

## Symposium 17 (S17): Advances in Vegetable Breeding and Crop Physiology

Monday · August 12

Location: Metro Toronto Convention Centre, Room 205AB

1100-1140

S17-0-1

### CONSERVATION AND USE OF VEGETABLES GENETIC RESOURCES: A EUROPEAN PERSPECTIVE

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The status of conservation of vegetable crops germplasm has always received less attention than that of the major staple crops such as cereals and legumes. Information on vegetables germplasm can however increasingly be obtained from on line international databases. Maintenance and updating of this information requires a high level of international collaboration. This can be exemplified by the activity of the European working groups on *Allium*, *Brassica*, *Solanaceae* and *Umbellifer* crops. Cost-effective and reliable ex situ conservation remains a challenge that can benefit from sharing responsibilities within crop networks. In these fora, the discussion of common problems (long-term storage, safety-duplication, regeneration) can lead to collaborative solutions. The databases, holding mainly passport data, can be analyzed for the identification of duplications and gaps among collections. International projects for the characterization and evaluation of vegetables germplasm, including with molecular tools, are generating new data and making them increasingly available. In this way, genebank material is becoming more attractive to breeders. At the same time, the management of collections can be based on better knowledge of the diversity in stock. Interest for potentially useful genes, carried by vegetable crops wild relatives, encourages the establishment of in situ conservation and management reserves in the areas where the genetic diversity is the highest. The enhancement of the links between germplasm conservation and use will continue to depend, inter alia, on easy access to the genetic material. The recently approved International Treaty on Plant Genetic Resources for Food and Agriculture established a Multilateral System for facilitated access to germplasm of a number of crops. This includes vegetables such as asparagus, beet, the *Brassica* complex, carrot and eggplant, but excludes tomato, pepper, cucurbits, alliums, etc., with possible implications on the use of these crops diversity in the near future.

1140-1200

S17-0-2

### MOLECULAR METHODOLOGIES FOR IMPROVED GENETIC DIVERSITY ASSESSMENT IN CUCUMBER AND MELON

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Morphological and biochemical descriptors have been used successfully in germplasm management. The role of molecular markers in genetic analysis is dependent on their effectiveness, the cost of their implementation, and the ease of their creation, reproducibility and application. Deployment of marker technologies is greatly enhanced if markers are codominant (increased information), consistent (transferable across laboratories), and amendable to high throughput operations. Interpretation of results is made more meaningful if diversity assessments are standardized by uniform marker arrays (UMA) and historically based, genetically defined, reference accessions (RA). Molecular marker technology has been applied to the assessment of genetic diversity of melon and cucumber. Sixty-three mapped RAPD markers have been converted to more stable SCARs markers, and tested in multiplexing reactions (duplex to pentaplex) to increase assessment efficiency. PCR kinetics and its optimization play a major role in the success of multiplexing. SSR markers have been constructed and evaluated for their effectiveness when compared to RAPD, AFLP, and isozyme markers. Data indicate that the effectiveness of dominant (RAPD, AFLP) and codominant (isozyme and SSR) markers are equivalent in this regard. Two UMA (RAPD & SSR) have

been developed based on their discriminatory power in *Cucumis* accessions of elite (commercial) and exotic (India, China, Mediterranean, Africa) origin. One UMA has been applied to the analysis of U.S., European, Spanish, and Japanese elite and African exotic germplasm to identify a unique set of RA in melon and distinct gene pools. Similarly, UMA and RA have been developed for cucumber to identify distinct African gene pools. This has allowed for development of databases that have been useful in the design of a Core collection for cucumber, and strategic planning for future germplasm assessment and collection in both species.

1200-1220

S17-0-3

### GENETIC STUDIES ON THE INHERITANCE OF DISEASE RESISTANCE IN TOMATO (*LYCOPERSICON ESCULENTUM* MILL)

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Interspecific crosses involving the wild tomato variety Cherry, *Lycopersicon esculentum* var. *cerasiforme* and the commercial cultivars: NRI, NR2, NR44 and NR46 were studied. Disease resistance or tolerance of the parents, F1, F2, B1 and B2 generations were studied. Diseases encountered in the field included damping-off, seedling blight, wilt, die back and viral diseases. In general, Cherry was found to be highly tolerant to many of these diseases and to drought when compared with the commercial parents. With the exception of seedling blight, which was observed to be controlled by duplicate dominant epistatic genes (F2 ratio of healthy to diseased plants was 15:1), other fungal diseases were observed to be controlled by a single dominant gene (F2 ratio of healthy to diseased plants was 3:1). F1 hybrids were observed to be as good as Cherry in disease tolerance and vigour. The hybrids, especially F1, B1, B2, and some F2 were observed to be close to the wild Cherry in most of the characters. The major problem with the use of Cherry in these crosses was on the size of the fruits, which was below marketable size. However, fruit size of F1s was improved through the use of commercial cultivars as donor parents (males) in a backcross to produce B2 progenies. In order to develop stable varieties with high disease tolerance and acceptable fruit sizes, it is suggested that single plant selection followed by backcrosses using the commercial varieties as recurrent parents may be followed.

1220-1240

S17-0-4

### GENETIC ANALYSIS OF RESISTANCE TO LETTUCE DROP CAUSED BY *SCLEROTINIA MINOR*

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Despite extensive germplasm screening, no lettuce accessions have been identified as possessing immunity to infection by *Sclerotinia* species. As previously reported, several genotypes have consistently shown a significant reduction in disease incidence compared with susceptible varieties in replicated field and greenhouse tests with *S. minor*. Many of these genotypes exhibit architectural features that may promote avoidance or escape from infection, such as upright growth and early bolting. Studies in the Leguminosae have revealed that some *Sclerotinia* resistance loci cosegregate with traits involved in avoidance, e.g., lodging and plant height, while others appear to confer physiological resistance (Kim and Diers, 2000; Miklas et al., 2001). To date, the genetic basis and mechanisms of resistance identified in lettuce remain unknown. If solely due to avoidance, it may be impossible to transfer resistance into commercial cultivars without simultaneous transfer of unacceptable plant morphology. In contrast, physiological resistance is likely to be more easily incorporated into acceptable cultivars. Our objectives were to develop lettuce cultivars with *S. minor* resistance and to ascertain the genetic basis of resistance from the primitive *L. sativa* accession 'PI251246'. Complementary objectives were to develop an improved greenhouse disease assay and to compare greenhouse and field evaluation results. We have established backcross breeding programs to transfer *S. minor* resistance from several genotypes into all major lettuce types. We have also developed recombinant-inbred lines (RILs) from a ('Salinas' x 'PI251246') F2 population to determine the heritability and action of genes involved in resistance derived from 'PI251246' and for mapping of quantitative resistance loci. Preliminary evaluation of F4 RILs was performed in replicated field and greenhouse trials. Breeding

progress, as well as results and implications from the evaluation of F4 RILs, will be discussed.

**1340-1440**

**S17-P-5**

**COWPEA [*VIGNA UNGUICULATA* (L.) WALP.] GERMPLASM RESISTANT TO BACTERIAL BLIGHT**

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Bacterial blight, incited by *Xanthomonas campestris* pv. *vignicola* (Burkholder) Dye, is a major disease of cowpea worldwide. The pinkeye-type of cowpea is the predominant type grown in the southern United States. Currently, there are no commercial pinkeye cultivars resistant to bacterial blight. An objective of the LSU AgCenter cowpea breeding program is the development of bacterial blight-resistant pinkeye cowpea germplasm and cultivars for fresh-market and processing use. F2 seedling plants from crosses between bacterial blight-resistant PI lines and susceptible commercial pinkeye cultivars are inoculated in a greenhouse using a leaf infiltration method and evaluated for reaction to bacterial blight. Resistant plants are identified for continued testing. Efforts have resulted in the development of bacterial blight-resistant cowpea germplasm possessing commercially acceptable horticultural attributes. Pinkeye breeding lines LA 00-39 and LA 00-61 are being proposed for release as germplasm lines. LA 00-39 was developed from the cross 'Coronet' x PI 382118. 'Coronet' is a commercial pinkeye cultivar grown primarily for processing. PI 382118 is a plant introduction from Nigeria. Bacterial blight resistance in PI 382118 is dominant. LA 00-39 has a vining plant-type, purple pods, and a pea with a pinkish-red hilum. Parents of LA 00-61 are 'Quickpick Pinkeye' and PI 382118. 'Quickpick Pinkeye' is a commercial pinkeye cultivar adapted for machine harvest and grown primarily for fresh-market. LA 00-61 possesses a bush plant-type, purple pods, and a pea with a pink hilum. LA 00-39 and LA 00-61 have considerable potential for use by cowpea breeders for development of bacterial blight-resistant cultivars.

**1340-1440**

**S17-P-6**

**UNEXPECTED SUSCEPTIBILITY OF NOVEL BREEDING LINES OF EUROPEAN RHUBARB (*RHEUM RHAPONTICUM*) TO LEAF AND PETIOLE SPOT DISEASES**

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Rhubarb is an important vegetable crop grown in Northern Europe, the USA, and Canada, with breeding lines lacking physiological dormancy being developed in the UK to extend seasonal production. Spotting diseases of leaves and the marketed, edible, petioles are observed on conventional cultivars of this crop with leaf disease being widespread across the cultivar range yet of little commercial significance, as leaves are non-edible and trimmed from the marketed product. Petiole spotting is a potentially serious, but typically limited, problem in conventional crops with material showing this symptom being rejected in the retail marketplace. Breeding lines selected for the absence of summer dormancy are as susceptible as conventional cultivars to leaf spot diseases, caused by *Ramularia rhei*. However, the petioles are also highly susceptible to petiole spotting resulting in market rejection of up to 70% of otherwise marketable sticks. The causal agent is *Ascochyta rhei* and the characteristics and pattern of infection, in vitro growth and likely control of these pathogens will be considered.

**1340-1440**

**S17-P-7**

**BREEDING OF LINES RESISTANT TO POWDERY MILDEW IN ORIENTAL SQUASH (*CUCURBITA MOSCHATA*)**

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Powdery mildew is a disease found wherever cucurbit crops are grown. Two organisms are reported as the causal agents of this disease, *Erysiphe cichoracearum* DC ex. Merat and *Sphaerotheca fuliginea* (Schlecht ex. Fr) Poll. The latter is the most prevalent pathogen in Korea. *Cucurbita moschata* varieties

are good in quality of fruit, but not resistant to powdery mildew. Hence, an interspecific cross was carried out in order to transfer the resistant gene of *Cucurbita martinii* to *Cucurbita moschata*. In 1991, the interspecific cross between the cultivar "Jacheonjaelae", *C. moschata*, and *C. martinii* was made for the first time. "Jacheonjaelae" was backcrossed to the hybrid in 1992. The selected individuals from the BC1F1 population were backcrossed successively to "Jacheonjaelae" three times. A line from the progenies was crossed with "Seoulmadi" (*C. moschata*), with good quality fruit, in 1994. The hybrid plants were backcrossed to "Seoulmadi" two times and selfed four times from 1995 to 2000. Selections were made for resistance to powdery mildew and for good quality of fruit at each generation. The two powdery mildew resistant lines that were finally selected are characterized by cylindrical and oblong fruit shape respectively. They ranged from 350 to 450 g in fruit weight and 10 to 15 cm in fruit length.

**1340-1440**

**S17-P-8**

**BREEDING LINES RESISTANT TO TYLCV DERIVED FROM *LYCOPERSICON CHILENSE***

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Tomato yellow leaf curl virus affects tomato growing in greenhouses and open air conditions. Crop losses reach up to 100% in many cases. TYLCV-Sr and TYLCV-Is isolates have been identified in Spanish growing areas. Due to the poor success of preventive measures, the development of resistant varieties seems the best solution to reduce losses caused by this disease. Breeding for resistance is based in the exploitation of wild relatives of tomato, due to the lack of resistance in the cultivated species. Inoculation trials carried out by our working group lead to the identification of *L. chilense* resistant sources. A group of resistant lines for fresh consumption were developed as a result of breeding programs. A trial was carried out in greenhouse during autumn-winter season in order to determine the level of resistance to TYLCV of these new breeding lines. Thirteen breeding lines of indeterminate growth habit and slightly flattened fruits of medium size, were tested. The tomato breeding line NE-1 was used as a susceptible control. The breeding line TY-197 (derived from *L. peruvianum*) and the commercial hybrids Anastasia and Boludo were used as resistant controls. The trial was performed with 4 replicates per genotype. Each replicate consisted of 5 plants. Two replicates were inoculated and the other two were not and cultivated in disease free conditions. Agroinoculation technique was performed. Each plant was agroinoculated with both isolates. Samples of leaf tissue were taken every 2 weeks for detection of viral DNA by molecular hybridization. Losses of yield due to infection were estimated by comparing the yield of healthy with infected plants in order to compare the resistance level. Breeding lines exhibited a variable behaviour. Some of them showed lower viral accumulation and lower yield losses than the resistant controls. These results confirm the interest of these lines for developing hybrids resistant to TYLCV.

**1340-1440**

**S17-P-9**

**SCREENING LETTUCE GENOTYPES FOR HIGH TEMPERATURE GERMINATION**

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Seeds of several types of lettuce (*Lactuca sativa*) were collected from various sources and germinated under various conditions: varying temperatures by using a thermogradient table (20–35 °C, DC) and varying wavelength by light emitting diodes. The plants were also grown in a summer greenhouse and the plant characteristics were recorded. Correlation was analyzed between several seed and plant characteristics obtained. Major results are as follows. Under the far-red light, there was no cultivar which showed higher than 50% germination rate at 20 °C. However, 12 out of 89 cultivars showed a limited germination (10% or higher) even under the far-red light. Thirty-four genotypes showed 50% or higher germination at 35 °C and eight showed 80% or higher at 35 °C. At 33.1 °C, 70/89 showed over 50% germination, thus suggesting the possibility of selecting or developing suitable cultivars for summer sowing. Various other results will be presented.

1340-1440

S17-P-10

**REACTIONS OF MELON POWDERY MILDEW RESISTANCE SOURCES TO RACE 2U.S.**

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Powdery mildew, incited by *Sphaerotheca fuliginea* (Schlecht ex Fr.) Poll. (SF) and *Erysiphe cichoracearum* DC ex Merat reduces yield and quality of melon (*Cucumis melo* L.) production worldwide. There are many sources of resistance to the 11 races of *S. fuliginea*, including two variants of race 2 (2France, 2U.S.), and two races of *E. cichoracearum*, but knowledge of their reactions to other races, inheritances and allelic relationships is often unknown, incomplete, or has not been verified. For example, Sowell and Corley (1974, HortScience 9:398-399) reported high level resistance in PI 234607 and 16 other accessions, and lower level resistance in PI 179901 to SF race 2 (prior to differentiation of the French and U.S. variants), yet the inheritance of resistance to race 2 in these 18 cultigens remains unknown. In the present study, 20 melon cultigens were evaluated for their reaction to SF race 2U.S. in a greenhouse. Ten race differentials reacted as expected to SF race 2U.S. Iran H, which had not been tested previously against race SF 2U.S., was susceptible. PI 234607, 'Perlita' and 'Seminole' were comparable to 'PMR 5', MR-1 and PI 124112 for resistance. PI 313970 was resistant. PI 179901 was rated intermediate. PI 236355, 'Amarillo', 'Negro', and 'Moscatel Grande', sources of resistance to SF race 1 only, were susceptible to SF race 2U.S. The resistance reactions of MR-1, PI 124111, PI 124112, and PI 313970 included water soaked spots, and, with the exception of PI 124112, resistant-blisters.

