medical importance, but a restricted cultivation. Natural introgressions produced a large number of phenodemes and topogenodemes (notomorpha) and an active speciation process. The case includes some priority species for in situ and ex situ genetic resource conservation; 2) The *Telekia* case: the splendid Teleki-flower (*Telekia speciosa* /Schreb./ Baumg., Asteraceae) is a plant pre-adapted for domestication. This taxon of Carpatho-Caucasian origin spread aggressively in Carpathian area, beginning with the Middle Ages and (according to our assumptions) especially during the Ottoman invasions. Teleki flowers followed a world wide process of "traditional domestication" beginning with the early 1800s as parklane ornamentals preferred mostly for leaf form, flower form, colour and a specific scent, attracting both humans and insects (e.g., butterflies). The species is a potential forage for large game, but also a potential invasive plant. Some gene-ecological, taxonomical and ethnobotanical problems connected with the use and conservation of Teleki-flower genetic resources are also discussed; and 3) The *Galanthus* case: snowdrops were recently "domesticated" both on local and global scale. The natural evolution of this geophyte was possibly influenced by postglacial plant migrations and genetic sedimentation along large rivers, such as the Danube in Szigetköz. Modern snowdrop evolution is now largely affected by human collection, selection, traditional domestication and by global commerce which resulted many unexpected introgressions in garden environment. All three cases were studied during some long term cultivation experiments performed between 1970-2000 in Transylvania (Western Romania) and in Pannonia (Western Hungary). This research was supported partly by the Hungarian Academy of Sciences (MTA/TKI)

1440–1520

S21–O–11

THE ROLE OF IN SITU CONSERVATION IN PROMOTING MORE EFFICIENT PLANT GENETIC RESOURCE CONSERVATION AND USE

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The conservation and use of plant genetic resources are introduced through a review of the diversity of plants, the causes of the loss of this diversity and the need, as highlighted by the Convention on Biological Diversity, to improve conservation and use paradigms. In situ genetic resources conservation in reserves and on-farm are defined and overviews are illustrated with case studies. Progress toward the equitable sharing of the benefits arising from the use of plant genetic resource, one of the pillars of the CBD, are reviewed, with examples. Various ways of promoting more efficient conservation and use are suggested, and in situ conservation activities are placed within the overall conservation and use framework.

1520–1540

S21–O–12

SPECIFIC FEATURES OF IN SITU CONSERVATION STRATEGY IN RUSSIA

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Problems of plant genetic resources conservation and utilization are of vital importance for Russia. The Vavilov Institute has been traditionally involved in collecting cultivated plants and their wild relatives and conserving them both in the genetic collection and within natural plant communities. After the adoption of the Convention on Biological Diversity, in situ conservation of plant genetic diversity has become a top priority. The strategy of in situ conservation in Russia has certain specific features, such as the choice of priority objects for conservation, based on the principle of inequality among species in regard to different characters, selection of the area for in situ conservation, conditions of monitoring and management. Development of a conservation strategy should be preceded by a detailed study of the objects to be conserved, as well as their morphological, taxonomic, biological, geographic, ecological and other features. Research materials include the seed and herbarium collections of VIR and other national institutes, archives of collecting missions conducted in different years, publications, etc. An important research instrument is the database of "Wild Relatives of Cultivated Plants in Russia" and the maps of species' areas of distribution throughout the country.

1540–1600

S21–O–13

ETHNOBOTANICAL DATABASES, ETHNOBIODIVERSITY STUDIES AND 'IN SITU' CONSERVATION OF HORTICULTURAL PLANT GENETIC RESOURCES IN ALP-BALKAN-CARPATH-DANUBE (ABCD) AREA

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Possibilities and limitations of ethnobotanical and ethnobiodiversity studies for promoting in situ plant genetic resource conservation in the Alp-Balkan-Carpath-Danube (ABCD) area are discussed using data collected between 1970–2000 during itinerary and stationary field studies, study of historical sources, ethnobiodiversity studies in a contact zone of different Indo-European (Slavic, Latin, German) and Ural-Altai (Hungarian) languages, as well as the experience gained by ethnobotanical database building. Case studies regarding 1) fruit trees (*Amygdalus*, *Prunus* and *Malus*: "The Alma-case"), 2) field crops of American origin (*Cucurbita*, *Helianthus*, *Phaseolus* and *Zea*: the "Bean-and-Corn case"), and 3) some ornamental, aromatic and medicinal plants of Mediterranean origin (*Cheiranthus*, *Dianthus*, *Matthiola*, *Ocimum*, *Satureja*, etc: "Viola-case") are analysed for factors potentially influencing the success of in situ conservation in the ABCD area. Case studies use data extracted from the Hungarian ethnobotanical database constructed in the "Lencsés György Biological Database Laboratory" summarising also traditional knowledge regarding horticultural plants accumulated in an area which still preserves high ethnobiodiversity especially on its Eastern (Transylvanian) and Western (Pannonian) sides. The following main phenomena of crucial importance for in situ conservation are briefly discussed: 1) ethnobotanical traditions and sustainability ("Alma-case"); 2) genetic sedimentation, ethnonomenclature and genetic diversity, the rediscovery of co-adaptedness and its importance for landrace conservation ("Bean-Corn case"); and 3) cultural erosion and ethnic diversity (including ethnic conflicts influencing in situ conservation), the possible role of poetry and music for in situ preservation of the traditional flower garden genetic resources (Viola-case). The paper is dedicated to the memory of N.I. Vavilov, arrested 60 years ago in the Northern Carpathians during field research in the ABCD area. Research was partly supported by the Hungarian Academy of Sciences (MTA/TKI).

1600-1620**S21-O-14****SALVATION OF OLD FRUIT LANDRACES IN THE CZECH REPUBLIC**F. Paprstein*¹, J. Kloutvor¹, V. Holubec²¹Research and Breeding Institute of Pomology Holovousy, 508 01 Horice v Podkrkonosi; ²Research Institute of Crop Production, Drnovska 507, 161 06 Praha 6-Ruzyně, Czech Republic

Changing of land ownership and setting of new agricultural priorities after political changes in the Czech Republic (CR) lead to abolishment of old orchards and alleys where mainly landraces were grown. Therefore, a program for conservation of still existing traditional fruit germplasm fragments was founded in 1994. Regularly organized collecting missions were oriented to border regions of CR, where there was the highest occurrence of landraces. Each expedition was prepared with cooperation of experts from national parks and protected landscape regions who provided us with maps of fruit occurrence. The sites were localized by GPS, the plant material was identified as to cultivars, their health was evaluated and the results were loaded to a dbf file connected to the digital map. For in situ conservation, altogether 239 items were chosen. The considered trees were between 80 and 200 years old. We succeeded to find rare old cultivars such as: 'Libinske' (frost-hardy); 'Kralicke' (for harsh climate); 'Halberstadske paneneske'; and many others with a good resistance to diseases and severe climate. In pears we found cultivars: 'Rihova bezjaderka' (fruits 200 g, seedless with missing endokarp); 'Jakubka ceska' (small fruits, very resistant to unfavourable conditions); 'Krvavka moravska' (red flesh); and two seedlings with red fruits and good commercial traits. In plums we found an interesting landrace 'Bila trnecka', which seems to be fully resistant to Plum Pox Virus. Several valuable seedlings of *Prunus avium* from altitudes 800 to 1000 m were in good health and had no frost damage. They were considered to be used in a timber industry. We found a sweet cherry 'Ladeho pozdni' which has the latest ripening of all known cultivars. At present we continue to work on projects regarding farm conservation of landraces and valuable wild accessions. The research was done with a support of Ministry of Agriculture EP6430 and QC0063 projects.

1620-1640**S21-O-14-A****TO BE ANNOUNCED****1640-1700****S21-O-14-B****TO BE ANNOUNCED****Tuesday · August 13****1100-1140****S21-O-15****EMPLOYING GENOMICS AND BIOINFORMATICS TO CONSERVE GENE, GENOME, AND GENEPOOL DIVERSITY**

Stephen Kresovich*

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Over the past century, genetic resources conservation has advanced based on fundamentals of botany, horticulture, agronomy, plant breeding, plant pathology, and entomology. In the future, some of the greatest opportunities for improved discovery, conservation, and use of the earth's biodiversity will occur because of our collective abilities to employ genomics and bioinformatics to understand and exploit variation of the gene, genome, and gene pool. The capabilities and insights provided through the application of genomics and bioinformatics will affect how we ask biological and agricultural questions, how we understand diversity, and how we utilize germplasm for the benefit of the global society. In this presentation, I will highlight how these new technology-driven disciplines impact management of both ex situ and in situ diversity.

1140-1200**S21-O-16****EVOLUTION OF GENE BANKS IN THE LIGHT OF MODERN MOLECULAR GENETICS**

Carmen de Vicente*

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Modern molecular genetics has made possible new and until recently, unimaginable approaches to solving a wide range of biological questions, including many in the agricultural sciences. In particular, both conservation and use of plant genetic resources can now benefit from the wealth of in-depth knowledge about genes and genomes gathered during the past decade. At the same time, initiatives are underway to conserve extracts of genetic material in "DNA banks," and even more sophisticated approaches are being taken to build and maintain collections of large inserts of DNA, and tissue-specific libraries. The implications of these recent developments in molecular genetics will be discussed in light of the concepts that initially prompted the creation of ex situ collections of agricultural germplasm, and continue to underpin their support.

1200-1220**S21-O-17****BIOINFORMATICS: A STRATEGY TO LINK IN SITU CONSERVATION AND TO REWARD PEOPLE**Dr. Tejaswini*¹, Teluve N. Prakash²¹Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bangalore 560089, Karnataka, India; ²Univ. of Agricultural Sciences, GKVK, Bangalore 560065, Karnataka, India

Horticultural crops whether it is fruits, vegetables, flowers, or medicinals are a part and parcel of farming families. Preferences of these horticultural crops is mainly based on taste and cultural heritage of people associated with it. Further, a vast variability is known to exist in horticultural crops, particularly when it is not commercially cultivated. In other words, homestead gardens are the major source of variability existing in these horticultural crops. Ex situ conservation can hardly take care of the vast diversity available in these crops. And thus strategies to encourage in situ conservation have to be widely aimed at. Meanwhile characterization of variability and accessibility of such variability for commercial exploitation is difficult under in situ conservation. Bioinformatics can play a vital role for bioprospecting by means of proper documentation of diversity as well as knowledge, thereby allowing for sorting, relating and assigning the farmers rights and also for better usage. We have considered genetic resources and advances made in soft ware industry as our strength and have tried to address and link points of 1) alternate employment, 2) involvement of youth, women and tribals, 3) better education, and 4) issues of patent rights. In the present model we have proposed involvement and networking of the following institutions to achieve the desired objective: 1) home gardens; 2) community based plant conservation; 3) consumers movement; 4) regional agricultural research stations and infrastructures of National Agricultural Systems; 5) government departments of agriculture, horticulture and veterinary; 6) local NGOs; 7) village panchayats; and 8) schools. This model has been developed keeping the existing situation of India. India is considered as one of the important twelve mega gene centers of the world. The same model can be extended across the globe linking several in situ conservation regions.

