

## Symposium 12 (S12): Breeding, Genetics, and Cultivar Development of Tree Fruits and Nuts

Monday · August 12

Location: Metro Toronto Convention Centre, Room 203BD

1100–1140

S12–0–1

### POME FRUITS

Susan K. Brown\*

Cornell Univ., NY State Agricultural Expt. Station, Geneva NY 14456

Similarities between *Malus* and *Pyrus* include their polyploid origin, diversity, prospects for interspecific hybridization and center of origin. Chimeras for enhanced fruit skin color and for increased or decreased russetting are common to both, as is a multi-allelic gametophytic incompatibility system. Resistance to the bacterial pathogen causing fire blight (*Erwinia amylovora*) is a breeding goal in both *Malus* and *Pyrus*. For fungal pathogens, resistance to apple scab (*Venturia inaequalis* (Cke.) Wint.) and pear scab (*Venturia pirina* Aderh.) are priorities. Breeding strategies are common across pome fruits, and traditional breeding and genetic studies are being enhanced by increased international collaborations. The identification and use of molecular markers and marker-assisted selection is more advanced in *Malus*, with genetic maps for important cultivars and advanced selections being used in genetic improvement. Simple sequence repeats (SSRs) cross-amplify in *Malus* and *Pyrus* suggesting further advances in this area. Regeneration and transformation techniques are well established in *Malus* and systems are being developed and optimized in *Pyrus*. Identification of genes is also progressing, with self-incompatibility alleles, allergens, and many other genes similar in apple and pear. Acceleration in both genetic improvement and the development of transgenic lines in pome fruits is being aided by research and by the development and use of new techniques.

1140–1200

S12–0–2

### PROGRESS AND PROSPECTS IN STONE FRUITS BREEDING

Françoise Dosba\*

ENSA.M–INRA UMR Biologie du Développement des Plantes Pérennes Cultivées  
2 Place Viala 34060 MONTPELLIER Cedex 1 (France)

During the last decade, important progress has been achieved in the breeding of stone fruits in order to obtain new cultivars adapted to different biotic or abiotic conditions as well as responding to consumer demands for quality. Most of the countries where the stone fruits are grown now combine the efforts of research institutions and private breeders to promote efficient strategies for selection. The level of knowledge has considerably increased, especially in genetics and biotechnology. Molecular biology developed for *Prunus* is a powerful tool to study the evolution of the genome, and the species. It has permitted an understanding of genome structure and of genetic diversity, particularly for cherries and plums. For most stone fruit species wide genetic variability exists and remains to be exploited. A better knowledge of *Prunus* genetics is emerging from analysis of inheritance of individual characters. The number of horticultural characters taken into account is constantly increasing. These include fruit characters (color, size, firmness) and yield (limitation of juvenile phase, early and regular productions, limitation of alternate bearing). More effort is needed in respect to quality (good flavor, aroma, nutritional compounds, storage quality, and elimination of different toxins). The largest challenge concerns disease resistance, especially for the quarantine pests present in different parts of the world. Work done on sharka disease (*Xanthomonas arboricola* pv *pruni*), continuing genetic, pathological and epidemiological approaches is an interesting example of the way to solve problems at the national, continental or world level. New sources of resistance are still required and different strategies of breeding are implemented from monogenic or polygenic resistance, genetic transformation or integrated management. A noticeable increase in availability of new resistant germplasm, although not always of commercial level, is foreseeable in the short and medium term. The capacity for combining different objectives could be greatly improved by increased knowledge of the species genomes and molecular approaches. The strategies developed on annual crops or a better knowledge of the synteny in the Rosaceae could be a new way to increase the efficiency of stone fruit breeding. New objectives for

the future development of stone fruits must be related to environmental adaptability as a consequence of climatic changes or with the necessity to adapt species and cultivars to new zones of cultivation. Environmental and economic plasticities should be the central objectives of stone fruit breeding for the future.

1200–1220

S12–0–3

### PROGRESS IN BREEDING SUBTROPICAL TREE CROPS

Louise Ferguson\*

Univ. of California, Kearney field Station, 9240 South Riverbend Avenue, Parlier, CA, USA, 93648

Cultivar improvement of subtropical tree fruit crops continues to be made with traditional breeding methods and selection, as opposed to newer biotechnology tools. Citrus is the only exception. These programs are generally focused on horticultural quality and yield, as opposed to disease or pest resistance. The current cultivar improvement programs in olive, fig, citrus, persimmon, and pomegranate will be covered.

1220–1240

S12–0–4

### PROGRESS AND PROSPECTS IN NUT BREEDING

Shawn A. Mehlenbacher\*

Dept. of Horticulture, Oregon State Univ., 4017 ALS Bldg., Corvallis, OR, USA, 97331

Efforts to genetically improve temperate nut crops began just a few decades ago. Progress, in some cases striking, has been made and efforts continue with generally modest levels of funding. The current status and prospects for the future will be discussed for each temperate nut crop, including efforts at mapping, marker-assisted selection, and transformation. Activity to improve tropical nut crops has been less intense, although vast genetic resources offer considerable potential for the future.

1340–1440

S12–P–5

### SELF-INCOMPATIBILITY IN SOUR CHERRY: CHARACTERIZATION OF THE NORMAL AND MUTATED S6-RNASE GENES

Hisayo Yamane\*, Ryutaro Tao, Nathanael R. Hauck, Amy F. Iezzoni, Akira Sugiura  
Laboratory of Pomology, Graduate School of Agriculture, Kyoto Univ., Kyoto, Kyoto, Japan, 606-8502

S-RNase is the stylar component of the gametophytic self-incompatibility in sour cherry as in other *Prunus* species. The expression of S-RNase is specific to the style and developmentally regulated during flowering. Cis-regulatory element and trans-activator could be present to regulate the expression pattern of the S-RNase gene. In an attempt to clarify the molecular basis of self-incompatibility in sour cherry, we happened to find a mutated S6-RNase gene in Erdi Botermo (EB) that could be distinguished from the normal S6-RNase gene by the size of a RFLP band. 2D-PAGE and RT-PCR analyses revealed that the mutated S6-RNase gene of EB was not transcribed and thus not expressed in the style. These observations could indicate that the coding region or the region that is responsible for the expression of the S6-RNase gene has been mutated so that it is not expressed in the style of EB. To further characterize the nature of the mutation, we cloned and compared the entire coding region with 5'- and 3'-flanking sequences of the normal S6-RNase gene of Rheinische Schattenmorelle (RS) and that of the mutated S6-RNase gene of EB by inverse PCR. Although no difference was observed in the coding sequences between them, there was an insertion of about 3 kb at about 800 bp upstream of the ATG initial codon of the mutated S6-RNase gene of EB, suggesting the presence of a cis-regulatory element in this region.

1340–1440

S12–P–6

### 'SUNHONG', A NEW APPLE WITH LARGE RED FRUITS AND HIGH SUGAR CONTENT

Jeong-Hwan Hwang\*, Yong-Uk Shin, Kwan-Jeong Song, Il-Sheob Shin, Whee-Cheon Kim

Dept. of fruit tree breeding, Horticultural Research Institute, 475, Imok-Dong, Jangan-Gu, Suwon, Kyonggi, Republic of Korea, 440-706

A promising new apple cultivar, 'Sunhong', was released from NHRI of Korea in 2000. This cultivar was finally selected from the cross combination between 'Hongro' and 'Chukwang' crossed in 1992 after regional adaptability test at 7 different places from 1998 to 2000. It has medium tree vigor and spreading branching habit and bears abundant flower buds on many spurs and axillary buds. This variety has no pre-harvest drop. Harvest time of this variety is late August, 5 days earlier than that of 'Tsugaru' in Suwon. Fruit shape is round conical and skin color is bright red. Fruit size is large weighing 300-350 g on an average and its fruits have 14-15% soluble solid and low acidity. The storable period at 4 °C is about 2 months. It is susceptible to *Alternaria* leaf spot (*Alternaria mali* Roberts) and *Glomerella* bitter rot (*Glomerella cingulata* Spauld. et Schr.). A slight crack occurs at the base or apex part of fruit on over ripened large fruits. Low nitrogen fertilization is recommended to avoid the fruits growing too big and early flower thinning is necessary to keep the tree growing with vigor. 'Sunhong' is expected to replace 'Tsugaru' owing to its better fruit quality compared with 'Tsugaru' which now is a main early ripening apple variety in Korea.

**1340-1440**

**S12-P-7**

**'GALARINA'® AND 'REINETTE RUSSET'®: TWO NEW HARDY SCAB RESISTANT APPLE CULTIVARS**

Shahrokh Khanizadeh\*, François Laurens, Yves Lespinasse, Yvon Groleau, Johanne Cousineau, Odile Carisse, Jennifer DeEil

Agriculture and Agri-Food Canada, HRDC, 430, Gouin Blvd., St-Jean-sur-Richelieu, Quebec, Canada, J3B 3E6

'Galarina' is a 'Gala' type apple (*Malus domestica* Borkh.). It is very attractive, has a pleasant taste and an excellent shelf-life. The tree is hardy and the fruit and leaves are resistant to the common races of apple scab (*Venturia inaequalis* (Cke) Wint.) due to the presence of the Vf gene derived from *Malus floribunda* 821. 'Galarina', tested as X4982, is a progeny resulting from a cross between 'Gala' and 'Florina Querina', made at the Fruit and Ornamental Plant Breeding Unit (FOPBU) of the Institut National de la Recherche Agronomique (INRA) located in Angers, France. X4982 was selected and tested at INRA. It was then sent to Quebec for further evaluation and is now being released by the Quebec apple breeding program (QAPB) located at the Agriculture and Agri-Food Canada (AAFC) station in St-Jean-sur-Richelieu (Quebec). 'Galarina' was evaluated by the QAPB at a sub-station located in Frelighsburg (Quebec) for 10 years as part of a group of genotypes sent by INRA for testing in Quebec. Compared to 'Gala', this new cultivar is hardier, it retains its fresh eating quality longer in storage and it is resistant to the common races of apple scab, reducing the need for fungicide applications. 'Reinette Russet' is being released by the QAPB as a replacement for 'Golden Russet', which is presently being grown in Eastern Canada for the production of apple cider and specialty markets. This new cultivar produces larger fruit than 'Golden Russet', is hardier and it is partially resistant to apple scab. The fruit has a pleasant flavor and it is very sweet, which should give it a market as a specialty item. 'Reinette Russet', tested as X4362, is a mutation of 'Reine des Reinettes'. It was first selected at the Fruit and Ornamental Plant Breeding Unit (FOPBU) of the Institut National de la Recherche Agronomique (INRA) located in Angers (France) and then sent to Quebec for further evaluation.

**1340-1440**

**S12-P-8**

**'MACEXCEL' APPLE**

Shahrokh Khanizadeh\*, Johanne Cousineau, Raymond Granger, Yvon Groleau, Gilles Rousselle, Lloyd P.S. Spangelo

Agriculture and Agri-Food Canada, HRDC, 430, Gouin Blvd., St-Jean-sur-Richelieu, Quebec, Canada, J3B 3E6

'MacExcel' produces a good yield of attractive apples (*Malus x domestica* Borkh.) on a columnar type tree. It has field immunity to apple scab (*Venturia inaequalis* (Cke) Wint.) and is resistant to powdery mildew (*Podosphaera leucotricha* (Eil. & Ev.) Salm.). 'MacExcel' is being released by the Horticultural Research and Development Centre of the Agriculture and Agri-Food Canada Research Station in St-Jean-sur-Richelieu. The fruit weighs an average of 121 g and grows on spurs along the very upright branches. 'MacExcel' is useful as a hardy, disease-resistant variety for home gardens with a limited amount of space.

**1340-1440**

**S12-P-9**

**FIRST GENERATION OF RECURRENT SELECTION IN APPLE: ESTIMATION OF GENETIC PARAMETERS**

N.C. Oraguzie\*, A. Alspach, C. Morgan, J. Fraser, C. Whitworth

The Horticulture & Food Research, Institute of New Zealand Limited, (HortResearch), Havelock North, Hawkes Bay, New Zealand, PB 1401

Increasingly complex breeding programs coupled with pressure on breeders to reduce costs and improve returns have made knowledge of the performance of breeding population imperative. Knowledge of genetic parameters including heritability, genotype x environment (g x e) interaction and phenotypic and genetic correlations is important for the interpretation of breeding and testing work as well as for the development of a selection index for multiple trait selection. Here, we report on the estimation of these parameters for major tree (including disease resistance) and fruit quality traits in a recurrent selection program in apple. To our knowledge, this is the first comprehensive report of estimation of genetic parameters in a breeding population in apple. In total, eight tree, three disease resistance, and 21 fruit quality traits were assessed in three of the sublines (91, 92 and 93), in this program. The families (520 in all in 4 sublines) were planted at three sites in a randomized incomplete block fashion. Fruit weight had the highest heritability of approximately unity. Heritability estimates for tree traits ranged from 0.48 to 0.87. Disease resistance traits had moderate (0.14-0.37 for fireblight) to high heritability (0.51-0.62 for scab). Heritability of fruit appearance was mostly moderate to high (0.26-0.54). Heritability of fruit texture ranged from 0.10 to 0.62. The range of heritability for mineral concentration was very wide, from 0.03 (magnesium) to 0.99 (calcium) and disorders; from 0.12 (chill injury) to 0.82 (superficial scald). Trait genetic correlations were moderate to high in subline 91, and mostly low in sublines 92 and 93. The estimates of genetic and phenotypic correlations were very similar ( $r=0.86$  and  $0.81$  for sublines 92 and 93, respectively). The genetic correlations between sites as well as between sublines (92 and 93) were generally high. The implications of these estimates for apple breeding are discussed.

**1340-1440**

**S12-P-10**

**INFLUENCE OF SOME FACTORS ON APPLE SEED GERMINATION REMOVED FROM FRUIT HELD IN COLD STORAGE**

Emilian Pitera\*, Slawomir Odziemkowski

Dept. of Pomology and Basic Na, Warsaw Agricultural Univ., Nowoursynowska 166, Warszawa, Poland, 02-787

The influence of temperature, cultivar and pollinator on the seed germination, removed from fruit held in cold storage, were studied. This seeds are used in diseases resistance apple breeding programme. Apple seeds from open pollinated and controlled crosses were removed from fruits stored until April 9 in common cold storage at 2 °C. The seeds were then sown directly to the seedbed and into the multipots. The multipots were filled with sphagnum peat with added mineral nutrition and placed in a greenhouse and an unheated plastic tunnel. All combinations were used only for seeds of 'Gloster' open pollinated. The germination of seeds was judged on the emergence of the cotyledons above the ground. In this experiment maximum (78%) germination percentage was reached in the unheated plastic tunnel and the lowest (52%) in the greenhouse. The remaining seeds were germinated in the plastic tunnel. Germination percentage of that seeds was generally high and was influenced by the cultivar and pollinator. The germination percentage of seeds of 'Elise' and 'Gloster' was significantly higher than that of the 'Golden Delicious'. It was the highest when clone U 211 was used as a pollinator and for the crosses 'Elise' x clone U 211-95%, 'Gloster' x clone U 211-93% and 81% for 'Golden Delicious' x clone U 211 in comparison to 70% for both 'Golden Delicious' x clone U 641 and 'Gloster' open pollinated. The rate germination of the seeds of 'Gloster' and 'Elise' was significantly lower than that of 'Golden Delicious' and was negatively correlated with the percentage germination. The growth of seedlings obtained from seeds removed from stored fruits in cold storage was equally good.

**1340-1440**

**S12-P-11**

**HARDY PEAR GERMLASM RESOURCES IN CHINA**

Mao-jun Zhang\*, Bing-bing Zhang, Li-hua Ding, QiangWan

Pomology Institute, Jilin Academy of Agricultural Sciences, Gongzhuling 136100, China

The genus *Pyrus* as well as cultivated pear originated in China. Pear germplasm resources are rich and include *P. pyrifolia* Nakai, *P. bretschneideri* Rehd., and *P. communis* L. which are adapted to temperate, subtropical, and tropical zones. Many cultivars of *P. ussuriensis* Maxim can be cultivated in cold areas. *Pyrus ussuriensis* has many desirable characteristics, such as high resistance to cold (wild species can withstand  $-52^{\circ}\text{C}$ , and cultivars can withstand  $-40^{\circ}\text{C}$ ), unique taste, fine flesh texture, heavy fragrance, rich juice, high content of sugar and acid, and is suitable for fresh consumption and processing. Thus the culture of *P. ussuriensis* has become important and development of the industry is rapid. Cultivars of *P. ussuriensis* have been used as parents in intra-specific crosses. Great improvement has been achieved in breeding for hardiness, high-quality, dwarfing rootstocks, and processing. As a result the pear production areas in cold regions have been increased.

**1340-1440**

**S12-P-12**

**BREEDING OF EARLY SEASON NEW PEAR CULTIVAR 'HANAREUM'**

Hae-Sung Hwang, Il-Sheob Shin, Whee-Cheon Kim, Yong-Uk Shin\*, Jeong-Hwan Hwang

Dept. of Fruit Tree Breeding, National Horticultural Research Institute, 475, Imok-dong, Suwon, Kyunggi, Republic of Korea, 440-706

'Hanareum' pear (*Pyrus pyrifolia* Nakai) originated as a cross between 'Niitaka' (non-patented, released from Japan in 1929) and 'Chuhwangbae' (patented, released from Korea in 1985). 'Hanareum' will be released as a high quality, large fruit, early-season pear for the fresh market by the National Horticultural Research Institute (NHRI) in Suwon, Rep. Of Korea. This cultivar was first selected in 1996, and its regional adaptability was checked out as 'Wonkyo Na-31' at 9 sites for 5 years from 1997. It was finally selected for its high fruit quality and large fruit size ripening in mid August in 2001. 'Hanareum' is vigorous in tree growth and upright in tree habit, and resistant to black leaf rot (*Alternaria kikuchiana*) and pear black necrotic leaf spot caused by apple stem grooving virus, Capilliviruses. It is higher yield (23% more) than 'Shinsui', because the tree has more spurs. It blooms same day as 'Shinsui' and one day earlier than 'Kosui'. Harvesting time is Aug. 20 in Suwon, 5 days later than 'Shinsui' and 10 days earlier than 'Kosui'. The fruit shape is round and the skin color is an attractive bright yellow brown. It has 420-600g fruit weight ranges and has 13-14 Bx of soluble solid contents. The flesh is soft, very juicy with light grit.

**1340-1440**

**S12-P-13**

**PERFORMANCE OF SWEET CHERRY CULTIVARS IN PIEDMONT, ITALY**

Ludovico Radicati, Maria Luisa Miaja\*, Marco Cehic

Via Leonardo da Vinci 44, Grugliasco, Torino, Italy, 10095

The agronomic behaviour of 21 recently released cultivars of sweet cherry (*Prunus avium* L.) was evaluated in order to assess their potential interest in a cherry growing area of Piedmont (Italy). Cultivars included: 'Badacsony', 'Big Tardif', 'Black Star', 'Blaze Star', 'Canada Giant', 'Celeste', 'Cristalina', 'Duron 3', 'Early Magjar', 'Early Star', 'Elisa', 'Garnet', 'Grace Star', 'Lala Star', 'Noire de Meched', 'Prime Giant', 'Rainier', 'Samba', 'Sumini', 'Sweet Early', and 'Verdel Ferbolus'. The main vegetative, phenological and productive traits were determined using 'Burlat' as a standard. Ripening period ranged from May 17 for 'Early Magjar' to June 18 for 'Rainier'. The earliest cultivars 'Early Magjar', 'Sweet Early' and 'Early Star' showed only average qualitative traits. Among the mid ripening cultivars, good qualitative traits of fruits were recorded for 'Canada Giant', 'Black Star' and 'Garnet' (fruit size, sugar content and overall quality). Among the late ripening ones, 'Duron 3', 'Elisa', 'Badacsony' and 'Rainier' reached the best quality of fruits.

**1340-1440**

**S12-P-14**

**CHARACTERIZING THE EVERGREEN PHENOTYPE IN PEACH**

Y. Wang\*<sup>1</sup>, R. Scorza<sup>2</sup>, T.C. Jenkins<sup>3</sup>, M.J. Line<sup>4</sup>, G.L. Reighard<sup>1</sup>

<sup>1</sup>Dept. of Horticulture, Clemson Univ., Clemson SC, 29634; <sup>2</sup>U.S. Dept. of Ag-

riculture/ARS, Appalachian Fruit Research Station, Box 45, Wiltshire Rd, Kearneysville, WV 25430; <sup>3</sup>Dept. of Animal & Veterinary Sciences, Clemson Univ., Clemson SC, 29634; <sup>4</sup>Environmental Chemistry Laboratory, Beltsville Agricultural Research Center, U.S. Dept. of Agriculture/ARS, Beltsville MD, 20705

'Evergreen' peach is a mutant phenotype that exhibits a different growing pattern in winter than that of the wild type deciduous peach. In temperate locations, the terminal apices on evergreen trees continue growing in winter until killed by low temperatures, whereas lateral buds become dormant. One single recessive gene (evg) controls this evergreen trait. Three experiments were designed to characterize this evergreen phenotype of peach. A grafting experiment confirmed that dormancy "signals" could not be transported from the dormant deciduous branches to the growing evergreen branches on the same tree. Foliage spraying of STC, an ABA-like chemical, slightly inhibited new growth on evergreen trees. Although this difference was not significant, it may indicate sensitivity to the exogenous ABA-like chemical treatment. Therefore, the evergreen gene may not be an ABA insensitive mutant. Budbreak percentages in a decapitation experiment suggested a paradormancy condition for the lateral buds on evergreen trees. In this decapitation experiment, both the saturated and unsaturated fatty acids in the evergreen terminal apices had different concentrations than those in the buds of deciduous trees. Considering the observed atypical concentrations of ABA and fatty acids in the buds and the continuous shoot growth in the terminal apices, evergreen peach may be a candidate model system for study of winter dormancy in woody plants.