1340-1440

S17-P-11

**QUALITY CHARACTERIZATION OF A GARLIC GERMPLASM COLLECTION**

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A U.S.D.A. germplasm collection of garlic (*Allium sativum*) and related species (*A. ophioscorodon*, *A. longicuspis*) has been evaluated for horticultural characteristics and yield under California production conditions for several years. In 1999, 2000 and 2001, characterization expanded to include compositional quality of 60-80 accessions. Bulbs were manually harvested late June to early July, cured about 3 weeks, shaded at ambient temperatures and the outer whorl of cloves manually peeled. Freeze-dried garlic powder was evaluated for alliin (precursor of flavor and health compounds) and allicin (major thiosulfinate responsible for flavor and pungency) concentrations by HPLC analysis. Dry weight, fructan concentrations, soluble solids, firmness and color data were also collected. Among the lines evaluated, alliin content varied from negligible to 20.9 mg per gram dry matter, allicin ranged from 1.7 to 5.7 mg per gram dry matter. Thiosulfinate concentrations were more highly correlated with alliin than allicin concentrations. Average dry weight was 37.2%, but varied by 10% between the highest and the lowest values. Dry weight was highly correlated with fructan concentrations. Soluble solids ranged from 34.5 to 43.7% and were also positively correlated to dry weight. Differences in peeled clove color (L\*, chroma) among accessions were minimal, but texture (rupture force) varied by 50%.

1340-1440

S17-P-12

**DEVELOPMENT OF DUAL-PURPOSE COWPEA [*VIGNA UNGUICULATA* (L.) WALP.] CULTIVARS FOR PRODUCTION OF BOTH SNAPS AND FRESH-SHELL PEAS**R. Fery\*<sup>1</sup>, B. Buckley<sup>2</sup>, D. Marsh<sup>3</sup>

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The cowpea [*Vigna unguiculata* (L.) Walp.] has a long history of use in the

United States as a vegetable crop. It is tolerant to drought and hot weather, and can be grown quite successfully under conditions that are totally unsuitable for such table legumes as the common bean [*Phaseolus vulgaris* L.] and the lima bean [*P. lunatus* L.]. Traditionally, home gardeners and farmers in the southern United States have grown cowpeas to produce fresh-shell peas and immature, fresh pods or snaps. One of the objectives of the U.S. Dept. of Agriculture (USDA) and Louisiana State Univ. AgCenter (LSU AgCenter) cowpea breeding programs is the development of a dual-purpose cultivar that can be used to produce both snaps and fresh-shell peas. Current efforts are directed toward incorporating the superior yield and seed characteristics of Asian "vegetable cowpea" lines into American snap-type cowpeas. Results of replicated field tests conducted over the past five years indicate that our effort to develop a high-yielding, dual-purpose cultivar has been successful. The breeding line US-905 has been identified as a candidate for release as a cultivar. This breeding line produces excellent yields of fresh snaps that can be harvested by a mechanical, reel-type, snap-bean harvester. The mature-green pods are long, exhibit an attractive yellow color, and are extremely easy to hand shell. The ease-of-shelling trait is important to home gardeners because most home gardeners must shell their harvest by hand. Fresh-shell peas are cream colored and kidney shaped. US-905 has considerable potential for use by market gardeners to produce snaps, mature-green pods, and fresh-shell peas for sale in farmers' markets.

1340-1440

S17-P-13

**ASSESSING THE PARENT-OFFSPRING REGRESSION ESTIMATE OF HERITABILITY FOR TWO DIFFERENT DISEASE ASSESSMENT SCALES AGAINST A GOLD STANDARD**

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Parent-offspring regression has been used to estimate the heritability of important traits. Some traits are continuously distributed and can be measured objectively, while other traits are harder to measure objectively. This is particularly true for disease assessments. The purpose of this study was to evaluate the agreement of the heritability estimates from two assessment scales, the equal distance (ED) and the Horsfall-Barratt (HB), with the estimate (the gold standard) from the continuous percent disease (PD) scale. Using computer simulations, percent disease values were generated for random samples (n = 5, 10, 25, 50, 75, 100) from normally distributed offspring populations with three heritability parameters (1.0, 0.5, 0.0) and six population variances (5, 10, 25, 50, 75, 100). For every heritability parameter, 200 samples were generated from each of the 36 sample-size population-variance combinations. The simulated percent disease values were converted to the two assessment scales. The ED scale divided the 0 to 100% disease interval into five 20% increments; whereas, the HB scale divided the disease interval into 12 unequal increments, with the increments being smaller at either ends of the scale and wider in the middle. In all cases where heritability = 0.5 or 0.0, HB was more highly correlated with PD than ED, especially when sample sizes and variances were small. In most cases where heritability = 1.0, HB was also more highly correlated with PD than ED, except when the population variances were small. These results indicate that the choice of rating scale in disease assessments can significantly alter the estimate of heritability for disease resistance, and that the results are much more likely to be over-estimates than under-estimates. Also, in most cases, HB is more closely correlated to the gold standard than ED, and would be the preferable rating method of the two studied.

1340-1440

S17-P-14

**ESTABLISHING THE ILLINOIS HORSE RADISH GERMPLASM COLLECTION IN VITRO**

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Illinois is the leading producer of horseradish (*Armorica rusticana*) in the United States. The Univ. of Illinois and the Horseradish Growers of Illinois have established the Illinois Horseradish Germplasm Collection, which consists of approximately 130 accessions from all over the world. For conserva-

tion purposes, we are duplicating this collection in vitro. For efficient in vitro conservation of a species, it is desirable to have a single method both to introduce and to maintain a wide variety of accessions. Preliminary results indicated that Murashige and Skoog medium with 1-naphthaleneacetic acid alone was sufficient to regenerate whole adventitious plants from horseradish leaf tissue. To adapt this technique to a wide variety of accessions, we tested the following conditions: regeneration in the light vs. the dark; leaf age (folded, unexpanded; unfolded, not fully expanded; fully expanded, not fully hardened; fully expanded, fully hardened); leaf size (equilateral triangular pieces 0.5, 1, or 2 cm a side); and presence or absence of veins. We have found more plants to regenerate in the light than in the dark. Unfolded, not fully expanded leaves formed more plants than other maturity stages. Leaf explant size has no obvious effect on regeneration rates, but a vein is essential for plant regeneration. Results from these studies will enable us to quickly and efficiently establish the Illinois Horseradish Germplasm Collection in vitro.

**1340-1440**

**S17-P-15**

**CRYOPRESERVATION OF DIVERSE POTATO GERMPLASMS (*SOLANUM TUBEROSUM* L.) USING VITRIFICATION TECHNIQUES**

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Shoot tips from in vitro grown buds of potato (*Solanum tuberosum* L.) were successfully cryopreserved by vitrification. Excised shoot tips from nodal segments cold-hardened at 10 C for 3 weeks were precultured on solidified MS medium supplemented with high concentrated sucrose for 1 day. After having been embedded with foils, shoot tips were osmoprotected by a mixture of 2 M glycerol plus 0.6 M sucrose for 90 min, then they were dehydrated with a cryoprotectant for 1 h at 0 C prior to a plunge into liquid nitrogen. Successfully vitrified shoot tips resumed growth within a week and developed shoots directly. The average survival rate of all tested cultivars were about 50%. This procedure was successfully applied to other cultivars. So, it appeared to be promising for the cryopreservation of various potato germplasms. In addition, the stability of vitrified plants was confirmed based on biochemical and molecular analysis.

**1340-1440**

**S17-P-16**

**BREEDING FOR RESISTANCE TO PEA LEAFMINER (*LIRIOMYZA HUIDOBRENSIS*) IN LETTUCE**

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The pea leafminer is a major pest that causes considerable damage to a wide variety of vegetable crops including lettuce, and resistant cultivars remain the most economic means of insect control. Eighty-four lettuce cultivars and introduction lines were grown in an insect cage with eight replications for resistance screening. Pea leafminer flies were released in the cage to feed on the plants. Significant genetic variation for leafminer stings per unit leaf area was observed among genotypes in repeated tests. Resistant lines with fewer leafminer stings were found in *Lactuca sativa*, *L. saligna*, *L. serriola*, and *L. virosa*, and the resistance was confirmed in a field experiment. Crosses were made to combine leafminer resistance and superior horticultural traits in crisphead, green leaf, red leaf, romaine, and butterhead lettuces. Leaf miner resistant plants were selected in F2 progenies of such crosses, and were backcrossed to restore horticultural type.

**1340-1440**

**S17-P-17**

**TRANSFER AND GENOMIC ANALYSIS OF ACYLSUGAR-MEDIATED PEST RESISTANCE IN TOMATO**

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The wild tomato (*Lycopersicon pennellii*) is resistant to numerous pests of tomato (*L. esculentum*), including armyworm, fruitworm, aphids, leafminers, and whitefly. The pest resistance of *L. pennellii* is mediated by the presence of

acylsugars, which constitute 90% of *L. pennellii* type IV trichome exudate. Transfer of the ability to accumulate acylsugars could result in pest resistant tomato cultivars, and thus a reduction in the dependence on synthetic chemicals for insect control for this crop. As described by this presentation, this transfer has been accomplished. A two pronged strategy was used to effect the transfer of acylsugar-mediated resistance to tomato: a breeding program with selection guided by a biochemical assay for acylsugars, and genomic analyses focused on determining the genetic regions that affect acylsugar production. QTL analysis of a *L. esculentum* x *L. pennellii* F2 population identified five genomic regions, on chromosomes 2, 3, 4 and 11, associated with acylsugar production. The location of one acylsugar biosynthetic gene, an acyltransferase, was also mapped on chromosome 10. However this information was insufficient to guide a marker-assisted breeding program in 1994-98, since the resulting lines produced only trace levels of acylsugars. From 1989 to date, a breeding program used the biochemical assay to guide selection and succeeded in generating several tomato lines fixed for production of moderate-high levels of acylsucroses. More complete genetic data resulted from the RFLP analysis of these acylsugar-producing lines. The genomes of these lines are 70 to 80% *L. esculentum* and have from 7 to 9 *L. pennellii* introgressions on up to 8 chromosomes. Comparison of the genomes of these lines also shows that the number and size of the introgressions could be reduced without loss of the trait, so that the plants would be at least 90% *L. esculentum* and have improved horticultural type.

**1340-1440**

**S17-P-18**

**BREEDING MUSKMELON FOR RESISTANCE TO VINE DECLINE**

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Melon vine decline is a major disease of melon. In Spain, *Acremonium cucurbitacearum* and *Monosporascus canoballus* are the main causal agents of this complex disease. Several sources of resistance have been identified in field and greenhouse assays conducted in USA and Spain. Specific resistance to the fungi along with a more vigorous root system has been proposed as mechanisms of resistance. We characterized the response to vine decline of the tolerant cultivars, Doublon and Deltex, selected in USA, and the wild accession *Cucumis melo* subsp. *agrestis* Pat81, selected in Spain. Plants were grown in naturally infested soil (NIS), in soil artificially infected with *Acremonium* (A), with *Monosporascus* (M), and in sterilized soil (SS). Lesions caused by fungi in hypocotyls (LH), lateral roots (LLR) and fine roots (LFR) were scored from 0 to 4. Other root parameters, such as the root fresh weight (RFW), were also measured. The Spanish cultivars Piel de Sapo and Amarillo Canario were used as susceptible controls. NIS and M treatments caused lesions significantly more severe than the A-treatment in all genotypes, at 30 days after inoculation. Pat81 exhibited the highest level of resistance to NIS and M, with scores of 0.2/1.3/1.8 for LH/LLR/LFR in NIS, compared to the susceptible controls (3.3/2.7/3). Doublon was also highly resistant to M inoculation, but developed more severe lesions in NIS (0/1.8/2.1). The response of Deltex was intermediate. Doublon had a heavier root than Pat 81 in SS. However, no significant differences in RFW were observed between SS and NIS for Pat 81, whereas Doublon suffered weight losses of 12% in NIS. The fact that Pat 81 was more resistant to pathogens occurring in naturally infected soils from Spain, where it has been selected, may have important implications in breeding for resistance to this complex disease.

**1340-1440**

**S17-P-19**

**SCREENING THE WATERMELON GERMPLASM COLLECTION FOR RESISTANCE TO GUMMY STEM BLIGHT**

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All available accessions from the USDA watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) germplasm collection, including var. *citroides*, were screened for resistance to gummy stem blight (*Didymella bryoniae* Auersw.). The experiment was a randomized complete block with 1585 cultigens (elite cultivars, obsolete cultivars, breeding lines, and PI accessions), two locations

(field and greenhouse) and two or four replications. Isolates used were collected from cucurbits and verified for virulence on watermelon. The best cultigens were significantly more resistant than the check, 'Charleston Gray'. The most resistant and most susceptible cultigens were retested along with check cultivars (including a set of cucumber cultigens). The retest was a randomized complete block with 75 (only 38 of those in 2000) cultigens, two locations (field and greenhouse), and three or four replications. Plants were rated using three systems: leaf only, stem only, and whole plant. The retest showed that the most resistant and most susceptible cultigens from the screening study were correctly classified in general. The most resistant cultigens were PI 189225, PI 211915, PI 271770, PI 482273, PI 482277, PI 482283, PI 482293, PI 482342, PI 500334, and PI 532809. The most susceptible cultigens were PI 113326, PI 169286, and PI 223764. Future research should use resistant and susceptible inbreds to determine inheritance of the disease resistance.

**1340-1440**

**S17-P-20**

**FRUIT AGE, FRUIT STORAGE, AND SEED STORAGE PERIOD AFFECT MANAGEMENT OF SEED IN A TROPICAL PUMPKIN BREEDING PROGRAM**

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A series of experiments tested the effects of fruit age [days post anthesis (PA)], fruit storage (FS), and seed storage on emergence in tropical pumpkin (*Cucurbita moschata*). The objective was to determine how these management considerations affect breeding program factors. Unlike in commercial seed production, high emergence might not be required for all conditions. We tested seed from fruit 21 to 50 days PA and stored 0 to 28 days post-harvest. Seed was stored from 0 days to 10 years in cold storage. For 90% or better emergence, fruits should be harvested no earlier than 45 days PA. Where perfect germination is not necessary, fruits can be harvested as early as 30 days PA and stored for several weeks. When seed was tested in 1991, percent emergence averaged 95.5%. After 10 years of cold storage, emergence dropped to 79.4%. Most treatments produced seed that remained highly viable after 10 years. Seed from 45 and 50-day-old fruit (with 0 to 20 days FS) had 100% emergence. Ten years later, these same treatments varied from 80 to 100% emergence. But seed from more immature fruits exhibited a much more severe drop in emergence from 1991 to 2001. Seed dormancy was not important in the tropical pumpkin populations we tested, especially when seed was harvested from mature fruits. In a breeding program where rapid cycling of generations is required, approximately 45 days is the minimum time needed between anthesis and planting the next generation to assure adequate emergence. Emergence would be excellent (>90%) if fruit was allowed to mature in the field, but less if fruits were harvested immature and stored. In tropical pumpkin the number of days from planting to anthesis varies greatly, but is typically about 65 days. For many types of tropical pumpkin, and probably for most genotypes of *Cucurbita moschata*, three generations/year could be generated in a tropical environment.