1220-1240**S21-O-18****DEVELOPMENT OF THE TECHNOLOGY OF PLANT GENETIC RESOURCES IDENTIFICATION AND DOCUMENTATION BASED ON PROTEIN MARKERS FOR EFFECTIVE GERMPLASM COLLECTION MANAGEMENT**

A.V. Konarev*

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To serve as an effective source for modern cultivar improvement, plant genetic resources (collections) should have rational organization and management. Each accession should be identified and registered. Preservation of the genetic constitution of accessions is also included into the list of basic problems. An important goal of genebank activities is to understand the genetic

structure of biodiversity (relationships inside a gene pool). Molecular markers are successfully used on all steps of the work with plant collections (in VIR protein markers are mainly used). Protein markers are, as a rule, inherited codominantly, and the analysis of a genotype is possible immediately by the protein phenotype. Seed proteins are widely used as marker systems for cultivar verification. The ISTA Working Group confirmed in 1997 the advantage of protein markers as standard methods for cultivar and species identification. The report will explicate how protein markers are used on various steps of the work with plant genetic resources. Scientists of VIR developed and proposed a system of identification and documentation based on seed storage proteins. This system has been successfully used for managing numerous crop collections of VIR. The system of registration includes the following aspects: nomenclature of electrophoretic components, model patterns and methods of recording components in the form of protein formulae, and development of databases based on protein formulae. By means of model patterns, cultivars or biotypes of the majority of crops have been recorded in the form of protein formulae; e.g. catalogues and databases of such formulae were released. For wider practical application of the above-mentioned approaches in genebanks, it is necessary to improve and develop all procedures, and adapt protocols for each given gene bank (key problems, dominant crops and other circumstances).

1340-1440

S21-P-19

HORTIVAR: HORTICULTURE CULTIVARS PERFORMANCE DATABASE

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Hortivar, the Horticulture cultivars performance information system has been developed by the Food and Agriculture Organization of the United Nations (FAO) as part of the World Agriculture Information Centre (WAICENT). It has been conceived to assist farmers and scientists to retrieve information on the yield and disease resistances of horticulture cultivars according to different agro-ecological areas and sites. It is designed to help and answer a difficult question often raised: which cultivar to grow in a specific site and season, to meet the requirements of the market. The paper describes the structure of the database which relates to six categories of horticultural crops: fruits, vegetables, roots and tubers, ornamentals, mushrooms, herbs & condiments. It develops the type of information that can be retrieved including general information on the cultivar itself, its standard phenotypic and genotypic characteristics, the basic cropping and yield data. The paper illustrates the additional information that can be retrieved in relation to a broad range of data which describe the context of the cultivar performance based on the prevailing climatic conditions, the nursery practices and field operations applied, including plant protection. Besides its principal goal for retrieval of information, the database can be used as a "professional and institutional memory" for national and international agricultural research stations and centres. Guidance is provided on how individual scientists or farmers can become editors of the FAO Hortivar database and log in data to be safeguarded. It is further illustrated how the templates can be used as a standard form for data logging of ongoing and future research activities for horticulture cultivars screening and evaluation.

1340-1440

S21-P-20

EVALUATION OF GENETIC DIVERSITY IN NEW GUINEA IMPATIENS USING AFLP MARKERS

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New Guinea *impatiens* (*impatiens* x *hb.*) is an economically important floral crop; however, little work has been conducted to further our understanding of the genetics of this crop. In this study, we attempted to use the amplified fragment length polymorphism (AFLP) technology to investigate the level of polymorphism present among 41 commercial cultivars of New Guinea *impatiens*, study their genetic relatedness, and assess the genetic diversity in this material. An efficient DNA extraction protocol was developed, and a total of 48 EcoR I and Mse I primer combinations were used for PCR amplification. The PCR amplification products were subjected to polyacrylamide gel electrophoresis. The AFLP analysis showed that all 41 cultivars generated between 73 and 130 scoreable polymorphic bands per primer combination. Gower's Genetic

Dissimilarity estimates for the entire set of cultivars ranged between 0.886 and 0.587. A dendrogram was generated from these dissimilarity data that revealed four groupings among these 41 cultivars. The implications of these results on genetic relationships and genetic diversity in New Guinea *impatiens* will be presented.

1340-1440

S21-P-21

MOLECULAR CHARACTERIZATION OF IRANIAN OLIVE (OLEA EUROPAEA L.) BY USE OF RANDOM AMPLIFIED POLYMORPHIC MARKERS

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Iran retains age-old, local cultivars of olive. These cultivars have not yet been systematically evaluated and classified for their genetic relationships. Following morphological traits evaluation, Random Amplified Polymorphic DNA (RAPD) analysis was performed on the main traditional cultivars of olive grown in Iran. Reproducible amplification fragments were identified using 80 decamer oligonucleotide random primers followed by agarose gel electrophoresis. A dendrogram based on unweighted pair-group (UPGMA) method cluster analysis was constructed using a similarity matrix derived from the RAPD amplification generated by the selected primers. Cluster analysis revealed presence of two main clusters. The major cluster is comprised of Dezful, Jenob and Rashid populations, the last two being joined to Dezful genotypes with some distance. The second major cluster is comprised of two sub-clusters, revealing variation among Zard genotypes. The shengeh cultivar was separated from the other genotypes on the basis of differences in RAPD bands.

1340-1440

S21-P-22

USE OF RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS FOR THE IDENTIFICATION OF GENETIC DIVERSITY IN CHINESE CABBAGE

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Chinese cabbage originated from China where it is one of the most popular vegetables. Based on its rich genetic and morphological diversity, hundreds of variations, cultivars and types of Chinese cabbage have been obtained by cross breeding, selection breeding and other breeding methods. In order to conserve the cabbage germplasm, efforts have been made to survey, collect, and identify the cabbage variety resources. It is crucial to develop effective methods and techniques for the identification of cabbage germplasm including their relatives, genetic diversity and categorization based on molecular biology. Genetic diversity of sixty-four germplasm accessions of Chinese cabbage were analyzed using RAPD markers with a Wuqing line and a Xiaobaicai line as controls to identify the feasibility and validity of the method. Thirty-one polymorphic primers were selected from four sets of primers (OPE, OPF, OPG, OPH) that have eighty primers. The percentage of polymorphisms was 38.8%. Among eighty primers, sixteen with sharp bands were selected to analyze the material. One hundred amplified bands were produced; six bands per primer were produced at average, ranging from two to eleven bands per primer. The length of the amplified fragments was between 400-2000 base pairs. Twenty-eight bands appeared in all 64 accessions. Other 72 bands were polymorphic; the percentage of polymorphisms was 72%. The primer OPF-16 had the highest percentage of polymorphism, i.e., 87.5%. The results can show the typical bands of Wuqing (*B. rapa*), Xiaobaicai (*B. chinensis* L.) and Chinese cabbage. These typical bands can be used as RAPD markers to identify these three species. Nei-Li similarities were computed by analyses of 72 polymorphic DNA markers and used in unweighted pair group method using arithmetic means (UPGMA) cluster analyses. All materials were clustered into groups corresponding to the eight types by similarity (0.721). Among them, 64 germplasm accessions of Chinese cabbage were clustered into six types, Wuqing type and Xiaobaicai type.

1340-1440

S21-P-23

EVALUATION OF GENETIC DIVERSITY IN EUROPEAN WILD AND CULTIVATED GENOTYPES OF *PRUNUS AVIUM* AND SOME RELATED SPECIES OF THE SUBGENUS *CERASUS* USING CPDNA MARKERS

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Prunus is a large genus including from 77 to 150 species (depending on the authors) divided into five subgenera. The subgenus *Cerasus* includes the cultivated cherry trees (sweet and sour cherry) and their related cherry species. The objective is to study the chloroplast DNA variation of those species in order to establish phylogenetic relationships between them. This diversity has been analyzed by PCR-RFLP. Eight pairs of primers and enzymes were used for this analysis. The sampling includes a large sample of wild and cultivated genotypes of *Prunus avium* accessions spread all over Europe, and smaller samples of *Prunus cerasus* and few other species. This study takes part in a larger programme analyzing the genetic diversity of cultivated and wild cherry trees (*Prunus avium*) with nuclear and chloroplast markers. Hypotheses on the domestication of cherry trees will be proposed. Relationships between *P. avium*, *P. cerasus* and some other species in the subgenus *Cerasus* will be discussed. The results will also provide a large knowledge of the chloroplast diversity and will help us in the management and conservation of genetic resources of *Prunus*.

1440-1500

S21-O-24

ANALYSIS OF GENETIC DIVERSITY AND POPULATION STRUCTURE WITHIN FLORIDA COCONUT (*COCOS NUCIFERA* L.) GERMPLASM USING MICROSATELLITE DNA, WITH SPECIAL EMPHASIS ON THE FIJI DWARF CULTIVAR

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Using fifteen simple sequence repeat (SSR) microsatellite DNA loci, we analyzed genetic variation within *Cocos nucifera* germplasm collections at two locations in south Florida, representing eight cultivars. The loci were also used in a parentage analysis of progeny of the 'Fiji Dwarf' variety at both locations. At total of 67 alleles were detected, with eight the highest number at any one locus. These loci uniquely identified 83 of the 110 individual palms. Gene diversity of the 15 loci ranged from 0.778 to 0.223, with a mean of 0.574. 'Fiji Dwarf', 'Malayan Dwarf', 'Green Niño', and 'Red Spicata' cultivars resolve as distinct clusters in a neighbor joining tree using modified Rogers distance, while the tall varieties form two aggregates. The highest gene diversity was found in the tall cultivars (0.583 cumulatively), and the lowest in the 'Malayan Dwarf' (0.202). After the tall coconuts, the 'Fiji Dwarf' was most genetically diverse (0.436), and had the largest number of unique alleles. Genetic identity is highest among the 'Malayan Dwarf' phenotypes, and between the tall varieties. The 'Red Malayan Dwarf' is genetically distinct from the 'Green' and 'Yellow Malayan Dwarf' phenotypes, which cannot be distinguished genetically. Off-type 'Malayan Dwarf' phenotypes (putative hybrids with tall) can be identified genotypically. Parentage analyses of thirty 'Fiji Dwarf' progeny propagated from five adults surrounded by other cultivars estimate that only 20% of the progeny were out-crossed to the other varieties, while 40-46% were possible selfs. This suggests that a seed production orchard of the variety maintained at reasonable distance from other varieties will likely yield only 'Fiji Dwarf' genotypes. Our data are discussed in the context of hypotheses of coconut dissemination around the world.