**1340-1440**

**S12-P-15**

**CLINGSTONE PEACH TRIALS IN ROMANIA**

L.M. Dumitru<sup>1</sup>, F. Stanica<sup>2</sup>, N. Cepoiu<sup>2</sup>, C. Gavai<sup>1</sup>

<sup>1</sup>Breeding Laboratory, Fruit Research Station, Constanta, Str. Pepinierei, 1, Valul lui Traian, Constanta, Romania; <sup>2</sup>Dept. of Pomology, Univ. of Agronomic Sciences and Veterinary Medicine, B-dul Marasti, 59, 71331, Bucuresti, Romania

In the last 20 years about 70 peach clingstone cultivars, hybrids, and clonal selections have been studied at the Fruit Research Station, Constanta. The harvest season lasts about 100 days from the 26th of June till the 5th of October. Recommended clones include: 'NJC 89', 'NJC 108', 'RR 51/32', 'Jolly 1 A', 'Baby Gold 6', and 'Excelsior'. A breeding program to obtain new varieties, having high quality fruits, high percentage of dry substances, well balanced acidity, and pleasant flavor was initiated and in 2001, a new clingstone cultivar, 'Catherine Sel. 1' was released.

**1340-1440**

**S12-P-16**

**INHERITANCE OF VENATION PATTERN IN *PRUNUS FERGANENSIS* X *PERSICA* HYBRIDS**

W.R. Okie\*<sup>1</sup>, M.W. Rieger<sup>2</sup>

<sup>1</sup>SE Fruit & Tree Nut Res Lab, USDA-ARS, 21 Dunbar Rd, Byron, GA, USA, 31008; <sup>2</sup>Dept. of Horticulture Univ. of Georgia, Athens, GA 30602 USA

*Prunus ferganensis* (Kost. & Riab) Kov. & Kost, is closely related to cultivated peach, *P. persica*, but is distinguished by very long, unbranched leaf veins which turn and run parallel to the leaf margin at the edge of the leaf. Also, the pits have longitudinal grooves. Otherwise the tree and fruit of this species (or sub-species) resemble those of our familiar commercial peach, *P. persica*. *P. ferganensis* is common in the dry Ferghana and Zeravshan Valleys in central Asia (now Tajikistan, Kyrgyzstan and Uzbekistan). In this region local varieties of *P. ferganensis* are widely grown for fruit. Several old accessions of *P. ferganensis* such as Plant Introduction 102705 ('Khodjent Kostokos') are in the United States and a few additional accessions have been brought in as seed in recent years. Fruit quality is edible but not of commercial standard, particularly in terms of fruit firmness, quality and skin color. The species has been little studied in the US. Hybrids of *P. ferganensis* (primarily nectarine P1102705) with commercial and experimental peaches have been produced, and segregating  $F_2$  populations obtained. These populations were evaluated for fruit, seed and tree characters. The distinct leaf-vein character segregates in a ratio of 3 normal vein: 1 long vein suggesting it is controlled by a single recessive gene. All of the long-veined progeny that fruited also had the grooves on the pit, in contrast to the normal seed of normal-veined seedlings. The preeminence of this species in its region of origin, where it is frequently cultivated, suggests

the leaf morphology may be advantageous, perhaps in terms of water relations. If the long-vein leaf type were found to be associated with superior water usage or photosynthetic characteristics, it would be relatively easy to backcross it into commercial type fruit.

**1340-1440**

**S12-P-17**

**KARYOTYPE ANALYSIS IN ALMOND**

Pedro Martinez-Gomez<sup>\*1</sup>, Yiftach Vaknin<sup>1</sup>, Federico Dicenta<sup>1</sup>, Thomas M. Gradziel<sup>2</sup>

<sup>1</sup>Dep. de Mejora y Patología Vegetal, CEBAS-CSIC, PO Box 4195, Murcia, Spain, E-30100; <sup>2</sup>Pomology Dept., Univ. of California, Davis, CA, USA

Knowledge of karyotype relationships is an important prerequisite for effective plant genetic and breeding studies. In *Prunus* species, karyotype analysis has been reported for mitotic cells from root tips or meiotic cells from flower buds, mainly from apricot and peach. These studies on *Prunus* karyotyping are frequently reported in diverse publications often having limited readership. In this study, different methods for the preparation of metaphase chromosomes have been evaluated using almond root tips. By modifying and updating these methods, an improved technique for counting chromosomes in almond has been developed. Root tips were first placed in cold water for 4 hours at 0 °C, and treated with 0.2% colchicine for 3-4 hours at 5 °C. They were then fixed in: 6 methanol, 3 propionic acid and 2 chloroform; for 24 hours at 5 °C, and stored in ethanol (70%). Root tips were hydrolyzed in 1N HCl at 60 °C for 20 minutes then stained in acetic acid orcein (45%) for 2 hours. Results allow the identification of almond chromosomes in the different stages of the mitosis. This technique has been successfully applied to other *Prunus* species including peach and apricot, utilizing either root tips or pollen mother cells.

**1340-1440**

**S12-P-18**

**FATTY ACID COMPOSITION OF EIGHTEEN NATIVE PORTUGUESE CULTIVARS OF CHESTNUT**

O. Borges\*, J.L. Soeiro de Carvalho, A.P. Silva

Direcção Regional de Agricultura de Trás-os-Montes, Quinta do Valongo, MIRANDELA, Portugal, 5370-078

In Northern Portugal sweet chestnut (*Castanea sativa* Mill.) is one of the most traditional and important crop. In this region the chestnut fruit area is about 17,000 ha and fruit production is near 17 500 t. There are three Protected Denomination Areas in Trás-os-Montes region: Castanha da Terra Fria, Castanha da Padrela e Castanha dos Soutos da Lapa. From these areas 18 cultivars were selected to evaluate fatty acids (FA) composition and content during a period of two years. Fatty acids methyl esters were determined by gas chromatography. For all analysed samples FA contents were determined as relative percentage of the total FA identified (fourteen). Unsaturated and saturated FA average accounted for 82.3% and for 16.7% respectively. The total of unsaturated FA corresponding to 62% polyunsaturated and 37% of monounsaturated. The saturated dominant FA was palmitic acid that corresponding to 91% of the total of saturated acid, followed by stearic acid. The analysis showed significant differences ( $P < 0.05$ ) among cultivars and also between Protection Denomination Areas.

**1340-1440**

**S12-P-19**

**CHARACTERIZATION OF PORTUGUESE CULTIVARS OF SWEET CHESTNUT USING AMINO ACIDS**

J.L. Soeiro de Carvalho\*, O. Borges, A.P. Silva

Direcção Regional de Agricultura, de Trás-os-Montes, Zona Agrária de Lamego, LAMEGO, Portugal, 5100

From three Protected Denomination Areas of sweet chestnut situated in the region of Trás-os-Montes, Portugal (Castanha dos Soutos da Lapa, Castanha da Terra Fria and Castanha da Padrela), eleven of the most important cultivars were selected to determined amino acids content and evaluate the influence of geographical origin. For the statistical analysis of total data was performed analyses of variance (ANOVA), followed by Scheffe's test with a significance level ( $P < 0.05$ ), principal components analyses (PCA) and cluster analyses. These analyses showed significant differences for the total of essential (seven)

and non-essential (ten) amino acids among cultivars with different geographical origin and allow separated varieties according to the Protected Denomination Areas. The cultivars from Soutos da Lapa and Terra Fria show a clear separation according to the amino acids content. Three sub clusters were separated and pairs of cultivars showed similar or very similar patterns. These results, although preliminary, indicate a clear relation between amino acid content and geographical origin.

**1340-1440**

**S12-P-20**

**IDENTIFICATION OF FEMALE PISTACHIO PHENOTYPES IN DAMGHAN REGION**

SM. Mortazavie<sup>\*1</sup>, A. Vezvaei<sup>2</sup>

<sup>1</sup>Damghan Pistachio Research Station, Damghan, Iran; <sup>2</sup>Dept. of Horticulture, College of Agriculture Univ. of Tehran Karaj Iran

The first and most important step on pistachio research are based on Identification of genetically capable of local germplasm potential which concern about environmental problems in a region. In addition, breeders are becoming educated concerning the available sources, after categorizing the concerned data, which are employed to genetic solution to female pistachio phenotypes, were collected based on morphological characteristics in a design. At first, 150 genotypes were collected, then 70 genotypes discarded in two stages, three characteristics categories were recorded from the remain genotypes. At first, characters such as, tree shape, vegetative, generative, fruit shape, color, inflorescence rachis, alternate bearing... characteristics and method of orchard management were evaluated in the orchard. In the second stage, after harvesting and preparing fruit crop of each selected genotype separately, their characteristics such as length, width, diameter, weight color nut and degree of suture opening nuts were measured. Finally, 24 genotypes from 80 pre selected genotypes were recognized favorite because of high producing, largeness suture opening nut, blank and low alternate bearing were selected. The 56 remain genotypes because of acceptable having characteristics will be employed in improved programs in pistachio nut, some of them such as resistance to psyllid (*Agonoscaena pistaciae*), frost, sustainable to shaking, very late, very early ripping, blind and very suture opening nuts were studied. Finally, 16 genotypes were selected. Fresh and dried pistachio fruit, their vegetative and generative characteristics are discussed in this paper.

**1340-1440**

**S12-P-21**

**WALNUT SELECTION 10/95**

Milislav Mitrovic, Miloljub Stanislavljevic\*, Slobodan Milenkovic

ARI "Serbia", Fruit and Grape Research Centre, Kralja Petra I 9, Cacak, Serbia, Yugoslavia, 32 000

Walnut selection has been underway at the Fruit and Grape Research Centre in Cacak for more than 40 years. More than 300 interesting walnut selections were selected, studied and described from natural populations in Serbia. The most interesting selections are in the collection plantings of the Center and are studied in the comparative trials Selection 10/95 has been singled out owing to its exceptional cropping. Tree is vigorous and a heavy cropper. Leaves are large and extremely healthy. Flowering it is protandrous. It ripens in the second half of September. Fruit is moderately large, averaging 10.6 g. The kernel percentage is 48.3%. Kernel is light yellow. Comparative trials indicate 10/95 is superior to standard cultivars.

**1340-1440**

**S12-P-22**

**PERSIMMON SELECTION FOR THE BLACKSEA REGION IN TURKEY**

Mustafa Akbulut\*

Ministry of Agriculture and R.A., Blacksea Agricultural Research Inst, (Karadeniz Tarimsal Aras. Enst.), Samsun, Turkey, 55000

This research is the second stage of persimmon selection in the Black-Sea Region. A total of 45 persimmon types (candidate cultivars) were planted in a 6x4 m row spacing, each with 3 trees. Phenological and pomological datas were recorded since 98 and 99. Types without brown endocarp taste sour. There were more non sour types than sour types. Clones 55 TH 03, 53 TH 01 and 55 Th 07 gave the highest yields.

1340-1440

S12-P-23

**EARLY RESULTS FROM THE KENTUCKY PAWPAP CULTIVAR TRIAL**

Kirk W. Pomper\*, Desmond R. Layne, R. Neal Peterson, Dwight Wolfe  
129 Atwood Research Facility, Land Grant Program, Kentucky State Univ., Frankfort, Kentucky, USA, 40601

Two pawpaw [*Asimina triloba* (L.) Dunal] cultivar trial orchards were established in Kentucky to evaluate suitability of various varieties for this region. The first orchard was planted in the fall of 1995 in Princeton, at the Univ. of Kentucky (UK) Research and Education Center as a joint Kentucky State Univ. (KSU)-UK research effort. A second orchard was planted in the spring of 1998 at the KSU Research Farm in Frankfort. A randomized block experimental design was used with both plantings with 8 replicates of 28 grafted scion selections. Cultivars being tested include 'Middletown', 'Mitchell', 'NC-1', 'Overleese', 'PA-Golden', 'Sunflower', 'Taylor', 'Taytwo', 'Wells', and 'Wilson'. The other 18 clones were selections from the PawPaw Foundation (PPF) orchards at the Univ. of Maryland Experiment Stations. In the Frankfort, KY planting, 95% of the trees have survived. Based on height and trunk diameter measurements taken from 1998 to 2001, most selections displayed excellent vigor, with the exception of 'Middletown', 'Taytwo', 2-10, 3-21, 5-5, and 11-5. 'PA-Golden' had the best early fruit production as evidenced by the fact that 5 of 8 trees had fruit in 2001. In the Princeton, planting, only 55% of the trees have survived. The selections, 'NC-1', 'PA-Golden', 'Sunflower', 'Wilson', 1-23, 8-20, and 9-58 showed the best fruit production and survival rates (>63%) in 2001. Based on limited data collected so far in the Kentucky trials, 'PA-Golden' has at least preformed well in the two locations and other cultivars and PPF selections show promise.

1440-1520

S12-O-24

**ANALYTICAL BREEDING**

Rodomiro Ortiz\*

International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria  
Mailing IITA c/o L.W. Lambourn & Co., Carolyn House, 26 Dingwall Road, Croydon, CR9 3EE, United Kingdom

Ploidy manipulations consist on scaling up and down chromosome numbers of a species within a polyploid series. Chromosome sets are manipulated with haploids, 2n gametes, and through interspecific-interploidy crosses. Analytical breeding schemes rely mainly on ploidy manipulations to 'capture' diversity from exotic (wild or non-adapted germplasm) and use 2n gametes to incorporate this genetic diversity through unilateral (USP;  $n \times 2n$  or  $2n \times n$ ) or bilateral (BSP;  $2n \times 2n$ ) polyploidization. Most interesting examples of analytical breeding in crop improvement are in vegetatively propagated species such as potato, sweetpotato, cassava, among roots and tubers, and plantain/banana among fruit crops. This breeding approach appears promising in blackberry, blueberry, strawberry and other fruits. An evolutionary crop breeding method was developed for further improvement of the plantain genome. This method ensued from the genetic knowledge accumulated during the analytical breeding of this triploid (3x) crop. Heterozygous 3x landraces are crossed with diploid (2x) wild or cultivated accessions showing the desired characteristic(s). Primary tetraploid (4x) hybrids are recovered after USP, i.e., 2n eggs from 3x x n pollen from 2x. Secondary triploids result by crossing selected 4x with selected 2x stocks, both producing n gametes. Triploid Musa hybrids may also occur due to USP among 2x, i.e., one 2x producing 2n gametes. Hybrids may result from artificial hand-pollination or through polycrosses among selected 4x and 2x parents according to their specific combining ability. Synthetic populations derived from the polycrosses may be tested in other locations to identify promising offspring for cultivar selection. Local selections may lead to dynamic conservation of genetic resources because farmers will preserve distinct locally adapted, improved genotypes across environments. Analytical breeding, coupled with this evolutionary breeding approach, offers an option for broadening the genetic base of fruit crops, enhancing their adaptation, and sustaining breeding gains in respective gene pools.

1520-1540

S12-O-25

**A NEW SELECTION STRATEGY**

Nnadozie C. Oraguzie\*

The Horticulture &amp; Food Research, Institute of New Zealand Limited,

(HortResearch), Havelock North, Hawkes Bay, New Zealand, PB 1401

Early plant breeders based their selection on phenotypic differences (mass selection) among individuals to develop distinctive races and cultivars. Rediscovery of Mendel's work in early 20th century and greater appreciation of Darwin's theory of natural selection provided a framework for understanding the genetic basis of inheritance and how selection can cause incremental changes within plant populations. Cyclical selection methods were then developed based on the principles of evolution, Mendelian genetics, and biometry. Emphasis was on capturing non-additive genetic effects (specific combining ability) and additive effects (general combining ability), and the exploitation of important heterotic groups (reciprocal recurrent selection). Depending on crop species, all methods have been successfully employed. Nevertheless, they may not seem to adequately answer the questions of the 21st century. Choice of parents at all stages of selection is often based on complex quality traits at the expense of descriptive traits. The latest consumer trends tend toward food for health, convenience and pleasure. There is also concern for genetic diversity. Integration of these mega trends in cultivar breeding would facilitate the sustainable development of cultivars relevant for the times. I propose a selection strategy whereby descriptive traits (for example, color, shape, habit, etc) will be used as foundation for developing more complex or "selection" traits. Initial parental selection to establish a breeding population will be based on descriptive traits (or genetic stocks) while subsequent selections will be on complex traits within each genetic stock. Each stock will be maintained as a separate subline in a recurrent selection program for general combining ability. Crosses will be restricted within rather than between sublines to maintain the purity and identity of each genetic stock while the population is undergoing improvement for selection traits. In the short term, mass selection can be used to identify outstanding individuals for immediate use in commercial breeding. New varieties emerging from the program will be promoted based on their genetic stock followed by the improved selection trait. The strategy will more likely ensure maximal production in a sustainable way.

1540-1600

S12-O-26

**HERITABILITY ESTIMATES IN PERENNIAL KIWIFRUIT [*ACTINIDIA DELICIOSA* (A. CHEV.) C.F. LIANG ET A.R. FERGUSON VAR. DELICIOSA]**

Hinga Marsh\*, Alan Seal, Thomas Paterson

Number One Rd, RD2 Te Puke 3071, Bay of Plenty, New Zealand, 3071

Genetic studies were conducted in kiwifruit (*Actinidia deliciosa* var *deliciosa*) to estimate narrow sense heritability in several important fruit characters. The objective of the experiment was to determine the utility of narrow sense heritability estimates derived from both individual and combined seasons' data. Fruit characters were measured in two separate factorial mating designs over three consecutive years from 1996 to 1998. Total fruit number and yield (kg) was recorded for each seedling and a random sub-sample of fruit was used to estimate mean fruit weight, shape and eating quality. Narrow sense heritabilities were estimated for 12 fruit characters based on data collected from 1996 to 1998 i.e. annual heritability estimates. Further analysis of the pooled data from the three consecutive years provided estimates of combined heritability for these data. Results showed the annual heritability estimates were well correlated to their respective combined years heritability estimates ( $r = 0.946$  to  $0.989$ ). Indicating data from any single year was sufficient for estimating narrow sense heritabilities for these characters. Low narrow sense heritabilities (<0.30) were reported for yield, total fruit number, flavour and texture. As a consequence these characters were more readily improved by combined recurrent selection strategies. In contrast those characters with moderate to high narrow sense heritabilities (>0.50) were most readily improved by individual recurrent selection strategies.

1600-1620

S12-O-27

**INTERSPECIFIC HYBRIDIZATION IN *PRUNUS*: ACCOMPLISHMENTS, BARRIERS, AND POTENTIAL**

Brian R. Smith\*

Dept. of Plant and Earth Science, Univ. of Wisconsin, River Falls, WI 54022

Interspecific hybridization (IH) of *Prunus* has been a technique used exten-

sively to introgress desirable traits not available from intraspecific germplasm, resulting in improved cultivars and useful breeding selections. Rootstocks developed via IH have exhibited such critical characteristics as size control, greater compatibility, environmental adaptation or tolerance and pest resistance expressed at levels that would be impossible with other hybridization strategies. The focus of interspecific introgression in the development of production cultivars has resulted in greatly improved winter hardiness, low-chill tolerance, pest resistance, later bloom and more recently, fruit quality. Genetic bridges have also been constructed by selection of widely compatible species that serve as a compatibility step between otherwise incompatible primary target species to be hybridized. Various barriers to successful IH include interspecific sterility, germplasm maintenance issues and problems associated with character quality recovery after crosses with wild germplasm. Two of the most ambitious past U.S. Prunus breeding programs that employed IH were located at South Dakota State Univ. and the Univ. of Minnesota in the early to mid-1900s. Interest in Prunus breeding for such severe climates in the U.S. became virtually nonexistent after the 1950s. A Prunus breeding program was initiated at the Univ. of Wisconsin-River Falls in 1991 to address this long-existing void, with the primary goal of plum, apricot and cherry cultivar development for areas in USDA Hardiness Zones 5 and below. IH has been a necessity for this program since required characteristics for adaptation were unavailable in traditional species. There appears to be nearly unlimited potential to exploit germplasm using IH for Prunus improvement. Reflection upon the past and current utilization of IH worldwide would indicate a continued bright future for this technique.