**1340-1440**

**S17-P-21**

**A STUDY ON DISEASE-RESISTANT CROSSING OF CHINESE HAMI MELON WITH AMERICAN MELON**

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Melon (*Cucumis melo* L ssp. *melo*) is one of the 10 most important fruits in the world, and its nutrient value is the second, especially the crisp fresh type of Xinjiang Hami. But the Hami melon is susceptible to disease. So, we must breed disease-resistant varieties. We obtained several varieties of American disease-resistant melons from Dr. Claude E. Thomas and Perry Nugent (USDA-ARS Vegetable Lab. Charleston, SC), and Dr. James McCreight (USDA-ARS Salinas Station, CA). We selected for three traits: 1. better quality; 2. no musk flavour; 3. good combining ability. Through cross and backcross breeding, it is easy to obtain a crisp flesh type. Finally, we selected three samples to cross with Hami melons. After inoculating and selection for three generations, we obtained three disease-resistant crisp flesh type lines; two are resistant to leaf

diseases, another is resistant to gummy stem blight, including one late maturing type with good quality, having better resistance than Jashi melon. These are now being grown in Kaskarl, Xinjiang.

**1340-1440**

**S17-P-22**

**BIODIVERSITY OF EGGPLANT IN TURKEY**

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Knowledge of the nature and extent of genetic variability in available germplasm is essential for a crop improvement programme. Genetic resources are the reservoir of variation that provides raw material for the breeder. Eggplant is an important vegetable in Central, Southeast and Southeast Asia, and in some African countries. Turkey is very rich in eggplant biodiversity. Collection of local ecotypes is of potential breeding value. However, there is further need for systematic evaluation and documentation of a large array of germplasm of eggplant, at various locations under certain conditions, so that promising lines can be tapped to meet the requirement of vegetable breeders working on this crop. Also, observations for morphological traits are described in this study.

**1340-1440**

**S17-P-23**

**BIODIVERSITY OF MUSKMELON IN TURKEY**

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Evaluation of germplasm is imperative to ensure its best use for crop improvement. With the development of modern cultivars, there is erosion of germplasm and thus primitive cultivars and wild taxa are becoming extinct. There is a need to collect and evaluate more local germplasm from the different parts of the world. Although *Cucumis melo* originated in tropical and subtropical Africa, which is the primary centre of diversity, Turkey is very rich in muskmelon diversity. There is great diversity in type with respect to fruit shape, size, color of flesh, vine growth and earliness. Also observations for morphological traits are given in this study.

**1340-1440**

**S17-P-24**

**GENETIC RESOURCES OF WILD *LACTUCA* SPP., THEIR NATURAL DISTRIBUTION AND REPRESENTATION IN EX-SITU COLLECTIONS**

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The broad survey of available world literature showed that at least 97 wild *Lactuca* spp. have been taxonomically described. In total 27 wild *Lactuca* species are reported in world gene bank collections according to the "International *Lactuca* database." The actual number of *Lactuca* spp. in collections is even lower due to incorrect taxonomic determination. The representation of taxa in the collections is poor and unbalanced with regard to both biogeography and distribution. The highest representations of wild taxa in collections are *L. serriola* (70%), *L. virosa* (12%) and *L. saligna* (10%). *L. serriola* is also the best represented species in collections as far as geographic variation and the spectrum of different habitats. Information relating to *Lactuca* spp. accessions is rather poor and sometimes misleading because the primary country of origin does not correspond with their natural distribution area. The secondary sources of origin data are generally donor sources (Institutes, Botanical Gardens). The collection and maintenance of more localised and autochthonous (area-specific) species, which are absent in the gene bank collections, is considered as a significant target for future research of the genus *Lactuca*. Future collecting strategy must be more intensively directed to the hotspots of *Lactuca* spp. biodiversity (Asia, Central and South Africa). The study of *Lactuca* spp. in natural habitats is valuable to progress the basic knowledge of taxonomy, ecobiology, phylogeny and evolutionary relationships.

1440–1500

S17–0–25

**CREATION OF A NEW GERMPLASM OF CMS NON-HEADING CHINESE CABBAGE**X.L. Hou\*<sup>1</sup>, S.C. Cao<sup>2</sup>, Y.K. He<sup>3</sup>

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A new Chinese cabbage germplasm ZS6(A)10 was created by asymmetric cell fusion. Its progeny plants were identified in both field and laboratory. Results were as follows: the material showed 100% sterility rate and 100% sterility degree and had 4 nectaries and no chlorosis at low temperature. Its seed-set rate was identical to that of the maintainer, which was notably higher than that of the parental sterile line. The chromosome number of the progeny plant was the same as the maintainer (2n=20). The POD isoenzyme of radicle and cotyledon and EST isoenzyme of hypocotyls were notably different from those of the maintainer and the parental sterile line. The cpDNA and mtDNA contents of the progeny plants were between those of the maintainer and the parental sterile line. PCR analysis of cpDNA and mtDNA confirmed that ZS6(A)10 was a somatic cell hybrid and its progeny 98HQiu-45 was a new germplasm of cytoplasmic male sterile (CMS) non-heading Chinese Cabbage.

1500–1520

S17–0–26

**GARLIC (*ALLIUM SATIVUM* L.) AND ITS WILD RELATIVES FROM CENTRAL ASIA: EVALUATION FOR FERTILITY POTENTIAL**R. Kamenetsky\*<sup>1</sup>, I. London<sup>2</sup>, F. Khassanov<sup>3</sup>, C. Kik<sup>4</sup>, H.D. Rabinowitch<sup>5</sup>

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Garlic (*Allium sativum* L.) is completely sterile, propagated only vegetatively, and is used as a popular condiment all over the world. Similarly, man also consumes its closely related wild species *A. longicuspis*. The latter is considered by taxonomists to be the ancestor of the domesticated garlic. The collection of a large number of accessions of *A. sativum* and *A. longicuspis* is the only means available to expand the genetic variability with regard to yield, quality, tolerance to biotic and abiotic traits as well as flowering and possibly fertility restoration. About 300 accessions recently collected in Kazakhstan and Central Asia (the main center of garlic diversity), were documented according to their geographic locations and environmental conditions, and thereafter evaluated and maintained in the field collections of vegetatively propagated alliums. The accessions studied were subdivided into two distinct sub-populations: semi-bolters (producing blind scapes) and bolters (producing a flower scape). Most of flower-producing accessions have fertile pollen and receptive stigma, and true garlic seeds were obtained from 11 accessions, collected in Kazakhstan in 1996–98. The garlic inflorescence is an umbel-like flower arrangement, and flower clusters (branches) arise from a common meristem. The flowers in the umbel have a distinct morphology typical of the genus *Allium*. Differentiation of topsets begins on the peripheral part of the apical surface only after floral differentiation occurs, and the size, number and rapidity of development of topsets vary significantly between genotypes. Further studies of flowering physiology and fertility restoration should focus on clones which can produce a large number of normal flowers with high flowers to topsets ratio.

1520–1540

S17–0–27

**STUDIES ON UNSTABLE FERTILITY OF CGMS IN F1 SEED PRODUCTION FOR CERTAIN GROUPS OF *CAPSICUM ANNUUM* L. AND SUGGESTION FOR ITS REMEDY**Do Hyeon Lee\*<sup>1</sup>, Moon Hwan Lee<sup>1</sup>, Hyo Guen Park<sup>2</sup>

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This study was conducted to elucidate possible causes of instability in expression of both male sterility and its restoring ability reported in certain groups of peppers (hot fresh and sweet fresh types), which has made the use of CGMS for F1 hybrid seed production impossible in these groups. Some morphological, histological and genetic studies were conducted to find out the causes of unstable fertility. We found a locus responsible for the instability of fertility in CGMS lines, which has been known putatively for many years as a modifier gene, in addition to a major restorer gene known as <sup>®</sup>Rf'. The new locus was tentatively designated as <sup>®</sup>St', for stability. This <sup>®</sup>St' is a clearly nuclear gene, independent from <sup>®</sup>Rf' and has multiple alleles. So far, we found three alleles, <sup>®</sup>St1', <sup>®</sup>St2' and <sup>®</sup>StU', respectively. While the alleles <sup>®</sup>St1' and <sup>®</sup>St2' seem to be responsible for increasing stability of fertility in maintainers as well as restorers, the allele <sup>®</sup>StU' makes unstable both maintainer and restorers. The <sup>®</sup>StU' appeared to be dominant to <sup>®</sup>St1', but recessive to <sup>®</sup>St2'. Actual conversions of unstable maintainers and restorers to stable restorers were attempted based on an assumptive genetic mechanism for the instability suggested from some genetic research in order to make the CGMS system available in F1 hybrid seed production to those groups of peppers in which it is so far not possible. When the differences in mtDNA between N- and S-cytoplasm were examined, some alteration in coxII, coxIII and atp6 genes have occurred in mtDNA of S-cytoplasm, and both the restorer gene (Rf) and the unstable allele (StU) seem not to cause any changes in molecular structure of coxII, coxIII and apt6 in S-cytoplasm.

1540–1600

S17–0–28

**TOMATO RESPONSE TO SALT STRESS**

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Thirteen tomato genotypes were subjected to salt treatment under hydroponics and their responses monitored in a set of two experiments with the objective of advancing them as potential salt tolerant tomato scions and/or rootstocks. Salt applications ranged from 0 to 2% NaCl with the resultant EC values of 1.4 to 37 ds·m<sup>-1</sup> respectively. Genotypes were cultured in the experimental solutions for up to four weeks in a three replicate completely randomised design in the greenhouse. Significant genotypic and/or salt treatment effects were registered on plant height, leaf green meter value and area, dry matter yield, Na<sup>+</sup> and Cl<sup>-</sup> accumulation in tomato tissues. Salt treatment at 2% NaCl stimulated chlorophyll production per unit leaf area but caused severe depression on dry matter yield and leaf area. These results revealed that some tomato genotypes consistently showed superior biological activity at higher salinity and others exhibited greater shift in the shoot:root ratio based on dry matter biomass production, thus displaying relatively greater adaptation to salt stress. Two tomato genotypes (Siozawa and Gambaru Ne-3) displayed superior performance based on these data. In a parallel investigation, production of tomato in pot experiments was examined and fruit yield production as well as fruit related parameters determined. A Kenyan landrace significantly produced sufficient fruits under this salt stress.

1600–1620

S17–0–29

**PHENOTYPE ISOLATION OF LINES OF SEEDLESS SQUASH (*CUCURBITA PEPO* L.).**D.A. Vasquez\*<sup>1</sup>, W.A. Warid<sup>1</sup>, J.J. Martinez<sup>2</sup>, J.M. Loaiza<sup>3</sup>

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The Dept. of Agriculture of the Univ. of Sonora, Mexico has been developing a mutant variety of *Cucurbita pepo* L. (squash) with naked seed for a period of 10 years because of the commercial importance that type of seed represents for nutritional value. The objectives of this work were: 1) to describe the morphologic characteristics and development of 24 lines of squash with naked seed and 2) to select the best lines showing the best seed characteristics. A computational digital system was used to identify morphological characteristics of seeds in the 24

lines. Protein and lipids were determined using the AOAC (1990) techniques and the characteristics from each seed line were used as criteria to classify the better lines: i.e. seed number and weight, color, and protein and lipid contents. The results showed a regular pattern of growth for seed and fruit development. Homozygosity for testa was also confirmed. Initial appearance of first female flowers was from 19 to 33 days. Fruit production by plant ranged from 1 to 9 with 0.86–7.9 Kg of fruit/plant, and 148.3–309.3 seeds/plant, with a weight of 17.5–51.5 g/seed/fruit. The range of seed weight was 0.1–0.22 g. The seed area ranged from 70.1–119.3 mm<sup>2</sup>. An interval from 3100 to 3400 pixels was registered as good color of the seeds. This means a green color. The protein and oil content varied from 26.2 to 34.8% and from 20.7 to 29.8%, respectively. Analysis of these data lead to the following conclusions. The best lines were numbers 1, 2, 3, 4, 5, 7, 8, 11, 13, 14, 16, 20 and 22. Finally, it is possible to cultivate these lines for commercial seed production.

**1620–1640**

**S17–0–29–A**

**TO BE ANNOUNCED**

**1640–1700**

**S17–0–29–B**

**TO BE ANNOUNCED**

**Tuesday · August 13**

**1100–1140**

**S17–0–30**

**ADVANCES IN COMMON BEAN IMPROVEMENT:  
SOME CASE HISTORIES WITH BROADER APPLICATIONS**

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Scientists in developing countries and the U.S. have made significant advances in breeding and genetics for multiple disease and stress resistance, and increased yield in common bean (*Phaseolus vulgaris* L.). It is an important commercial crop in many areas of the world, as well as a staple food crop for the poor in Latin American and East Africa. This paper will, through specific case histories, review some highlights of the work that led to these advances in the U.S. and other countries. Implications for bean breeders of the domestication genetic syndrome, two major gene pools, and breeding pyramid will be first outlined. Four case histories will be examined: 1) archetype breeding to improve yield per se or to provide a canopy avoidance mechanism to reduce losses due to white mold disease; 2) classical and molecular pyramiding of major genes for resistance to anthracnose, bean common mosaic virus, rust, and QTL for resistance to common bacterial blight to provide for enhanced durability of resistance; 3) the mapping of anthracnose and rust resistance gene clusters, and associations with the co-evolution of both pathogens in the two gene pools; and 4) approaches to alleviate biotic and abiotic stresses that limit bean production in Latin America. Some major challenges in bean improvement for the future will be presented.

**1140–1200**

**S17–0–31**

**PYRAMIDING GENES FOR DISEASE RESISTANCE IN *CUCURBITA***

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Genes from *Cucurbita ecuadorensis* for resistance to zucchini yellow mosaic virus (ZYMV), papaya ringspot virus (PRSV), and cucumber mosaic virus (CMV) were combined with powdery mildew (PM) resistance from *Cucurbita okechobeensis* subsp. *martinezii* to breed the summer squash cultivar 'Whitaker', which is resistant to those four diseases, and multiple disease resistant pumpkin germplasm. 'Whitaker' was crossed with *C. pepo* breeding lines of interspecific origin with resistance to watermelon mosaic virus (WMV) in order to develop germplasm homozygous for resistance to five diseases: WMV, ZYMV, PRSV,

CMV, and PM. Genes from different sources of resistance to ZYMV were combined to reduce vulnerability to new pathotypes of that virus.