1500-1520

S21-O-25

UNIBASE®: A UNIVERSAL DATABASE FOR ANY TYPE OF HORTICULTURAL CROP, PEST, INSECT, OR CHEMICAL PRODUCT

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Unibase® is a Windows based (95, 98, 2000 or NT) user friendly software package that was developed for those who are interested in creating their own instant database. The program is partly derived from the software package Pedigree which was developed by S. Khanizadeh in 1997. Unibase® allows the user to create a new database by importing existing data and images. Field names can easily be changed, images and pedigrees of any horticultural crop can be viewed instantly and password protection can be added to make the database a read-only program. The database can be searched using various criteria and the use of operators such as "and", "or", 'begin with', 'equal to', 'greater than', 'less than', and 'contains' makes the search option very flexible and efficient. Unibase® was originally designed to be used with ornamentals. Users can view images of trees, shrubs, flowers, etc. along with botanical descriptions of the plants in the images. People who presently use Pedigree (DOS, Windows) can transfer their Pedigree data into Unibase® and take advantage of the expanded features associated with the new software. There are no limitations to the number of entries that can be incorporated into a database and to the number of different databases that can be created. An unlimited number of images can be stored for each entry and several graphic formats including BMP, JPEG, GIF, TIFF, etc. can be used. The professional version of Unibase® comes with the ability to make a personal database re-distributable (e.g. a personalized logo can be added to the database and it can then be sold to third parties). Unibase® is very useful for germplasm inventory (fruit crops, vegetables, ornamentals, agronomic crops, weeds, chemicals, insects, pests, etc.) and can be used in any breeding program (animal, horticulture, agronomy, etc.) to trace pedigrees and view images and characteristics of progenies. Additional information on Unibase® can be obtained from www.universaldatabase.com

1520-1540

S21-O-26

USE OF THE CHALCONE SYNTHASE INTRON IN CHARACTERIZING *PETUNIA* TAXA

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Most molecular markers measure genetic distance and may not be related to evolutionary distance because of selection pressure. Introns are under very little selection pressure and should be more closely related to evolutionary distance than most of the techniques currently being used. A method was developed to characterize the genetic heterogeneity of the chalcone synthase A gene (Chs A) intron within the *Petunia integrifolia* (Hook.) Schinz & Thell. species complex. The DNA from wild species collected from known locations were used to amplify the chalcone synthase gene intron through the polymerase chain reaction (PCR). The resulting PCR product was then characterized by Rsa I restriction. In addition, the sequence of the intron was used to develop an evolutionary tree of the gene. This study showed that the variation in the intron of the Chs A gene could be used to characterize closely related *Petunia* taxa.

1540-1600

S21-O-27

MARKER-ASSISTED REDUCTION OF REDUNDANCY IN GERMPLASM COLLECTIONS: GENETIC AND ECONOMIC ASPECTS

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Germplasm collections invariably contain duplicate accessions, both within and between genebanks. These redundancies are a burden for curators because they do not contribute to the diversity in the collection, but do require genebank budget for maintenance. Thus, both from a genetic and economic point of view, identification and elimination of redundancies should be an important genebank objective. Molecular analysis can complement traditional approaches towards identifying duplications. Interpretation of molecular data is, however, by no means straightforward because various genetic relationships among potential duplicates may occur. Since in all collections, even for self-fertilizing crops intra-accession variation is often observed, the question is not so much whether two accessions are identical, but rather whether they

are sufficiently different to consider them distinct. To address this question, statistical methods can be applied to estimate and test molecular variance components. Genetic issues related to the answering of this question are illustrated by experimental data from rationalization studies carried out in various crop collections, including flax and potato, of the Centre for Genetic Resources, The Netherlands. In addition, economic aspects of rationalization studies are discussed. It is concluded that, considering the high costs of molecular analyses, the potential economic benefits of rationalization with the help of molecular technology should not be taken for granted and indeed strongly depend on the crop involved. In contrast, the added value obtained by molecular characterization in improving insight in the genetic composition of collections and the quality of genebank operations can be regarded considerable. Examples of spin-off from such studies are presented.

1600–1620

S21–0–28

MOLECULAR GENOME ANALYSES AS TOOLS FOR EFFICIENT EX SITU CONSERVATION AND UTILIZATION OF PLANT GENETIC RESOURCES

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The potential of molecular markers in augmenting the information available on plant genetic resources is applicable to several aspects of ex situ-genebank work. Gaps in the passport data on taxonomic status and geographic origin of the accessions are a primary target, being especially present in material collected in earlier times and/or exchanged several times between various donors. In addition, molecular analyses offer insight into the diversity present within collections and even into the evolution of certain cultivated plant species. With regard to taxonomy and geographic origin of accessions, species from the very variable and closely related *Solanum nigrum* complex were studied at the IPK by SSRs and AFLPs. Both contributed to a classification of more than a dozen formerly undetermined accessions, with AFLPs also unravelling *S. americanum* as being rather unrelated to the other species of the complex and as exhibiting unexpected high levels of infraspecific variation. Simultaneously, they detect geography-correlated subclusters in the species *S. americanum* and *S. villosum*. Similar links between geography and molecular clusters were observed in *Malus sieversii* as (one of) the main progenitor species of cultivated apple from Central Asia: PCR markers lead to a mainly population-specific grouping, the molecular distances between the clusters being even in rather good accordance with their geographic origin. In the genus *Amaranthus*, genetic diversity assessment confirmed the existence of three genepools for grain amaranth breeding. The detected species-specific clusters also offer potentials for a future, DNA-based classification of material from morphologically similar species, while in respect to the evolution of the grain amaranths, additional USDA/ARS reference material is currently examined. Together with accessions of known provenance, they will be employed in a next step to search for geography-correlated, infraspecific subclusters.

1620–1640

S21–0–28–A

TO BE ANNOUNCED

1640–1700

S21–0–28–B

TO BE ANNOUNCED

Thursday · August 15

1100–1140

S21–0–29

PLANT GENETIC RESOURCES MANAGEMENT AND CONSERVATION STRATEGIES: PROBLEMS AND PROGRESS

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The conservation of plant genetic resources has developed into an important technical, socio-economic and political concern over the past forty years or so. With the successes of the Green Revolution in the sixties and the concomitant losses of landraces of the major food crops, especially in the developing countries, it became apparent that coordinated efforts to collect and conserve these threatened resources needed to be initiated. Genebanks were established in almost every country based on a two-tiered conservation concept that was developed for the storage of orthodox seed-producing cereal crops. However, vegetatively propagated and recalcitrant seed producing species, as well as other materials for which the genebank concept did not work, became increasingly threatened and also needed to be conserved. New techniques and strategies were called for. With the ratification of Convention on Biological Diversity in 1992, considerable awareness was created about the importance of conserving biodiversity, its sustainable use and the need for equitable benefit sharing arrangements. The discussions which led to the CBD and thereafter gave a real boost to in situ and on-farm conservation and brought to light the realization that adequate management practices for genetic resources conserved in farmers' fields and home gardens were badly needed. This paper deals with important PGR management and conservation approaches taken by both public and non-governmental institutions, assesses their constraints and describes the progress made towards their further development.

1140–1200

S21–0–30

DEVELOPMENT OF PLANT CRYOPRESERVATION AND ITS FUTURE PROSPECTS

Akira Sakai*

1-5-23, Azabu-cho, Kita-ku, Sapporo, Hokkaido, Japan, 001-0045

Cryopreservation is becoming a very important tool for long-term storage of plant genetic resources for future generations with a minimum of space and maintenance requirements. Recently, cryopreservation was reported to offer a real hope for long-term conservation of endangered and rare species in the advent of catastrophe. Cryopreservation in LN2 appears to be logical choice for long-term storage of plant germplasm. However, the availability or development of simple, reliable, cost-effective protocols, and subsequent plant regeneration, are basic requirements for plant germplasm conservation. Almost 12 years ago, some new cryogenic procedures such as vitrification with or without encapsulation, and the encapsulation dehydration technique were presented. These new procedures dehydrate a major part of the freezable water of specimens at non-freezing temperatures and enable them to be cryopreserved by direct plunging into LN2 without the need for a freeze-induced dehydration step. These alternative dehydration procedures have simplified cryogenic protocols, and have provided high levels of recovery growth and greater potential for broad applicability, especially non-hardy tropical plants. The vitrification protocol utilizes a highly concentrated vitrification solution, which sufficiently dehydrates explants without causing injury so that both cells and the surroundings solution turn into a stable glass when plunged into LN2. We have developed a glycerol-based vitrification solution, PVS2. Our vitrification protocol, using PVS2 and loading solution (a mixture of 2 M glycerol and 0.4 M sucrose) has successfully been applied to a wide range of plant materials of temperate and tropical plants totaling nearly 200 over the last 12 years. For many vegetatively propagated species or cultivars of temperate origins, cryopreservation techniques are sufficiently advanced to envisage their immediate utilization of large-scale experimentation in genebanks. Research is much less advanced for tropical wild species. This is because of the comparatively limited level of research activities aiming at improving the conservation of these species. However, various technical approaches can be explored to improve the efficiency and increase the applicability, provided that the tissue culture protocols are sufficiently operational for the species. It is hoped that new findings on critical issues such as understanding and control of dehydration tolerance will contribute significantly to the development of improved cryopreservation techniques for difficult species or cultivars.

1200–1220

S21–0–31

POTATO CRYOPRESERVATION IN GERMANY—USING THE

DROPLET METHOD FOR THE ESTABLISHMENT OF A NEW LARGE COLLECTION

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Potato germplasm has been stored in cryopreservation since 1997. The droplet method is applied using 10% dimethyl sulfoxide as cryoprotector. Explants are fixed on pieces of aluminium foil and frozen ultra-rapidly. Regeneration rates depend on the genotype and range from 20 to 100% per accession. The average survival rate is 71.5%, the mean regeneration is 48.4%. The explants are obtained from a collection based on in vitro cycles including storage of microtubers. Donor plantlets are grown from microtubers on MS medium without hormones. Once the plantlets have reached lengths of 5 cm, apical explants are dissected for cryopreservation. A comparison has been made with plantlets grown as permanent shoot cultures for several years. Microtuber-derived plantlets gave significantly better results. Controls have been transferred to soil conditions and compared with the donor plants. No changes have so far been observed. To further improve the regeneration rates, experiments have been performed using different culture vessel types. Technological considerations will be presented concerning the principal management of a large cryo-collection in the framework of the reorganisation of the German potato genebank.