1620-1640

S12-0-28

#### BREEDING AND CHARACTERISTICS OF SYMMETRIC INTERGENERIC HYBRIDS BETWEEN APPLE AND PEAR

Kiyoshi Banno\*, Y. Hirano, H. Ishikawa

Shinshu Univ., Faculty of Agriculture, Lab. of POMOLOGY, 8304 Minami-Minowa, Kamiinagun, Nagano, Japan, 399-4598

The cross-pollinated embryos of apple cv. 'Fuji' x pear cv. 'Oharabeni' were cultured in the half-strength MS medium supplemented with 0.5 mg/L BA, 0.1 mg/L IBA and 70 g/L coconut water. The shoots of these hybrids after the multiplication were directly grafted onto pear rootstock (*Pyrus calleryana*) and bred. These hybrids were analyzed for S-genotypes by S-gene-specific PCR, RAPD markers, isozyme phenotypes and chromosome number. These results suggest that all of the plants are symmetric intergeneric hybrids receiving both genome equally. Morphological characteristics of the leaves and shoots generally resembled to those of the pollen parent (pear). The disease response to apple blotch, apple scab, pear black spot and pear scab was evaluated among the 5 hybrids, respectively. All of the hybrids showed the resistance against these disease. These results offer a new breeding strategy for multiple-disease resistance using the intergeneric hybrids.

1640-1700

S12-0-29

#### STUDY OF MALE STERILITY ALLELISM BETWEEN PEACH AND ALMOND

J.M. Alonso, Rafael Socias i Company\*

Unidad de Fruticultura, SIA-DGA, Apartado 727, Zaragoza, Zaragoza, Spain, 50080

Male sterility is a reproductive abnormality consisting in the plant inability to produce functional pollen. Peach male sterility was described long time ago and showed to be a monofactorial recessive trait, with a single Mendelian inheritance. Probably the mostly known male sterile cultivar is 'J.H. Hale', which was used in many old breeding programmes, transmitting the male sterility allele a great number of cultivars. Almond male sterility was discovered in 1975 in the cultivar 'Rof', when used as a pollinizer for 'Marcona', resulting in very poor production of the pollinated cultivar. The genetic proximity between peach and almond allowed to presume that almond male sterility could show the same inheritance behaviour than peach and even that the male sterility locus could be homologous between the two species. This hypothesis is being checked by pollen viability assessment in a hybrid progeny obtained by pollinating 'Rof' with pollen of a heterozygous peach for male sterility, from the cross 'J.H. Hale' x 'Maluenda', as well as in some progenies obtained by self-pollinating some of the F<sub>1</sub> peach x almond hybrids. If male sterility allelism were present between the two species, half of the hybrid progeny would be male sterile and the other half male fertile. Pollen viability

results have shown that these almond x peach hybrids are male fertile, implying that there is no allelism for male sterility between the two species.

## Tuesday · August 13

1100-1140

S12-0-30

#### USING GENETIC MODIFICATION TO IMPROVE FRUIT QUALITY: BENEFITS FOR THE GROWER, THE CONSUMER AND THE ENVIRONMENT

David J. James\*, Andrea Massiah, Andrew Passey, Sean Bulley, Simon Vaughan  
Plant Breeding & Biotechnology Dept, Horticulture Research International, East Malling, West Malling, Kent, UK, ME19 6BJ

Genetic modification (GM) of fruit crops at HRI, East Malling has been part of an ongoing programme of crop improvement since 1985. Since the fruit crops we deal with are perennial by nature, (primarily apple and strawberry) breeding programmes are of necessity long term. GM can, in certain circumstances, shorten these programmes by adding just a few desired characters at a time. In recent years we have been able to use gene technology methods to (a) delay the ripening of apples by downregulating ACC synthase and ACC oxidase (b) dwarf apple trees apples by downregulating GA20 oxidase to open the way for the non chemical methods of reducing tree vigour (c) induce *Botrytis* resistance in strawberries by overexpression of a pear polygalacturonase inhibitor protein (PGIP), and (d) investigate the possibility of using fruit plants to produce edible vaccines for the treatment of tooth decay. This talk will summarise the progress made in these areas and discuss future uses of the technology.

1140-1200

S12-0-31

#### GENE SILENCING-BASED RESISTANCE TO PLUM POX VIRUS

R. Scorza\*<sup>1</sup>, M. Ravelonandro<sup>2</sup><sup>1</sup>USDA-ARS Appalachian Fruit Research Station, 45 Wiltshire Rd., Kearneysville, WV 25443, USA; <sup>2</sup>UMR GDPP-Virologie, INRA-Bordeaux, France

Plum pox virus (PPV) is one of the most devastating diseases of *Prunus* (stone fruit) species. Since the first report of PPV in Bulgaria in the early 1900s PPV has spread throughout Europe, into parts of Asia and Northern Africa, and more recently to Chile, the U.S. and Canada, where eradication efforts are currently underway. Breeding for resistance is an important control strategy, but few sources of high-level resistance have been identified, and these are multigenic, requiring long-term breeding efforts for their incorporation into commercial cultivars. Transgene-based resistance offers a complementary approach to developing PPV-resistant stone fruit cultivars. Transgenic plum clone C5 carrying the PPV coat protein (CP) gene was shown to be highly resistant to PPV in greenhouse graft-inoculation tests (Ravelonandro et al., Plant Dis. 81:1231-1235, 1997). Scorza et al (Transgenic Res. 1021-1029, 2001) demonstrated that the C5 clone displayed CP transgene methylation and post-transcriptional gene silencing, a plant defense described in herbaceous plant models. Field tests of C5 in Poland, Romania, and Spain have demonstrated not only the high level resistance to graft inoculation of PPV, but also an apparent immunity to natural aphid-vectored infection. C5 has been shown to be resistant to all of the major PPV strains (Ravelonandro et al., Acta Hort. 550: 431-435, 2001). The transgene, which appears to be a complex multicopy repeat and rearrangement of the original gene cassette, is inherited in crosses to *Prunus domestica* and *P. spinosa* as a single dominant locus. All progeny carrying the insert are resistant to PPV (Scorza et al., Acta Hort. 472: 421-427, 1998). These results with C5 indicate the efficiency of transgene-mediated resistance to PPV, the effectiveness of gene-silencing in a woody perennial tree crop, and provide new and useful transgenic germplasm for developing PPV-resistant lines through hybridization.

1200-1220

S12-0-32

#### DEVELOPMENT OF FIRE BLIGHT RESISTANT APPLE CULTIVARS BY GENETIC ENGINEERING: PRESENT AND FUTURE

Herb Aldwinckle\*

Dept. of Plant Pathology, NYSAES, Cornell Univ., Geneva, New York, USA, 14456

To prove the concept that genetic engineering (GE) could be used to create fire blight (FB) resistant strains of 'Royal Gala' (RG) apple were transformed using *Agrobacterium* with genes for several heterologous lytic proteins (LP), driven by constitutive promoters. RG lines transgenic for attacin LP showed elevated FB resistance and normal RG fruit quality during up to 4 years of field trials. Attacin-transgenic lines of 'Galaxy' and 'M.26' rootstock have also shown increased FB resistance in the field. The fruit color of 'Galaxy' was maintained in the transgenic lines. RG lines transgenic for LP's SB-37, and avian and T-4 lysozyme had increased FB resistance, but were generally less resistant than attacin-transgenic lines. The GE technology is now being applied with genes designed for ready acceptance by regulatory agencies, industry and the consumer. The FB bacterium, *Erwinia amylovora*, produces an effector protein harpin, which induces resistance when applied topically to apple flowers. Some apple lines transgenic for the harpin gene (HrpN), driven by an inducible promoter were shown to have increased FB resistance in the growth chamber and in preliminary field tests. The NPR1 protein is thought to be a pivotal in the plant disease resistance cascade, and when overexpressed may have increased resistance in *Arabidopsis*. Lines transgenic for the apple MpNPR1 gene are being evaluated for resistance in the growth chamber. *E. amylovora* secretes the DspE protein, which must interact with protein(s) in apple for fire blight disease to result. Four DspE-interacting kinases have been identified, and sequences. Sense sequences have been transferred to 'M.26' with the goal of silencing the kinases and preventing disease development. Transgenic regenerants are now being propagated.

**1220-1240**

**S12-0-33**

**CANDIDATE RESISTANCE GENES FROM AN EST DATABASE PROVE A RICH SOURCE OF MARKERS FOR MAJOR GENES CONFERRING RESISTANCE TO IMPORTANT APPLE PESTS AND DISEASES**

Susan Gardiner<sup>1</sup>, Erik Rikkerink<sup>3</sup>, Sarah Meech<sup>1</sup>, Joanna Murdoch<sup>1</sup>, Heather Bassett<sup>1</sup>, Vincent Bus<sup>2</sup>, Rachel Rusholme<sup>1</sup>, Michael Cook<sup>1</sup>, Andrew Gleave<sup>3</sup>, Ross Crowhurst<sup>3</sup>, Gavin Ross, Ian Warrington

<sup>1</sup>HortResearch, Palmerston North Research Centre, Private Bag 11 030, Palmerston North, New Zealand; <sup>2</sup>HortResearch, Hawkes Bay Research Centre, Private Bag 1401, Havelock North, New Zealand; <sup>3</sup>HortResearch, Mt Albert Research Centre, Private Bag 92 169, Auckland, New Zealand

Our apple EST database containing sequences from over 44 cDNA libraries representing several cultivars and a range of tissues has provided an excellent resource for genetic markers linked to previously identified resistances to apple scab, powdery mildew and woolly apple aphid (including the Vf, PI2, PIMIS, and Er3 genes). Candidate ESTs were mined from our apple database on the basis of homology to genes from 5 resistance (R) gene classes and a number exhibited linkage to major R genes. EST markers do not need to be derived from varieties that carry recognised R genes. Linkage analysis suggested that these ESTs often cluster around the R gene in a region of several cM. These clusters can contain candidates from more than one R gene class. Some R genes have genetic markers in common. We have used this targeted strategy to efficiently obtain additional markers for a number of resistance genes that are candidates for marker assisted selection in our apple breeding programme. Techniques used in the targeted strategy include Southern analysis with mini-population blots to identify linkage, screening of enlarged populations to confirm linkage, and then conversion of the more closely linked markers to PCR based markers (SCAR, SNP) to enable high throughput population screens.

**1340-1440**

**S12-P-34**

**APPLICATION OF DEVELOPED MOLECULAR MARKERS FOR PRACTICAL APPLE BREEDING IN THE UKRAINE**

Volodymyr V. Radchuk\*, Kira M. Kopan, Volodymyr P. Kopan

Institute for Plant Genetics and Cr, Corrensstrasse 3, Gatersleben, Germany, 6466

The programme aimed to improve apple cultivars by introducing in their genomes some monogenes was initiated in Ukrainian Institute of Horticulture several decades ago. There were used following genes: Vf, or Vm as the sources for resistance against scab, Co as a source for columnar habit of trees, and some others. Twenty years effort was realized in releasing of 22 new cultivars with very valuable commercial traits. Among them, 4 cultivars possess the gene Vf, one-

Vm, and three cultivars show columnar habit (Co gene). Meanwhile, several elite lines were selected, which carry in their genomes both the Vf and Co genes. In developed cultivars and lines, resistance to scab was estimated visually during plant growth in hybrid orchard without chemical treatment of trees against fungus. No artificial inoculation of pathogen was applied. Despite of high natural scab disease pressure on hybrids in Ukraine, breeders should be sure that selected lines really possess a corresponding resistance gene. Recently, several SCAR and other markers were developed by different groups for Vf, one PCR marker for Vm, and one SSR marker for Co genes. The aim of present work was to test applicability of developed molecular markers for practical apple breeding. Among tested markers, the reliable results were achieved by using of SCAR markers ACS-3, ACS-7 (Xu et al., 2001) and S5 (Hemmat et al., 1998). These markers indicates the availability of Vf gene on the chromosome from different sites. All ukrainian apple cultivars, resistant to scab, showed the corresponding fragments in amplification products, confirming the presence of region with the scab resistance gene in these cultivars. Molecular marker usage in apple breeding is not effective on the seedling stage because of labour and cost demands but it makes sense in stage of elite hybrids for verification of existence of corresponding genes in the hybrid genome.

**1340-1440**

**S12-P-35**

**GRAFT-INDUCED CHANGES OF SEVERAL CHARACTERISTICS IN APRICOT**

Xiuju Li\*, Shengyao Fan, Yongsheng Liu

Dept. of Biochemistry, Univ. of Alberta, Edmonton, Alberta, Canada, T6G 2H7, Edmonton, Alberta, Canada, T6G 2H7

In order to confirm the truthfulness of graft mentor method founded by Michurin, a bud taken from a full-grown pissard plum (*Prunus cerasifera* cv. pissardii) was grafted on a one-year apricot (*Prunus armeniaca* L.) seedling in 1965. The branches and leaves of apricot were removed in Spring 1966, then the bud of pissard plum sprouted and grew vigorously. A tillered plants was produced from the root of apricot by using root pruning and transplanted in 1980, and began to blossom in 1985. The tillered plant was exactly like the scion of pissard plum but very different from its mother plant, apricot in leaf color, leaf shape, flowering habit and many other characteristics. The characteristics which are induced by grafting are stable when the branches taken from the tillered plant were grafted on the stocks of peach and plum. Most of the RAPD (randomly amplified polymorphic DNA) markers that are present in the tillered plant occur in the scion of pissard plum, but are absent from the stock of apricot. The detection of scion DNA in the tillered plant produced from the stock indicates that the direct transfer of DNA from the scion to the stock was the cause of the changes. The tillered plant is actually a graft hybrid between the two species. This furnishes a fresh evidence for graft mentor method founded by Michurin.

**1340-1440**

**S12-P-36**

**EFFICIENT PLANT REGENERATION CULTURE FROM THE LEAF EXPLANTS OF IN VITRO GROWN SWEET CHERRY**

Tadashi Takashina\*, Ryouichi Katoh, Hideaki Nakano

Yamagata Hort. Exp. Sta., 423 Shimaminami, Sagae, Japan, 991-0043

Sweet cherry is one of the most important deciduous fruit trees in Yamagata, because about 80% of the products in Japan are produced in Yamagata. Our objective is the establishment of a gene transfer system to the sweet cherry. However, regeneration from somatic tissue has not been established until now. We then developed an efficient regeneration culture system. Four cultivated varieties, *Prunus avium* 'Benisyuhou', 'Benitemari', 'Benisayaka' and 'Satonishiki' were used in these experiments. Beni-series have been bred at the Yamagata Hort. Exp. Sta. The shoots of these cultivars were subcultured in the modified MS basal medium which contained 1mM Phloroglucinol (PG) supplemented with 0.5 mg/L 6-benzylaminopurine (BA) and 0.1 mg/L indolebutyric acid (IBA). The expanded and/or furled leaves were collected from the shoots. Each leaf was cut several times just across the midrib, and put in Woody Plant (WP) liquid medium supplemented with 5 mg/L 2,4-D for 1 day. After soaking, the leaves were placed on the regeneration medium, the WP agar medium supplemented with 5 mg/L thidiazuron (TDZ). The regeneration rate (adventitious shoots formatted leaves/cultured leaves) and number of adventitious shoots were scored after culturing for 2 months. The furled leaf explants had a higher shoot regeneration rate (77.3 ± 5.1%) than the

expanded leaves ( $26.2 \pm 5.6\%$ ) in 'Benisyuhou'. Also the number of adventitious shoots increased in the furled leaf explants from 0.6/leaf to 2.7/leaf. The younger leaf explants indicated a higher regeneration response than the old leaves. In addition, the pre-culture treatment including 2,4-D is effective for inducing the adventitious shoots from the leaf explants. Comparing the regeneration ability among the four cultivars using the furled leaf explants, 'Benisyuhou' and 'Benitamari' had the higher regeneration rates (about 80%) than 'Satonishiki' and 'Benisyayaka' (20-30%). These adventitious shoots are able to easily grow in acclimated plants.

#### 1340-1440

##### S12-P-37

#### SSR MARKERS FOR PRUNUS DEVELOPED FROM A SMALL EST DATA SET

Steven Van Nocker\*, Audrey Sebolt, Amy Iezzoni

Dept. Horticulture and, Program in Plant Breeding/Genetics, Michigan State Univ., E. Lansing, MI, USA, 48824

We analyzed a small (~1000 nonredundant sequences) EST database generated from ripening fruit of sour cherry (*Prunus cerasus*) for di- or tri-nucleotide SSRs that could be useful to develop a linkage map emphasizing fruit-related traits. As a theoretical base for this work, we cataloged the type, frequency, and polymorphism of SSRs that occur within transcribed and coding sequences of the model plant *Arabidopsis thaliana*, through an analysis of EST databases, the complete genomic sequence, and a compilation of insertion-deletion sequences polymorphic between the Landsberg erecta and Columbia strains. We found that the most abundant di- and tri-nucleotide repeats in cDNAs were (AG), (ATC), and (AAG), together occurring at a frequency of ~47/10E6 bp. Analysis of genomic DNA indicated that ~50% of (ATC) repeats and ~35% of (AAG) repeats were found within predicted gene coding regions. Surprisingly, those repeats that were polymorphic occurred at a similar high frequency within coding regions. (AG) repeats were found almost exclusively outside of coding regions. We identified 78 potentially useful SSRs in our cherry EST database, and our sequence data was sufficient to allow primer design from 56 of these. A subset of these markers were evaluated for potential to detect polymorphisms both within *P. cerasus* and between various *Prunus* species, including sweet cherry, black cherry, apricot, peach, and almond.

#### 1340-1440

##### S12-P-38

#### GENETIC DIVERSITY OF CHESTNUT GERMPLOASM, CULTIVATED AND WILD

Roberto Botta\*, Daniela Marinoni, Aziz Akkak, Gabriele Beccaro, Giancarlo Bounous

Dipartimento di Colture Arboree, Univ. of Torino, Via Leonardo da Vinci 44, Grugliasco, (TO), Italy, 10095

SSR (Simple Sequence Repeats) markers were developed within the European CASCADE (Securing gene conservation, adaptive breeding potential and utilisation of a model multipurpose tree species (*Castanea sativa* Mill) in a dynamic environment) project to study gene flow between different chestnut domestication levels (orchard, coppice, naturalised forest) and to assess the genetic diversity within the chestnut germplasm. Bud samples were collected in winter from stands located in France, Italy and Greece. DNA was extracted and analysed at 6 SSR loci by multiplex PCR using a ABI-PRISM 377 genetic analyser and Genescan software. A total of 36 alleles has been found so far and the highest diversity was detected for wild populations and between the most distant stands. Ongoing studies on gene flow has shown that pollen flow from orchards is often limited due to the high presence of sterility of male flowers in the cultivated germplasm

#### 1340-1440

##### S12-P-39

#### IDENTIFICATION OF JUGLANS CULTIVARS BY INTER-SIMPLE SEQUENCE REPEATS (I-SSR) ANALYSIS

Suk-In Hwang\*, Kyung-Jin Cho, Moon-Ho Lee, Yong-Pyo Hong, Byoung-Sil Lee

44-3 Omokchun-dong Suwon Kyonggi-do, 441-350, Republic of Korea, Korea Forest Research Institute, Suwon, Kyonggi, Korea, 441-350

Inter-simple sequence repeats (I-SSR) markers were used to identify and evaluate genetic relationships among Juglans varieties. Eighty five varieties including *Juglans sinensis* from Korea and *J. regia* from China, Japan, USA, Russia, France, Germany and Nepal, *J. sieboldiana* and *J. mandshurica* were used for this study. Out of one hundred and thirteen amplicons were generated by 9 primers, 105 were polymorphic. Each species or variety could be identified on the basis of each DNA fingerprint. Genetic relationships were evaluated by cluster analysis using UPGMA. Species specific bands were found in *J. mandshurica* but not in *J. sinensis* and *J. regia*. *J. mandshurica* showed clear genetic differences from other species. *J. sieboldiana* was located between *J. mandshurica* and *J. sinensis*. Among eight varieties, which were regarded as *J. sinensis*, only one cultivar, 'Chooknae', appeared to be *J. sinensis*, the others were very similar to *J. mandshurica*. Two hybrids between *J. sinensis* from Korea and *J. regia* from U.S.A. were closely grouped with Chinese and Japanese *J. regia* cultivars. Some Korean *J. sinensis* cultivars, which were bred by selection were distantly related to Chinese and Japanese *J. regia* cultivars. Dendrogram for hybrids of *Juglans sinensis* showed they were more closely related to maternal tree than to pollen donor. Cluster analysis of the varieties representing each nation demonstrated that they could be divided into two groups. Although most oriental varieties were loosely grouped together, some Japanese appeared to be close to Europeans. This is consistent with the fact that European and Persian walnuts were imported to Japan earlier. The results obtained in this study suggested that DNA fingerprints generated by I-SSR PCR be used to identify very closely related crops or plants and manage varieties in clone banks. They could also be sieved as markers in registering new varieties. The genetic relationships revealed by similarity assessment may provide us with markers for finding suitable genetic combination among parents plants.