**1200–1220**

**S17–0–32**

**INHERITANCE OF ADULT-PLANT RESISTANCE TO DOWNY MILDEW [*PERONOSPORA PARASITICA* (PERS. EX FR.) FR.] IN BROCCOLI**

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The objective of this study was to determine the mode of inheritance of field resistance to downy mildew [*Peronospora parasitica* (Pers. ex Fr.) Fr.] in broccoli (*Brassica oleracea* var. *italica*) at adult plant stage. The F<sub>1</sub>, F<sub>2</sub> and BC progeny of resistant (line A) and susceptible (line B) plants of broccoli were tested in the field under natural infection in central Portugal from August to December in three successive years. The plants were evaluated for resistance to downy mildew at maturity using a five class scale of increasing susceptibility to the disease, which took into account the number of infected leaves and the size of the sporulating lesions. The F<sub>2</sub> segregated a clear 3 resistant: 1 susceptible, and the backcross to the susceptible parent segregated 1:1 suggesting a dominant character controlled by a single locus. Self-pollinated lines of the resistant parent (line A) and of the susceptible parent (line B) were tested with two different *P. parasitica* isolates in a greenhouse using a single-leaf inoculation method to evaluate the specificity of the resistance. Each leaf was sprayed with a spore suspension, enclosed for 24 h in a plastic bag for infection, enclosed again 8 days later to induce sporulation, and then evaluated for resistance using a six class scale. Resistant leaves were those scoring in non-sporulating classes. Line A was resistant to isolate P523 (collected from the testing field in Portugal) and to isolate P005 (from the UK), while line B was resistant to isolate P005 and susceptible to isolate P523. This study demonstrated the existence of race-specific resistance to downy mildew in adult plants of broccoli and demonstrated the horticultural value of the resistance in line A since it is controlled by a single dominant gene and it is effective against two different *P. parasitica* pathotypes.

**1220–1240**

**S17–0–33**

**BREEDING EGGPLANT FOR VERTICILLIUM WILT RESISTANCE**

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Resistance to Verticillium wilt was found in *Solanum incanum* accessions from Kenya and in *Solanum* species more distantly related to eggplant. Interspecific hybrids with eggplant were produced with the aid of embryo culture for the crosses with distantly related species. The authenticity of the interspecific hybrids was verified on the basis of morphology and RAPD analysis of the hybrids and segregation of the next generation. Breeding lines with Verticillium wilt resistance and with good fertility and horticultural type were developed from interspecific crosses with eggplant.

**1340–1440**

**S17–P–34**

**HOST SPECIFICITY OF THE RESISTANCE TO DOWNY MILDEW [*PERONOSPORA PARASITICA*] IN *BRASSICA OLERACEA* AT THE SEEDLING STAGE**

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The high variability of *Peronospora parasitica* (Pers. ex Fr.) Fr., the causal agent of crucifer downy mildew, includes pathotypes that are resistant to fungicides, or overcome the resistance genes of *Brassica oleracea*. The aim of this work was to identify sources of resistance related with the pathogenic variability of different *P. parasitica* isolates and to identify the existence of plants with differential reaction to the isolates. We inoculated seedlings of 11 accessions of *B. oleracea*, by depositing a spore suspension of isolates P501 (Portugal), P005 (UK) and P006 (UK) on the cotyledons, under controlled environment. Acces-

sions HRI4302, HRI5389, HRI6226, HRI5443 and ISA207 were resistant to the three isolates, with 15 to 93% of resistant seedlings per accession. Accessions HRI 5555 and HRI 6254, were susceptible to P501 and resistant to P005 and P006. In the second experiment we inoculated seedlings of 16 accessions with 8 isolates of diverse origin: P501, P502 and P517 (Portugal), P005 and P006 (UK), FP06 (France), P-Italiano (Italy) and P-Murcia (Germany). There was a clear accession x isolate interaction which suggested several response groups: A—CrGC 3.4 and KB62/00; susceptible to all eight isolates; B—KB01/00, KB14/00, KB091, KB092 and KB566R resistant to only one different isolate; C—KB4/00 and KB13/00 resistant to three and five isolates, respectively; D—KB10/00, KB207/00 susceptible to P502 and P517; E—KB85 and KB87 susceptible only to P501; and F—KB5/00, KB10/00 and KB14A/00 resistant to all isolates used in the experiment. This study recognised common genes for specific resistance to downy mildew in various genotypes and will be used in the development of a set of differential plants for pathotype discrimination. In parallel, the crosses between resistant individuals and a susceptible rapid cycling line are also expressing putative differential responses.

#### 1340–1440

##### S17–P–35

### GENETIC ANALYSIS OF IMPORTANT FRUIT CHARACTERS OF TOMATO BY INVOLVING LINES POSSESSING MALE STERILITY GENES

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The present investigation was carried out at the Vegetable Research Farm, Punjab Agricultural Univ., Ludhiana to study the worth of male-sterile lines of tomato in combination with already identified superior performing male parents. The plant material comprised 40 F1 hybrids obtained by crossing four genetic male sterile (pollen abortive type) lines with 10 male parents in a line x tester fashion. Observations were recorded on number of locules, pericarp thickness, equatorial diameter, polar diameter, TSS, fruit weight and total yield. Analysis of variance for combining ability revealed that the MS due to hybrids was significant at  $P = 0.01$  for all the characters studied. Partitioning of total genetic variability into different components revealed significance of GCA lines, GCA testers and SCA hybrids for all the characters. The ratio of SCA/GCA indicated a greater role of non-additive gene effects for all the characters except equatorial diameter where additive and non-additive gene effects were, more-or-less, equally important. None of the parents studied exhibited good GCA effects for all the characters studied. Two parents, 'P 259' and 'W 321', proved to be good combiners for TSS and total yield. Based upon the inferences drawn, parents 'L 211', 'P 259', 'W 321' and 'W 322' have been recommended for their utilization in genetic improvement of tomato through pure line breeding. The cross 'ms 45 VFN 8 x S 282' was identified as the best combiner. The new hybrid not only out-yielded two commercial checks 'TH 802' and 'TH 2312' by a margin of more than 50 percent, but was also either superior or at par with the better check for rest of the characters.

#### 1340–1440

##### S17–P–36

### RELATIONSHIPS OF VIRUSES, SYMPTOMS AND CULTIVARS TO LETTUCE BIG-VEIN DISEASE

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Lettuce big vein is an important soil-borne virus disease, and causes great losses in lettuce in the world. Recently, lettuce big vein virus (genus *Varicosavirus*) or/and Mirafirori lettuce virus (genus *Ophiovirus*) is/are assumed to be a causal agent or agents of this disease. For lack of specific detection methods of these viruses, the resistance has been evaluated only by symptoms. Therefore, the relations between viruses and cultivars of lettuce were not clear. We developed a specific immunoassay to detect these two viruses, and compared the relations of these viruses, symptoms and lettuce cultivars to lettuce big-vein disease. About 50 cultivars of lettuce plants, which were crisphead, cos, butterhead, leaf and stem lettuce, were grown on a big vein-infested field from 30 Oct. 2000 to 12 Jan. 2001. Lettuce leaves with or without symptoms were used to detect the two viruses by Western blotting analysis using monoclonal or polyclonal antibodies against these viruses. Concerning crisphead lettuce plants, symptoms of resis-

tant cultivars were apparently less and weaker than those of susceptible ones, while the viruses were detected from some resistant cultivars without symptoms. Many butterhead lettuce plants without symptoms contained these viruses. The relationship of two these viruses to the expression of big vein symptoms were not revealed in this trial. However, the detection of viruses ought to be introduced as a selection criterion for lettuce breeding to big-vein disease. Our results open a new chapter on lettuce big-vein disease, a classical and commercial important but still elusive disease.

#### 1340–1440

##### S17–P–37

### CLASSIFICATION AND PRODUCTIVITY OF INDUSTRIAL TOMATO CULTIVARS

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The present work aimed to study the productivity and classification of 28 tomato cultivars for industrial processing. The experiment was carried out in Jaboticabal-SP, Brasil, at 21°15'22" South, 48°18'58" West, at an elevation of 575 m, in Haplorthox soil, from June to December. The cultivars H 7155, Hypeel 108, Andino, U 573, H 9036, Ipa 6, H 9494, AG 33, Yuba, RPT 1294, AG 72, Peelmech, Curico, Hypeel 45, RPT 1478, H 9492, H 9498, H 2710, Hitech 45, Halley, Botu 13, H 9553, U 646, NK 1570, AG 45, RPT 1095, RPT 1570 and PSX 37511 were evaluated. The experimental design was randomized blocks with five plants per plot, replicated four times. Fruits harvested from each plot were counted, classified by transversal diameter (great, medium, small, smallest, and reject) and weighted posteriorly. As for total number of fruits yielded, the cultivars H 9498, Curico, Hypeel 45, RPT 1095 and AG 72 presented an average above 70 fruits per plant. The total production per plant of cultivars AG 72, H 9498, Hypeel 45, H 7155, Hypeel 108, Halley, Hitech, RPT 1095, H 9494, H 9036 and Curico was higher than 4 kg. It was observed that the cultivars H 2710, Botu 13, U 573, Hypeel 45, Yuba, RPT 1294 and Ipa 6 presented values above 50% for production, considering the weight of great and medium fruits, categories which are important for in natura market.

#### 1340–1440

##### S17–P–38

### UNEXPECTED SUSCEPTIBILITY OF NOVEL BREEDING LINES OF EUROPEAN RHUBARB (*RHEUM RHAPONTICUM*) TO LEAF AND PETIOLE SPOT DISEASES.

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Rhubarb is an important vegetable crop grown in Northern Europe, the USA and Canada, with breeding lines lacking physiological dormancy being developed in the UK to extend seasonal production. Spotting diseases of leaves and the marketed, edible, petioles are observed on conventional cultivars of this crop with leaf disease being widespread across the cultivar range yet of little commercial significance, as leaves are non-edible and trimmed from the marketed product. Petiole spotting is a potentially serious, but typically limited, problem in conventional crops with material showing this symptom being rejected in the retail marketplace. Breeding lines selected for the absence of summer dormancy are as susceptible as conventional cultivars to leaf spot diseases, caused by *Ramularia rhei*. However, the petioles are also highly susceptible to petiole spotting resulting in market rejection of up to 70% of otherwise marketable sticks. The causal agent is *Ascochyta rhei* and the characteristics and pattern of infection, in vitro growth and likely control of these pathogens will be considered.

#### 1340–1440

##### S17–P–39

### MUSKMELON VARIETY EVALUATION IN SOUTHWESTERN INDIANA, TRENDS FROM A DECADE OF RESEARCH

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Indiana continues to be a leading producer of muskmelons, and southwest-

ern Indiana is the center of the industry in the state. This area is marked by several unique soil and climatic features including large areas of sandy, well drained soils and early-season warm temperatures. These conditions combine to allow for the production of high quality fruit. Independent and objective evaluation of new cultivars and advanced experimental genetic material has been a cornerstone of Purdue's outreach effort in this area for over a decade. An examination of the performance and quality of these materials over several years is presented and discussed. Trends emerged to show that typically the highest quality varieties, and thus the highest ranking in these trials, have been high yielding, early maturing types with a large uniform fruit size. Market preference tends toward fruit with heavy netting and distinct ridges. In addition, years of evaluation on the internal and eating quality of these melons have also been carried out. These variety trial results are examined in light of a recent survey revealing producer rankings of the importance of various evaluation characteristics. The influence of climatic conditions on variety performance is explored across growing seasons. There is over a century of combined muskmelon evaluation experience in the staff members of the Southwest Purdue Agricultural Program and Center which allows them to continue to be at the forefront of muskmelon variety evaluation.

1340-1440

S17-P-40

#### GENETIC PARAMETERS OF MEAN FRUIT WEIGHT AND THEIR COMPONENTS OF TOMATO

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Tomato breeding in Mexico has been oriented to increase yield and to improve earliness, growth habit, and tolerance or resistance to environmental stresses, pests and diseases, but varieties with firm fruit and high quality are necessary. The present research determined gene action for mean fruit weight, pericarp weight, and locule content weight. A complete diallel using 10 experimental lines was evaluated during Spring-Summer 1998 in a greenhouse at Lomas de Cristo, Mexico, and in a non-recirculating, open hydroponic system using Steiner's Universal solution applied via drip irrigation at 0.7 atm osmotic pressure. The experimental design was a 10 x 10 partially balanced lattice with two replications. To estimate mean fruit weight, pericarp weight and locule content weight, fruit were collected mature, weighed individually, cut equatorially to extract locule contents and fruit parts weighted separately. A genetic variance analysis was done following Griffing's method 1. Additive genetic effects prevailed; narrow sense heritability was low, 18% to 25%. Improvement of these characters in selection requires the appropriate breeding method, using a low pressure selection index. The best parents (CJPL-8-7-4, CJPL-7-8-4, CJPL-2-2-1) were equal in their general combining ability for the three characters studied. A consistent response is expected when these characters are used as selection criteria. Mean fruit weight components permit improvement for soluble solids and fruit flavor along with increased fruit weight. Significance of reciprocal effects indicates mean fruit weight and its components were affected by the male parent. Parents with the highest reciprocal effects estimates for crossing should be identified before initiating a selection process. An equilibrium exists between pericarp weight and loci weight content, an increase in one lowers the other.

1340-1440

S17-P-41

#### EFFECT OF SILVER NITRATE ON INDUCTION OF STAMINATE FLOWERS IN GYNOECIOUS CUCUMBER LINE (*CUCUMIS SATIVUS* L.)

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Cucumber is the second largest vegetable cultivated under greenhouse in Albania. Being so important for our country, the Vegetables and Potato National Research Institute is working intensively to create and introduce new hybrids suitable for the Albanian climate. Our breeding work is based on the creation of new hybrids from crosses of different gynoecious lines by inducing staminate flowers. The present study was carried out to investigate the effect of silver nitrate (AgNO<sub>3</sub>) concentration and number of sprays on sex expression of a gynoecious,

parthenocarpic cucumber line. The initial sprays were applied at the first true leaf stage of growth, and subsequent treatments were applied at weekly intervals. Treatment effects were evaluated through anthesis at the 10th node. Induction of staminate flowers was dependent upon AgNO<sub>3</sub> concentration and number of sprays. All treatments using one spray were ineffective in producing staminate flowers. The treatments with 100 ppm failed to induce staminate flowers. The greatest numbers of staminate nodes were produced on plants sprayed 2x or 3x with 400 ppm to 500 ppm. Plants showing injury a few days after spraying with 400-500 ppm recovered within 7 to 10 days. These results demonstrate that commercial seed production of gynoecious hybrids is feasible when the staminate parent is gynoecious, which permits maintaining homozygous gynoecious inbreds.

1340-1440

S17-P-42

#### GENETIC ANALYSIS OF YIELD IN TOMATO BY INVOLVING GENETIC MALE STERILE LINES

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Thirty-six F1 tomato hybrids, developed from crosses of three genetic male-sterile lines and 12 superior performing male parents, were grown along with parents and two check hybrids, TH 802 and TH 2312, to study combining ability effects of parents and hybrids. The experiment was laid out in an RBD using three replications and observations were recorded on fruit weight (g), marketable yield (kg/plant) and total yield (kg/plant). The ANOVA for the experimental design revealed significant differences among genotypes, parents, hybrids and parents v/s hybrids. Combining ability analysis revealed the greater importance of additive gene effects for fruit weight and non-additive gene effects for total yield and marketable yield. Among lines, ms 45 was a good general combiner for fruit weight and total yield. Among testers, I 181, I 183 and S 286 were good general combiners for marketable and total yield. These parents are recommended for their utilization in hybridization program to develop high-yielding, true-breeding lines. The crosses ms 1036 x I 181, ms 45 x I 181 and ms 1547 x U 301 proved good specific combiners for total yield. These hybrids also proved significantly higher yielding compared to the check hybrids and are therefore, recommended for multi-location testing before their commercial use.