1220-1240

S21-O-32

CRYOPRESERVATION OF SOME TEMPERATE FRUIT SPECIES

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A scientific cooperation program was established between the International Plant Genetic Resources Institute (IPGRI), the Fruit Tree Research Institute in Rome and two Research Institutions of People's Republic of China and Jordan. The objectives were to study the most proper cryopreservation methodologies and consequently to start activities of gene bank cryopreservation of temperate-fruit species. Strong reasons for implementing such an activity were the need of reducing costs for maintaining large field collections (already existing at the three Institutions) and to avoid risks of losses due to disease and pest attacks. The most important temperate fruit species were used for the experiments: apple, almond, peach, strawberry, kiwi, walnut, plum and others. The source materials consisted of nodal buds or apices of micropropagated plantlets; for strawberry also organogenic callus and cell suspensions were used. Three methods were adopted for the experiments: two-step freezing, vitrification and encapsulation-dehydration; this latter gave the most satisfactory results (50–60% regrowth), while two-step freezing was successful for cells (80% survival). After the procedures of conservation, which were performed at LN temperature, the surviving plants were tested to confirm their identity types through enzymes, protein patterns and molecular-marker analysis. So far, variations were not detected. Total protein profiles during the different steps were done; a new band was found at 18.7 kDa after cryoconservation, this band at the moment is considered to be a cold shock protein. The Institutes in China and in Jordan have begun to establish a cryo-bank while in Rome research activities concerning molecular aspects of the genetic stability are routinely done.

1340-1440

S21-P-33

THE SPANISH FRUIT GERMPLASM BANK OF ALMOND, PEACH AND PEAR

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The temperate fruit tree genebank of the Servicio de Investigación Agroalimentaria (SIA) of the Diputación General de Aragón (DGA) is located in Montañana (Zaragoza), in the Ebro Valley Area, a cold climatic zone of the country. It consists on three field collections of the species *Prunus amygdalus* Batsch, *P. persica* (L.) Batsch and *Pyrus communis* L. These are the reference collections in the Spanish network of genetic resources as well as for the Spanish Plant Variety Office. The almond collection holds more than 250 accessions, most of them originated in Spain. A quite important number of selections from different almond breeding programmes are also held while others are traditional and commercial cultivars coming from the most important almond growing areas in the world. A small collection of wild species of almond coming mainly from an exploration in Iran and Afghanistan is also maintained. The peach collection contains mostly clingstone peaches (118), both of yellow and white flesh and flat peaches (11); most of them of Spanish origin, and other new and old foreign commercial peach and nectarine cultivars (194), used as reference for characterization. For the pear collection, there are 47 Spanish accessions with eight of them commercial cultivars, and 76 foreign cultivars used as reference for characterization. The objectives of this bank: 1) The characterization and preservation of the variability of the three species, with special attention to the Spanish forms; and 2) The use of this germplasm in active breeding programmes and other research and transference projects.

1340-1440

S21-P-34

LOW TEMPERATURE STORAGE AND CRYOPRESERVATION OF THE GRAPE ROOTSTOCK "KOBER 5 BB"

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Grapevine germplasm consists of a large number of cultivars and rootstocks, many of which are typical for small and remote environments, and therefore important for biodiversity conservation and the reduction of genetic erosion. The creation of a clonal collection is a reliable method to preserve the germplasm of fruit tree species, but it involves high maintenance and management costs, and is not completely free from dangers, due to the possibility of the spread of grave plant pathogens. Biotechnology offers valid alternatives to the traditional methods of germplasm conservation. This study had the task of exploring the potential for grapevine preservation, both at low temperatures and by means of cryopreservation (in liquid nitrogen, at -196 C). The plant material utilized in our trials was the grape rootstock "Kober 5 BB" (*Vitis Berlandieri* x *V. riparia*). As regards slow growth storage, the variables studied were the temperature of conservation (4 and 10 C), the photoperiod (darkness and 8 h light), the sucrose concentration (15 and 30 g/L) and the presence/absence of activated charcoal in the storage medium. After four months of storage, the results indicate a strong influence of temperature; shoots kept at 10 C having higher survival (80%) than those at the lower temperature. Cryopreservation trials have been carried out with shoot tips, by utilizing different vitrification techniques (use of the PVS2 vitrification solution, encapsulation-dehydration, encapsulation-vitrification) before directly plunging the explants into liquid nitrogen. Encapsulated and cryopreserved explants have shown survival and regrowth, although the percentages are still low.

1340-1440

S21-P-35

GERMPLASM PRESERVATION IN ALLIUM SPECIES-AN INTEGRATED APPROACH TO STORE MORPHOLOGICALLY CHARACTERIZED VIRUS-FREE PLANT MATERIAL VIA CRYOPRESERVATION

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A large collection of *Allium* crop and wild species is maintained at Gatersleben. Additionally to the field maintenance, in vitro culture and cryopreservation are used to increase the maintenance safety and plant quality. One third of the 3000 *Allium* accessions is held vegetatively. Vegetative main-

tenance of germplasm is usually accompanied by virus accumulation. OYDV, LYDV, GCLV, SLV and allexiviruses have been detected by ELISA, tissue print and dot blot technique. Virus susceptibility is species-specific. Together cultivated *A. albidum*, *globosum*, *hymenorrhizum*, *lineare*, and *obliquum* were more infected than *A. rubens*, *saxatile*, and *senescens*. Similar differences were found in their hybrids with *A. cepa*. Virus elimination is performed by meristem culture partly together with thermo- and chemotherapy. Virus elimination is high in garlic (50.9% of 108 tested plants), but so far low in shallots. Here, in 144 plants screened by tissue print, four viruses were detected. In garlic, it was possible to establish a virus-free core collection of the most important accessions. This collection has been described by internationally standardized morphological descriptors. Cryopreservation methods are in development for garlic: the vitrification and the droplet method. The cryoprotector PVS3 (50% glycerol + 50% sucrose) is used. For cryopreservation, meristematic regions of the plants are used. Large differences have been found in plantlet regeneration with respect to the source organs—ripe cloves, basal plates of bulbs in the sprouting phase, bulbils of different age and size, in vitro cultures. Explants from cloves regenerate to 75%, but they suffer from contamination. Therefore, the mostly used organs are bulbils. Finally, in vitro cultures offer the chance to use virus-free material for storage, but cryopreservation of them is still difficult. Therefore, several pre-treatments are necessary such as dehydration and cold hardening.

1340–1440

S21–P–36

CRYOPRESERVATION OF APPLE GERMPLASM: RESULTS USING A WINTER VEGETATIVE BUD METHOD

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The *Malus* germplasm collection at the USDA, ARS Plant Genetic Resources Unit (PGRU), Geneva, NY, is being processed for long-term preservation at the USDA, ARS National Center for Genetic Resources Preservation (NCGRP), Fort Collins, CO. Scions harvested at PGRU in mid-winter are sent directly to NCGRP where they are cut into nodal sections, desiccated to 30% moisture, cooled at 1 C/hr to –30 C and held for 24 h before being transferred to the vapor phase over liquid nitrogen (ca. –160 C). Samples are thawed at + 4 C. At Geneva, samples are rehydrated and viability is measured by budding to seedling rootstock. To date 96% of 1665 *Malus* accessions tested showed some survival and 91% percent had viabilities of 40% or greater, the level for which we considered an accession successfully cryopreserved. *Malus xdomestica* comprised 65% of the accessions tested and of these 95% had 40% or greater viability. For species other than *M. domestica*, 83% met this criterion. Some species are very tolerant of the procedure (examples *M. robusta* and *M. pumila*) whereas others are sensitive (examples *M. angustifolia* and *M. tschonoskii*). Eight lines have been processed each year since 1995; data from this group suggest that mean fall temperature in Geneva NY influences survival. Sixty-four accessions processed in 1988–92 on average have shown no decline over 8 years of storage. A few lines have shown either a slight increase in survival with storage or a slight decline. Lines have been reestablished in the field from this cryopreserved collection to replace trees lost to fire blight. This simple cryopreservation method has been very useful for germplasm management of *Malus* species.

1440–1500

S21–O–37

THE CONSERVATION ACTIVITY ON FRUIT TREE GERMPLASM IN ITALY

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The Istituto Sperimentale per la Frutticoltura (ISF), with the support of the Ministry for Agricultural and Forestry Policy (Mi.P.A.F.), responsible in Italy for plant genetic resources for food and agriculture (PGRFA), is carrying out and co-ordinating a project on plant genetic resources. One of the two actions of this project—aimed at coordinating and harmonising the ex situ collection, conservation, characterization, evaluation and utilization activities on PGRFA achieved in Italy by different Institutions and entities—is particularly focused on

the assessment and study of the management and the safeguard of fruit tree genetic resources present in most of the Italian research institutes belonging to Mi.P.A.F., Universities, the National Research Council and regional research centres. Among the 21 Institutes interviewed, 27 species of fruit trees for a total number of 13,027 accessions are conserved ex situ. Considering the number of varieties, it amounts to 8,835, 39% of which are of Italian origin. Most of the fruit tree varieties collected consists of cultivars and obsolete varieties (74.6%). Breeder's selections amount to 2.8%, while wild material and rootstock cultivars count 2.3% and 1% of the varieties, respectively. For 19.3% of the varieties it was not possible to acquire this type of information. All the data concerning the accessions conserved were collated according to a descriptor list (passport and preliminary characterization and evaluation data) and, in order to spread the relative information and to allow a wider use of this material, an on-line searchable database was developed and it is going to be available for any kind of users. This project has also permitted to identify a list of varieties of different species, which will be the starting material for the establishment of the Centro Germoplasma Frutticolo-CGF (National Fruit Tree Germplasm Centre) at ISF.