#### 1440-1500

##### S12-O-40

#### ADVANCES IN THE USE OF MOLECULAR MARKERS IN POME FRUIT BREEDING

Stefano Tartarini\*, Silviero Sansavini

Dipartimento Colture Arboree, Via Fanin 40, Bologna, Emilia Romagna, Italy, 40100

A great deal of research effort over the last decade has gone into the identification of molecular markers linked to important agronomic traits both to improve and to speed up selection procedures. Despite the different strategies used for their identification, including BSA, gene and QTL mapping, many markers have been found in apple but few are available in pear. Most of the currently available RFLP, RAPD, SSR and AFLP markers are generic, i.e. their sequence is only genetically linked to the trait of interest and usually no functional relationship can be inferred. In apple, most of the markers identified so far are linked to monogenic traits, mainly forms of resistance. The best known system -the Vf gene for scab resistance- is discussed in detail as the introgression of the floribunda genome in advanced apple cultivars derived from breeding programs can be investigated by the use of the Vf-linked molecular markers and an optimized marker-assisted selection (MAS) approach has been developed. Markers linked to other scab, mildew, *Dysaphis devector* and *Eriosoma lanigerum* resistance genes are also available. In apple, too, a few markers are available for the selection of such agronomic and fruit quality traits as columnar tree habit, fruit colour and flesh firmness. Recently, the construction of different molecular maps, mainly SSR-based, will make it possible to identify more QTL markers linked to agronomic and fruit quality traits. In the last several years more attention has been dedicated to the identification of functional markers, i.e. DNA sequences responsible for the expression of given traits. This work was made possible by the recent availability of DNA sequences in databases that can be used to design specific primers to isolate by PCR analogous sequences in other species or genotypes. This approach has successfully been used to characterize, for example, genes involved in gametophytic incompatibility in both apple and pear and in apple ethylene biosynthesis. These functional markers will be useful in inferring their map location and possible involvement in the expression of various complex traits.

#### 1500-1520

##### S12-O-41

#### IDENTIFICATION AND MAPPING OF DNA MARKERS LINKED TO GENES (VA, VB, VR AND VX) CONFERRING RESISTANCE TO SCAB IN APPLE

Minou Hemmat\*<sup>1</sup>, Susan K. Brown<sup>1</sup>, Norman F. Weeden<sup>2</sup>, Shawn A.



Mehlenbacher<sup>3</sup>

<sup>1</sup>Dept. of Horticultural Sciences, Cornell Univ., NYSAES, Geneva, NY 14456; <sup>2</sup>Dept. of Plant Science, Montana State Univ., Bozeman, MT; <sup>3</sup>Dept. of Horticulture, Oregon State Univ., Corvallis, OR

The identification of two new races of apple scab (races 6 and 7) that are virulent on material derived from *Malus floribunda* 821 (Vf) has made the pyramiding of scab resistance genes of even higher priority. Environmental and genetic effects on phenotypic expression of resistance have made selection and interpretation of resistance difficult. The ability to pyramid sources of resistance using molecular markers for genotyping is highly desirable. Bulked segregant analysis identified RAPD markers closely linked to genes conferring qualitative resistance to apple scab: Va derived from 'Antonovka' (PI 172623), Vb from *M. baccata* and Vr and Vx from Russian seedling R12740-7A. Detailed linkage maps were developed for Va, Vb, Vr and Vx and the map location of these genes were identified. These markers are being used for pyramiding genes for more durable resistance to apple scab.

**1520-1540****S12-0-42****MARKER ASSISTED SELECTION (MAS) IN STONE FRUITS**

Raffaele Testolin\*

Dipartimento di Produzione Vegetale, Univ. of Udine, Via delle Scienze 208, Udine, UD, Italy, 33100

The first peach linkage maps that appeared in 1994 include markers associated with traits of horticultural interest, such as vegetative habit, fruit skin pubescence (fuzz), and redleaves. Many breeders predicted a rapid development of marker-assisted selection (MAS), based on the analysis of marker tightly associated to the character rather than to the character itself, which is often not expressed in seedlings during their juvenile phase. Since then, diverse molecular markers have been developed including: isozymes; RFLP; markers produced by means of PCR and arbitrary primers, such as RAPD and AFLP; markers based on the length polymorphism of repetitive DNA, such as SSR; markers based on single point mutations such as SNPs and others obtained from either cDNA sequences (ESTs); and databases (CGAs, Cloned Genes Analogs). Different approaches to the analysis of marker-trait association include the use of mapping populations segregating for the characters of interest, bulk segregant analysis (BSA), and linkage disequilibrium (LD). The most important characters and quality trait loci (QTL) tentatively mapped in several stone fruits (peach, almond, cherries, common and Japanese apricot, and myrobalan plum), some of which are used in early progeny screening, include blooming time, pollen sterility, self-incompatibility, double flower, fruit shape, skin hairiness, flesh color, acidity and sweetness, pillar and weeping tree architecture, red leaves, resistance to powdery mildew, leaf curl, root-knot nematodes and other pests and diseases. There are many advantages offered by the high degree of genome synteny found in *Rosaceae*, which allows transferring sets of markers and coding sequences between species.

**1540-1600****S12-0-43****MOLECULAR MARKER FOR SELECTING POLLINATION-CONSTANT NON-ASTRINGENT (PCNA) TYPE PERSIMMON AT JUVENILE STAGE**K. Yonemori\*<sup>1</sup>, S. Kanzaki<sup>1,3</sup>, A. Sato<sup>2</sup>, M. Yamada<sup>2</sup>, A. Sugiura<sup>1</sup>

<sup>1</sup>Graduate School of Agriculture, Kyoto Univ., Sakyo-ku, Kyoto 606-8502, Japan; <sup>2</sup>Dept. of Grape and Persimmon Research, National Institute of Fruit Tree Science, Akiitsu 729-2494, Japan; <sup>3</sup>Faculty of Agriculture, Kinki Univ., Nakamachi, Nara 631-8505, Japan

Japanese persimmon (*Diospyros kaki* Thunb.) cultivars are classified into four types depending on the nature of astringency-loss; 1) pollination-constant non-astringent (PCNA), 2) pollination-variant non-astringent (PVNA), 3) pollination-variant astringent (PVA), and 4) pollination-constant astringent (PCA). However, based on the mechanism of astringency-loss, persimmon should be divided into two groups; 1) PCNA and 2) non-PCNA. In addition, the trait of natural astringency-loss in PCNA-type is qualitatively inherited and is recessive to other three types (non-PCNA-type). So far, as the breeding objective for persimmon has been focused on obtaining PCNA-type offspring with better eating qualities and early maturation, crossings have been restricted

among PCNA genotypes to yield PCNA offspring in F<sub>1</sub> generation, but it has caused a serious problem of inbreeding. To overcome it, non-PCNA-type should be included in the breeding project. However, when the crossings were performed between PCNA-type and non-PCNA-type, all plants in F<sub>1</sub> progenies became non-PCNA-type. To yield PCNA-type in the breeding population, these F<sub>1</sub> plants have to be backcrossed to PCNA-type. This backcrossed population yields only around 15% of PCNA type due to polyploid nature of Japanese persimmon. So, molecular marker is needed for selecting PCNA type efficiently from these breeding populations. Until now, we have found two RFLP markers for distinguishing PCNA-type from non-PCNA-type with 100 accuracy in breeding population tested. Since non-PCNA-type persimmons have either one of these two markers or both of them, we assumed that the trait of natural astringency-loss is controlled by two allele pairs and the genotype must be recessive in all alleles to be PCNA-type. We are now trying to design two primer pairs to detect both sequences of these two RFLP markers and apply PCR analysis using these primer pairs to breeding population for establishment of easier practical marker-assisted selection.

**1600-1620****S12-0-44****SYNTENY WITHIN THE PRUNUS GENOMES DETECTED BY MICROSATELLITE MARKERS**E. Dirlwanger<sup>1</sup>, P. Cosson<sup>2</sup>, C. Poizat<sup>3</sup>, M.J. Aranzana<sup>2</sup>, M.T. Dettori<sup>1</sup>, I. Verde, R. Quarta, P. Arús, F. Laigret\*

<sup>1</sup>Unité de Recherches sur les Espèces Fruitières et la Vigne, INRA, BP 81, 33883 Villenave d'Ornon Cedex, France; <sup>2</sup>Departament de Genètica Vegetal; IRTA, Carretera de Cabriels s/n; 08348 Cabriels (Barcelona), Spain; <sup>3</sup>ISF, Via Fioranello, 52 Ciampino Aeroporto 00040 Roma, Italy

Several intraspecific and interspecific *Prunus* maps were constructed or saturated using common microsatellite markers. Here, we compare the maps build from three intraspecific populations (i) an F<sub>2</sub> peach (*Prunus persica* (L.) Batsch) population from the 'Ferjalou Jalousia' x 'Fantasia' cross, (ii) an F<sub>1</sub> sweet cherry (*Prunus avium* L.) population from the 'Regina' x 'Lapins' cross, (iii) an F<sub>1</sub> almond (*Prunus amygdalus*) population from the 'Ferragnès' x 'Tuono' cross. Additional maps were build from three interspecific populations (i) an F<sub>2</sub> interspecific population from the cross between 'Texas' almond and 'Earlygold' peach from which the reference *Prunus* map was obtained (Joobeur et al., 1998), (ii) an F<sub>1</sub> population from the cross between the Myrobalan plum (*Prunus cerasifera*) clone 'P.2175' and an hybrid between the almond 'Garfi' and the peach 'Nemared' and (iii) a BC1 progeny [*Prunus persica* x (*P. persica* x *P. ferganensis*)]. The order of most of the markers is the same in all the maps suggesting a high level of synteny within the *Prunus* genus. The homology between *Prunus* species should then allow a rapid transfer of the results obtained in one species to another.

**1620-1640****S12-0-45****SPECIES COMPOSITION OF CALIFORNIA AND SOUTHEASTERN DIPLOID PLUM FOUNDING CLONES AS REVEALED BY RAPD MARKERS**Unaroj Boonprakob<sup>1</sup>, David H. Byrne\*<sup>1</sup>

<sup>1</sup>Dept. of Horticulture, Kasetsart Univ., Kamphaengsaen, Nakhonpathom 73140, Thailand; <sup>2</sup>Dept. of Horticultural Sciences, Texas A&M Univ., College Station, TX 77843-2133, USA

Early domestication of diploid plums in the United States was focused on native North American plum species until Luther Burbank imported several Japanese plum (*P. salicina* Lindl.) seedlings from Japan and intercrossed these with Chinese plums (*P. salicina* and *P. simonii* Carr), Eurasian plums (*P. cerasifera* Ehrh.), and native American plums (*P. americana* Marsh., *P. hortulana* Bailey, *P. angustifolia* Marsh., *P. maritima* Marsh, and *P. subcordata* Benth). His released plums, which later become founding clones of Japanese-type plums in the United States, were mainly multispecies hybrids. The major founding clones for Japanese-type plums for the California gene pool are 'Santa Rosa', 'Eldorado', and 'Gaviota'; and for the southeastern USA are 'Methley', 'Santa Rosa', and 'Mariposa' (Byrne, 1989). These founding clones contributed about 70% and 50% of their genetic background to the California gene pool and to the southeastern US gene pool, respectively. However, the parentage and consequently the species composition of these multispecies hybrids is poorly docu-

mented and has been based on their morphological traits. The objective of this study was to estimate species composition of California and southeastern diploid plum founding clones with 158 RAPD markers generated with eight primers (C10, E6, G6, J5, J8, K3, K18, and N10). The species composition was estimated by calculating the sum of probabilities that a particular RAPD marker possessed by a founding clone came from the putative species and weighing this by the number of markers present in the founding clone. This analysis confirms that *P. salicina*, *P. simonii*, and *P. cerasifera* are in the backgrounds of these founding clones but raises questions about the *P. americana* parentage proposed in the development of the founding clones 'Santa Rosa' and 'Gaviota'.

**1640-1700**

**S12-0-46**

**EVALUATING GENETIC RESOURCES IN MINOR FRUITS**

Hilde Nybom\*

Dept. of Crop Science, Swedish Univ. of Agricultural Sciences, Fjalkestadsvagen 123-1, Kristianstad, S-291 94, Sweden

Proper evaluation of genetic resources in native material is especially important for plant species at the initial stages of domestication like dogrose, lingonberry, sea buckthorn, black chokeberry, Japanese quince, false banana and papaw. However, there is increasing interest in widening the available gene pool also for more well-known crops in the quest for genes that can improve e.g. disease resistance and climatic adaptation. In lesser known species, the first step may consist of assessing the amount and distribution of genetic variability in native populations using molecular markers like e.g. RAPD, AFLP or microsatellite DNA loci. Various life history traits have proven to be closely associated with the variability parameters. Among these traits, breeding system is especially important. This is also a trait for which the most important fruit and berry family, Rosaceae, contains a tremendous range of variation. I shall here shortly describe some recent results obtained using DNA markers in two rosaceous crops, black chokeberry (*Aronia melanocarpa*) and dogroses (*Rosa* sect. *Caninae*). (1) RAPD markers first demonstrated total identity among several named cultivars of black chokeberry. Subsequent analyses conducted on newly collected material from N America showed that there were two morphologically very similar entities: one diploid outcrossing taxon and one tetraploid, apomictic and probably hybridogenous taxon. (2) Due to their aberrant meiosis, dogroses have a truly unique reproductive method resulting in comparatively low levels of variability. Microsatellite DNA analyses of seedlings from interspecific crosses indicate that each dogrose plant has 2, 3 or 4 (depending on ploidy level) nuclear, haploid genomes (with 7 chromosomes each) that are inherited only on the maternal side, and one nuclear, diploid genome (14 chromosomes) which is biparentally inherited. These two examples clearly indicate the importance of studying the reproductive system and its effects on genetic variability before designing strategies for collecting and utilizing germplasm in a plant breeding program.

---

**Thursday · August 15**

---

**1100-1140**

**S12-0-47**

**RESISTANCE TO BIOTIC STRESS**

Yves Lespinasse\*

INRA-C.R. d'ANGERS, Unité d'Amélioration des Espèces Fruitières et Ornamentales, B.P. 57-49071 BEAUCOUZE Cedex-France

Resistance to pests and diseases is a very desirable objective in fruit breeding but is a long-term endeavor. It requires appropriate tests for early screening and an analysis of host-parasite interactions for durability of resistance. Host resistance is considered durable when it remains effective for a long period despite wide exposure to the parasite. Non-durable resistance is usually characterised by a hypersensitive reaction (HR) and major gene resistance which often occur in multiple allelic series and/or complex loci. Resistance of a more durable nature against fungi and bacteria is often quantitative and based upon the additive effects of some to several genes not eliciting a hypersensitive reaction. Durability has to be the key-point of any fruit breeding program for resis-

tance. HR resistance or race-specific resistance is usually rendered ineffective; the pathogen population is shifted genetically to avoid the resistance gene. The current situation of fruit crops—monovarietal orchards established for several years—enhances the selection pressure on the pathogen population and results in population shifts which could be dramatic. Guidelines have to be proposed to predict the evolutionary potential of pathogen populations based on analysis of their genetic structure; the most important parameters to consider are reproductive/mating systems and gene/genotype flow. Pathogens that pose the greatest risk of breaking down resistance genes are those that possess a mixed reproduction system, with one sexual cycle per growing season and asexual reproduction during the epidemic phase, and a high potential for gene flow. Several examples of different strategies used by fruit breeders will be presented mainly on *Malus*, *Prunus*, *Coffea* and *Musa*. The more complex the genetics of the resistance, the more difficult it is for the pathogen to evolve to a form that can overcome the resistance. Polygenic resistance is usually associated with a quantitative expression that is characterised by a continuous variation between susceptibility and resistance. To approach the number of genes involved in polygenic resistance (QTL) and the relative effect of each of these genes, they have to be mapped on the genome. Marker Assisted Selection (MAS) gives the possibility to incorporate QTL for resistance; major genes could be associated with QTL. The combining of resistance genes may be desired to: acquire a higher level of resistance against a particular pathotype, obtain resistance against a broader range of pathotypes, retain defeated genes, and combine different mechanisms of resistance. Fruit breeders can use the lessons learned from deploying resistance genes in annual crops and selecting resistance in forest trees and apply these to their strategies for fruit tree improvement.

**1140-1200**

**S12-0-48**

**GENE ACTION OF PMR1 AND OTHER POTENTIAL SOURCES OF RESISTANCE TO SWEET CHERRY POWDERY MILDEW**

J.W. Olmstead\*, G.A. Lang

Michigan State Univ., Dept. of Horticulture, A338-E Plant and Soil Science Bldg., East Lansing, Michigan, United States, 48824-1325

Many sweet cherry (*Prunus avium* L.) cultivars grown commercially are susceptible to powdery mildew (PM), including all leading North American cultivars ('Bing', 'Van', 'Rainier', 'Lapins', 'Sweetheart') as well as 'Stella', the progenitor of all current self-fertile cultivars worldwide. We previously confirmed the first source of genetic resistance to PM in the sweet cherry selection PMR-1. Resistance was conferred to progeny from crosses of PMR-1 with susceptible parents through a single gene (Pmr1), although the gene action was not elucidated. The objective of this research was to determine: 1) the gene action of PM resistance from Pmr1; and 2) the inheritance of PM resistance from other potential, unrelated sources that we identified previously ('Chelan', 'Hedelfinger', and 'Moreau'). Reciprocal crosses were made between two highly susceptible cultivars, 'Bing' and 'Van', used previously to develop segregating progenies with PMR-1. The seedlings were screened for reaction to PM colonization after natural infection in a greenhouse. All progenies proved to be susceptible; this result, combined with our previous segregating progenies, indicates Pmr1 follows a dominant gene action model, and is, in PMR-1, in the heterozygous allelic state. In addition, one-way crosses were made between 'Bing' and 'Chelan', 'Hedelfinger', and 'Moreau'. Following similar greenhouse screening, segregation for PM reaction within all progenies fit a 1 resistant : 1 susceptible segregation ratio ( $P > 0.05$ ), indicating resistance to PM derived from each of the parents is also conferred by a single dominant gene in the heterozygous allelic state. Whether the resistance genes in these cultivars are allelic to, or completely different from, Pmr1 has yet to be determined, though genomic analysis strategies are now underway. The implications of these genetic sources of PM resistance, for existing as well as future sweet cherry cultivar breeding, will be discussed.

**1200-1220**

**S12-0-49**

**RESISTANCE TO BROWN ROT DISEASE IN PEACH IS DETERMINED BY MULTIPLE STRUCTURAL AND BIOCHEMICAL COMPONENTS**

Thomas M. Gradziel\*, Richard M. Bostock, James E. Adaskaveg  
Dept. of Pomology, Univ. of California, Davis, CA 95616

A multi-year evaluation of USDA and UC peach (*Prunus persica*) germplasm for resistance to fruit brown rot as caused by *Monilinia fructicola* has identified the Brazilian cultivar 'Bolinha' as well as several peach breeding lines derived from almond (*Prunus dulcis*) as the most promising sources for the transfer of disease resistance to processing peach. Fruit flesh or mesocarp resistance was often associated with elevated levels of the phenolic compounds chlorogenic and caffeic acids. Elevated levels of these phenolics were also associated with greater susceptibility to fruit bruising making them undesirable for cultivar development. Usable and heritable levels of epidermis-based resistance were recovered following a series of controlled backcrosses. The epidermis of resistant progeny typically possessed thicker cuticles and greater amounts of epicuticular waxes, and higher levels of pectin, phenolics, chlorophyll, and other biochemical compounds associated with immature tissue. Structural components, particularly cuticular and epicuticular waxes were significantly influenced by growing season environment. The concurrent selection for epidermis-based resistance combined with a high (CIE  $L^*a^*b^*$ ) 'a' color value has been successful in breeding resistant genotypes possessing good horticultural and processing quality.

1220-1240

S12-O-50

**CLIMATIC ADAPTATION IN FRUIT CROPS**W.B. Sherman\*<sup>1</sup>, T.G. Beckman<sup>2</sup><sup>1</sup>Dept. of Horticultural Science, 1143 Fifield Hall, PO Box 110690, Gainesville, FL 32611-0690 USA; <sup>2</sup>USDA-Byron, GA

Fruits have varying amounts of climatic adaptation. Most grow only in either the tropics, subtropics, or temperate zones. Fruits such as mango grows best in a tropical climate without frosts, citrus grows best in a subtropical climate without hard winter freezes, and apricot grows best in a temperate, Mediterranean climate of uniformly cool winters and dry summers. However, strawberry has adaptation from the equator to the arctic circle and some apple genotypes will grow in low chill, subtropical climates while others will grow in high chill, temperate climates. Clearly, some fruits have more specific adaptation limitations than others as seen by their specialized areas of production. Fruit breeding is human directed evolution in desired tree and fruit characteristics. Climatic adaptation precedes breeding for commercial fruit qualities. Without climatic adaptation, the breeder may not be able to make hybrids and cannot adequately fruit and evaluate them. Once the breeder finds climatic adaptation for tree growth and fruiting, selection for more specific climatic requirements is possible, and primary attention can then be given to fruit characteristics necessary for making the crop economically viable. Adaptation factors for tree growth, flower bud formation, flowering, and fruit growth and maturation are photoperiod, light intensity, chilling and heat units, soil type, and temperature and water tolerance. These topics are discussed with examples of fruit species that respond to each. Future prospects in breeding for adaptation are presented.