1340-1440

S17-P-43

#### BREEDING STUDIES ON PEPPER

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Heterosis, combining ability and inbreeding depression for some characters were studied in pepper. The study was conducted under unheated plastic houses conditions. Hybrid vigor was detected for both early and total fruit yield, and significant positive average degree of heterosis values were obtained. Both additive and non-additive gene effects were involved in the inheritance of the studied traits. The additive gene effects were more important than the additive ones in the genetic mechanism. The best combiner cultivars or lines were: Feherzon, 25-1, Yolo Wonder and Greyga for early yield; Sweet Banana, Marconi Rosso, Casca Dura and Avelar for total yield as fruit number and weight. The best F1 hybrids were: Feherzon x Sweet Banana and Avelar x Marcony Rosso for early yield; 5-27 x Yolo Wonder, Suptol x Avelar and 5-27 x Casca Dura for total yield. Regarding inbreeding depression, all F2 populations were lower than their corresponding F1 crosses in early and total yield.

1340-1440

S17-P-44

#### EVALUATION OF FRESH MARKET TOMATOES FOR RESISTANCE TO EARLY BLIGHT INCITED BY *ALTERNARIA SOLANI*

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*Alternaria solani*, or early blight is the major pathogen affecting tomato. It occurs with devastating effects throughout the U.S. wherever high temperatures (24 to 27 °C) and RH (75%) prevail. A high dew point exacerbates the problem.

Early signs of infestation are dark, girdling lesions around the base of the stem and circular lesions on older leaves. As the foliar lesions enlarge, concentric rings appear, forming a target pattern. Eventually the entire plant is defoliated. While varying levels of tolerance have been observed, immunity to early blight is not known in *Lycopersicon esculentum*. Resistance to *A. solani* is controlled by multiple genes and is affected by epistasis, or gene interactions within a genotype. The complexity of this disease has discouraged efforts to develop genetic tolerance. However, a few cultivars are available that express tolerance to *A. solani*. Growers control this disease by the application of 8–15 fungicide sprays each season, by long crop rotations, and field sanitation. Increased use of genetically resistant plants could reduce the amount of fungicides applied. For this study 15 fresh market tomato cultivars were evaluated for *A. solani* under field-grown conditions. Cultivars were evaluated when approximately 50% of the fruit were ripe, and again 10 days later. Stem-, leaf-, fruit-, and whole-plant evaluations were conducted. Varying levels of tolerance to *A. solani* were observed. In whole-plant evaluations, cultivars showing the greatest tolerance to the pathogen included Mountain Fresh and Better Boy, while those showing the least tolerance were Red Rider and Sunstart. Whole-plant and leaf evaluations yielded similar results. Fruit were not severely affected, except for 'Red Rider', 'Mountain Spring', and 'Fabulous'. Of these three, 'Red Rider' was most severely affected. 'Sunrise' had the greatest tolerance in stem evaluations, while 'Red Rider' was least tolerant.

**1340–1440**

**S17–P–45**

**SCREENING SHORT-DAY ONION LINES FOR FUSARIUM BASAL ROT RESISTANCE**

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Fusarium basal rot (FBR), causal organism *Fusarium oxysporum* f. sp. *cepae*, is a worldwide soil-borne fungal disease that affects bulb onions (*Allium cepa* L.). Short and intermediate-day onion cultivars that are resistant to FBR are lacking. Breeding efforts are underway to develop resistant cultivars. The goal of this project was to screen short-day onion germplasm for FBR resistance using an inoculated seedling screening in a growth chamber and a mature bulb field screening. In growth chambers, forty-two short-day onion lines were seeded in silica sand infested with  $4.0 \times 10^4$  spores·g<sup>-1</sup> sand. At two weeks, the number of germinated seedlings were counted and the chamber temperature was increased from 22 to 28 °C. At four weeks, the number of surviving seedlings were counted and a percent survival rate was calculated for each line. The same onion lines were grown in a field known to produce a high incidence of FBR-infected bulbs. When all the bulbs in a plot were mature, the basal plates of 30 bulbs were cut transversely and each plate was rated for disease severity on a scale of 1 to 9. The FBR incidence was calculated from the number of bulbs with FBR out of total bulbs tested. In growth chamber studies, 'NuMex Luna' and NMSU 00-32 had the highest survival percentages (23.6% and 20.4%, respectively). In field studies, 'Cardinal' was found to have the highest FBR incidence (90.8%) and the highest FBR severity (4.9). NMSU 00-13-1 was found to have the lowest FBR incidence (10%) and the lowest FBR severity (1.11). A strong, positive correlation existed between FBR incidence and severity while both traits were weakly correlated with seedling survival.

**1340–1440**

**S17–P–46**

**VARIETY EVALUATION OF CONTAINERIZED CHERRY TOMATO (*LYCOPERSICON ESCULENTUM* MILL.)**

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Gardening is the number one hobby in the United States, and container balcony gardening is becoming more and more attractive to people living in high-density urban areas. The objective of this study was to evaluate different varieties of cherry tomatoes (*Lycopersicon esculentum* Mill.) grown in containers under

South Florida conditions. Seven cherry tomato varieties were grown in fall of 2000 in a complete randomized block design. All varieties were germinated in a Styrofoam flat and then transplanted into seven-gallon containers (one plant per container). Data collection included percent germination, plant height at transplant, days to flower, number of fruit per cluster, number of clusters per plant, and total yield. A three-judge panel rated the varieties for flavor and appearance. The highest percent germination was obtained from 'Sweet Million FT-R', while 'Sweet Million FNT' and 'Naomi' had the highest plant heights at transplant. 'Sweet Million FNT', 'Camelia', 'Supersweet 100 VF' and 'Sweet Million FT-R' took the least number of days to flower. There were no significant differences among varieties in total yield, due to differences in the number of fruit per cluster. There were also no differences among varieties for flavor and appearance test. The best overall varieties were 'Sweet Million FNT', 'Sweet Million FT-R' and 'Camelia'.

**1340–1440**

**S17–P–47**

**BREEDING MUSKMELON FOR RESISTANCE TO VINE DECLINE**

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Melon vine decline is a major disease for melon crop. In Spain, *Acremonium cucurbitacearum* and *Monosporascus canonballus* are the main causal agents of this complex disease. Several sources of resistance have been identified in field and greenhouse assays conducted in USA and Spain. Specific resistance to the fungi along with a more vigorous root system has been proposed as mechanism of resistance. We characterized the response to vine decline of the tolerant cultivars, Doublon and Deltex, selected in USA, and the wild accession *Cucumis melo* subsp. *agrestis* Pat81, selected in Spain. Plants were grown in naturally infested soil (NIS), in soil artificially infected with *Acremonium* (A), with *Monosporascus* (M), and in sterilized soil (SS). Lesions caused by fungi in hypocotyls (LH), lateral roots (LLR) and fine roots (LFR) were scored from 0 to 4. Other root parameters, such as the root fresh weight (RFW), were also measured. The Spanish cultivars Piel de Sapo and Amarillo Canario were used as susceptible controls. NIS and M treatments caused lesions significantly more severe than the A-treatment in all genotypes, at 30 days after inoculation. Pat81 exhibited the highest level of resistance to NIS and M, with scores of 0.2/1.3/1.8 for LH/LLR/LFR in NIS, compared to the susceptible controls (3.3/2.7/3.0). 'Doublon' was also highly resistant to M inoculation, but developed more severe lesions in NIS (0/1.8/2.1). The response of 'Deltex' was intermediate. 'Doublon' had a more greater root weight than Pat 81 in SS. No significant differences in RFW were observed between SS and NIS for Pat 81, whereas 'Doublon' suffered weight losses of 12% in NIS. The fact that Pat 81 was more resistant to pathogens occurring in naturally infested soils from Spain, where it has been selected, may have important implications in breeding for resistance to this complex disease.

**1340–1440**

**S17–P–48**

**EVALUATION OF ABILITY OF COMBINATION AND HETEROSIS FOR CHARACTERISTICS OF MUSKMELON FRUITS**

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The objective of this work was to estimate the general and specific ability combining (GCA and SCA) between five cultivars of muskmelon, to identify occurrence of reciprocal effects (RE) of the characteristics associated with fruit quality, and to evaluate the heterosis expressed by the F1 hybrids. The hybrid seeds were produced in a greenhouse of the experimental area of the Dept. of Crop Production at FCAV/UNESP-Jaboticabal-SP-Brazil. Reciprocal crosses among the five cultivars produced 10 hybrids and 10 reciprocal hybrids. The five cultivars, and their 10 hybrids and 10 reciprocal hybrids were evaluated in a greenhouse using a randomized block design with three replications. Each plot consisted of three plants on a 0.8 m x 1.0 m spacing. The fruit characters evaluated were: weight, transversal and longitudinal diameter, thickness and color of flesh and skin, transversal and longitudinal locule diameter, seed cavity dryness (dryness), total percentage of soluble solids (°Brix), pH, and total acidity. The GCA effects showed that the progenitors JAB-22 e JAB-23 stood out from the others for mean longitudinal diameter. Based on GCA, SCA and RE, the best hybrid combination was JAB-20 x JAB-21 for dryness and longitudinal diameter of fruit. Reciprocal ef-

fects were observed for dryness and color of epicarp and endocarp. Positive heterosis was observed for longitudinal diameter and dryness.

**1340-1440**

**S17-P-49**

**EVALUATION OF PRODUCTION PERIOD FOR TOMATO CULTIVARS OF DETERMINATE GROWTH**

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The present work was carried out in Jaboticabal-SP, Brazil, at 21°15'22" South, 48°18'58" West, at an elevation of 575 m, in Haplorthox soil, during June–December. The objective of this work was to study the productivity of 28 tomato cultivars for industrial processing at three harvest stages (119, 149 and 179 days after seeding). The cultivars were: H 7155, Hypeel 108, Andino, U 573, H 9036, Ipa 6, H 9494, AG 33, Yuba, RPT 1294, AG 72, Peelmeh, Curico, Hypeel 45, RPT 1478, H 9492, H 9498, H 2710, Hitech 45, Halley, Botu 13, H 9553, U 646, NK 1570, AG 45, RPT 1095, RPT 1570 and PSX 37511. The experimental design was a randomized block with five plants per plot, replicated four times. There were no significant differences in productivity among the cultivars at the first stage of harvest. At the second stage, AG 72 cultivar produced the highest total yield per plant (5.76 kg) followed by the cultivars Curico, H 9498 and Hypeel 45. At the third stage, Ipa 6 and H 9036 produced statistically higher yield per plant than the other cultivars. The second harvest stage was the most productive among the three stages. Cultivars noted for their earliness (>90% of total production at the first and second harvest stages) were: Curico, RPT 1095, U 573, H 9492, H 2710, Halley, Botu 13, U 646, NK 1570, AG 45, RPT 1570 and PSX 37511

**1340-1440**

**S17-P-50**

**CELL-TO-CELL INTERACTIONS IN ARTIFICIAL INTERGENERIC CHIMERAS BETWEEN RADISH AND RED CABBAGE**

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We have studied cell-to-cell genetic interaction in grafting, i.e., graft transformation, in vegetable crops for 10 years. We have obtained many genetic changes and gene transfer by in vivo grafting in red pepper and other crops, and are now trying to obtain intergeneric transformants using an in vitro chimera system. Recently, we investigated graft transformation using artificial chimeras synthesized by in vitro grafting between radish and red cabbage to study the intercellular interactions between at morphological, physiological and molecular levels. Morphogenetical and physiological interactions were clearly observed in the chimeras as well as in interspecific *Brassica* chimeras. Generally, chimeral tissues were intermediate state depending on the contributed tissues (or cell layers). Irregular behavior was observed, for example, four layer structure appeared in revertant radish type of chimera instead of three layer one. Pollen and pod fertility was distorted either negative or positive according to the layer constitutions. Cabbage tissue in particular was negatively affected for pollen and pod fertility. A new, highly branching type appeared in chimeras. However, clear genotypic change in the progenies derived from chimeras has not been obtained. Interestingly, new amplified fragments specific for chimeras were obtained in PCR experiment, suggesting the existence of genetic or gene interactions in chimeral tissue itself.

**1340-1440**

**S17-P-51**

**SCREENING METHOD OF RESISTANCE TO TIPBURN IN CHINESE CABBAGE**

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Tipburn is a physiological disease caused by drought, calcium deficiency, excessive salt, or excessive nitrogen. Typically, it shows as tipburn of new head leaves which may then rot. Tipburn may cause serious loss of product. Four Chinese cabbage cultivars were evaluated for resistance to tipburn at the seedling stage of growth when grown in perlite and watered with standard and modified Hoagland solution. Tipburn was induced using Hoagland solution without calcium and with high level

nitrogen (2X). Tipburn symptoms were divided into seven classes (0, 0.5, 1, 3, 5, 7, 9). Symptoms occurred quickly and became more serious with increased ammonium nitrate in the absence of calcium. Furthermore, the seedlings were dwarfish and yellow. Tipburn occurred earlier in solution short of both calcium and trace elements. The calcium content of young leaves in the calcium deficient treatment was 0.157% of dry leaf weight, which was 8.3% that of the check. 'Jing Spring King' was resistant, and the line 99-481 was highly susceptible. The results of the seedling test were consistent with field results.

**1340-1440**

**S17-P-52**

**SCREENING METHOD OF BOLTING RESISTANCE IN CHINESE CABBAGE**

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Bolting resistance is very important character for spring cultivars in Chinese cabbage, and serious yield loss of may be caused by bolting before harvest. Eighteen Chinese cabbage lines were evaluated for bolting resistance using seed vernalization and supplemental light to provide longer days. The best treatment combination for identification of bolting resistance in this study was obtained by vernalizing the seeds at 3 °C for 20 days for, then sowing them and growing in a greenhouse at 20–22 °C and 16 hours photoperiod using supplementary light (6000-8000 lx). Time (days) to the appearance of buds and length of dwarf stem were suitable indexes for identification of bolting resistance. Four classes were identified based upon bud appearance: extra late: >40 days; late: 31–40 days; medium: 25–30 days; early: <25 days. Three classes were identified based upon length of dwarf stem: strong: <2 cm; medium: 2–5 cm; weak: >5 cm. The results of seedling identification were consistent with those of a field test.