1500–1520

S21–O–38

CRYOPRESERVATION OF PELARGONIUM SHOOT TIPS BY ENCAPSULATION–DEHYDRATION: EFFECTS OF SUCROSE CONCENTRATION, DEHYDRATION, DURATION AND GENOTYPE

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In order to guarantee a safe long-term conservation of the INH *Pelargonium* collection, meristem cryopreservation studies were undertaken. Survival and regeneration were obtained using an encapsulation–dehydration process involving meristem preculture in a liquid medium progressively enriched in sucrose (up to 1 M) prior dehydration with silica gel. In order to optimize the process the effect of different sucrose concentration on meristem dehydration and cryopreservation was studied with the cultivar *P. xpellatum* 'Ville de Paris Lilas'. First, the *Pelargonium* meristem natural tolerance to dehydration has been investigated. After one day of culture on standard medium (0.088 M sucrose), meristem water content was 1130 % (with respect to dry weight). Without preculture, natural survival was near to 100% up to a water content of 450%. After that, survival decreased to 0% for a water content of 33%. Then, meristem tolerance to a direct high sucrose concentration was studied. *Pelargonium* meristems were directly precultured for 48 h in liquid medium with sucrose concentration from 0.088 M to 1.25 M. Up to 0.75 M, 100% of survival was obtained, and more than 60% survived with 1.25 M. With 0.75 M for 48h, water content was about 258%. Cryopreservation using a direct preculture with 0.75 M or 1 M sucrose were then realized. Survival rate as good as the one obtained with progressive preculture was obtained (more than 60%). This result permitted a simplification of the process. But, the percentage of regeneration was still low due to the development of hyperhydric tissues. Studies are carried on to improve the regeneration rate and to test the process on other genotypes.

1520–1540

S21–O–39

UPOV REFERENCE COLLECTION OF HYDRANGEA: GENETIC RESOURCES CHARACTERIZATION

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Many species of the genus *Hydrangea* (Saxifragaceae) are appreciated for their great ornamental value. The UPOV reference collection of this genus (13 species, according to McClintock classification, and over 500 accessions), is located in Angers (France) and represents a large part of the European genetic resources. Genetic knowledge is essential in order to manage this collection and to valorize the different species. All the more so as the existing classifications do not agree as to the number of species and subspecies in the genus. Therefore, we analyzed the inter and intraspecific relationships among species and subspecies. 1) Concerning the floral biology of *Hydrangea*, we have examined the reproductive regime and the prezygotic crossing barriers of different species and subspecies. Alloamy is the general reproductive system. Many

crosses between species and subspecies are compatible although the number of chromosomes between the parents can differ significantly. The results on the progeny of the different crosses tested will help to understand the taxonomic status of the species/subspecies. 2) Concerning genetic diversity, we chose to develop ISSR markers because previous studies had shown that they could be more reliable than AFLP, for species where high quality DNA can not be obtained. Seven primers were chosen which yielded over one hundred polymorphic markers on the cultivars of the subsections *Macrophyllae* (350 clones) and *Asperae* (47 clones). The genetic proximity found using ISSR markers closely reflected what was known from the pedigree of the varieties. Confirmation of previous identification of varieties (achieved with 35 morphologic markers) was obtained and in some cases, mislabellings were detected. This study on inter and intraspecific relationships among *Hydrangea* is the first done for this genus and will be helpful for plant breeding programs, as well as for the management of the reference collection.

1540-1600

S21-O-40

EVALUATION OF FRUIT TREE GENETIC RESOURCES IN A MEDITERRANEAN SECONDARY CENTER OF BIODIVERSITY

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A large group of uncultivated or underutilized plant species, as well as major staple crops, represent a source of genetic variability which can ensure the plant sustainable use for human consumption. For each crop there are one or more primary centers of origin, from where crops were dispersed long-range thus originating secondary centers of genetic variability in new diffusion areas. The presence of wild relatives in each diversity area and the continuous flow of genes among and within plant species determined crop evolution and the rise of new genetic variability. Recently loss in genetic diversity has been outlined mainly in intensively cultivated areas, while reduced erosion has been observed in protected habitat such as islands. Sardinia is one of the secondary diversity centers of plant species that have evolved by adaptation to the Mediterranean environment, where a large number of genotypes of different fruit tree species have been collected and described. In this work results are reported for a long-term survey carried out to improve knowledge on the diversity of the genetic resources for food. Eleven fruit tree species have been evaluated in the level of their genetic diversity. Some are major staple crops such as olive and grape, others such as almond, apricot, cherry, plum, fig, apple and pear are presently less cultivated, and others more recently introduced including citrus and cactus pear. The degree of conservation of Sardinian landraces and local varieties was the highest in grape, olive, almond and fig. A complete inventory of most of the species has been carried out and the Sardinian germplasm of fig, cactus pear and olive were included in the databases of the European collection. It was established by the working groups of the UE Projects on Conservation, evaluation, exploitation and collection of minor fruit tree species (RESGEN CT95-29) and Conservation, characterization, collection and utilization of genetic resources in olive (*Olea europaea*) (RESGEN CT96-97).

1600-1620

S21-O-41

BIO-DIVERSITY: INTEGRATED CONSERVATION STRATEGY IN THE JNANABHARATHI CAMPUS OF BANGALORE UNIV.

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With an objective of conserving threatened and endangered plant species and to improve ecology and environment of the Jnanabharathi Campus (headquarters of Bangalore Univ.) spread over an area of 1200 acres, a strategy has been conceived where in plants of economic and medicinal importance collected from Western Ghats and also from different parts of Karnataka were planted. In the first phase in 2000, an area of 100 acres was planted. In the second phase in 2001, another plot of 100 acres was covered by planting saplings of trees, shrubs, creepers and climbers of 300 species. The approach adopted is "Integrated Conservation," Mortality of saplings was minimized by feeding them with rainwater harvested through contour trenches, contour bunds,

basins, and check dams. More than 95% of the saplings have survived the severe hot and dry seasons of summer. Recharge of the ground water was ensured by construction of minor checkdams and gullyplugs. Existing fauna and flora have been saved by not disturbing them during land preparation and also by protecting them from wild fire. Fauna populations including birds, rodents, reptiles and insects, have increased after one year. Around 1725 National Service Scheme (NSS) volunteers, at the rate of 100 to 300 for a period of 10 to 15 days at a time, drawn from the affiliated colleges of the Univ., were deployed for developing the Biodiversity Park. They were imparted educative training and had undergone physical labour. They were also given skills of theory and practice in nurturing the plants, their utility to society, their contribution to ecology and environment. This unique strategy involved both ex situ and in situ conservation. The Biodiversity Park is a demonstration center for not only students, but also for farmers in particular and people in general.

1620-1640

S21-O-41-A

TO BE ANNOUNCED

1640-1700

S21-O-41-B

TO BE ANNOUNCED

Friday · August 16

0800-0900

S21-P-42

EVALUATION OF IRANIAN ONION GENOTYPES USING MULTIVARIATE ANALYSIS

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Onion is an important vegetable crop in Iran where it has grown for thousands of years. Iran is one of the centers of genetic diversity of onion cultivars. Onion cultivars and landrace collections from different parts of Iran and stored at the National Plant Genebank of Iran were characterized and evaluated based on agromorphological characters to determine patterns of germplasm variation. Significant correlations were found between pair characters such as presence of leaf wax and susceptibility to thrips that is correlated with foliage color. Accessions with light green color or glossy foliage are more resistant to thrips than darker colored genotypes. Factor analysis has shown that the first five factors gave eigen values greater than 1.0 and altogether account for 62.0% of the accumulated variation. The first factor explained 22.6% of the variation and was associated mainly with susceptibility to thrips at three development stages. The second factor accounted for 15.7% of the variation and was associated mainly with presence of bulbils, foliage color, and anther color. The third factor explained 8.4% of the variation and was associated with the ability to flower and the shape of fully-grown bulbs. The fourth factor explained 8.1% of the variation and was associated with the nature of storage organs. The fifth factor explained 7.3% of the variation and was associated with bulb skin color. By cluster analysis, the Iranian onion genotypes were grouped into six clusters, each of which contained genotypes that were highly similar based on characters and geographical locations.

0800-0900

S21-P-43

INVESTIGATION OF FRUIT GERmplasm RESOURCES WITH COLD RESISTANCE IN JILIN PROVINCE CHINA

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Jilin Province is located in the central part of Northeast China, where the yearly average temperature ranges from 2 to 6 C and it may drop to -42 C in the winter. In Jilin Province, there are large collections of hardy fruit tree germplasm. Studies on collection, preservation, characterization and utilization of germplasm

resources of hardy fruit trees have been carried out in the Pomology Institute of the Jilin Province Academy of Agricultural Sciences for 50 years. Thirteen families, 25 genera, 2 subgenera, 63 species, and seven varieties of fruit trees were identified, and the National Fruit Tree Germplasm Center (Gongzhuling Hardy Fruit Nursery) was established. Important traits, ecological distribution and utilization of germplasm resources of hardy fruit trees are presented in this paper. Based on investigation of problems in the utilization and studies of germplasm resources of hardy fruit trees in Jilin Province of China, several suggestions will be presented as follows: (1) to obtain a wide-ranging collection of wild species of hardy fruit trees; (2) to construct a descriptive system and a data bank of hardy fruit tree germplasm; (3) to establish a genetic bank of hardy fruit tree germplasm in vitro using tissue culture techniques; (4) to study the genetic diversity of hardy fruit tree germplasm using molecular markers; and (5) to create new germplasm with unique hardy fruit tree resources.

0800-0900

S21-P-44

IDENTIFICATION OF GENETIC STRAINS OF "DEGLET NOOR" AND "MEDJOOL" DATE (*PHOENIX DACTYLIFERA* L.) VARIETIES USING AFLP MARKERS

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Date palm (*P. dactylifera* L.) is one of the most important fruit crops in North Africa and Middle East. There is limited production of date palm in California and Arizona. "Deglet Noor" and "Medjool" are two of the most important and widely grown date varieties around the world and in the U.S. It is difficult to identify date palm variety based on morphological characteristics, isozymes or RAPD markers. It is even more difficult to identify genetic strains of commercial variety based on those markers. Genetic strains of clonally propagated fruit crops are very common, but it is challenging to identify different genetic strains within the same variety. We have developed PCR based amplified fragment length polymorphism (AFLP) analysis with near Infrared fluorescence labeled primers for the identification of date varieties in California. The AFLP markers generate large number of polymorphic bands among different date varieties and allow easy identification of different varieties. We now use the AFLP markers to identify genetic strains of "Deglet Noor" and "Medjool" date varieties. A total of 17 "Deglet Noor" samples and 24 "Medjool" samples collected from the USDA date germplasm collection and commercial gardens in California were included in the study. We are able to identify large number of genetic strains in "Deglet Noor" variety and fewer strains in "Medjool" variety using AFLP markers. The potential application of AFLP markers in identification of date variety or genetic strains is very feasible. The identification of genetic strains of date varieties using AFLP markers will enhance the decision for future date germplasm collection and maintenance. The information also can be used in future date variety breeding and improvement.