1340-1440

S12-P-51

**RESISTANCE TO PEAR PSYLLA NYMPHAL FEEDING OF GERMLASM FROM CENTRAL EUROPE**

Richard L. Bell\*

U.S. Dept. of Agriculture, Agricultural Research Service, 45 Wiltshire Road, Kearneysville, WV, USA, 25430-9425

Pear psylla (*Cacopsylla pyricola* Foerster) is the most serious pest of the European pear (*Pyrus communis* L.) in the production regions of Europe and North America. Nine plant germplasm introductions of pear from Central Europe recently released from plant quarantine were evaluated for nymphal feeding antixenosis, a primary mode of resistance known to be correlated with ovipositional antixenosis and antibiosis (i.e. nymphal mortality and reduced developmental rate). Five single-shoot budded trees were grown in the greenhouse without pesticide application. The top two youngest fully expanded leaves were infested with ten 2nd and 3rd instar nymphs from a young laboratory colony. The number of surviving nymphs and the number of actively feeding nymphs was recorded after two days. Three cultivars from Yugoslavia, 'Karamanka', 'Jeribasma', and 'Vodenjac', plus NY 10353 (a resistant control of *P. ussuriensis* Max. ancestry) were significantly more resistant to nymphal feeding than the susceptible control, 'Bartlett', and the cultivars 'Junsko Zlato', 'Lida', 'Orlovskaya',

'Oranzhevaja', 'Nadejda', and the selection IV 12. These objective data confirm field observations made in Europe of the Yugoslavian cultivars, and increases the number of psylla-resistant genotypes available for breeding new cultivars.

1340-1440

S12-P-52

**COMPARATIVE ANALYSIS OF THREE DIAGNOSTIC METHODS FOR THE EVALUATION OF PLUM POX VIRUS (PPV) RESISTANCE IN APRICOT BREEDING PROGRAMS**

Pedro Martinez-Gomez\*, Manuel Rubio, Federico Aparicio, Vicente Pallas, Federico Dicenta

Dep. de Mejora y Patologia Vegetal, CEBAS-CSIC, PO box 4195, Murcia, Murcia, Spain, E-30100

Plum pox potyvirus (PPV), is the causal agent of the Sharka disease, which is the most destructive viral disease of *Prunus* stone fruits, mainly apricot, in Europe. No control means have already been developed except for the complete destruction of infected trees and the application of strict quarantine control measures. On the other hand, the develop and growth of new resistance cultivars could be the definitive solution to the problem. In this moment search for PPV resistance is one of the most important objectives in all the European apricot breeding programs. The routine application of an adequate detection method during the evaluation of PPV resistance is a critical step in these breeding programs. During last years, a large number of serological and PCR-based methods have been described for their application in these programs, whereas methods based on the molecular hybridization techniques have been less considered despite that have recently shown to be a very good alternative for routine diagnosis. In this work, the comparison between non-radioactive molecular hybridization, ELISA-DASI with monoclonal antibodies, and IC-PCR, was performed in terms of sensitivity, reliability, cost, and routine application. Results showed the higher sensitivity of the IC-PCR although was more time consuming and expensive. Molecular hybridization and ELISA showed similar sensitivity, reliability and routine application, but the cost of the molecular hybridization was lower than ELISA-DASI.

1340-1440

S12-P-53

**USE OF A DETACHED LEAF BIOASSAY FOR SCREENING SWEET CHERRY CULTIVARS FOR BACTERIAL CANKER RESISTANCE**

K.E. Bedford\*, P.L. Sholberg, F. Kappel

Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, 4200 Highway 97, Summerland, BC, Canada, V0H 1Z0

Bacterial canker, caused by the bacterium, *Pseudomonas syringae* pv. *syringae* is a serious disease of sweet cherries world wide. The ability to readily discriminate relative resistance or susceptibility of sweet cherry seedlings or selections would be of benefit to cherry breeding programs. In this study, detached leaves harvested from sweet cherry trees in an orchard setting were used for an in vitro assay of resistance to bacterial canker of sweet cherry. Two methods of inoculation were tested, a leaf disc infiltration technique and a mid-rib leaf injection technique. Variables tested included age of leaves, sample date, and concentration of inoculum. Harvested detached leaves were surface sterilized, inoculated with known pathogenic strains of *Ps. syringae* pv. *syringae*, a saprophytic strain of *Pseudomonas fluorescens* or sterile distilled water. Inoculated leaves were incubated for 7-14 days at 25 C with a 12 hour photo period. Symptom development was rated using a 0-4 (leaf infiltration) or 0-3 (leaf injection) scale with 0 indicating no symptom development and the highest numbers indicating expanding chlorotic and necrotic leaf tissue. Cultivars tested were of known susceptibility and included 'Merpet' (resistant), 'Merchant' (resistant), 'RoyalAnne' (susceptible), 'Sweetheart', 'Lapins' and 'Bing'. The leaf disc infiltration technique was successful in confirming the pathogenicity of the *Ps. syringae* pv. *syringae* strains used. It did not allow discrimination of levels of resistance of the cultivars tested. The mid rib needle injection technique offered more useful results. Mature leaves were better subjects for inoculation than younger succulent leaves primarily because of sensitivity to the surface sterilization procedures. An inoculum concentration of 106 colony forming units/mL gave the best results of the concentrations tested. A refined protocol for using this method for larger scale screening is being developed.

1340-1440

S12-P-54

**BIOCHEMICAL CHANGES AT SOME PEACH AND NECTARINE VARIETIES AND HYBRIDS LINKED WITH THE RESISTANCE LEVEL TO SPHAEROTHECA PANNOSA VAR. PERSICAE**

Stefania Toma, Antonia Ivascu\*, Cristina Petrisor, Veronica Lazar  
Research Station for Fruit, Tree Growing Baneasa-Bucharest, Sos.Ion Ionescu de la Brad, #4, sec1, Bucharest, Romania, 71592

The project had in view the study of some biochemical compounds such as: free, total and linked water content, dry matter, nitrogen and protein content along with tannin level at some peach and nectarine varieties and hybrids to prove the relation between these biochemical traits and the biotic stress resistance degree. Studies have been done at the Research Station for Fruit Tree Growing Baneasa-Bucharest situated in the south area of Romania during 1997-2000. The south zone of Romania has extremely favorable ecological conditions for peach and nectarine growing being affected in several years by various fungi. One of most aggressive pathogen is *Sphaerotheca pannosa* var. *persicae*. We proved that this agent has a great influence on plant metabolism. Total water content was significantly increased in contrast with the dry matter and tannin content which was reduced in case of resistant cultivars ('Victoria', 'Nectared 7', 'HB11-40'). Total nitrogen and protein level has less influence on resistance behaviour to powdery mildew at all the biological material analyzed. All the genetic material found as resistant to powdery mildew is used in the present breeding peach program in Romania.

1340-1440

S12-P-55

**EVALUATION OF SOME BIOCHEMICAL COMPOUNDS IMPLICATED IN BIOTIC STRESS AT SOME PEACHES AND NECTARINES GENOTYPES**

Antonia Ivascu\*, Viorica Balan, Cristina Petrisor, Veronica Lazar, Stefania Toma  
Research Station for Fruit Tree Growing Baneasa, Bd. Ion Ionescu de la Brad, No. 4, Bucharest, Romania

Our aim was to try to understand the resistance to viruses and some peach and nectarine varieties and hybrids; this representing an essential factor for the improvement of pathogen infection control. The amount of some biochemical compounds leaves had been extracted such as: a chlorophyll, b chlorophyll, carotene, xanthophyll and also dry substance was determined. These compounds had been chosen taking in account the essential role of a chlorophyll, b chlorophyll, carotene, xanthophyll in photosynthesis and nevertheless the well known involvement of phenolic compounds in plant disease resistance. We saw a great increase in phenolic compounds level in case of the PPV affected leaves comparative with the healthy ones. Concerning the chlorophyll level we remarked the opposite the amount was less in the infected samples due to decoloration phenomenon which is present on leaves. In case of the other two assimilation pigments (carotene and xanthophyll) the same diminution was observed. The ratio between "a+b/x+c" indicate a strong sensitiveness of the leaves to the viral infection. A diminution of the dry substance content was also observed in the infected leaves compared to the healthy ones, the explanation is that the leaves have a low level of resistance to the viral infection

1340-1440

S12-P-56

**THE FAST SELECTION TECHNOLOGY OF SOME PEACH CULTIVARS WITH GENETIC RESISTANCE TO CYTOSPORA CINCTA**

Marioara Trandafirescu\*<sup>1</sup>, V. Spita<sup>2</sup>, Georgeta<sup>3</sup>

<sup>1</sup>Ovidius Univ. B-dul Mamaia 124; 8700 Constanta-Romania; <sup>2</sup>Fruit Research Station, Pepinierei 1, 8763, Valu lui Traian- Romania; <sup>3</sup>Fruit Research Institut, 0300 Pitesti Jud.Arges-Romania

The fungus *Cytospora cincta* Sacc. produces great damage and is incriminated as one of the agents responsible for short life and tree decline. Rapid selection for increased resistance genitors has been devised after Crossa-Raynaud (1969). This test which consisting of artificial inoculation of tree-branches with mycelium reduces observation time to 3-4 years compared to the natural infection. By comparing the length of the infection peach and apricot entries were divided into four classes of resistance. Springold, Cardinal, Collins, and Flamekist were classified as resistant.

1340-1440

S12-P-57

**SPREAD OF PLUM POX VIRUS IN NEW PLUM ORCHARDS OF THE CZECH REPUBLIC AND RESISTANT CULTIVARS TO THE DISEASE**

J. Blazek\*, F. Paprstein, R. Karesova

Research and Breeding Institute of Pomology, Holovousy 1, Horice, O. Jicin, Czech Republic, 508 01

A majority of the territory of the Czech Republic is infested by plum pox. Wild growing plums are almost completely infected by PPV. Trees in plum orchards, which were established by using virus free planting material, were contaminated by plum pox at a rate fluctuating from 0 to 3 % per year in a dependence on infection pressure of the pathogen from surrounding. If a part of the planted trees was already infected, the rate of plum pox spreading was much higher. There is a relation between distance of trees from a source of infection and rate of their contamination by PPV. If the distance was less than 5 m the average rate was 43.2%, whereas at distances 5-10 m this rate was equal to 20.8% and at distance greater than 30 m to only 5.8%. With 'Domestic Prune', that is very sensitive to PPV, these rates were nearly doubled while in the case of the other cultivars frequencies of infection were proportionally lower (from 5.3 to 19.5%). No significant difference was found between Myrobalan and St. Julien A rootstocks. Contamination of a tree significantly increased the risk of infection of neighbouring trees even if infected trees were discarded. Those within the same row increased their hazard by approximately threefold and those between rows doubled in comparison to the average rate of contamination of trees by PPV. Timely grubbing of affected trees immediately after an emergence of symptoms of this viral disease is recommended. The highest level of resistance to PPV was found in 'Bila Trnecka', 'Francja Naranes', 'Large Sugar Prune', 'Reine Claude Diaphane', 'Renkloda Jandacek' and one seedling.

1340-1440

S12-P-58

**NEW RESULTS ABOUT THE HYPERSENSITIVE REACTION OF PLUMS AND PRUNES TO PLUM POX VIRUS**

W. Hartmann\*

Hohenheim Univ., Institut fuer Obst-, Gemuese- und W, Emil-Wolff-Str. 25, Stuttgart, Germany, D-70599

The plum pox virus (PPV) causes significant yield loss in *Prunus*, yield and fruit quality are reduced. Only few genotypes in *Prunus domestica* can be regarded as resistant. There are two different types of PPV resistance: qualitative and quantitative. The qualitative resistance is visualized as necrotic symptoms and is based on a hypersensitive reaction (HR), a widely occurring active defence mechanism. The qualitative resistance in plums was regarded as a yes or no reaction (Kegler et al. 1998). However new results shows that there is a gradual reaction, depending upon the genetics of the plant and the infection dose. Tests for HR were made by grafting on infected trees or rootstocks. Hypersensitive hybrids react with tip necrosis. The earlier we found the reaction the higher will be the HR. Infection method affects reaction. Budstick infections give different results than from chip or aphid infection. One year old potted trees are more sensitive than two year old or older trees in the field. From our resistance breeding effort we observed hybrids which are field resistant. Durable absolute resistance can be achieved by combining qualitative and quantitative resistance in hybrids.

1340-1440

S12-P-59

**DISTRIBUTION AND TRANSPORTATION OF WITCHES' BROOM-RELATED PHYTOPLASMA (MLO) IN CHINESE JUJUBE**

Mengjun Liu\*, Xiuling Wang, Lijuan Liu

Research Center of Chinese Jujube, College of Horticulture, Agricultural Univ. of Hebei, Baoding, Hebei, P.R. China, 71001

Chinese jujube is an important multi-purpose fruit tree both in China and South Korea. Witches' broom disease is a destructive disease of Chinese jujube caused by phytoplasma (MLO). The distribution of witches' broom-related phytoplasma in 'Fuping Dazao' (an important commercial Chinese jujube cultivar) was studied in a systematic way with fluorescence microscope. The result showed that the distribution of phytoplasma in Chinese jujube tree had some specific properties, such as wide-spread, unwell-distribution and corresponding distribution (under ground and above ground). In different seasons, witches'

broom-related phytoplasma concentrated in different parts of the same organ. The property of unwell-distribution could be observed easier in the trees that symptoms were just found. The infected branches can be divided into six grades according to the obvious symptoms. The relevant microscopic characteristics (concentration of phytoplasma) of different grades were pointed out respectively. In addition, the results that a great amount of phytoplasma existing in branches during whole winter season and seed containing phytoplasma did not support the traditional belief that phytoplasma could not be transferred by seed and concentrated in root during winter.

**1340-1440**

**S12-P-60**

**VIRUS INFECTED TOLERANT PAPAYA MAINTAINING PN CAPACITY AS GOOD AS THE HEALTHY CONTROL**

Loong-sheng Chang\*, Tzong-Shyan Lin, Ren-Hoang Wang

Dept. of Horticulture, National Taiwan Univ., No. 1, Sect. 4th, Roosevelt Rd., Taipei, Taiwan

Papaya ringspot virus (PRV-P) is a limiting factor of papaya industry worldwide. Field tolerant papaya is needed to control the disease. Effects of the virus on photosynthetic rate (Pn) of papaya leaves were used to characterize the susceptibility of the papaya populations in the study. The photosynthetic parameters of tolerant hybrid 'Tainung No. 5', and a susceptible 'Tainung No. 2' were used to estimate the capacity of endurance the virus. The Pn of virus infected 'Tainung No. 2' was 38% less than the control, but there was not significant difference of Pn of the infected tolerant hybrid 'AE' compared to that of the healthy control. The variable fluorescence (Fv) was dramatically decreased on susceptible papayas 14 weeks after inoculation, photoinhibition was further occurred. However, the ratio of variable to maximum fluorescence was not changed of the infected tolerant hybrid 'AE' to the control check. The virus significantly reduced leaf area among papaya populations; however, the leaf duration period, chlorophyll meter reading (CMR) and leaf number of the hybrid 'AE' remained as the control. The virus limited radiation absorption and utilization of the susceptible papaya, but the tolerant one was able to counteract the viral effects. Breeding for field tolerance of papaya ringspot is possible.

**1340-1440**

**S12-P-61**

**INHERITANCE OF APPLE SCAB RESISTANCE FROM POLYGENIC SOURCES IN THE GREENHOUSE AND FIELD**

H.A. Quamme, C.R. Hampson\*, J.W. Hall, P.L. Sholberg, K.E. Bedford, P. Randall  
Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, BC, Canada, V0H 1Z0

The resistance of fifteen apple (*Malus x domestica* Borkh.) progenies (three females mated with five males) to apple scab (*Venturia inaequalis*) was determined by inoculation in the greenhouse and natural infection in the field. Five of the parents were reported to carry polygenic resistance ('Antonovka Monasir', 'Discovery', 'Akane', 'Rosu de Cluj', and 'Spartan') and two were susceptible to scab ('Royal Gala' and 'Summerred'). The field test was conducted at a site with heavy scab pressure in the Fraser Valley of British Columbia (Agassiz). Estimates of general and specific combining ability (GCA and SCA) of categorical data were provided by Chi-square analysis using the SAS procedure CATMOD. GCA was low and SCA absent in the greenhouse, but GCA was high and SCA present in the field. Chi-square analyses indicated that the greenhouse scab resistance scores were related to the field scores in only three of the progeny. After three years in the field, only 'Antonovka Monasir' and 'Discovery' positively contributed to the inheritance of complete resistance. In the third year, the resistance of five 'Antonovka Monasir' progenies segregated in a way consistent with control by a single dominant gene. The resistance (% leaves with sporulating lesions) of infected offspring of 'Antonovka Monasir' or 'Discovery' was also greater than those of other parents, indicating the possible presence of minor resistance genes.

**1340-1440**

**S12-P-62**

**LOW SUSCEPTIBILITY TO MILDEW IN APPLE PROGENIES OF THE SCAB-RESISTANT CLONE U 211 AND MILDEW SUSCEPTIBLE CULTIVARS**

Emilian Pitera\*

Dept. of Pomology and Basic Na, Warsaw Agricultural Univ., Nowoursynowska 166, Warszawa, Poland, 02-787

Progenies of scab resistant clone U211 (Primula open-pollinated, selected at Dept. of Pomology Warsaw Agricultural Univ.), cultivars with different degrees of mildew susceptibility and others progenies were evaluated for natural mildew (*Podosphaera leucotricha*) for up to 6 years in the field. Mildew infection of seedlings in the field greatly varied with weather conditions. Clone U 211 progenitor transmitted low level of susceptibility to mildew in a considerably higher proportion comparing to the cultivars. In progenies obtained from the crosses of susceptible cultivars such as 'Jonared', 'Blackjon', 'Idared' and 'Granny Smith' with clone U 211, the percentage of non infected and tolerant seedlings ranged from 38% to 67%. In two other hybrid families (without clone U 211 as a progenitor), the percentage of non infected and tolerant seedlings was 7% and 15%. Screening for mildew incidence during the second year in the nursery was not always effective; under Polish climate conditions further screening should be continued in successive years. These studies have confirmed our earlier observations that scab resistant clone U 211, is a good source for breeding scab resistant apple cultivars combined with the tolerance to mildew, particularly when crossed with cultivars sensitive to mildew. Clone U 211 should be also useful for an increased durability of resistance to mildew when crossed with different sources of resistance.

**1340-1440**

**S12-P-63**

**EFFICIENT MULTI-LOCATION TESTING OF SCAB RESISTANT CULTIVARS FOR ORGANIC APPLE PRODUCTION IN SWITZERLAND**

Franco-Peter Weibel\*, Andi Schmid, Andreas Haeseli

Research Institute of, Organic Agriculture (FiBL), Ackerstrasse, Frick, AG, Switzerland, CH-5070

Since 1994 supermarket retailers of Switzerland began selling organic apples. To fulfill this sudden additional demand a sharp increase in organic apple production was necessary: An almost 5-fold increase was achieved mainly by the conversion of conventional fruit farms to organic production. Consequently the major part of the Swiss organic apple production consists of scab (*Venturia inaequalis*) sensitive varieties such as 'Golden Delicious', 'Maigold', and 'Jonagold'. With these varieties scab control with biological products such as copper, clay powder and sulphur is very demanding and, depending on weather conditions, of questionable efficiency, economy but also ecology. For this reason organic fruit growers prefer to use scab resistant varieties. However the 'old' scab resistant cultivars such as 'Florina', 'Prima' etc. do not reach the demands of agronomic and sensorial performance, and from the numerous recent selections no data exist on their suitability for—especially organic—production. To achieve the necessary knowledge as rapidly and as farmer-applicable as possible we conducted, since 1994, a cultivar testing method combining precision trials and on-farm trials. In the precision trials we test interesting looking selections/cultivars (56) with and without blossom thinning and with/without aphicides (fruit thinning and powdery apple aphid (*Dysaphis plantaginea*) are key problems). The trees are distributed completely randomised in 3 blocks (n = 6). The most promising cultivars (16) out of the precision trials are distributed on up to 11 commercial organic farms in all important growing regions of Switzerland. The design of this «Ring Trial» is that each cultivar is planted on two blocks per orchard (n = 12 to 20), allowing proper statistics. Management consists of good farm practice with instructions from us on pruning, training, and fruit thinning. The paper reports the concrete results and a critical but mainly positive reflection on methodology.