**1340-1440**

**S17-P-53**

**EXTENDING THE RANGE OF TROPICAL ZAVORYR PEPPER (*CAPSICUM CHINENSE*) BY BREEDING AND HIGH-TUNNEL CULTURE**

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One potential benefit from use of season-extending high tunnels is the environmental niche they may offer for growth of tropical plants being introduced or bred for northern adaptation. We are breeding South American Aji dulce (*Capsicum chinense*), a very low pungency relative of ultra-hot pepper, Habanero, for growth in eastern U.S. The potential benefit is that unique flavors previously hidden in capsaicin heat will become available to the culinary industry. This breeding work has involved a recurrent backcross program to introduce genes for earliness from *Capsicum annuum* and from selected strains of *C. chinense*. The end-product, which we are calling Zavoryr® Pepper has been partially successful in producing good yields of quality peppers consistently at Penn State Univ.'s South-East Station in the Piedmont region near Lancaster, Pa. Typically it has failed to yield well near State College, Pa. in the mountainous central part of the state, where the season is shorter and cooler. In an effort to see whether high tunnel culture could make this pepper available for growers in areas of this sort we have raised strains of Zavoryr® Pepper in high tunnels near State College for two years for comparison with growth of the same strains under field conditions in State College and near Lancaster. Results have been encouraging: Seedlings transplanted to high tunnels in mid-April produced four pickings of mature red-orange fruits between mid-August and mid-September yielding well into the commercial range. Data will be presented comparing yields under the three conditions and economic potentials for the product.

**1340-1440**

**S17-P-54**

**GENETIC ANALYSIS OF IMPORTANT FRUIT CHARACTERS OF TOMATO BY INVOLVING LINES POSSESSING MALE-STERILITY GENES**

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The present investigation was carried out at the Vegetable Research Farm, Punjab Agricultural Univ., Ludhiana to study the worth of male-sterile lines of tomato in combination with already identified superior performing male parents. The plant material comprised 40 F1 hybrids obtained by crossing four genetic male-sterile (pollen-abortive type) lines with 10 male parents in a line x tester fashion. Observations were recorded on number of locules, pericarp thickness, equatorial diameter, polar diameter, TSS, fruit weight and total yield. Analysis of variance for combining ability revealed that the MS due to hybrids was significant at  $P = 0.01$  for all the characters studied. Partitioning of total genetic variability into different components revealed significance of GCA lines, GCA testers and SCA hybrids for all the characters. The ratio of SCA/GCA indicated a greater role of non-additive gene effects for all the characters except equatorial diameter where additive and non-additive gene effects were, more-or-less, equally important. None of the parents studied exhibited good GCA effects for all the characters studied. Two parents, 'P 259' and 'W 321', proved to be good combiners for TSS and total yield. Based upon the inferences drawn, parents 'L 211', 'P 259', 'W 321' and 'W 322' have been recommended for their utilization in genetic improvement of tomato through pure line breeding. The cross 'ms 45 VFN 8 x S 282' was identified as the best combiner. The new hybrid not only out-yielded two commercial checks 'TH 802' and 'TH 2312' by a margin of more than 50%, but was also either superior or at par with the better check for the other characters.

#### 1340-1440

##### S17-P-55

#### BREEDING OF LATE BOLTING CRISPHEAD TYPE LETTUCE 'NAAES NO. 1'

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'NAAES No. 1' was developed at New York State Agricultural Experiment Station, Geneva from a cross of 'Montello' and 'Saladcrisp', and advanced using pedigree selection to the F7 generation. It was planted in a greenhouse during winter for seed propagation in 1999. In the summers of 2000 and 2001, it was planted in an alpine area (elevation 800 m) of Korea for evaluating adaptation and comparison with other lines and commercial cultivars. It showed good growth, was late in bolting, and produced greater head weight and higher yield (45.8 t-ha<sup>-1</sup>) each year compared to another inbred lines and 'Urake', which was the most popular variety in Korea.

#### 1340-1440

##### S17-P-56

#### GROWTH PATTERN OF CAULIFLOWER AND BROCCOLI IN RELATION TO ACCUMULATED DAILY TEMPERATURES

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A simple measure of the rate of increase in plant weight, i.e., growth rate, is the slope of the plot of total weight per plant against time (HUNT, 1982). This theoretical approach uses destructive measurements. For horticultural practice, non-destructive, easily measured parameters are needed, which allow to generate a model for harvest forecast. In the present work, results from two cultivars of cauliflower and broccoli in 2000 and 2001 are presented. In both years, plants were grown at three transplant dates (beginning, middle, and end of July), and measurements were taken at weekly intervals. The correlation of stem diameter and plant weight (equals total biomass), and curd diameter and curd weight were both significant ( $r^2 = 0.954-0.966$ ). Stem diameter and curd diameter, proved to be useful for describing plant growth and generating a plant growth model. Summarizing all available data (years, transplanting dates, cultivars), stem diameter correlates significantly with accumulated day degrees (ADD) (cauliflower:  $r^2 = 0.921$ ; broccoli:  $r^2 = 0.919$ ). The coefficients of regression are even greater when data are split by cultivar ( $r^2 = 0.916-0.953$ ), year ( $r^2 = 0.908-0.964$ ) and transplanting date ( $r^2 = 0.889-0.993$ ). Similar results were obtained for curd diameter

and ADD (cauliflower:  $r^2 = 0.694$ ; broccoli:  $r^2 = 0.709$ ), which when split by transplanting date fitted best ( $r^2 = 0.771-0.977$ ). This indicates that curd diameter shows higher genotypic variation and is more sensitive to environmental factors than stem diameter. On the basis of this regression, the required ADDs can be calculated for curd initiation and harvest date. Using data from weather forecast, prediction of harvest dates are possible. The knowledge of growth patterns in relation to ADDs also allows to qualify regions for suitability to cultivate different horticultural crops.

#### 1340-1440

##### S17-P-57

#### ESTIMATION OF GENETIC VARIANCE FOR ANTHRACNOSE RESISTANCE IN TOMATO USING RECOMBINANT INBRED AND INBRED BACKCROSS LINES

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Anthracoze is a fruit rot disease of tomato caused primarily by *Colletotrichum coccodes*. Rainfall, warm temperatures, and high humidity which occur at harvest in the midwestern U.S. and south-central Canada favor disease development. If left uncontrolled, serious crop losses and reduced crop quality occur in these production regions. Recombinant inbred tomato lines derived via single seed descent of F2 individuals from a cross of the anthracnose resistant *Lycopersicon esculentum* accession PI 272636 and the susceptible tomato cultivar US28 were utilized for a genetic analysis of tomato anthracnose resistance. Inbred backcross lines developed from the same cross were similarly evaluated. Heritability estimates, gene number and variance components for anthracnose resistance were estimated. After sufficient generations of inbreeding to achieve homozygosity, the recombinant inbred lines and inbred backcross lines become fixed for short linkage blocks of progenitor alleles. Since a genotype is represented by an inbred line, rather than an individual, a more accurate estimation of the genetic components can be made to evaluate quantitatively inherited traits such as anthracnose resistance. Estimates of genetic components derived from these lines are discussed in the context of prior estimates obtained using F2 and backcross populations.

#### 1440-1500

##### S17-O-58

#### RELATIONSHIP OF WHITE ROT RESISTANCE TO PYRUVATE AND S-ALK(EN)YL-L-CYSTEINE SULFOXIDES IN ONION ROOTS.

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*Sclerotium cepivorum* causes white rot and is a serious threat to the onion industry worldwide. *S. cepivorum* sclerotia are stimulated to germinate by *Allium* root organosulfur exudates. *Allium* organosulfur compounds are often quantified by a simple method measuring pyruvate. The objective was to determine if differences in white rot resistance levels were due to differing organosulfur profiles found in *Allium* roots. If so, pyruvate analysis of onion roots could be used as a disease resistance screen for plant breeders. Putative onion white rot resistant (RBL) and susceptible breeding lines (SBL) were grown in naturally infested fields in 1999 and 2000 (New Zealand) and in 2000 (Canada). Significant differences in disease incidence at harvest were found. The analysis of root juice from greenhouse-grown plants showed that garlic had significantly more pyruvate (20.5  $\mu$ moles/mL of juice) than leek (3.5) and the 8 onion breeding lines tested (5.0 to 2.7). The contrast comparing pyruvate concentration of roots between the 3 SBL and the 5 putative RBL was not significant. Root juice pyruvate concentration could not be used to distinguish the SBLs from the RBLs. The pyruvate data was used as a covariate to predict disease incidence in the field. Similar results were found for both countries. Pyruvate was not a good predictor of disease incidence. The interaction of pyruvate and onion breeding line was significant, highlighting the complexities of the relationship between organosulfur compounds and disease resistance. HPLC will be used to analyze S-alk(en)yl-L-cysteine sulfoxides (ACSOs) in and exuding from onion roots. The results will determine if differences in root ACSOs exist between SBL and RBL onions and the extent to which they predict field disease incidence among lines and can be used to screen for resistance.

1500-1520

S17-O-59

**DEVELOPMENT OF S1 FAMILIES IN GARLIC**

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Production of true seed in garlic (*Allium sativum* and *A. longicuspis*) has been known for several years. Although release of seed-derived varieties may be nearing reality, there are no reports on inheritance patterns for this species. One of the reasons for the lack of information may be due to difficulties associated with self-pollination of garlic plants and establishment of inbred families. From 1999 to 2001, over 500 garlic plants were self-pollinated to generate S1 progenies for genetic studies. In all years, the number of S1 seed harvested was low. About 10% of the self-pollinated plants produced from 10 to 71 seeds each. The seed germination rate averaged 8%, and the number of S1 plants established in field plots was even lower. Many seedlings had severe chlorophyll deficiencies, truncated roots, or did not grow beyond the first leaf stage. Several field-established plants showed stunted growth, or their bulbs deteriorated without senescence of foliage. Among plants of the S1 families, different phenotypic characteristics included the presence or absence of viable pollen; purple, white or yellow anther color; different intensities of chlorophyll degradation; and different plant habits and maturities. Despite these deleterious characteristics, S1 bulbs of a few families were successfully harvested and they represent valuable materials for studies on garlic genetics.

1520-1540

S17-O-60

**ESTIMATION OF VARIANCE COMPONENTS WITH LIMITED SEED PRODUCTION OF THE CROSSES**

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For those crop species in which a seed increase is required for evaluation of the crosses among individuals from a random sample taken to estimate the variance components of the sampled population, the selfing of the crosses has been suggested. Although this procedure assures the necessary amount of seed for the evaluation which yields the required information to assess the breeding potential of the population under study, it might be expensive and laborious. In addition, the theory for panmictic populations with multiple alleles has not been developed. This study was designed to derive a cheap and simple estimation method of genetic variance components of populations under these circumstances. From a sample of m males and h females the mh possible crosses were considered (each male was crossed with each female). From the crosses of each male, the seed was composited to evaluate m half-sib families. S1 seed from the selfing of each family was considered as well. The common parent of each half-sib family was also selfed. Thus, 3m families were considered for field evaluation. On the basis of the experimental information from this evaluation, estimators were derived for the variance of the additive and dominance effects and for the dominance deviation effects of the genotypes with identical-by-descent alleles. Estimators were also derived for the covariance between the additive and the dominant effects, the mean inbreeding depression of the population, and for the square of this mean. The described procedure makes possible the estimation of six parameters, and requires less resources than North Carolina designs I and II.

1540-1600

S17-O-61

**A PSEUDOEMBRYO WITH HIGHLY STAINABLE CELLS INDUCES FRUIT GROWTH OF PARTHENO-CARPIC TOMATO**

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The pseudoembryos are formed in the parthenocarpic tomato fruits genetically induced in 'Severianin' or can be auxin-induced also. We investigated the relationship between pseudoembryo development and parthenocarpic fruit growth. We defined in this report a thickening of endothelial integument cells as the beginning of the pseudoembryo formation. All fruits of the non-parthenocarpic tomato cultivar 'Kyoryoku-Kyokkou' treated with 15 mg·L<sup>-1</sup> 4CPA 0, 5 and 10 days

after anthesis began to grow immediately following the treatment. Endothelial integument cells did not thicken at anthesis. They thickened, stained poorly and remained undivided 5 and 10-days after anthesis. In the ovules treated with 4CPA 0, 5 and 10-days after anthesis, we observed that endothelial integument cells thickened and started cell division, or well-developed pseudoembryos were formed 5, 10 and 15-days after anthesis, respectively. Two parthenocarpic tomato lines originated from 'Severianin', 'MPK-1' and 'HOK-12' were investigated. 'MPK-1' strongly exhibits parthenocarpy and often starts the ovary growth before anthesis. In the growing ovary of 'MPK-1', the pseudoembryo began to form or occupied the embryo sac cavity. The ovary with well-developed pseudoembryos never failed to grow. In the same cluster, the pseudoembryo developed as the stage of the ovary advanced. 'HOK-12' can usually set fruits without developing. One day before anthesis, the endothelial integument cells thickened, stained poorly and did not divide. Ten days after anthesis, they were in a similar state. Treatment with 4CPA at anthesis induced ovary growth, and well-stained pseudoembryo occupied the embryo sac cavity 7-days after the treatment. As a result, it was suggested that the well-developed pseudoembryo with highly stainable cells induced sufficient fruit growth, and the fruit setting required thickening of endothelial integument cells, whether they were highly stainable or not.

1600-1620

S17-O-62

**NO ABSTRACT PROVIDED**

1620-1640

S17-O-62-A

**TO BE ANNOUNCED**

1640-1700

S17-O-62-B

**TO BE ANNOUNCED**

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**Thursday · August 15**

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1100-1120

S17-O-63

**RECENT ADVANCES IN MOLECULAR BREEDING: THE EXAMPLE OF TOMATO BREEDING FOR FLAVOR TRAITS**Mathilde Causse\*<sup>1</sup>, Laurent Lecomte<sup>1</sup>, Angélique Gautier<sup>1</sup>, Michel Buret<sup>2</sup>, Frédéric Hospital<sup>3</sup>

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With the development of molecular markers, genetic maps have been constructed in plant species, which allowed the location of major loci and QTLs controlling agronomical trait variation. Molecular markers were widely used for the introgression of major loci, but marker assisted selection for quantitative trait breeding is more rarely used. Both theoretical and applied aspects of marker assisted backcross will be presented, with special emphasis on a program of tomato breeding for flavor traits. Improving organoleptic quality of fresh market tomato fruit has become an important objective for tomato breeders. Several QTLs controlling the variation of tomato quality traits have been detected in the progeny of a cross between a cherry tomato chosen for its good flavor and a line with bigger but less tasty fruits. 37 traits involved in fruit quality were evaluated. Physical traits included fruit weight, color and firmness. Chemical traits were dry matter weight, titratable acidity, pH, and the contents of soluble solids, sugars, lycopene, carotene and 12 aroma volatiles. The lines were also evaluated by descriptive sensory profiling. Taste and aroma were analyzed through sweetness, sourness, overall aroma intensity, together with several specific aromas. Texture was also assessed. A number of QTLs were detected for all the traits, some with strong effects. Co-localizations of QTLs controlling several traits were found. Most of the favorable alleles came from the cherry tomato parent, showing the potential usefulness of this line for tomato organoleptic quality improvement. A marker

assisted selection scheme was thus initiated in order to transfer into elite lines the five most important QTLs involved in fruit quality. Three recurrent lines were chosen in order to study the effect of genetic background on QTL expression. The backcross scheme was first optimised taking into account both theoretical and practical aspects. The application of the scheme will be presented.