0800-0900

S21-P-45

SEGREGATION OF RESISTANCE TO ROOT-KNOT NEMATODES IN A *VITIS VULPINA* HYBRID POPULATION

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The root-knot nematode (*Meloidogyne* spp.) resistance of a seedling population derived from *Vitis vulpina* L. was evaluated to investigate the genetic control of nematode resistance in this grape species. The female parent of the population is the phylloxera resistant grape rootstock 161-49C, a *V. riparia* x *V. berlandieri* hybrid. This rootstock is known to be homozygous for the alleles conferring susceptibility to *Meloidogyne incognita* and also does not contribute resistance to Harmony virulent root-knot nematodes to its progeny. The male parent is an accession of *V. vulpina* (accession DVIT 1280) held in the collection of the U.S. National Plant Germplasm System. The nematode resistance of this *V. vulpina* accession has not been determined, but root-knot nematode resistance has been reported in grape rootstocks with *V. vulpina* in their parentage. Resistance was assessed in greenhouse pot culture with nematode reproduction measured by counting egg masses present on seedling roots six weeks after inoculation with second stage juvenile nematodes. Three nematode populations were used to evaluate seedling resistance. Two of the nematode populations are virulent on Harmony, a grape rootstock that is resistant to most *Meloidogyne incognita* popula-

tions. The third nematode population is a *Meloidogyne incognita* population that is avirulent on Harmony. In each of the three nematode population screenings the grape seedlings segregated in a pattern consistent with a 1:1 ratio of resistant:susceptible. However, since each seedling was challenged by only a single nematode population, it cannot yet be determined if the resistance to Harmony virulent and Harmony avirulent nematodes is due to the same or different alleles. The *V. vulpina* parent of the population, accession DVIT 1280, is heterozygous for at least one dominant allele conferring resistance to root-knot nematodes.

0800-0900

S21-P-46

RESPONSE TO ROOT-KNOT NEMATODES IN A *VITIS MONTICOLA* HYBRID POPULATION

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Accessions of the grape species *Vitis monticola* Buckley have been reported to be resistant to a root-knot nematode, *Meloidogyne incognita*, with resistance conditioned by a single dominant allele. New sources of root-knot nematode resistance are needed in grape rootstocks because of the emergence of nematode populations that are virulent on rootstocks with resistance derived from *V. x champinii* Planch.; these nematodes are termed "Harmony virulent" populations in reference to their diagnostic grape rootstock host. Resistance against two types of root-knot nematodes was evaluated in seedlings of a cross of *V. monticola* and a grape rootstock. The male parent is an accession of *V. monticola* (accession DVIT 1376) held in the collection of the U.S. National Plant Germplasm System. The nematode resistance of this *V. monticola* accession has not been determined. 161-49C, a *V. riparia* x *V. berlandieri* hybrid, is the female parent of the population. This phylloxera resistant rootstock is known to be homozygous for the alleles conferring susceptibility to *Meloidogyne incognita* and also does not contribute resistance to Harmony virulent root-knot nematodes to its progeny. Resistance was evaluated in greenhouse pot culture using egg mass counts as a measure of nematode reproduction. *Meloidogyne incognita* (Harmony avirulent) and Harmony virulent nematodes (*Meloidogyne* sp.) were used to separately challenge the seedlings. The seedlings demonstrated segregation for resistance to Harmony avirulent *M. incognita* nematodes in a pattern consistent with a 1:1 resistant:susceptible ratio. *Vitis monticola* accession DVIT 1376 is heterozygous for resistance to *M. incognita*. However, the seedlings were very susceptible to Harmony virulent root-knot nematodes. *Vitis monticola* is a source of nematode resistance, but accession DVIT 1376 does not offer resistance superior to that available in contemporary grape rootstock varieties.

0800-0900

S21-P-47

LACK OF ASSOCIATION BETWEEN GENETIC AND GEOGRAPHIC ORIGIN CHARACTERISTICS FOR THE WILD POTATO *SOLANUM SUCRENSE* HAWKES

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Collecting germplasm to broaden breeding resources is an essential activity of genebanks. Research to understand how genetic diversity is partitioned in nature might help to identify collections rich in diversity. Previous studies among wild populations of *S. fendleri* (disomic polyploid selfer) and *S. jamesii* (diploid outcrosser) revealed no significant associations between genetic and ecogeographic variation. Even physical separation did not predict genetic differences. In this study, 28 populations of *S. sucrensis* Hawkes (2n = 4x = 48), a Bolivian species with a third breeding system (polysomic polyploid outcrosser) were evaluated. The objective was to assess whether genetic differences between populations are predicted by differences in geographic parameters at the natural site of origin. Genetic differentiation was estimated by using 216 polymorphic Random Amplified Polymorphic DNA (RAPD) markers. The average genetic distance (GD) found between pairs of populations was 31% (ranging from 8% to 44%). Correlations of GD with latitude, longitude, altitude and distance were not

significant. Multiple regression analysis also confirmed that GD was not explained by the geographic parameters used. This is now the third species and breeding system in wild potato for which we conclude that geographic origin data may not very useful in gauging interpopulation genetic diversity in the genebank.

0800-0900

S21-P-48

APPLES OF NORTH EASTERN AMERICA

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One of the major problems facing apple growers in Eastern Canada is low temperature injury during the winter and spring seasons. A survey was conducted in 1995–96 to identify factors responsible for apple tree mortality during the particularly severe winter of 1993–94 in Quebec. Three hundred and thirty (330) apple orchards were visited and information on more than 50 characteristics were evaluated via a questionnaire that included topics such as hardiness, shelf life and end use of the fruit, etc. A large diversity of cultivars and rootstocks were observed in Quebec orchards. The survey work carried out in 1995–96 lead to the establishment of a database containing important agronomic information on the cultivars evaluated. Some of the more important information, such as hardiness, end use, shelf life, scab resistance, etc., along with 265 apple images, were put together on a CD and a poster. A copy of the "Apples of North Eastern America" CD and the poster is available from <http://www.pgris.com>.

0800-0900

S21-P-49

GENETIC DIVERSITY OF CHINESE JUJUBE (*ZIZIPHUS JUJUBA* MILL.)

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Chinese jujube (*Ziziphus jujuba* Mill.) is a native fruit tree and medicinal plant of China and has been introduced to more than 20 countries. It is becoming increasingly important for its wide adaptation, easy management, early bearing, rich nutritional value, and multi-use. Reasonable repayment can be expected when planting it in the temperate, especially arid and semi-arid zone. There are about 700 cultivars of Chinese jujube in China. To better use and conserve the species with brilliant prospect, its genetic diversity was systematically studied at different levels. It can be commercially cultivated (with proper cultivar) under the condition of annual average temperature (5.5 to –22 °C) soil pH (4.5–8.4), and annual rainfall (87–2000 mm). It has a high diversity in chromosome numbers (2n = 24, 36) and karyotype (1A, 2A, 3A, 1B, 2B, 2C); shape, size and surface sculpture of pollen; leaf length (2.3–10.1 cm) and flower diameter (2.9–10 mm); especially the shape, color, weight (2–46 g), growth period (60–145 d), soluble solid (17%–45%), Vc content (61 mg/100–1174 mg/100 g.fw), and cAMP content (2 nmol/g.fw–302 nmol/g.fw). In addition, the RAPD and isoenzyme (7 kinds) patterns of different cultivars of Chinese jujube were also revealed. Basing on the above data, a tree diagram and a core germplasm collection of Chinese jujube cultivars were constructed.

0800-0900

S21-P-50

DEVELOPING WEAR-RESISTANT PLANT CULTIVAR FOR USE ON MILITARY TRAINING LANDS

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Military land managers in the US try maintain and improve the sustainability and native biological diversity of terrestrial and aquatic ecosystems while supporting human needs, including the military mission. We are using plant genetics to (1) to better understand and evaluate genetic diversity on military

lands and (2) to breed new cultivars (varieties) of existing range-land plants that will be better able to maintain healthy plant communities on training lands, while also increasing the morphological diversity of the ecosystem. We are using the Amplified Fragment Length Polymorphic DNA (AFLP) genetic marker technique to identify markers associated with desired traits. In one example, we used degrees of genetic diversity within adjoining and geographically distinct populations of the same native plant species by combining AFLP with new statistical tools to identify degrees of diversity within adjoining and geographically distinct populations of little bluestem [*Schizachyrium scoparium* (Michx.) Nash]. In our plant-breeding program we have assembled a broad genetic base and initiated a breeding program to develop and evaluate improved native and naturalized grasses and forbs. We are selecting plants for reduced seed dormancy and increased seedling vigor. An independent panel has determined that the new germplasms being developed are not invasive to other habitats. Germplasm Release Notices and Crop Science Registration Articles will be prepared prior to formal release of these germplasms. These combined diversity and breeding programs will provide a better return on the military investment in its Land Repair and Maintenance Program. Land managers will have better information on what types of plants are best suited to rehabilitate lands.

0800-0900

S21-P-51

VARIATION IN PLOIDY LEVEL, FERTILITY, AND BREEDING BEHAVIOR IN CULTIVATED *SCHLUMBERGERA* (CACTACEAE)

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Chromosomes were counted in pollen mother cells and root tips of seven *Schlumbergera* clones. Microscopical analysis revealed that two of the clones were diploid (2n = 2x = 22), two were triploid (2n = 3x = 33), and three were tetraploid (2n = 4x = 44). Female fertility was assessed by percent fruit set and numbers of viable seeds per fruit, and pollen viability was assayed by the fluorochromatic reaction (FCR). All seven clones produced viable ovules and pollen. The diploid and triploid clones were self-incompatible (SI) whereas the three tetraploid clones were self-compatible and yielded S1 progeny when selfed. Pollen was collected from a diploid, triploid, and tetraploid clone and 200 pollen grains were measured per clone using an ocular micrometer. There was a positive correlation between pollen diameter and ploidy level. Pollen diameter was more uniform in the diploid clone than in the triploid or tetraploid clones. Numbers of viable seeds per fruit were greatest in 2x x 2x (female parent x male parent) matings, but viable seeds were also obtained in 4x x 4x, 4x x 2x, 3x x 4x, 3x x 3x, 3x x 2x, 2x x 4x, 2x x 3x matings. The significance of these findings with regard to breeding of cultivated cacti and chromosome evolution of the Cactaceae will be presented.