**1340-1440**

**S12-P-64**

**INFLUENCE OF CLIMATIC CONDITIONS ON YIELDS AND FRUIT PERFORMANCE OF NEW APPLE CULTIVARS FROM THE CZECH REPUBLIC**

J. Blazek\*, I. Hlusickova

Research and Breeding Institute of, Pomology, Holovousy 1, Horice, O. Jicin, Czech Republic, 508 01

Yields, fruit size and some other fruit characteristics of apple trees on M 9 rootstock were monitored in 35 orchards located in different climatic conditions of the Czech Republic between 1996-2000. Altogether 31 cultivars, mostly

newly bred in the country and some standard ones, were ranged according to their average yield per tree, specific productivity (based on a unit of canopy volume), and mean fruit weight in three groups of orchards with different climatic conditions. These three groups were based on average annual mean temperature like: cold (below 7.5 °C), medium (7.5–9 °C) and warm (above 9 °C), which roughly corresponded to decreasing altitude: over 400 m, 200–400 m, and less than 200 m above sea level respectively. Different climatic conditions in the case of some cultivars (i.e. 'Resista', 'Topaz', 'Zuzana') also influenced an extent of over colour, an amount of russeting and incidence of some physiological disorders. The most productive cultivar that also gave the highest average yield per tree was 'Produkta'. However in the cold climatic conditions the best cropper was 'Jonalord'. 'Rajka', 'Selenia' and 'Otava' were also generally very productive. On the contrary the lowest yields were observed in case of 'Rubin', 'Bohemia', 'Rubinola' and 'Julia'. 'Angold', 'Rubin', 'Bohemia', 'Melrose', 'Jonalord', 'Zuzana' and 'Vanda' belonged among cultivars with very big or big fruits. Above-average size of fruits was further typical for 'Jarka', 'Gloster', 'Delor', 'Goldstar', 'Glockenapfel' and 'Produkta'. On the other hand round 'Julia' and 'Karmina' had on the average the smallest fruits. Beside them small fruits sometimes appeared also in 'Otava', 'Florina', 'Resista' and 'Elstar'. In the case of these cultivars the variability of fruit size was greatest, being dependent on climatic conditions and on general level of orchard management in particular farms.

**1340–1440**

**S12–P–65**

**THE ADAPTATION OF SOME APRICOT VARIETIES FROM NORTH AMERICA IN THE SOUTH-EAST PART OF ROMANIA**

Elena Topor\*

Fruit Research Station Constanta, Pepinierei 1, 8763 Valu lui Traian, Romania, 8700

In the south-east part of Romania, there is a rich germplasm "in situ" for apricot including 152 cultivars from north America. All these cultivars have been studied in regards to growth, vigor, fruit production and quality, and disease. In the south-east part of Romania the yearly precipitation's quality is reduced, in average 400 mm, sometimes even smaller under 300 mm. Very reduced quantities fall during the activity period of vegetation (April–September), among 200–250 mm. Thus the humidity deficit must be completed through irrigations. The mean yearly temperature is 10,7 °C, the absolute minima not decreasing under –20 °C, during the winter especially spring periods, great variations of temperature are registering. American cultivars have some very good traits including resistance to *Monilinia laxa* and *M. fructigena*; precocity of bearing; and high productive potential. However, poor characters include very early blooming, 7–10 days before European cultivars, and self-sterility.

**1340–1440**

**S12–P–66**

**VARIABILITY OF SOME AGRONOMIC TRAITS WITHIN GERmplasm OF CORNUS MAS L.**

Paulina Mladin\*, Gh. Mladin, Evelina Rudi, Camelia Mutafa

Fruit Research Institute, Pitesti-Maracineni, Pitesti, Arges, Romania, 300

Fruit Research Institute, 0300 Pitesti, Romania

The cornell tree, (*Cornus mas*) is a potential new crop based on the wide range of fruits and wood utilization and ornamental use. In the last twenty years studies in the wild populations of *C. mas* L. were carried out in various areas of Romania in order to identify and select the most valuable biotypes to be grown. Over 220 biotypes were evaluated, mainly for fruits, of which 64 were then propagated by grafting and planted in an experimental plot (3 plants per selection). There is an uneven development of fruit yield and canopy development in the first 7 years of fruiting. Average fruit yield per tree varied from 0.150kg/tree (1st cropping year) to 3.2 kg (8th years) and the highest yield was 2.5–4.5 kg per tree. The mean fruit weight varied from 1.10 g to 3.9 g; most below 2.0 g (only 14% biotypes had very large fruit). Fruit shape (l/d) index was between 0.85–1.92. There was wide variability in fruit characters: 22.3 to 167.8 mg% vitamin C, 10.2–24.9% dry weight; 5.0–13.76 g% sugars; 1.10–3.91 g% acidity; 0.395–1.800 g% pectines; 0.196–1.091 g% tannins; 0.22–0.78 g% row proteins; 0.53–1.15 g% minerals, of which 259–589 mg% K, 30–99 mg% Ca, 8–14 mg% Mg; 0.23–1.07 mg% Fe.

**1340–1440**

**S12–P–67**

**STUDY ON POLLINATION AND COMPATIBILITY AND DETERMINATION OF BEST POLLINIZER FOR IRANIAN AND FOREIGN CULTIVARS OF OLIVE (OLEA–EUROPEAL)**

M.R. Naini\*<sup>1</sup>, H. Sadeghi<sup>3</sup>, A. Boland Nazar<sup>3</sup>

<sup>1</sup>Soil and Water Research Division of Qom, Iran; <sup>2</sup>Department of Horticulture, Faculty of Agriculture, Mazandaran Univ., Sari, Iran; <sup>3</sup>Manager of Fadak Research Orchard, Iran

Research at the Fadak research orchard, Qom, during 1999–2000 was carried out to determine the best pollination treatments for seven cultivars of olive ('Zard', 'Shengeh', 'Roughani', 'Manzanilla', 'Kroneiki', 'Conservolea', and 'Mission'). The treatments were open and self-pollinations, and crosses with 'Mari' and 'Beldy' as pollinizers. Flowering branches of each variety were bagged at the white bud stage. The experimental design was a randomized complete block design with 6 replications. Bloom sequence, compatibility, and final fruit set were determined. Statistical analysis showed that there were significant differences among pollination treatments. The best pollination treatments for olives were 'Beldy' open-pollination and 'Mari'. The highest rate of pollination was observed in 'Kroneiki' and the lowest with 'Roughani'.

**1340–1440**

**S12–P–68**

**INHERITANCE OF CHILLING REQUIREMENT IN APRICOT VEGETATIVE BUDS**

R. Tzonev\*, A. Erez

Institute of Horticulture, The Volcani Center, ARO, Bet-Dagan, Israel, 50250

The aim of this work was to study the pattern of vegetative bud dormancy in hybrid populations of apricot and to evaluate the inheritance of chilling requirement. Vegetative bud breaking (BB) was estimated by evaluating 3 parameters (the level, the pattern and the timing of BB) on each of 1529 hybrids obtained from 44 cross-combinations or open pollination. The study was done in Israel, in a region with mild climate, under natural conditions after two consecutive unusual warm winters. A most striking result was the extremely high level of vegetative bud break in progenies of all cultivars and selections including ones with high chilling requirements. On the other hand, a non-uniform vegetative development and a late bud break were characteristics found in crosses with high chill parents. From the data obtained we concluded that the chilling requirement in apricot generative buds is controlled by at least two genes. One gene (or group of genes) controls qualitatively the level of bud break, and the other gene (or group of genes) is responsible for the vigour of subsequent bud growth. The inheritance pattern of the first gene seems to be low chilling dominant while the second exhibits a non-dominant intermediate response between the parents.

**1340–1440**

**S12–P–69**

**DEVELOPING LOW CHILL, HIGH QUALITY PLUMS IN SUBTROPICAL TAIWAN**

Ien-chie Wen\*

189 Cheng-cheng Rd. Wufeng, Taicheng, Taiwan R.O.C., Taicheng, Taiwan, R.O.C., 413

Taiwan is situated on the western coast of the Pacific Ocean, traversed by the tropic of cancer and has a tropical and subtropical climate with a warm winter—the limiting factor for producing high quality deciduous fruits. The planted area of plums in Taiwan were 9150 and 4733 ha. in 1990 and 1999 respectively. Shorting of good low chill cultivars that could grow in lowland area is the reason of decreasing in planted area. About 35 ha. of the high quality plums cultivars are planted in limited mountain areas more than 1500 m above sea level. But growing deciduous fruit in high elevations led to water erosion of soil in the higher slopes and had not encouraged by Taiwan government since 1980. The breeding objective was to develop cultivars with high fruit quality and low chilling requirement. 24 native low chill plum cultivars that collecting form all over the Taiwan island and 10 low chill plum cultivars which introducing from Univ. of Florida were evaluated the tree and fruit characteristics in Rona repository. Three sweet skin cultivars were selected as par-

ents in breeding program. One selection with good quality and low chill requirement were selected from the progenies of 'Hwa ro' x 'Sungold' for advanced testing.

**1340-1440**

**S12-P-70**

**EARLY SPLITTING IN IRANIAN PISTACHIO CULTIVARS**

A. Tajabadipour\*, B. Panahi

Dept. of Breeding, Iranian Pistachio Research Institute, P.O. Box 77175-435, Rafsanjan, Iran

During 1998 and 1999, 10 fruit clusters from each of 48 pistachio cultivars were randomly selected before harvesting and number of early split fruits, fruits with irregular-cracked or intact hull were determined. 'Ghazvini-motevasetras', 'Ebrahimi', 'Sabz-pestehnooghi', 'Ghazvini-dirras', 'Italiaii-dirras', 'Fandoghi-riz', and 'Badami-zarand' had no early split pistachio fruits. Early splitting in major Iranian pistachio commercial cultivars was less than 5% (1.06% 'Owhadi', 1.36% 'Kaleghouchi', 2.48% 'Ahmad Aghai', and 4.25% 'Akbari'). The greatest early split percentage was observed for 'Javad-aghahi' and 'Lahijani' (about 20%), and 95% of the cultivars had less than 10% early splitting. 'Seifaddini', 'Loksirizi', 'Khanjari-damghan', 'Italiaii-dirras', 'Badami-nishkalaghi' and 'Sabz-pestehnooghi' had the minimum irregular-cracked-hull pistachios (less than 4%). The highest irregular-cracked-hull pistachios were observed in 'Fandoghi-zoodras', 'Behesht-abadi', and 'Amiri' (about 50%).

**1340-1440**

**S12-P-71**

**SF-RNASE AND ITS RELATION TO SELF-COMPATIBILITY IN JAPANESE APRICOT**

Ryutaro Tao\*, Azusa Namba, Tsuyoshi Habu, Hisayo Yamane, Akira Sugiura  
Laboratory of Pomology, Graduate School of Agriculture, Kyoto Univ., Kyoto, Kyoto Prefecture, Japan, 606-8502

Self-compatible cultivars of Japanese apricot (*Prunus mume* Shieb. et Zucc.) have a common S-RNase (Sf-RNase) gene that can be used as a molecular marker for self-compatibility. In this study, inheritance of the Sf-RNase gene and self-compatibility was investigated using the progenies from controlled crosses. In all the crosses examined, the Sf-RNase gene was inherited to the progenies as one of the pistil S-alleles in a non-functional S-haplotype. In addition to the inheritance study, we characterized Sf-RNase by comparing S-RNases of self-compatible 'Kensak' (SfSf) and self-incompatible 'Nanko' (S1S7). cDNA libraries from the styles with stigmas of these two cultivars were constructed and cDNAs encoding Sf-, S1-, and S7-RNases were cloned. Deduced amino acid sequences from these cDNAs all contained two active domains of the T2/S type RNase family and five conserved regions of the rosaceous S-RNase. RNA blot analysis showed that the Sf-, S1-, and S7-RNase genes were transcribed in the pistil but not in the leaf as with other S-RNase genes of *Prunus*. Furthermore, 2D-PAGE analysis revealed that Sf-RNase had Mr, pI, and immunological characteristics similar to other S-RNase. These results could indicate that the pollen-S gene supposed to be tightly linked to the Sf-RNase gene may be responsible for the self-compatibility observed in the Sf-haplotype.

**1340-1440**

**S12-P-72**

**GALA APPLE TRANSFORMED FOR SCAB (*VENTURIA INAEQUALIS*) RESISTANCE WITH CLONED VF GENE REGION CONSTRUCT**

Silviero Sansavini\*, M. Barbieri, E. Belfanti, S. Tartarini, B. Vinatzer

Dipartimento di Colture Arboree Univ. of Bologna via Filippo Re 6 Bologna 40126 Italy

Scab is the most serious disease of apple in many districts throughout the world and can require more than 15-20 treatments per year. The monogenic resistance conferred by the Vf gene against *Venturia inaequalis* has been employed in traditional breeding programs for over fifty years. Despite the many cultivars that have been released from these efforts, the problem has not yet been resolved because the resulting fruit quality is less than satisfactory and because this kind of vertical resistance has been overcome by *V. inaequalis* races 6 and 7 in several European countries. Eight years ago, Bologna's DCA and Zurich's ETH undertook the cloning of the Vf gene starting from a saturated

map; the markers AL07 SCAR and M18 CAPS proved to be closely linked to the Vf gene. The BAC library derived from cv. Florina extended more than five times the size of the apple haploid genome itself. Chromosome walking was then used to screen this library with Vf markers and yielded a contig of the Vf locus of 550 kb. Recombinant analysis of the seedling population enabled the restriction of the contig to 350 kb made up of 5 BAC clones, including the Vf region. The next step was the construction of a cDNA library from Florina leaves elicited with *V. inaequalis conidia*; this library's subsequent screening yielded more than one hundred hybridizing cDNAs. A cluster of receptor-like genes homologous to Cf *Cladosporium fulvum* resistance gene family of tomato was identified, sequenced and isolated from the Vf region. A plasmid construct of the HcrVf2 sequence (about 2,000 base pairs), selected among several of the same cluster, was introgressed mediated by *Agrobacterium tumefaciens* into Gala leaf explants using the binary vector pCambia2301 (containing two nptII genes and a GUS reporter gene with its promoter CaMV 35s). PCR assays on about 50 regenerated plantlets after 15 months on selection medium showed that almost 90% had HcrVf2 and the control genes. The acquired resistance was corroborated by repeated in vitro infection with *V. inaequalis*.

**1440-1500**

**S12-0-73**

**CURRENT SITUATION AND PROSPECTS IN BREEDING FOR TROPICAL AND SUBTROPICAL FRUITS**

J. Ganry<sup>1</sup>, P. Ollitrault<sup>1</sup>, F. Bakry<sup>1</sup>, J.P. Horry<sup>2</sup>

<sup>1</sup>CIRAD-FLHOR : TA 50/PS4, Bd de la Lironde, 34398 Montpellier Cedex 5 (France); <sup>2</sup>CIRAD-FLHOR : B.P. 153, 97202 Fort-de-France, Martinique

This review of research undertaken on the most important tropical and subtropical fruit species includes current research objectives, breeding methods, leading research groups, and main achievements for banana, citrus, pineapple, mango, and papaya. Important progress has been made during the last decade on banana and citrus, combining studies on genetic diversity as well as conventional breeding and research on genetics and biotechnology, including genomics. For banana, genetic resources management and improvement are strongly supported internationally by INIBAP (International Network for the improvement of Banana and Plantain). Pineapple receives less international effort, but has a special focus on genetic resources management and conventional breeding. Mango and papaya breeding is undertaken by a few countries around the world with mostly a conventional breeding approaches, but some noticeable progress in biotechnology including virus resistance for papaya. A common challenge for these species is dealing with resistance to pests and diseases which have a strong impact in tropical and subtropical conditions. Increasing attention is being paid to improving quality in order to meet marketing objectives and consumer expectations. Efforts are being made to improve genetic diversity utilization, as this is crucial for enriching the pool of parental material for generating new fruit types with improved taste and nutritional value. Finally, an attempt is made to predict some trends for the future in terms of economic and social demand, scientific aspects, and international cooperation.

**1500-1520**

**S12-0-74**

**TREE SIZE AND ARCHITECTURE**

C. Fideghelli\*

Istituto Sperimentale per la Frutticoltura, Via di Fioranello 52, 00134 Rome, Italy

Fruit tree size control and tree architecture to improve the efficiency of the hand labor has been achieved for centuries through pruning, whose highest sophisticated expression was reached in the 18th century by La Quintinie, gardener Louis XIV of France. During that time many tree training systems were developed (palmette, horizontal and vertical cordon, fan), mainly for ornamental purposes. Due to the high efficiency and increased fruit quality of these training systems, some were introduced into the commercial fruit industry. Palmette, with all its variations, is probably the most important application of the historical tree training systems singled out by the royal orchardists in commercial orchards, followed by cordons. These have been adapted to controlling tree size and shape. Based on the fundamental studies of Hatton at East Malling (UK) between 1920 and 1938 the tree size control was obtained through the adoption of dwarfing rootstocks in combination with training system and prun-

ing technique. Attention to the genetic control of the tree size of scion cultures and architectures began in the 1970s. Numerous studies showed great variability of these traits in different fruit species. During the last decades, genetic control of tree size and innovative tree architectures have been important objectives of several breeding programs around the world with substantial breeding activity. Three main genetic traits for tree size are dwarf, semi dwarf, and compact. Non-conventional tree architectures includes columnar and weeping habits.

**1520–1540**

**S12–0–75**

### **BREEDING FOR FRUIT QUALITY**

Ann Callahan\*

USDA-ARS, Appalachian Fruit Research Station, Kearneysville, WV 25430 USA

Fruit breeding programs have many different goals, including disease resistance, cold tolerance, tree size, precocity and productivity. They all have in common the need to develop high quality fruit. Programs either insure that acceptable fruit quality is attained or they work to enhance the existing acceptable fruit quality. Fruits come in a wide spectrum of size, flavor, color, firmness, and texture. Quality is defined differently for each fruit species and consists of many attributes. For some species, high quality flesh texture is crisp while in others it is soft and melting. Some fruit require a balance of acidity and sweetness while quality in others is simply defined by the degree of sweetness. A survey of fruit quality traits across a variety of fruit species that are currently being improved will be presented with a concentration on texture, aroma/taste and volatiles and sugar/acid ratio. Commonalities and differences will be discussed in terms of improvement objectives for the various species. Data on the physiological and genetic basis for fruit quality traits will be presented.

**1540–1600**

**S12–0–76**

### **INCOMPATIBILITY IN TREE FRUIT CROPS AND NUTS**

Paul A. Wiersma\*

Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, British Columbia, Canada V0H 1Z0

Self- and cross-incompatibility are important breeding concerns in many of our fruit and nut cultivars, where fruit set and nut filling require efficient and predictable fertilization. The past decade has seen a rapid increase in our understanding of the molecular basis of incompatibility. Gametophytic self-incompatibility is one of the best understood and very widely distributed systems. Based on the understanding of this system (largely from model systems) identification and breeding for incompatibility traits have rapidly progressed in important cultivars, particularly in the *Rosaceae* (e.g. pome and stone fruits). Recent results from the Brassicaceae provide the same type of molecular understanding for sporophytic self-incompatibility and can hopefully be applied in the near future. New methodologies will be discussed which can now add to traditional breeding methods in first analyzing and then helping to select for desired incompatibility traits. Types of desired traits, which will be addressed this millennium, include self-fertility, sterility, increased fruit-set, dioecious plants (kiwi, pistachio), timing of flowers (reduced dichogamy in walnut, cherimoya).

**1600–1620**

**S12–0–77**

### **S-ALLELE GENOTYPE OF APPLE CULTIVARS AND SELECTIONS**

Shogo Matsumoto\*<sup>1</sup>, Kentaro Kitahara<sup>2</sup>, Hiromitsu Komatsu<sup>3</sup>, Hirokazu Fukui<sup>4</sup>, Junichi Soejima<sup>5</sup>

<sup>1</sup>Dept. of Biology, Faculty of Education, Gifu Univ., Gifu 501-1193, Japan; <sup>2</sup>The United Graduate School of Agricultural Science, Gifu Univ., Gifu 501-1193, Japan; <sup>3</sup>Nagano Fruit Tree Experiment Station, Nagano 382-0072, Japan; <sup>4</sup>Laboratory of Horticulture, Faculty of Agriculture, Gifu Univ., Gifu 501-1193, Japan; <sup>5</sup>Apple Research Center, National Institute of Fruit Tree Science, Morioka 020-0123, Japan

Apple (*Malus x domestica* Borkh.) exhibits gametophytic self-incompatibility, controlled by a single multiallelic locus, the S-locus. In this type of self-incompatibility, pollen tube growth is arrested in the style when the pollen

shares the same S-allele with the pistil. The S-alleles in the pistil encode ribonucleases, called S-RNases. Within the 27 apple S-alleles reported, 13 S-RNases from S1- to S5-, S7-, S9-, S10-, S20-, S24-, S25- to S27-allele have been cloned and sequenced. In Japan, Sa- to Si- and Sz-alleles were temporary used for S-alleles designation, and except Se-allele, all alleles were corresponded to one of the 13 S-alleles based on the S-RNase sequence comparison. Since the 13 S-alleles and the Se-allele possess their own S-RNases sequence, each S-allele-specific PCR-RFLP method has been developed based on the sequences. Using the method, we investigated the S-genotypes of more than 100 apple cultivars and selections.