**1120-1200**

**S17-0-64**

**DEVELOPMENT OF RAPD MARKERS LINKED TO THE MALE STERILITY ALLELE, MS-3, IN *CUCUMIS MELO* L.**

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The popularity of hybrid varieties for commercial production of western shipper melons can be associated with increased vigor and earliness compared to open-pollinated lines. The production of hybrids requires laborious emasculation of seed parents and leads to expensive seed. Genic male sterility, conditioned by the single recessive allele, ms-3, provides a potentially stable and effective means to generate larger quantities of hybrid seed with less contamination and much less labor. Several families were developed at the Weslaco Experiment Station using sterile (ms-3/ms-3) plants as seed parents and mildew resistant western shipper lines as pollen parents. The goal was to employ backcrossing to introgress the ms-3 allele into several, high quality inbred western shipper lines. These lines could then be used as parents to produce hybrid seed in field plots. One F<sub>2</sub> family of the cross ms-3/ms-3 x 'Dulce' was utilized to develop RAPD molecular markers linked to the sterility allele. All F<sub>2</sub> plants were grown in plastic pots in a greenhouse. Each individual plant was phenotyped for sterility and DNA was extracted from young leaf tissue. All fertile plants were selfed and F<sub>3</sub> progenies were planted in the greenhouse to confirm the homozygous or heterozygous nature of the F<sub>2</sub> plants. Bulked segregant analysis was performed with 7-10 plants of both homozygous fertile and sterile genotypes. Several markers were identified as linked to the ms-3 allele and several linked to the fertility (MS-3) allele. These should be useful in the process of marker-assisted selection to expedite the inbreeding of lines carrying the ms-3 allele. Expansion of the number of RAPDs screened and addition of AFLP markers have been undertaken as well.

**1200-1220**

**S17-0-65**

**OPTIMISATION OF CUCUMBER (*CUCUMIS SATIVUS* L.) DIHAPLOID LINE PRODUCTION USING IN VITRO RESCUE OF IN VIVO INDUCED PARTHENOGENIC EMBRYOS**

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Production of haploids through androgenesis or parthenogenesis is used frequently in modern breeding programs. Haploids facilitate the recovery of recessive mutations and unique genetic recombinations. Furthermore, chromosome doubling of haploids allows the production of homozygous dihaploid lines (DHLs), which can be used directly in hybrid production. The protocol developed involves the following: 1) in vivo induction of parthenogenic embryos by pollination with pollen irradiated at 0.5 KGy with a <sup>60</sup>Co gamma ray source; 2) in vitro rescue of putative parthenogenic embryos identified by their morphology and localized under a dissecting scope or X-ray radiography; 3) discrimination of undesirable zygotic individuals from the homozygous plants using cucumber and melon SSR markers; 4) determination of ploidy level from homozygous plants by flow cytometry; and 5) in vitro chromosome doubling of haploids. Codominant markers and flow cytometry confirmed the gametophytic origin of plants regenerated by parthenogenesis, since all homozygous lines were haploids. No spontaneous doubled haploid plants were rescued. Chromosome doubling of haploid plants was accomplished by an in vitro treatment with 500 mM colchicine. Rescue of diploid or chimerical plants was confirmed by flow cytometry, previous to their acclimation and plant growth in the greenhouse. Selfing of colchicine-treated haploid plants allowed the perpetuation by seed of homozygous lines. Seeds were harvested from almost all lines after selfing in the greenhouse. The high rate of seed production facilitated the recovery of inbred lines. Despite some limiting factors, parthenogenesis is routinely used in a cucumber-breeding program to achieve complete homozygosity in one generation, and accelerate breeding for new commercial varieties. So far, DHLs have been used as parental lines for the produc-

tion of commercial hybrids.

**1220-1240**

**S17-0-66**

**A NEW PARADIGM FOR THE BREEDING OF LONG-GENERATION HYBRID CROPS**

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Many economically important horticultural crops possess longer generation times, including the biennial vegetables, woody ornamentals, and tree crops for the production of fruits, nuts, and wood products. The genetic improvement of these long-generation crops is a slow process requiring long-term commitments of time and resources. As a result, breeders cannot quickly address changes in consumer preferences or production environments, such as the loss of pesticides. In spite of massive public and private investment in biotechnologies, the predominant approach to the genetic improvement of these crops remains pedigree breeding with backcrossing to introduce desirable disease resistances and cytoplasmic male sterilities (CMS). In this presentation, I describe a breeding scheme using new and previously described technologies to reduce the time and investment required to breed competitive hybrids of long-generation crops. The approach is based on population improvement by recurrent selection to increase the frequency of favorable alleles and linkages; the extraction of haploids and their doubling to produce uniform inbreds; the testing of these inbreds to identify superior parents for hybrid production; transformation of the nuclear genome to introduce simply inherited disease resistances or other value-added traits; and transformation of the mitochondrial genome to produce CMS lines for hybrid-seed production. I will review salient literature on each step of this breeding approach and identify the research challenges to the implementation of this new paradigm.

**1340-1440**

**S17-P-67**

**EVALUATION OF SNAP BEAN BREEDING LINES FOR HEAT TOLERANCE**

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Heat stress is a limiting factor in snap bean production which can result in the failure or reduction of pod set and can have effects on the uniformity of pod shape and sieve size. Heat tolerant snap bean breeding line '8333' was crossed to the variety 'Venture' and advanced to the F<sub>5</sub> generation, screening for heat tolerance in the F<sub>2</sub> and F<sub>3</sub> populations. A total of 122 F<sub>5</sub> breeding lines were evaluated for heat tolerance during 2001 field and greenhouse trials. The twelve most tolerant lines were selected based on yield, set and type under heat stress. Replicated greenhouse tests were undertaken to evaluate these lines for heat tolerance using day/night temperatures of 35 °C/32 °C with a 12-hour photoperiod from seven days prior to anthesis through senescence. Components of heat tolerance were examined including abscission rates, pod set, pod fill, malformed pods and yield. Crosses of the most tolerant lines have been undertaken to improve the type and generate populations for evaluating genetic components controlling heat tolerance in snap beans.

**1340-1440**

**S17-P-68**

**REPRODUCTION AND CYTOGENETIC CHARACTERIZATION OF INTERSPECIFIC HYBRIDS BETWEEN *CUCUMIS HYSTRIX* CHAKR. AND *C. SATIVUS* L.**

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An interspecific hybrid between *Cucumis hystrix* Chakr. (2n = 24) and *C. sativus* L. (2n = 14) was reproduced by means of embryo rescue and subsequent chromosome doubling. Hybridity was confirmed using both genomic in situ hybridization (GISH) technique and chromosome counts. The amphidiploid was

selfed and backcrossed to cucumber to produce genetically enhanced cucumber germplasm. An investigation of pollen grain shape, stainability and germination rate, and fruit set indicated that fertility was increased as progeny were produced as diploids ( $2n = 19$ ), amphidiploids ( $2n = 38$ ), and BC1F1 ( $2n = 12-14$ ). Cytogenetic characterization (metaphase (M) and telophase (T)) was performed on these progeny, and it was determined that the duration between MI to TII was considerably shorter than the duration between prophase I to MI. Univalents (19) were observed at diakinesis and metaphase I in pollen mother cells (PMCs) in diploid progeny of diploid hybrids. Chromosome anomalies such as "fry-pan" trivalent, laggards, and spindle mis-orientation were observed in diploid preparations. Normal meiotic procedures, however, were observed in PMCs of the amphidiploids, which resulted in the production of viable pollen grains and fertility restoration. More than 98% of the observed amphidiploid M I configurations possessed 19 bivalents. Configurations in the remaining PMCs were multivalents (trivalents + quadrivalents). Chiasma percentage at diakinesis in amphidiploid PMCs decreased from 10 in 300 cells to 1 in 100 at MI, indicating a high degree of preferential pairing and the existence of distinct parental genomes in these progeny.

**1340-1440****S17-P-69****NO ABSTRACT PROVIDED****1340-1440****S17-P-70****MAPPING OF P-LOOP (KINASE-1A) CONTAINING GENES FOR DISEASE RESISTANCE IN *PHASEOLIS VULGARIS* L.**

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Plant diseases are major production constraints, causing yield and quality losses. Breeding for resistance based on inoculation and selection for phenotypic reaction has been a slow and challenging process. However, use of molecular markers tightly linked to known plant resistance genes is expected to expedite and increase the precision of the selection process. The objective was to clone resistance genes and/or to find markers tightly linked to known resistance genes for breeding purposes. Phosphate-binding domain (P-loop) is conserved in 13 protein families, including the NBS-LRR type plant resistance gene class containing Kinase-1a domain (Traut WT, 1994). Degenerate primers based on conserved domains were used to pull out fragments with kinase-1a domain targeting plant resistance genes (Chen et al, 1998; Collins et al, 1998). Sequence analysis indicated that about 20 clones contain NBS-LRR type disease resistance signature at and around the conserved domains. Thirty-three common bean lines/cultivars, resistant to different diseases, including the common bacterial blight (CBB) caused by *Xanthomonas campestris* pv *phaseoli* (Xcp), were inoculated with Xcp isolates. Then leaf samples were taken at different times. The mRNA was then used in bulk for initial amplification of the kinase-1a containing fragments that were cloned subsequently. RFLP mapping of these fragments using the BAT93 x JALO EEP558 RIL population which was used originally to create the integrated map of common bean indicated that this gene family was mostly conserved in four different chromosomes (B2, B3, B4, B7) and absent in three chromosomes (B8, B9, B10). Mapping also showed the distribution.

**1340-1440****S17-P-71****MAPPING OF QTL FOR LEAFHOPPER RESISTANCE IN COMMON BEANS (*PHASEOLUS VULGARIS* L.)**Dermot P. Coyne<sup>1</sup>, Jorge W. Gonzales<sup>1</sup>, Dale T. Lindgren<sup>2</sup>, Kent Eskridge<sup>3</sup>, Steve Kachman<sup>3</sup>, Nedim Mutlu<sup>1</sup><sup>1</sup>377 Plant Science Hall, Univ. of Nebraska, Agronomy & Horticulture Dept. Lincoln, NE 68583-0724; <sup>2</sup>461 W. Univ. Dr., Univ. of Nebraska, North Platte, NE 69101; <sup>3</sup>101 Miller Hall, Dept of Biometry, Univ. of Nebraska, Lincoln, NE 68583

The potato leafhopper (LH) *Empoasca fabae* Harris is the most important *Empoasca* species attacking dry beans (*Phaseolus vulgaris* L.) in North America. Yield losses of about 20% were reported on susceptible bean varieties in North

Platte (NP), NE. Resistance (R) to LH injury has been identified but genes or quantitative trait loci (QTL) for R have not been reported. The objective was to map QTL for R to LH (*E. fabae*) injury in F2-derived and recombinant inbred line (RIL) dry bean populations. Ninety F2 progenies from the cross resistant (R) dry bean pinto 'Sierra' and the susceptible (S) great northern 'Starlight', and 55 RILs from the cross BelnebRR-1 (R) x A-55 (S) were evaluated for leafhopper injury during 1999 and 2000 under field conditions at NP, NE. Visual scores from 1 (= no injury) to 5 (= severe injury) were used to rate LH injury. SAS statistical procedures were used to analyze the phenotypic data. Molecular (103 RAPDs for the F2 population; 240 RAPDs and 1 SCAR for the RIL population) along with phenotypic data were used to detect QTL associated with R to LH injury. QTL associated with leafhopper injury were identified in both populations using the composite interval mapping procedure. QTL on linkage groups (LG) 5 and 8 were common to both populations for R to leafhopper injury. Low heritability estimates for this trait indicated that molecular markers linked to QTL for R to LH injury may be useful for marker-assisted selection.

**1340-1440****S17-P-72****GENETIC LINKAGE MAP OF BROCCOLI BASED ON AFLP, RAPD, SSR AND ISSR MARKERS INCLUDING MARKERS LINKED TO RESISTANCE AGAINST THE DOWNY MILDEW**M. Farinhó<sup>\*1</sup>, J. Carlier<sup>1</sup>, D. Svetleva<sup>2</sup>, A. Monteiro<sup>3</sup>, José M. Leitão<sup>1</sup><sup>1</sup>FERN, Universidade do Algarve, Campus de Gambelas, 8000-117 Faro, Portugal; <sup>2</sup>Dept. of Genetics, Agricultural Univ.-Plovdiv, 12, D. Mendeleev Str, Plovdiv 4000, Bulgaria; <sup>3</sup>Departamento de Horticultura, Instituto Superior de Agronomia, Tapada da Ajuda, 1300 Lisboa, Portugal

A genetic linkage map of broccoli (*Brassica oleracea* var *italica*; n=9) is being constructed using an interspecific F2 population generated from self-pollinating a single F1 plant from a cross between a CrGC downy mildew susceptible double-haploid line and a resistant line of broccoli. The map currently comprises thirteen linkage groups with 129 markers (39 RAPD, 70 AFLP, 14 ISSR, 5 SSR and one disease resistance marker). Two RAPD markers are linked to the downy mildew resistance gene. Eight groups have at least 9 markers, one group has 5 markers, two groups have only three markers and one group has two markers. The average distance between two adjacent markers is 7 cM. Thirteen markers remained unlinked. The total map distance covers about 90% of the total genome, estimated to be approximately 917.8 cM in length. Significant deviation from the expected 3:1 segregation ratio was observed for 27 markers (21%). This map will be used for marker-assisted selection and map-based cloning of the downy mildew resistance gene and other agronomically important genes in the future.

**1340-1440****S17-P-73****ISSUES IN APPLYING DIHAPLOID TECHNOLOGIES TO BROCCOLI BREEDING**

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The development of dihaploid lines from cultured microspores has become a relatively standard practice of broccoli (*Brassica oleracea* L., Italica Group) breeders. Dihaploids of broccoli were first produced from anther cultures, and direct culture of microspores was refined later. Both culture techniques are presently used, but exact procedures that individual programs employ differ. The USDA-ARS, broccoli breeding program has conducted anther and microspore culture techniques and examined thousands of plants regenerated from these techniques to better understand the development of dihaploids. A primary consideration in regenerating plants derived from microspores is that regenerants have variable ploidy. Flow cytometry procedures have been applied efficiently in the ARS program to elucidate ploidy of individuals. Although an average of 60% diploids are identified among regenerants, tetraploids (about 30% on average) and haploids (less than 10%) are commonly observed. In general, the ploidy makeup of populations arising from anther cultures is not different than the makeup of those arising from microspore cultures. However, the ARS program has often observed a higher frequency of diploids in anther-derived populations. Since tetraploids and haploids will not set seed and have little intrinsic value, breeders must identify these so they can be eliminated

before plants are selfed for development of dihaploid line seed. Mutants and aberrant plants are not uncommon among dihaploids. A lack of fertility and seed set in nearly 20 to 30% of dihaploids probably occurs due to mutagenic properties associated with culture. Refinement of dihaploid techniques allows broccoli breeders to generate large numbers of dihaploid lines. These highly homozygous lines are produced in about one year, saving a breeder several years that would be spent in a conventional inbreeding program. These lines readily serve as inbred parents for production of hybrids.