0800-0900

S21-P-52

MARKETABLE YIELD EVALUATION OF ELEVEN HEIRLOOM TOMATO VARIETIES

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Many New England growers are producing heirloom tomato varieties in order to attract consumers to retail farm operations. In 2001, we tested eleven different heirloom varieties of tomato (*Lycopersicon esculentum* Mill.) for production characteristics and fresh market suitability in Vermont. Tomato seedlings were transplanted into a well-drained sandy soil at the Horticulture Research and Education Center in South Burlington, VT. A completely randomized design was used with four replicates for each variety. Each replicate consisted of 12 plants (total of 48 plants per variety). In row spacing was 0.9 m and between row spacing was 1.5 m. 'Amish Paste,' 'Brandywine,' 'Cherokee Purple,' 'Cosmonaut Volkov,' 'Costoluto Genovese,' 'Green Zebra,' 'Ida Gold,' 'Mosvich,' 'Purple Calabash,' 'Prudens Purple,' and 'Yellow Brandywine' varieties were produced organically using plastic mulch beds and drip irrigation. 'Better Boy' served as a hybrid control. Plants were fertigated weekly using a balanced organic liquid supplement (3–3–3) or nitrogen (16–0–0) based on extension recommendations for New England. Tomatoes were harvested weekly (9 total harvests) and every fruit was individually graded according to USDA standards.

Sample findings include: 'Costoluto Genovese' produced significantly greater total marketable yield by weight when compared to 'Brandywine' (DMRT, n = 36), 'Mosvich' produced the greatest amount of US#1 large fruit (DMRT, n = 36), and 'Cherokee Purple' had a significantly greater amount of culls by weight when compared to 'Cosmonaut Volkov,' 'Green Zebra,' and 'Ida Gold' (DMRT, n = 36). Interestingly, several heirloom varieties outperformed 'Better Boy' in certain instances during this trial. For example, the round red variety 'Mosvich' produced significantly more U.S. No. 1 fruit (11.35 kg) than 'Better Boy' (2.26 kg) (DMRT, n = 36).

0800-0900

S21-P-53

FIRST REPORT OF OCCURRENCE AND CONFIRMATION OF A NATURAL ABBB TETRAPLOID BANANA (*MUSA SPECIES*) FROM INDIA

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South and South-east Asia is believed to be the one of the centers of origin and diversification of banana and plantains. Though Thailand, Malaysia and Myanmar are rich in *Musa acuminata* and its species, India harbours much diversity for *M. balbisiana*. Close proximity and natural tendency for introgression has resulted in speciation and diversification in North Eastern and peninsular India. Explorations conducted by National Research Center for banana in the interior forests of Arunachal Pradesh (N-E state) adjoining China and Myanmar has resulted in the identification of a unique accession. Evaluation and field assessment for 3 years in the NRCB field genebank using Shepherd and Simmond's 15 character classification chart and modified score card of Singh and Uma (2000) has classified this accession to be a tetraploid with ABBB genomic constitution. Flow cytometry studies at IAEA, Vienna have confirmed its tetraploid status. In nature triploid bananas are preferred over the diploids and tetraploids. Natural selection has slowly wiped out natural tetraploids which have played a key role in the evolution of triploid bananas. This accession has been evaluated for its yield, quality, reaction to biotic and abiotic traits and most importantly for its male and female fertility status. The paper deals with its superior traits which contributed for its possible survival against selection pressure in nature.

0800-0900

S21-P-54

HYDROXYCINNAMOYL ESTER CONTENT IN FRUIT OF WILD AND CULTIVATED EGGPLANT SPECIES

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Eggplant (*Solanum melongena* L.) is ranked among the top ten vegetables in terms of ORAC (oxygen radical absorbance capacity) value. This is attributed to the fruit's high phenolic content. When consumed regularly in the human diet, the protective effects of polyphenol antioxidants may help to prevent diseases such as atherosclerosis and cancer. Although research to date has been scant, there is evidence that the complete compliment of phytonutrients, rather than any single constituent, determine the potential health benefits of a fruit or vegetable. Various hydroxycinnamoyl esters of quinic acid and other organic acids and sugars comprise most of the polyphenol antioxidants in flesh of eggplant fruit. The content and distribution of these phenolic esters in fruit flesh from 16 accessions of the cultivated species *S. melongena* and from accessions representing 4 related wild species (*S. aethiopicum*, *S. anguivi*, *S. incanum* and *S. macrocarpon*) were determined by HPLC analysis with PDA detection. On a dry weight basis, the content of total phenolic esters differed as much as 9-fold among species. One accession of *S. anguivi* had the highest content, about twice that of the average for *S. melongena*, whereas *S. aethiopicum* generally had the lowest content. Chlorogenic acid (5'-caffeoylquinic acid) was invariably the principal phenolic, typically ranging from 70 to 80% of the total. However, in fruit from one accession of *S. anguivi* it made up only 44%, and these fruit also contained much higher levels of dicaffeoyl and di-p-coumaroyl quinic acid esters. Overall, we found considerable variation in fruit flesh hydroxycinnamoyl ester content and composition

among eggplant species and accessions included in the USDA germplasm core collection. However, there were also instances of wide variation in fruit from different plants of the same accession, suggesting that physiological parameters such as fruit maturity can strongly influence phenolic ester accumulation.

0800-0900

S21-P-55

GROWING PLUM CULTIVARS IN EASTERN CANADA: A COMPILATION OF DATA FROM 3 EXPERIMENTAL SITES

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Winter hardiness is one of the major problems facing plum growers in Eastern Canada. Several experiments were conducted over many years at three Agricultural and Agri-Food Canada research centres (The Central Experimental Farm in Ottawa (Ontario) "latitude: 45.3832, longitude: -75.7182", the La Pocatière (Quebec) station "latitude: 47.3624, longitude: -69.9951" and the Frelighsburg (Quebec) sub-station "latitude 45.0465, longitude: -72.7837", which is associated with the Horticulture Research and Development Centre in St-Jean-sur-Richelieu). The objective of the experiments was to evaluate the performance and hardiness of over 300 different plum cultivars. A detailed description of 80 of these cultivars as well as their performance in terms of hardiness, flowering dates and yield was compiled and published in a bilingual book entitled "Our Plums/Les Pruniers de chez nous". The information contained in the book was used to prepare a poster showing images of the fruits, flowers and leaves. The poster includes symbols identifying cultivars that are hardy, self-fruitlet, freestone, or those that can be dried to make prunes, and symbols indicating the origin of the plums (American, European, Japanese or hybrids). Additional information on the plum book and plum poster and also on the computer program "Pedigree: a Genetic Resource Inventory System", which lists descriptions of over 250 plum cultivars, is available at <http://www.pgris.com>.

0800-0900

S21-P-56

A TWO-YEAR/TWO-LOCATION EVALUATION OF TRIPLOID WATERMELON GENOTYPES IN MISSISSIPPI

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Twenty-one entries of triploid watermelons of the 'Tri-X 313' class were evaluated during the summers of 2000 and 2001 in northern and central Mississippi. A higher than normal plant density of 7173 plants/ha (2904 plants/ac) was used. This density was equivalent to 1.4 m²/plant (15 ft²/plant). Seed was sown into 72-cell flats containing a commercial potting mix in the greenhouse and transplanted to the field on 15 May 2000 and 30 April 2001. Germination of triploid seed in the greenhouse was excellent in 2000 and fair to excellent in 2001. 'Charleston Grey', was the pollinator and was planted at a 1:1 pollinator:triploid ratio. Individual melon weight, soluble solids content, and incidence of rind necrosis and hollow heart were measured in these studies. In 2000, SXW-5052 (Sunseeds) and 'Constitution', (Sunseeds) were the highest yielding entries in northern and central Mississippi, respectively. Melons from the northern location exhibited more problems with hollow heart and rind necrosis than melons from the central location in 2000 and 2001. A combined analysis of results from both locations and both years will be presented.

0900-0940

S21-O-57

EVALUATION AND UTILIZATION OF VEGETABLE GENETIC RESOURCES FOR TROPICAL ENVIRONMENT

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AVRDC holds in trust one of the largest collection of vegetable germplasm. The collection is preserved in long-term and complemented with an active collection for distribution and utilization. Germplasm distribution averages 25,000 accessions annually: 20,000 improved genetic material and 5,000 germplasm

accessions. The materials are used by NARS for evaluation and selection of varieties for release or for use in their own vegetable improvement programs. Requests are for sources of resistance to pests and diseases and abiotic stresses and various researches. A limited quantity finds its way to private commercial seed companies and individuals. Center scientists evaluate germplasm for their reaction to biotic and abiotic stresses as well as for other desirable traits. AVRDC focuses its work on the development of varieties adapted to tropical conditions. Breeding lines that are heat tolerant and resistant to common pests and diseases in the tropics have been developed in mungbean, soybean, tomato, chinese cabbage and pepper. Developing countries have used them as sources of desirable traits or have selected them for official release. In all the crops, the emphasis has been on stable high yield during the hot summer season and resistance to diseases and insects. In addition to these traits, mungbean lines are selected for determinate growth habit, early and uniform maturity, bold seeds; vegetable soybeans for sweet and less beany flavor as well as aroma. Tomatoes are bred for the fresh market and the processing industry. Special cherry types are also developed. High beta carotene tomato lines are available. Examples of how various germplasm have been used in the improvement of tomatoes, pepper, mungbean and vegetable soybean are given. The use of wild species in the improvement of tomato is highlighted.

0940-1000

S21-0-58

CHARACTERIZATION OF SWEETPOTATO GERmplasm THROUGH GENETICALLY INHERITED BIOCHEMICAL RESISTANCE COMPOUNDS

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Sweetpotato [*Ipomoea batatas* (L) Lam.] is a highly heterozygous, heterogamous, self-incompatible, hexaploid crop with 90 chromosomes. These characteristics make it a difficult species to use DNA markers in plant breeding and taxonomy research. A more straightforward approach is direct selection for gene products. Fourteen genetically diverse sweetpotato genotypes were characterized for allelopathy and for relative resistance to several soil insect species, root knot nematodes, and Fusarium wilt. These resistances were determined for these genotypes using greenhouse screening and field evaluation. Although these evaluation methods are effective, the identification and quantification of the gene products that confer these resistances could result in a more rapid and reliable method to quantify resistance to pests in sweetpotato germplasm. Extracts from sweetpotato periderm were found to be highly inhibitory to yellow nutsedge. They were identified as resin glycosides and accounted for 90% of allelopathy in the multiple pest resistant cultivar 'Regal'. These glycosides also reduced insect larval growth and survival. Both resin glycosides and caffeic acid from sweetpotato periderm interfered with hyphal growth of 4 sweetpotato root-rotting fungi. Root cortex was found to contain at least 16 secondary compounds that contribute to resistance (phenolic acids, phenolic acid esters, coumarin derivatives and high molecular weight compounds, with unknown structures). In vitro assays with these compounds generated dose-response relationships showing their biological activity in growth and survival of disease and pest organisms. Semi-automated HPLC techniques were developed for quantification of these compounds in a large number of genotypes. These techniques can be used to quantify these compounds in potential parent lines, and to screen large seedling populations. An F1 population was developed to determine the efficacy of selection for multiple pest and disease resistant seedlings by direct selection for these genetically determined resistance compounds.