**1620–1640**

**S12–0–78**

### **IDENTIFICATION OF SELF-INCOMPATIBILITY ALLELES IN ALMOND AND RELATED PRUNUS SPECIES USING PCR**

Pedro Martinez-Gomez\*<sup>1</sup>, Merce Lopez<sup>2</sup>, Jose Manuel Alonso<sup>3</sup>, Encarnacion Ortega<sup>1</sup>, Thomas M. Gradziel<sup>4</sup>

<sup>1</sup>Dep. de Mejora y Patologia Vegetal, CEBAS-CSIC, Murcia, Spain; <sup>2</sup>Dep. d'Arboricultura Mediterranea, IRTA, Reus, Spain; <sup>3</sup>Unidad de Fruticultura, SIA, Zaragoza, Spain; <sup>4</sup>Dept. of Pomology, Univ. of California, Davis, USA

In almond flowers, self-incompatibility is of the gametophytic type and acts to prevent self-fertilization. This trait is controlled by a single locus with multiple codominant alleles and is expressed as S-RNases within the styles. These glycoproteins are responsible of the inactivation of pollen tube growth. Self-incompatibility alleles (S-alleles) can be identified through controlled crosses with a series of known S-genotypes. Molecular methods have recently been developed allowing stilar S-RNases electrophoresis and S-allele specific amplification using PCR. In this study, the identification of S-genotypes for almond cultivars and related Prunus species was achieved using the specific PCR primers AS111 and AmyC5R (Tamura et al., 2000, Theor Appl Genet 101: 344-349). Plant material analyzed included 40 almond cultivars and selections from different geographical origins and 16 Prunus species. Results showed the identification of 8 unique S-alleles in almond and 6 in related Prunus species. Findings also allow the clarification of genetic relationships among almond and related Prunus species. The nucleotide sequence of these genomic amplified fragments appears to be highly conserved in almond and its close relatives. The applications of these PCR markers in almond breeding for self-compatibility are discussed.

**1640–1700**

**S12–0–79**

### **APPLE SELF-INCOMPATIBILITY GENOTYPES: AN OVERVIEW**

Wim Broothaerts\*<sup>1</sup>, Ilse Van Nerum<sup>2</sup>, Radovan Boscovic<sup>3</sup>, Ken Tobutt<sup>3</sup>

<sup>1</sup>Better3Fruit N.V. Willem de Croylaan 42, B-3001 Leuven, Belgium; <sup>2</sup>Fruittelcentrum K.U.Leuven, Willem de Croylaan 42, B-3001 Leuven, Belgium; <sup>3</sup>Horticulture Research International, Plant Breeding and Biotechnology Dept., East Malling, West Malling, Kent ME19 6BJ, United Kingdom

Apple (*Malus x domestica* Borkh.) flowers express an effective self-incompatibility system that reduces self-fertilization by arresting the growth of self-pollen tubes inside the pistil. Many alleles of the S-gene controlling the female "receptivity" to self-pollen have been identified in previous years through either protein separation techniques (IEF, NEPHGE, 2D-PAGE) or DNA-based methods (including cDNA cloning and sequencing). Some of the proposed 'new' S-alleles have been shown to be identical to already known alleles on the basis of further investigation and can be retired. Confusion is also created by the two different labeling codes used for S-alleles, based on either numbers (S1, S2, etc.) or letters (Sa, Sb, etc.). Moreover, data on cross-incompatibility between varieties, tested by pollination studies, do not always reflect the true genetic incompatibility mechanism. Here we propose to use the S-genotype assignment originally introduced by Kobel and coworkers (1939) consistently and number new alleles from there on. We have assayed the S-alleles of a large number of apple varieties by analysis of SCARs (Sequence Characterized Amplified Regions) for each individual S-allele and by S-RNase staining following style protein separation. An extensive table will be presented of apple incompatibility genotypes of current and old apple varieties. Calculation of allele frequencies reveals that a few S-alleles, particularly S3, are predominant in the apple gene pool.



## Friday · August 16

0800-0900

S12-P-80

**FIRE BLIGHT RESISTANCE OF NEW PEAR ROOTSTOCK CLONES**

Richard L. Bell\*

U.S. Dept. of Agriculture, Agricultural Research Service, 45 Wiltshire Road, Kearneysville, WV, USA, 25430-9425

New pear rootstocks have been developed by programs in North America and Europe as replacements for pear seedlings and quince (*Cydonia oblonga* L.). Resistance to fire blight (*Erwinia amylovora* [Burr.] Winsl. et al.) is an important requirement for any pear rootstock. Liners of eight pear (*Pyrus communis* L.) rootstock clones were inoculated with the pathogen by cutting the unexpanded leaves, plus the top two expanding leaves, on the leader shoot of each replicate plant with scissors which had been dipped in a suspension of inoculum. The inoculum consisted of a mixture of two isolates (Ea273 and AFRS 554), each at a concentration of approximately  $2 \times 10^8$  cfu ml<sup>-1</sup>. Length of infection was recorded one, two, four, and six weeks after inoculation, at which time lesion development had reached a maximum. Length of infection was divided by the total current season shoot length to compute proportional lesion length used as an index of resistance/susceptibility. 'Winter Nelis' seedlings were used as the susceptible control. Clones were significantly different in total shoot length, and in total lesion length, and proportional lesion length on all dates. 'Old Home' x 'Farmingdale' ('OHxF') 40 was the most vigorous, with a mean shoot length of 80cm, while 708-36 was the least vigorous, with a mean shoot length of 25 cm. 'OHxF 87' had the smallest proportional lesion length (0.23), followed by 'OHxF 97', 'OHxF 40', 708-2, 708-12, and 'Winter Nelis' seedling, 'Fox 11', and 708-36.

0800-0900

S12-P-81

**PERFORMANCE OF SOUR CHERRY CULTIVARS AND ROOTSTOCK COMBINATIONS**

Milica Fotiric\*, M. Milutinovic, D. Nikolic, Vera Rakonjac

Dept. of Fruit Science and Vit, Faculty of Agriculture, Nemanjina 8, Zemun, Yugoslavia, 11080

Four sour cherry cultivars ('Meteor', 'Rexelle', 'Heimanns Konservenweichsel' and 'Kelleris 14') on rootstocks ('Colt', 'Mazzard', seedling of mahaleb cherry and 'Mazzard' with 'Oblacinska' sour cherry as an interstem) were characterized. 'Meteor' and 'Rexelle' had the largest fruit size on 'Mazzard' rootstock, while 'Heimanns Konservenweichsel' and 'Kelleris 14' had the lowest size on seedling of mahaleb cherry. 'Mazzard' influenced large fruit weight in all cultivars. Stone weight in 'Meteor', 'Rexelle' and 'Heimanns Konservenweichsel' was the highest on 'Mazzard', but stone weight in 'Kelleris 14' was the highest on 'Mazzard' with 'Oblacinska' sour cherry as interstem. Variability of all investigated properties was significantly influenced by cultivar, rootstock, and interaction.

0800-0900

S12-P-82

**BIOAGRONOMIC CHARACTERISTICS OF 'SUNCREST' PEACH GRAFTED ON NINE ROOTSTOCKS IN THE TUSCANY COASTAL AREA OF ITALY**

Filiberto Loreti\*, Rossano Massai, Carlo Fei

Dipartimento di Coltivazione e, Difesa delle Specie Legnose, Via del Borghetto, 80, Pisa, PI, Italy, IT-56124

Evaluation of nine peach rootstocks (Rubira, P.S.A5, P.S.A6, Ishtara-Ferciana, Julior-Ferdor, Jaspri-Fereley, Citation-Zaipime, Barrier 1 e GF 677), grafted with 'Suncrest', has been carried out in Tuscany coastal area, inside the targeted project "National list of recommended rootstocks and fruit varieties", sub-project "Rootstocks", in order to assess the bioagronomic characteristics of the rootstocks introduced on the Italian nursery market. The orchard was planted in 1995, with 15 trees per each rootstock, at the distance of 5 x 5 m on a silty-clay loam and trained to open vase. This report highlights

the main results obtained after 7 years of growth (4 years of production). Data on vegetative and productive activity and on fruit quality are reported. GF 677 and Barrier 1 rootstocks appeared to be very vigorous and productive, with positive effect on mean fruit weight. The last clone constantly delays (5-7 days) bud burst, bloom, harvest and leaf fall time. Peach seedling rootstocks Rubira, P.S.A5 and P.S.A6 performed quite well in that soil but they showed vigour, yield and fruit quality lower than that of trees grafted on peach x almond hybrids. Diffuse symptoms of graft incompatibility with 'Suncrest' have been observed on the two plum rootstocks Citation and Jaspri, while the other two, Julior and Ishtara, performed quite well as regard yield per tree and fruit size. Julior and Jaspri showed an important sucker ability on almost 50% of trees observed. Peach seedlings and Ishtara appeared to be very interesting for high density plantings because their vigor that allows an increase planting density up to 30%.

0800-0900

S12-P-83

**DETERMINATION OF SUITABLE ROOTSTOCK FOR TURKISH PISTACHIO CULTIVARS UNDER ARID CONDITIONS**

Halit Seyfettin Atli\*, Selim Arpaci

Pistachio Research Institute, Gaziantep, TURKEY, Gaziantep, Gaziantep, TURKEY, 27060

This study was carried out to determine of suitable rootstock and pistachio cultivar combination for arid conditions between 1998-2001 years in Gaziantep in Turkey on 25 years old trees. Five pistachio cultivars ('Siirt', 'Ohadi', 'Uzun', 'Halebi' and 'Kirmizi') were budded on three Pistacia species (*Pistacia atlantica* Desf., *Pistacia khinjuk* Stocks and *Pistacia vera* L.). These rootstocks and cultivars combinations have been used as material. Yield, fruit number per 100 g, splitting rate, kernel rate and trunk diameter have been determined. 'Siirt' budded on *P. khinjuk* was the best combination for arid conditions.

0800-0900

S12-P-84

**PISTACHIO ROOTSTOCKS INFLUENCE SCION GROWTH AND ION RELATIOS UNDER SALINITY AND BORON STRESS**L. Ferguson\*<sup>1</sup>, J.A. Poss<sup>2</sup>, S.R. Grattan<sup>3</sup>, C.M. Grieve<sup>2</sup>, C. Wilson<sup>2</sup>

<sup>1</sup>Univ. of California, Kearney Agr. Center, Parlier, CA, USA; <sup>2</sup>USDA-ARS George E. Brown, Jr. Salinity Lab., Riverside, CA, USA; <sup>3</sup>Univ. of California, Dept. of Land, Air, and Water resources, Davis, CA, USA

The performance of pistachio trees (*Pistacia vera*, cv. 'Kerman') on three rootstocks (*P. atlantica*, *P. integerrima* and UCB-1, a *P. atlantica* x *P. integerrima* hybrid) was evaluated with two-year-old trees grown in sand-tank lysimeters under combined sulfate-chloride salinity and boron stress for six months. Four salinity treatments were imposed by dS/m each containing 10 mg-L<sup>-1</sup> boron (B). 'Kerman' growth response was evaluated based on increase on total leaf area, increase in trunk diameter and total above-ground biomass production. All growth parameters decreased as salinity increased, but were not significant until ECiw exceeded 12dS/m. However, growth of 'Kerman' on *P. atlantica* and UCB-1 was considerably better than on *P. integerrima* at 16 dS/m. The onset and severity of foliar injury differed among scions and treatments and was attributed primarily to B toxicity rather than the effects of salinity. Concentrations of B in injured leaf tissue ranged from 1000 to 250 mg·kg<sup>-1</sup>. Leaf injury decreased with increasing salinity, although leaf-B was not significantly reduced, suggesting an internal synergistic interaction between B and other elements. However for *P. vera* on *P. integerrima*, the highest level of salinity produced the greatest injury, possibly as a combination of B plus Cl and/or Na toxicity. Leaf transpiration, stomatal conductance, and chlorophyll concentration of *P. vera*, determined by steady-state porometry, were also reduced to a greater degree by combined salinity and B when budded on *P. integerrima* than on the other two rootstocks.

0800-0900

S12-P-85

**PERFORMANCE OF 25 CORNELL-GENEVA ROOTSTOCKS WITH 'LIBERTY' AS THE SCION ACROSS NORTH AMERICA**

Terence Robinson\*, L. Anderson (UT), A. Azarenko (OR), B. Barritt (WA), G. Brown (KY), J. Cline (ONT), R. Crassweller (PA), P. Domoto (IA), C. Embree

(NS), A. Fennell (SD), E. Garcia (VT), A. Gaus (CO), G. Greene (PA), P. Hirst (IN), E. Hoover (MN), S. Johnson (CA), M. Kushad (IL), R. Moran (ME), C. Mullins (TN), R. Perry (MI), C. Rom (AR), J. Schupp (ME), M. Warmund (MO) Dept. of Hort. Sci., NYSAES, Cornell Univ., Geneva, NY, USA, 14456

Two multi-site uniform rootstock trials of new Cornell-Geneva (CG) rootstocks with Liberty as the scion cultivar were planted at 13 locations in North America in 1992 and at 14 locations in 1993. At each site the rootstocks were grouped into categories (dwarf, semidwarf and vigorous) and separate plots of each group were planted. Each site had from 4-7 single tree replications of each rootstock. The experiments were laid out as randomized complete block designs with blocking done by initial trunk diameter. Several sites were terminated after 5 years but the rest were continued through year 9. In the 1992 plots 'CG.3029', and 'Geneva.11' had the highest cumulative yield efficiency, good tree survival and also had good average fruit size. They had similar tree size as 'M.9' but exceeded the yield performance of 'M.9'. 'G.65' was more dwarfing than 'M.9' but had significantly lower cumulative yield efficiency and smaller fruit size than 'M.9'. Among semi-dwarf stocks, 'Geneva.30', 'CG.6210', 'CG.4222', and 'CG.5179' were top performers. They exceeded the performance of 'M.7'. 'G.30' generally had good survival; however, in a few sites several trees broke off at the graft union. In the 1993 plots 'CG.4247', 'CG.3041', 'CG.3902', and 'CG.3007' had the highest yield efficiencies and had good tree survival. All were similar in size to 'M.9' but performed significantly better than 'M.9' or 'M.26'. Among this group 'CG.3041' has also been tested on several grower's farms where it has been a top performer and will likely be introduced by Cornell Univ. in 2003. Among the semi-dwarf stocks top performers were 'G.30', 'CG.6210', 'CG.222' and 'CG.4202'. All performed significantly better than 'M.7'. Among this group 'CG.4202' has also been tested in New Zealand where it has been a top performer and will be introduced by Cornell Univ. In 2002. Among vigorous stocks, 'CG.6239', 'CG.6253', 'CG.7707', were top performers. These stocks exceeded the performance of 'MM.111'.

#### 0800-0900

##### S12-P-86

#### CHARACTERS OF SOME APPLE CULTIVARS ON M.9 ROOTSTOCK AND THEIR ADAPTABILITY WITH DAMAVAND REGION, IRAN

Rafii Yeganeh-Mazhar\*, Mostafa Mostafavi, Zabihollah Zamani  
Ministry of Agriculture, Agricultur, Karaj, Tehran, Iran, 31587

Eleven apple cultivars including: 'Red Elstar', 'Elstar', 'Elise', 'Golden Rinders', 'Golden Clon B', 'Braeburn', 'Gloster', 'Jonagold', 'Jonagored', 'Gala Royal Prince' and 'Granny Smith' on M.9 Rootstock were introduced to Iran at 1995 and cultivated in Damavand, an important apple growing region at Iran. Characteristics of these cultivars and their adaptability to the region were evaluated at 1999. 'Braeburn' and 'Granny Smith' with their long growth duration being respectively 180-210 days and 168-175 days after full bloom were not the appropriate cultivars for Damavand due to the short growth season of the region. 'Elstar', 'Red Elstar' and 'Gala', which picked in mid-Shahriyar (early September), can be introduced to farmers as high quality late summer ripening apples. 'Elise', 'Gloster', 'Jonagold' and 'Jonagored' can be introduced to farmers as very high quality early Autumn apple cultivars which benefit from an attractive appearance as well as high production potential.

#### 0800-0900

##### S12-P-87

#### FRENCH APPLE BREEDING PROGRAMS: FIRST RESULTS ABOUT A PARTNERSHIP BETWEEN INRA AND FRENCH NURSERYMEN

Francois Laurens\*

Unité Amélioration Fruit, INRA Centre d'Angers, BP 57, Beaucouzé, F, France, 49070

INRA Angers genetic improvement of dessert and processing apples started in 1960. The main objective is to combine high fruit quality with disease and pest resistance, and to obtain trees that allow high and regular cropping. Each year, 10 000 to 20 000 seedlings are planted and inoculated in glasshouse with a mixture of scab strains collected in INRA's orchards. The resistant seedlings are then planted in nursery condition for mildew assessment. In 1996, a new collaboration started with the French group of nurserymen "Novadi." After the mildew tests, budwood of the scab resistant and mildew tolerant trees are delivered to the nurserymen to be grafted; the trees are planted in 6 nursery sites where fruit evaluation is performed. The tree distribution between the sites follows a complex experimental design including the sharing of the progenies between the sites and the duplication of all the

hybrids in French Northern and Southern sites. First fruits of this new design have been tested in 2000; some hybrids appear promising. In addition, this new design allows us to estimate genetic parameters on the assessed fruit traits. Preliminary genetic results will be presented and discussed.

#### 0800-0900

##### S12-P-88

#### ANCESTRY OF APPLE SELECTIONS AT THE UNIV. OF SASKATCHEWAN

Robert H. Bors\*

Univ. of Saskatchewan, Dept. of Plant Sciences, 51 Campus Drive, Agriculture Building, Saskatoon, SK, Canada, S7N 5A8

Since the mid 1960s, 30,297 seedlings from controlled crosses have been evaluated in our apple breeding program. Young seedlings were selected following artificial freezing in a deep freezer or natural conditions in a nursery where -40C lows are common each winter. Only 8717 seedlings showed superior cold hardiness and were selected for field planting. From this population, 68 advanced selections have been propagated for further study. The most important parents for producing advanced selections were 'Brookland' and 'Haralson', which contributed 28.4 and 23.7%, respectively. Tracing ancestry revealed the most important founders to be 'Heyer 12', 'McIntosh', 'Ben Davis', and 'Malinda' which contributed 17.6, 14.6, 12.2, and 11.8%, respectively. An additional 13 founders contributed 20.85% while up to 11 accessions contributed 22.9% through open pollination. Nine of the 51 cultivars developed through the Prairie Fruit Breeding Co-operative contributed 66% of the gene pool. The 20 cultivars developed at the Univ. of Saskatchewan between 1923 and 1960 have not resulted in promising offspring and make up only 0.4% of the advanced selection gene pool. Crab-apple cultivars have contributed only 2.0%, while cultivars of Russian origin contributed 23.8%. Of the advanced selections, 56 are third generation crosses while 12 are fourth generation. None of the advanced selections have inbreeding in their lineage. Hardiness and fruit size was emphasized in previous generations. In the current generation those two attributes are more common and selection has been for fruit quality and storage life.

#### 0800-0900

##### S12-P-89

#### SWEET CHERRY BREEDING AT SUMMERLAND, CANADA

Frank Kappel, Richard MacDonald, Darrell-Lee McKenzie, Cheryl Hampson\*

Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, B.C. Canada V0H 1Z0

The sweet cherry breeding program has been ongoing at the Pacific Agri-Food Research Centre (PARC) Summerland, B.C. since 1936. An important contribution was the release of 'Stella' in 1968, the first self-fertile sweet cherry cultivar with reasonable commercial quality. 'Stella' has served as a source of self-fertility in our breeding program, as well as programs in other countries. The current objectives of the program are: 1) diversification; 2) environmental adaptation; and 3) reducing production costs. A number of cultivars have recently been introduced, including: 'Santina', 'Sumpaca Celeste', and 'Sumnue Cristalina' (early to mid-early season); 'Sumste Samba', 'Sandra Rose', and 'Sumleta Sonata' (mid-season); and 'Skeena' and 'Staccato' (late season). They span the cherry ripening season from 8 days before 'Van' to about 26 days after 'Van'. All these cultivars are red to dark red when ripe, and all but 'Santina' have average fruit weights greater than 10 g. Most of them have good fruit firmness, and some have natural rain-cracking levels lower than the standard cultivars 'Van' and 'Bing'. Total soluble solids range from about 16% to over 19%. All but 'Cristalina' and 'Samba' are self-fertile.