1000-1020

S21-0-59

UTILIZATION OF APPLE GERmplasm COLLECTIONS VIA RECURRENT SELECTION

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In apple, breeders tend to use only a small portion of the genetic diversity available within the genus for new cultivar development. It is believed that this practice has resulted in the narrowing of the genetic base. This necessitated the establishment of a recurrent selection program at the Horticulture and Food Research Institute New Zealand, to run alongside their commercial breeding. The objective of the program was to increase genetic variability and at the same time study the genetics of horticulturally important tree and fruit characters. The breeding population was constituted with mostly open pollinated seed of primitive cultivars, cider apples, landraces and wild species obtained from North America, United Kingdom, Europe, Australia, South Africa and Kazakhstan (Kazakhstan is believed to be the center of diversity of cultivated apples). In total, there were 520 families, and these were divided over four sublines (91, 92, 93 and 94) and planted out in randomized incomplete blocks of 20 single trees at 3 different sites. We have now completed the first generation (cycle 0) in all sublines and parents have been selected for the next cycle using family means. All traits were considered neutral in the selection process. That is, both exceptionally low and high values were of potential interest except for pest and disease resistance (resistant ones only were selected). At this stage, individuals are selected based on single traits instead of a combination of traits to minimise linkages. We will be looking to combine traits in subsequent generations. A plot of frequency distribution of the traits indicated that the population has been improved and diversity was maintained. Out of the original 217 families in subline 91, 149 in subline 92, 72 in subline 93, and 86 in subline 94, 148, 125, 63 and 74 individuals, respectively were selected for advancement to the next cycle. The challenges and prospects of this program are discussed.

1020-1040

S21-0-59-A

TO BE ANNOUNCED

1400-1420

S21-0-60

COMPARISON OF GENETIC DIVERSITY BETWEEN CUCURBITA MOSCHATA ACCESSIONS FROM THE PAIRMANI BOLIVIA AND USDA GERmplasm BANKS

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Prior to the colonization of the Americas, *Cucurbita moschata* was thought to be distributed from northern south America into Mexico and the southern United States; thus, it was surprising to find that accessions had been collected by the Pairumani Germplasm Bank in southern South America, in Bolivia. The dates of the collection were unknown, but were thought to be since late 1980. Did these accessions represent a secondary center of diversity or were they feral types or escapes from lines that had been introduced? Forty-two *C. moschata* accessions from the Pairumani Germplasm Bank, Cochabamba, Bolivia were compared to a random sample of 48 accessions from the U.S.D.A collection, USDA-ARS, Ames, Iowa. The 90 accessions were characterized for 100 polymorphic RAPD molecular markers. Genetic distance was calculated based on the proportion of shared bands (Jaccard). Permutation analysis of band frequencies indicated a significant difference in genetic distance between the two groups of accessions. In addition, the genetic diversity, based on Nei's estimator of gene diversity at a locus, indicated that the accessions from the Pairumani Germplasm bank were less diverse than the random accessions from the USDA collection. The results suggest that the accessions from Bolivia may represent a unique source of genetic diversity in *C. moschata*.

1420-1440

S21-0-61

EVALUATION OF VITIS AESTIVALIS AND RELATED TAXA AS SOURCES OF RESISTANCE TO ROOT-KNOT NEMATODES

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Development of rootstocks with resistance to root-knot nematodes (*Meloidogyne* spp.) is a top priority in grape breeding. Accessions of *Vitis aestivalis*

Michx. resistant to root-knot nematodes have been identified. *Vitis aestivalis* is native to eastern North America and has historically been more important in breeding fruiting varieties than in rootstock development. This species is very difficult to propagate from cuttings, essentially precluding its direct use as a rootstock. Hybridization with easily propagated rootstock selections will be required to utilize any nematode resistance found in *V. aestivalis*. Progeny testing was used to assess the breeding value of potential sources of nematode resistance, including *V. aestivalis* and two related taxa. Three *V. aestivalis* accessions, all held in the U.S. National Plant Germplasm System collection, were evaluated. *V. x slavini* Rehder is a natural hybrid of *V. aestivalis* and *V. riparia* that has been used in breeding rootstocks resistant to the dagger nematode *Xiphinema index*. *Vitis nesbittiana* Comeaux is native to Mexico; little evaluation of the nematode and disease resistance of this species has been reported. *Vitis aestivalis*, *V. x slavini*, and *V. nesbittiana* were crossed with the rootstock varieties Riparia Gloire, 1616 Couderc, and Dog Ridge. Hybrid seedling resistance was measured by counting the stained nematode egg masses visible per root system. Roots were stained in an eosin-Y solution (0.25 g/L for one hour) six weeks after inoculation with approximately 1500 second stage *Meloidogyne* spp. juveniles. Two populations of nematodes were used, representing populations either avirulent (*M. incognita*) or virulent (*Meloidogyne* sp.) on the grape rootstock Harmony. Several accessions showed useful levels of nematode resistance in their hybrid seedlings, but *Vitis nesbittiana* seedlings demonstrated especially high levels of resistance; this species has great potential for use in rootstock breeding.

1440–1500

S21–0–62

UTILIZATION OF THE INTERNATIONAL CACAO GERmplasm COLLECTIONS: PROSPECTING FOR DISEASE RESISTANCE GENES

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The USDA-ARS cacao genetics program is based at the Subtropical Horticulture Research Station in Miami, Florida. The primary goal of the program is to develop a biotechnology-based approach to solving two destructive disease problems, witches broom and frosty pod rot, in Central and South America. In addition, the USDA-ARS and M&M Mars Corporation are coordinating an international bioinformatics project that feeds information into national and regional breeding programs. Using a candidate gene approach (CGA) we have isolated 74 resistance gene homologues (RGH) from cacao. These 74 RGH can be placed into 11 different groups based on sequence homology. Some of the groups represent a single locus with multiple alleles while other groups contain multiple loci. The CGA has also been used to isolate 16 WRKY genes from cacao. WRKY gene products are transcription factors that regulate the hypersensitive response to pathogen attack. We are using RGH and WRKY genes as markers in populations segregating for disease resistance and among certain accessions in the germplasm collections. Disease resistance genes are often clustered allowing the identification of blocks of genes that co-segregate. The use of RGH and WRKY genes as markers has advantages over randomly distributed markers like simple sequence repeats. These advantages and the usefulness of these types of markers will be discussed.

1500–1520

S21–0–63

EVALUATION OF GENETIC RESOURCES OF PEACH AND NECTARINE FOR POWDERY MILDEW RESISTANCE BY PHYSIOLOGICAL PARAMETERS

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The knowledge of plant physiology has a great importance for a better understanding of the resistance mechanisms of peach to *Sphaerotheca pannosa* var.

persicae. During 1997–2000, studies on the physiological changes due to this fungus have been carried out on three cultivars belonging to different resistance classes, at the Research Station for Fruit Tree Growing Baneasa, Bucharest, located in the southern part of Romania. Research has been focused on ion transport through membranes, permeability index, total electrolyte content, photosynthesis and respiration intensity along with chlorophyll and anthocyanin levels. The catalase level in plant tissue was also analyzed. There was a correlation between the speed of ion transport and the resistance to powdery mildew with high speed observed in an infected cultivar ('Crimsongold'). The total electrolyte content was always higher in healthy plants ('Victoria'). A decrease in the permeability index value was observed in infected cultivars such as 'Crimsongold' compared with the uninfected ones such as 'Victoria'. Photosynthesis was also reduced in infected phenotypes. Moreover, the amount of chlorophyll and anthocyanins were reduced. Catalase proved to be less intense in the infected plants.

1520–1540

S21–0–64

BIODIVERSITY OF BEAN ON THE COAST OF THE MEDITERRANEAN IN ANYALYA, TURKEY

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Diverse germplasm is the basic material on which most breeding programs depend. The operation and reconstruction of the genotype depends upon the genepool. Several primitive varieties with superior genes are being eroded and it is feared that such valuable material may be lost and these types may become extinct in due course. There was a need to collect and evaluate specific *P. vulgaris* genes from our region. Ten genotypes were collected and evaluated in this study. These were evaluated for quantitative traits such as plant height, leaf size, leaf color, flower color, fruit color, fruit length (cm), and yield per plant(g).

1540–1600

S21–0–65

DIVERSITY OF PHENOLIC ANTIOXIDANT CONTENT AND RADICAL SCAVENGING CAPACITY IN THE APPLE GERmplasm CORE COLLECTION

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Regular consumption of fruits and vegetables containing naturally occurring antioxidants has been recommended to intervene in the onset and development of lifestyle diseases, such as cancer and cardiovascular diseases. Apples contain significant quantities of vitamins and other potent antioxidant compounds such as anthocyanins, flavonoids and phenolic acids. While apples have long been recognized as beneficial to human health, analytical data on antioxidant content and radical scavenging activity, and particularly on the extent of biodiversity in the germplasm pool has been sparse. We examined juice and fruit tissues from a 'core collection' of 321 species, selections, and cultivars considered representative of the genetic diversity of apple in the USDA-ARS Plant Genetic Resources Unit maintained at Geneva, NY. We also examined fruit from a subset of the same 'core collection' grown in Excelsior MN. This 'core collection' was found to be an extremely diverse source of phenolic antioxidants, ranging from a low of 14 to a high of 4606 mg/L, gallic acid equivalents. Red wines, considered one of the most potent sources contain 1500–2500 mg/L phenolic antioxidants. MN grown apples were consistently higher than the same cultivars grown in NY. Species content varied considerably: *M. asiatica*, Nakai = 169; *M. baccata*, L. Borkh. = 600–1180; *M. brevipes*, Rehder = 513; *M. floribunda* Siebold ex van Houtte = 1454; *M. hartwigii*, Koehne = 595; *M. mandshurica*, (Maxim) Kom = 192; *M. micromalus*, Makino = 640–3437; *M. platycarpa*, Rheder = 2706; *M. pumila*, Mill = 184–1533; *M. rockii*, Rheder = 4606; *M. sieversii*, (Ledeb.) M. Roem = 731; *M. sylvestris*, Mill. = 847–1108; *M. toringoides*, (Rheder) Hughes = 3873; *M. transitoria*, (Batalin) C.K. Schnied = 2465; *M. yunnanensis* var. *veitchii* (Veitch) Rheder = 2802 mg/L. Cultivars contained the lowest levels ranging from 14 (Gingergold) to 241 (Cox's Orange) mg/L. Crabapple cultivars varied from 212 (Dolgo) to 2360 (Prairie Fire). Juice yield varied from 25 to 71 mL per 100 gm fruit, the highest for the largest fruit.