#### 0800-0900

##### S12-P-90

#### ALMOND BREEDING PROGRAMS IN IRAN

A. Vezvaei\*

Horticulture Agriculture Faculty, Tehran Univ., Karaj Tehran 31587-11167, Iran

The Iranian almond breeding program is started from 20 years ago with aim to produce late blooming cultivars adapted for local conditions. Recently breeding program started for produce cultivars with superior characteristics for all parts of Iran. Classical hybridization involving controlled hand cross-pollination is aimed at increasing quality. Parents include local Iranian selection and American and Australian cultivars. Hybridization was carried out in Australia from 1990-1994. First

isozyme markers for identify the hybrids. Seedling were evaluated for the physical and chemical characters in horticultural research station of the agricultural faculty of Tehran Univ. 2001, Also, the correlation between morphological and horticultural characters were evaluated. Iranian cultivars as well as wild species showed new alleles for IDH, AAT, PGM and GPI, which recognize this area as a gene pool of almond. At the end the history of almond breeding and the aims were discussed.

**0800-0900**

**S12-P-91**

#### **SELECTION OF SUPERIOR OLIVE CULTIVARS**

Jenny Guerin, Genet Mekuria, Shubiao Wu, Graham Collins, Margaret Sedgley\*  
Dept. of Horticulture, Viticul, Adelaide Univ., Waite Campus, Plant Research Centre, Glen Osmond, South Australia, Australia, 5064

Olive trees were first planted in South Australia in 1836. Since then, feral progeny have spread from abandoned orchards and now grow, untended, across large areas of southern Australia. Part of the research into olive improvement conducted at Adelaide Univ. is focused on the selection of superior olive trees from this unique and diverse gene pool. Within the last five years there has been renewed interest in olive production, and this current revival of the Australian olive industry will need improved varieties to help sustain it. We expect that selections from feral populations will provide the basis for new cultivars that are adapted to local conditions and possess distinct oil flavors. Many qualities contribute to the performance of an olive variety and we are using a range of techniques that have been developed in our laboratories to assist in the selection of superior feral trees. A reliable DNA fingerprinting method based on RAPD markers has been used to study genetic diversity and gene flow within an isolated feral population. A sequence-tagged-site (STS) has been developed to identify a genetic marker linked to resistance of olive leaf spot, which is caused by the pathogen *Spilosea oleaginea* (syn. *Cycloconium oleaginum* Cast.). Studies on the biology of olive pollination have revealed some of the reasons for low fruit set, and in addition, have enabled us to assess both self-fertility and the potential for a cultivar to be an effective pollen donor. Oil quality is determined using fatty acid profiles and polyphenol contents of oils, and a trained sensory panel is used for organoleptic assessment. Clonally propagated replicates of superior ferals will be planted in a field trial to further assess their potential as new varieties.

**0800-0900**

**S12-P-92**

#### **NATIVE APPLE GERMPLASM IN ROMANIA**

Gica Gradinariu\*, Felicia Gradinariu, Istrate Mihai, Marius Dascalu, Aleea M. Sadoveanu

nr.3, B-dul C.A. Rosetti, B-dul C.A. Rosetti, Iasi, Iasi, Romania, 6600

In Romania, apple germplasm consists in more than 1100 genotypes. More than 700 varieties and local selections are genetically disease resistant. The collection from Univ. of Agronomic Sciences and Veterinary Medicine Iasi contains over 200 cultivars. Among these, there are 65 local cultivars and biotypes which are disease resistant. This genetic material is mainly used in the breeding program of our Univ.. From 250 new selections 16 were confirmed to be disease resistant and released as new cultivars: 'Aromat de Vara', 'Frumos de Voinești', 'Auriu de Bistrita', 'Rosu de Cluj', 'Delia, Ancuta', 'Pionier', 'Voinea', 'Generos', 'Romus 1', 'Romus 2', 'Romus 3'. These represent 10% of all cultivars grafted in nursery. Based on annual pomological studies we establish the characteristics of each cultivar or biotype, the ways to use them, and the most appropriate methods to create new cultivars and hybrids. Valuable cultivars are recommended for multiplication and for replacing unsuitable ones.

**0900-0940**

**S12-O-93**

#### **NEW CITRUS ROOTSTOCKS VIA PROTOPLAST FUSION**

J.W. Grosser\*

Univ. of Florida, Institute of Food and Agricultural Sciences, Citrus Research and Education Center, Lake Alfred, FL, 33850, USA

Citrus rootstock improvement is challenging because so many traits must be packaged into any successful new hybrid. In Florida, these include: resistance/tolerance to blight, citrus tristeza virus, *Phytophthora* spp., nematodes, Diaprepes (Sugarcane root weevil), and in some cases salinity; adaptation to challenging soils; tree size control; nucellar embryony for seed propagation; good nursery performance;

and the ability to consistently produce high yields of quality fruit. No existing rootstock meets all of these criteria. During the past 15 years, we have produced somatic hybrid plants via protoplast fusion from more than 120 parental combinations, including more than 70 for rootstock improvement. Many of these have been propagated and entered in replicated commercial rootstock trials. Our primary strategy has been to produce allotetraploid somatic hybrids that combine diploid rootstocks with complementary traits. A secondary strategy has been to combine citrus with sexually incompatible or difficult to hybridize related species exhibiting important traits. Production of such hybrids and performance in field trials will be discussed. Smaller trees are desirable to facilitate harvesting and to maximize cold protection. Tree size and yield efficiency data from somatic hybrid field trials indicate that somatic hybrid rootstocks have excellent potential for use in high density plantings (due to polyploidy). Several somatic hybrid rootstocks are performing well in field trials, and some of these are producing adequate nucellar seed for standard nursery propagation. Fertile somatic hybrid trees are also providing a new opportunity for citrus rootstock improvement by breeding and selection at the tetraploid level.

**0940-1000**

**S12-O-94**

#### **ROOTSTOCKS FOR POME FRUITS**

Anthony D. Webster\*

1, Pine Grove, Maidstone, Kent, UK, ME14 2AJ

Rootstocks have been used as an aid to propagating desirable cultivars of apples and pears for more than a thousand years. Most scion cultivars do not come true-to-type from seed and are difficult to propagate using conventional vegetative techniques of propagation. Rootstocks provide an inexpensive and reliable method for scion propagation. The rootstocks used for these two crops today confer many attributes to the scion, as well as facilitating propagation. Rootstocks may be used to control the vigour of the scion tree, as well as its precocity, abundance and consistency of cropping and fruit size/quality. Rootstocks may also provide the scion with tolerance/resistance to soil-borne pests and diseases as well as to unfavourable abiotic (climatic and edaphic) conditions. The presentation will describe the range of beneficial characteristics currently achievable with the aid of apple and pear rootstocks and discuss the objectives required in their future breeding. The problems associated with traditional methods of breeding apple and pear rootstocks will be described and possible solutions discussed. The opportunities for using modern breeding techniques based on molecular biology will also be considered.

**1000-1020**

**S12-O-95**

#### **ROOTSTOCK BREEDING FOR STONE FRUITS**

Thomas G. Beckman\*<sup>1</sup>, Gregory A. Lang<sup>2</sup>

<sup>1</sup>United States Dept. of Agriculture, Agricultural Research Service, 21 Dunbar Road, Byron, Georgia, 31008, United States; <sup>2</sup>Michigan State Univ., Horticulture Dept., A338D Plant and Soil Science Bldg., East Lansing, MI 48824, United States

Over the last 20 years stone fruit rootstock development has begun shifting from seedling to clonal types, many of interspecific origin. Publicly funded breeding programs produced most of the old line stocks due to the extremely long development time, cost, and risk associated with rootstock development; however, private industry is emerging as a significant contributor of many of the new rootstocks. Particularly noteworthy among recent releases has been the incorporation of resistance to soilborne diseases, nematodes, waterlogging and vigor control, the latter most notably in recent cherry rootstocks. Nevertheless, despite the remarkable progress in the development of clonal stocks, seedling rootstocks still dominate most stone fruit industries around the world, if only because of their relatively low cost, ease of propagation, and proven utility. Many opportunities and challenges remain to be addressed in the areas of disease and insect resistance, adaptation to abiotic stresses, graft compatibility, and rootstock influence on scion performance and fruit quality. Biotechnology is just now beginning to show potential in accelerating rootstock development. With the development of markers to assist selection for difficult to evaluate traits, new rootstocks with resistance to multiple diseases are feasible. Future prospects for breeding are presented.

**1020-1040**

**S12-O-95-A**

**TO BE ANNOUNCED**

**1400-1420**

**S12-0-96**

**ROOTSTOCK DEVELOPMENT IN TEMPERATE NUT CROPS**

L.J. Grauke\*, Tommy E. Thompson

USDA ARS Pecan Breeding & Genetics Rt. 2 Box 133, Somerville, TX, 77879, USA

The driving force behind the development of rootstocks for nut crops has been the solution of specific problems, often related to the presence of pests or the need for adaptation to particular sites. The use of interspecific hybrids as rootstocks has led to increased appreciation for the contribution genetic diversity can make to orchard profitability in the face of site specific challenges. The past decade has seen dramatic increases in access to germplasm resources, while technological developments in molecular genetics have contributed to genetic characterization and utilization in some crops. The focus on clonal propagation through tissue culture has been somewhat abated by the slow pace of nursery incorporation of available techniques, by challenges with anchorage of some clonal rootstocks, and by the recognition of the vulnerability inherent to a monoculture susceptible to an unsuspected root pest. Increased application of spatial analysis systems (GIS) may contribute to prescription use of site-specific rootstocks, although public database development and access may be limited by proprietary or confidential information. As global boundaries become less of a barrier to the movement of information and germplasm, and as the linkage between generations of family farmers is broken, the ability to accurately prescribe appropriate rootstock-scion combinations with precision may become a proprietary commodity on the market. The role of public sector research and development is rapidly changing.

**1420-1440**

**S12-0-97**

**THE GENEVA SERIES OF APPLE ROOTSTOCKS FROM CORNELL: PERFORMANCE, DISEASE RESISTANCE AND COMMERCIALIZATION**

Genaro Fazio\*<sup>1</sup>, Terence Robinson<sup>2</sup>, Herb Aldwinckle<sup>3</sup>, Todd Holleran<sup>2</sup>

<sup>1</sup>Plant Genetics Resource Unit, USDA, New York State Agricultural Experiment Station, Geneva, New York, 14456 USA; <sup>2</sup>Dept. of Hort. Sciences, New York State Agricultural Experiment Station, Cornell Univ., Geneva, New York, 14456 USA; <sup>3</sup>Dept. of Plant Pathology, New York State Agricultural Experiment Station, Cornell Univ., Geneva, New York, 14456 USA

The Geneva series of apple rootstocks has been bred for tolerance to fireblight and Phytophthora root rot, high yield efficiency and good tree survival. Three clones from the program have been commercialized. 'Geneva 30' rootstock which produces a tree about 50% the size of seedling has continued to show high yield efficiency in several field plantings on growers farms and in the US national rootstock testing program. However, it has shown graft union brittleness with 'Gala'. Breakage tests have confirmed that the graft union of 'G.30' is weaker than similar unions with 'M.26' or 'M.7' with several varieties. 'G.30' also has the deficiency of producing many lateral spines on stoolbed shoots. This has limited its production by commercial stoolbed operators. 'Geneva 16' which produces a tree about 30% the size of seedling has been slightly more vigorous than 'M.9NAKB337' but has been equally productive. It has had excellent performance in the nursery except where virus infected scionwood has been used. Tests have shown that 'G.16' is sensitive to apple stem pitting virus but is not sensitive to apple stem grooving virus. Tests with apple chlorotic leaf spot virus were inconclusive. Its sensitivity to other viruses is unknown. 'Geneva 11' rootstock which produces a tree about 40% the size of seedling has shown very high productivity and good tree survival but not complete resistance to fireblight. A field planting of 3rd year Gala which was inoculated with fire blight in 1999 and evaluated for tree survival in 2000 showed that most Geneva rootstocks had high survival rates while most 'M.9' and 'M.26' trees were killed. 'G.11' gave intermediate survival. Greenhouse inoculations with 4 strains of fire blight showed that the Geneva stocks are largely resistant. The Geneva breeding program expects to release a new apple rootstock, 'Geneva 4-202', in 2002 in New Zealand. This stock is resistant to woolly apple aphid. In 2003 we expect to release two additional rootstocks: 'Geneva 3-41' and 'Geneva 5-935'.

**1440-1500**

**S12-0-98**

**LOW CHILL BREEDING OF DECIDUOUS FRUITS AT THE UNIV. OF FLORIDA**

W.B. Sherman\*

Horticultural Sciences Dept., Univ. of Florida, Gainesville, FL 32611

Florida's low chill fruit breeding program was initiated by Ralph Sharpe in the early 1950s. The peach program utilized South China peaches from the descendants of importations through Charleston, South Carolina, the Hawaiian group, and Okinawa as sources for local adaptation. These were inter-hybridized with the best commercial genotypes, mostly at USDA, Ft. Valley, Georgia, and segregating and backcross generations provided the melting flesh varieties upon which the low chill industry was founded. Non-melting flesh was introduced from North Carolina in 1970, from Mexico in 1975, and from Brazil in 1982. Semi-freestone, low chilling genotypes have been obtained from the 3 sources. Development of the high density fruiting nursery, identifying early ripening from red anthocyanin in autumn leaves, and selection for less blind nodes and bud drop has led to major improvements in the peach breeding program. Undesirable characteristics associated with nonmelting flesh such as long fruit development period, high chill, lack of red skin, off flavor, and low aroma have been overcome. Improvement in firmness, tree ripe flavor, red skin development as fruit were allowed to ripen on the tree, round fruit shape, short pubescence, tree ripen flavor, and lack of red at the pit were possible with the non-melting flesh. Advances in tree structure, resistance to bacterial spot and leaf rust, and development of ornamental flower and novel fruit types such as peento and anthocyanless fruits have been made. Subtropical plums were developed by crossing a low chill Japanese plum from Taiwan with high chill genotypes at USDA, Byron, Georgia, and because of self incompatibility were carried through 5 polycross generations to produce the 'Gulf-' prefix cultivars. The search for subtropical apricots has centered on a low chill mume from Thailand [(*P. mume* x apricot) F<sub>2</sub>], to produce 2 selections which have been open pollinated and backcrossed again to apricots. These seedlings are expected to produce home garden apricot varieties. Subtropical sweet cherry development is less promising, but a selection [(*P. pleiocerasus* x 'Black Tartarian') x *P. campanulata*] 4 open pollinated generations) has been crossed with sweet cherry and resulting F<sub>2</sub> seedlings may produce a home garden cultivar. 'Anna' and 'Dorsett Golden' subtropical apples have been used in breeding 'TropicSweet' in FL and others in Mexico such as 'Granny Mex'. Subtropical pears were mainly "sand" pears. 'Flordahome', bred in Florida, has "buttery" flesh texture, and resembles a European pear.

**1500-1520**

**S12-0-99**

**APPLE BREEDING PROGRESS IN JAPAN**

N.C. Oraguzie\*, J. Soejima, T. Fukusawa-Akada, H. Komatsu, N. Kotoda

The Horticulture & Food Research, Institute of New Zealand Limited, (HortResearch), Havelock North, Hawkes Bay, New Zealand, PB 1401

Apple is the second largest fruit crop after citrus cultivated in Japan. It has a history of cultivation dating back to late 1800s when the first apple cultivars were introduced from the USA. The total area currently under cultivation is approximately 45,000ha, with 'Fuji' contributing half the entire production. There are six major apple growing areas but only three research institutes from these regions have large breeding programs for apple. More than a hundred apple cultivars have been released from these breeding programs and about 30 of these are available mainly on Japanese markets. The main breeding objectives are texture, storage ability and resistance to pests and diseases. Rootstock breeding started in 1972 with the aim to develop rootstocks suitable for high density planting, adaptability to wet soil conditions and ease of propagation by hardwood cutting. The breeding efforts led to the release of the "JM" series in 1996/97. These rootstocks combine dwarfing attributes with high productivity and resistance to several diseases and pests hence, are considered good replacements for 'M9' and 'M26', in Japan. Until a decade ago, apple breeding methods and selection techniques were largely conventional. Through Agrobacterium-mediated transformation system, genes encoding sorbitol and antifungal proteins such as chitinase, glucanase and sarcotoxin have been transferred into apple cultivars and rootstocks. Transgenic lines of 'Orin' and 'JM 7' are currently being evaluated in the glasshouses for resistance to several diseases. Five RAPD markers linked to the susceptibility locus for Alternaria leaf blotch (*Alternaria mali*) have been identified using cultivar Kaori ('Delicious' x 'Ralls Janet'). High susceptibility to the disease has also been observed in 'Indo' and many cultivars derived from 'Delicious' x 'Ralls Janet' parentage. A linkage map approximately 950cM, has been constructed with 300 markers including RFLP, RAPD and CAPS. Loci for self-incompatibility linked RNase gene are also being mapped. Studies are underway for QTL mapping of fruit traits using segregating populations of several Japanese apple cultivars.

1520–1540

S12–O–100

**I.N.R.A. FRUIT BREEDING PROGRAMS**

Yves Lespinasse\*

INRA–C.R. d'ANGERS, Unité d'Amélioration des Espèces Fruitières et Ornementales, B.P. 57–49071 BEAUCOUZE Cedex–France

INRA breeding programs involved scion cultivars of apple, apricot, cherry, chestnut, peach, pear, plum, mandarin, olive, strawberry and walnut and rootstocks of *Prunus*, chestnut, pear and walnut. Genetic resources are characterised for resistance to biotic stress, adaptation to environmental constraints, tree architecture, and fruit quality. Works on resistance to biotic stress are concentrated on the genetic and molecular bases of plant x bio-aggressor interactions on the different pathosystems: apple (*Venturia inaequalis*, *Erwinia amylovora*), pear (*Erwinia amylovora*), *Prunus* (Plum Pox Virus, nematodes, *Myzus persicae*, *Sphaerotheca pannosa*), strawberry (*Colletotrichum*, *Phytophthora*). The main objective is to identify the different genes involved in resistance and to propose breeding strategies for durability of resistance. Quality of fruit is studied through flesh texture (apple), sugar and acidity contents (peach), aroma, epidermal color and process of maturation (apricot). The tree architecture approach is based on the analysis of successive architectures taken by the tree throughout its life span (apple and apricot). The objective is to integrate morphological criteria, linked with yield factors into breeding schemes and to suggest improvements in fruit tree management based on a more comprehensive knowledge of their growth and fruiting behavior. There are different programs aim to map the most important genes (major genes and QTLs), to identify and co-localise candidate genes with QTLs of specific traits, to obtain fruit specific EDNA libraries for various stages of tree and fruit development, and finally to develop marker assisted selection. Trials are performed in experimental farms where genetic resources are maintained, seedlings are created and evaluated, pre-selections are studied in various pedo-climatic conditions for the different traits concerned, i.e. fruit quality, disease and pest resistance, regularity of production. The INRA fruit group has a narrow link with

technical organizations of the fruit industry and also the nursery industry. The INRA fruit breeding group is involved in many international projects, particularly with European partners.

1540–1600

S12–O–101

**THE FUTURE: RESISTANT APPLE CULTIVARS**M. Fischer\*<sup>1</sup>, M. Geibel<sup>1</sup>, C. Fischer<sup>2</sup>

<sup>1</sup>IPK Gatersleben, Fruit Genebank Dresden-Pillnitz, D–01326 Dresden, Germany; <sup>2</sup>BAZ Quedlinburg, Institute of Fruit Breeding Dresden-Pillnitz, D–01326 Dresden, Germany

Integrated and biological cultivation methods are becoming increasingly important. The situation concerning the authorisation of pesticides is becoming more critical as increased attention is focussed on the conservation of the environment. An alternative solution here is the cultivation of resistant cultivars which can be grown with much less pesticides. It is still the aim of the Pillnitz apple breeding to combine in new cultivars improvements in fruit quality + yield + resistance to different pathogens. Early-, mid-, late-season apple cultivars were selected in two series, Pi- and Re-cultivars<sup>®</sup>. The Re-cultivars<sup>®</sup> guarantee a high degree of resistance. Triple and multiple resistant cultivars are selected with resistance to scab, mildew and fire blight: 'Remo', 'Regia' 'Rewena', and 'Rebella'. 'Rebella' was found with resistance also to bacterial canker, red spider mite and abiotic damages. Scab infection on vf-resistant cultivars has been observed since 1984 at different degrees in Northern and Central Europe. No infections were found in cultivars with other as vf sources: 'Reglindis' (VA), 'Reka' (Vr), 'Regia' (Vr). New sources for resistance breeding especially for pyramiding of resistance genes were found in the Fruit Genebank in some *Malus* species and old apple cultivars. However, the future needs new resistance sources and cultivars with two or more different sources of resistance to stabilise healthiness in the field, if the vf-gene is overcomes and not working any longer. The future lies in resistant cultivars. New breeding material is in field tests.