**1340-1440**

**S17-P-74**

**EFFECT OF CULTURE MEDIUM AND TEMPERATURE ON GYNOGENESIS OF IRANIAN ONIONS, *ALLIUM CEPA* L.**

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Iranian onions have good horticultural characteristics, but their yields are lower than those obtained using foreign hybrid seeds. However, there is risk of losing the Iranian germplasm due to displacement by hybrids. Therefore, production of F1 hybrid seed using Iranian germplasm is necessary and necessitates the generation of inbred lines. Production of inbred lines using a traditional system takes many generations, while gynogenesis offers the possibility of haploid and dihaploid line production in shorter time. In this research, the response of six Iranian cultivars, Ghermez-e-Azarshahr, Sefid-e-Kashan, Sefid-e-Kamare-e-Khomain, Sefid-e-Qom, Dorcheh-e-Esfahan, Gholigheseh-e-Zanjan to in vitro gynogenesis and factors affecting in vitro gynogenesis were investigated. Factors included: 1) F6 medium containing BDS; 2) macro salts and B5; 3) micro salts, 2,4-D, BA, sucrose; 4) JAF medium containing MS macro and micro salts, 2,3,5-triiodobenzoic acid (TIBA), glucose; and 5) effect of 17 °C and 24 °C treatments applied to flowers in culture. The F6 medium produced more embryos, while the JAF medium regenerated more plants. The most responsive Iranian onion was 'Gholigheseh-e-Zanjan' (0.56% of gynogenic embryos), while the least responsive was Sefid-e-Kamare-e-Khomain' (0.07%). The embryo rate in two Italian onions, 'KLR' and 'Borettana', used as controls, was 1.56% and 0.09%, respectively. The JAF medium with TIBA and glucose at 17 °C produced two new findings. The first was inhibitory effect of low temperature (17 °C) on gynogenic yield; the second was induction of high frequency of diploid ovule-derived plants in 'Ghermez-e-Azarshahr'. The diploid/haploid ratio found in this factorial combination was 36/1, while in a normal process of onion gynogenesis at 24 °C it usually ranges between 1/8 to 1/9.

**1340-1440**

**S17-P-75**

**SCAR PRIMERS WHICH DISCRIMINATE AMONG THE SIX CULTIVATED *BRASSICA* SPECIES**

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We have developed 16 species-specific SCAR primers (appendix) that are capable of distinguishing among the diploids *Brassica rapa* (AA, n=10), *Brassica nigra* (BB, n=8), *Brassica oleracea* (CC, n=9) and amphitraploids *Brassica juncea* (AABB, n=18), *Brassica napus* (AACC, n=19), *Brassica carinata* (BBCC, n=17) morphotypes of the Brassicaceae family. The PCR amplification products (bands) can be visualized by agarose gel electrophoresis. These primer sets show two types of polymorphism, either the presence or absence of a particular band or length polymorphism based on the number of base pairs amplified. Seven of our primer sets distinguish *B. rapa* (presence of a band) from *B. oleracea* and *B. nigra* (absence of a band). Four of our primer sets distinguish *B. oleracea* (presence of a band) from *B. rapa* and *B. nigra* (absence of a band). Five of our primers reveal length polymorphism between *B. rapa* and *B. oleracea*. As for the amphitraploids, the primers are capable of revealing which genome, i.e., if A, B, or C, is being amplified. These primers were developed as part of instructional material (educational kit) devoted to aid the visualization of biological concepts using Wisconsin Fast Plants. We consider that these primer sets constitute an excellent tool for teaching molecular biology and evolutionary concepts from the high school to the college level.

**1340-1440**

**S17-P-76**

**IN VITRO CULTURE REGENERATION OF APICAL AND AXILLARY MERISTEMS FROM ICEBERG LETTUCE DEPENDS ON HEAD MATURITY BUT NOT STORAGE DELAY**

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Iceberg lettuce (*Lactuca sativa* L. 'Ithaca') was transplanted on 2 May 2001 on black plastic mulch with either a row cover or no row cover in a randomized complete block design with 4 blocks. On 20 June, lettuce grown under the row cover was more mature and had longer cores (46 ± 0.8mm) than those from the control (30 ± 0.7mm). The cores were stored for 0, 2 or 13 days at 2 °C. Apical and axillary buds were then removed from the cores and placed in a Murashige and Skoogs medium for in vitro culture. Survival rates of explants were highest with apex from short stems (90%), independent of the time of delay in storage of the core. Meristems from short lettuce stems had a significantly higher survival rate (83%) compared with meristems from long stems (71%). Twice as many leaves were produced in the tubes from apical compared with axillary meristems. The effect of core length on the rooting percentage depended on the type of meristems. Stem length had a highly significant effect on rooting for the apical, but not for axillary meristems. Three times more explants from apical meristems from short stems rooted than from apical meristems from long stems or from axillary meristems (long or short stems). Storing the meristems for 0, 2 or 13 days did not affect the rates of survival, the rate of rooting, or the number of leaves.

**1340-1440**

**S17-P-77**

**MAPPING QTLs ASSOCIATED WITH PHYTOPHTHORA ROOT ROT RESISTANCE IN CHILLI (*CAPSICUM ANNUUM*)**

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For mapping and characterizing the QTLs related to *Phytophthora capsici* (PC) resistance, a molecular linkage map was constructed with RAPD and AFLP markers in an intraspecific BC1F1 population. An introduced accession YCM334 is highly resistant to PC and the local variety Taeon is susceptible to PC. A total of 43 BC1F1 plants from the cross between YCM334 and Taeon were used for identification of DNA markers linked to PC resistance. Twenty-eight linkage groups were constructed using 37 RAPDs and 192 AFLP markers. Average density of the map is approximately one marker for every 12.0 cM. ANOVA between DNA marker genotypes and resistance identified 7 markers. Five of them were located on two linkage groups and the other 2 were not linked. Three markers mapped on LG 9 had a major effect on PC and explained 27.9% of phenotypic variance in one-way ANOVA and 61.8% with AF56 marker in two-way ANOVA. AF56 marker showed a negative effect on resistance when each plant had the YCM334 allele. Interval analysis detected two QTLs associated with PC resistance. The interval of AF191-AF300-RA5 on LG9 showed a 3.15 LOD score with resistance. This was also detected using the ANOVA model. Another interval of AF138-AF316 on LG24 showed LOD 2.22, thus it was considered to have a minor effect on PC resistance.

**1340-1440**

**S17-P-78**

**ESTABLISHMENT OF GENETIC TRANSFORMATION SYSTEM AND INTRODUCTION OF MADS BOX GENE IN HOT PEPPER (*CAPSICUM ANNUUM* L.)**

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In vitro plant regeneration of inbred lines of hot pepper (*Capsicum annuum* L.) was established using leaf and petiole segments as explants. About 28-day-old plants were excised and cultured on MS medium supplemented with TDZ and NAA or in combination with Zeatin. In all of the media compositions tested, combination of TDZ 0.5 mg·L<sup>-1</sup>, Zeatin 0.5 mg·L<sup>-1</sup>, and NAA 0.1 mg·L<sup>-1</sup> was found to

be the best medium for shoot bud initiation. A young petiole was the most appropriate explant type for plant regeneration as well as genetic transformation in hot pepper. In this study, HpMADS1 gene isolated from hot pepper was introduced using an Agrobacterium-mediated transformation system. Based on the analysis of Southern blot and RT-PCR, HpMADS1 gene was integrated in the hot pepper genome. It has been known that floral organ development is controlled by a group of regulatory factors containing the MADS domain. Morphological characteristics in these transgenic plants, especially flowering habit, however, were not significantly altered, indicating this MADS gene, HpMADS1 may be non-functional in this case.

1340-1440

S17-P-79

**HIGH PLANT REGENERATION AND ECTOPIC EXPRESSION OF OSMADS1 GENE IN ROOT CHICORY (*CICORIUM INTYBUS* L. VAR. *SATIVUS*)**

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We have established the optimal conditions for shoot regeneration of 'Cesare', a chicory cultivar (*Cichorium intybus* L. var. *sativus*). Leaf explants were co-cultured with *Agrobacterium tumefaciens*, which contained a neomycin phosphotransferase II (NPT II) as a selectable marker and a rice homeotic gene, OsMADS1, that encodes a MADS-domain-containing transcription factor. After one day of co-cultivation, explants were transferred to selection media consisting of MS basal medium supplemented with 0.5 mg·L<sup>-1</sup> BAP, 0.1 mg·L<sup>-1</sup> IAA, 70 mg·L<sup>-1</sup> kanamycin, and 250 mg·L<sup>-1</sup> cefotaxime. PCR and Southern blot analyses revealed stable integration of the OsMADS1 gene in the chicory genome. Fourteen T0 plants were acclimatized in the greenhouse and examined for their morphological characters. Most of the transgenic plants showed altered morphologies, such as short, bushy, and early-flowering phenotypes with reduced apical dominance. Additionally, half of the transgenic plants exhibited altered leaf shapes, and 4 out of 14 plants were sterile. These phenotypes were inherited by the next generation. Northern blot analysis confirmed expression of the OsMADS1 gene in both floral and vegetative organs.

1340-1440

S17-P-80

**PLANT REGENERATION AND TRANSFORMATION USING *AGROBACTERIUM TUMEFACIENS* IN BROCCOLI (*BRASSICA OLERACEA* VAR. *ITALICA*)**

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Two inbred lines of *Brassica oleracea* var. *italica*, KW12 and KW13, were genetically engineered using *Agrobacterium tumefaciens* to express the bar gene which confers resistance to the broad spectrum herbicide of glufosinate. Southern blot analysis of seven putatively transgenic plants indicated the integration of the NPTII gene which encoded neomycin phosphotransferase. Three of seven putative transgenic lines, two KW 12 and one KW13, were selected by painting glufosinate 3000 mg·L<sup>-1</sup> on their leaves. Foliar application of basta had little or no effect on agronomic performance of offspring derived from a transgenic KW13 line, while the progenies of the other two KW12 plants at the 5 to 7 leaf stage were killed within 7 days after 3000 mg·L<sup>-1</sup> of basta applications. The stable expression of the bar gene based on Northern blot analysis was observed in all four plants chosen randomly from these herbicide resistant T1 individuals.

1340-1440

S17-P-81

**DEVELOPMENT OF HOMOGENEOUS TRANSGENIC BROCCOLI (*BRASSICA OLERACEA* VAR. *ITALICA*) LINES WITH STABLE EXPRESSION OF HERBICIDE RESISTANCE USING *AGROBACTERIUM TUMEFACIENS***

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Inbred lines of *Brassica oleracea* var. *italica*, KW13, were genetically engineered using *Agrobacterium tumefaciens* to express the bar gene, which confers resistance to the broad spectrum herbicide glufosinate. Transgenic broccoli were selected based on their kanamycin resistance (T0 generation). Progenies of transgenic broccoli were obtained by selfing and artificial crossing, and these were tested for response to herbicide (Basta) treatment at high concentrations. Stable expression of herbicide resistance up to the third (T3) seed generation has been investigated and homogenous lines have been selected. Molecular analysis of T2 and T3 generations showed that Basta resistance was inherited. By using T3 individuals with herbicide resistance introduced, it was shown that a purity assay of F1 hybrid seed could be tested in field.

1340-1440

S17-P-82

**PLANT REGENERATION AND GENETIC TRANSFORMATION OF RADISH (*RAPHANUS SATIVUS* L.) USING BOLTING RELATED GENE RSCO**

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Radish has been known as a very difficult crop to be regenerated. Explants used for plant regeneration and transformation were cotyledons and hypocotyls of seedling grown in MS medium for 5–6 days. The basal medium for shoot regeneration was MS with 2% sucrose and 0.8% agar added. Various levels of BAP and NAA combined with different degrees of silver nitrate were tested. Shooting took place in the medium supplemented with BAP 2.5–5.0 mg·L<sup>-1</sup> and NAA 0.5–1.0 mg·L<sup>-1</sup>. To induce the late-bolting type of the radish cultivars, we introduced the RSCO gene in anti-sense direction into the radish cultivar 'JinjuDaePyeong' which is known as a very early bolting cultivar under normal field growing conditions. We obtained several transgenic plants, and progenies of these plants were tested for the stable integration of the gene. T0 plants showed a delay in bolting under normal field conditions compared with the control plants. Northern blotting also confirmed expression based on the NPT II gene as a probe. PCR analysis of T1 showed an approximate 3:1 ratio of segregation. T2 plants were obtained by self-pollinating, and resulting PCR-Southern blots from T2 plants showed the transmission of RSCO gene in progenies. T2 plants were tested for the treatment of herbicide, Basta (0.03%) in the field, and they showed herbicide (Basta) resistance after 7 days. Based on the date of flower bolting, transgenic plants flowered 15–20 days later than the control plants.

1340-1440

S17-P-83

**CHARACTERIZATION AND PRODUCTION OF SOMATIC HYBRIDS WITH CYTOPLASMIC MALE STERILITY BETWEEN *B. JUNCEA* (LEAF HEADING MUSTARD) AND *B. OLERACEA* (BROCCOLI) THROUGH PROTOPLAST FUSION**

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Ogura types of Cytoplasmic male sterility (CMS) in *Brassica oleracea* were successfully transferred to *Brassica juncea*. Leaf heading mustard (*B. juncea*) and broccoli (*B. oleracea*) were used as experimental materials. Protoplast fusion was performed by PEG mediated method. Fused protoplasts were cultured in a modified K8p medium supplemented with 0.3 M sucrose, 0.1% agarose, and plant growth regulators (1 mg·L<sup>-1</sup> 2,4-D, 0.5 mg·L<sup>-1</sup> BAP, 1 mg·L<sup>-1</sup> NAA and 0.2 mg·L<sup>-1</sup> Kinetin), until reaching a density of 5 × 10<sup>5</sup> protoplasts·mL<sup>-1</sup>. These cultures were kept under dim light with day length of 16 h, at 25°C. Small calli, about 2–3 mm in diameter, were transferred to MS medium containing plant growth regulators to obtain regenerated shoots. The calli were retransferred to new media every two weeks. Regenerated plants were analyzed by PCR to detect CMS using CMS specific-primers, and also assessed for flower morphology and male fertility. Twelve plants derived from fused cells were identified to be somatic hybrids with CMS. They had normal petals and stamens but produced no pollen. Only two plants produced pollen and set seeds. These all showed intermediate phenotypes. ([www.potatokorea.com](http://www.potatokorea.com))

1340-1440

S17-P-84

**MORPHOLOGICAL, CYTOLOGICAL AND MOLECULAR CHARACTERIZATION OF PROGENIES DERIVED FROM TWO SOMATIC HYBRIDS BETWEEN *B. CAMPESTRIS* AND *B. OLERACEA***

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Somatic hybrids between *B. campestris* and *B. oleracea* were synthesized through protoplast fusion. Five somatic hybrids were obtained from the protoplast fusion between from *B. campestris* and *B. oleracea*, and they were analysed for their nuclear content. The DNA content was measured by flow cytometry. All of the regenerated plants were confirmed as somatic hybrids based on RAPD analysis and morphological features. All regenerated plants were successfully transferred to the soil, and they showed normal flowers. Although seed set was low after self-pollination, some seed were obtained from selfing, open-pollinations, and back-crossing. No difference was observed within the somatic hybrids and their progenies. Genomic in situ hybridization patterns indicated that *B. campestris* or *B. oleracea* signals were detected on the chromosomes of the putative somatic hybrids. The regenerated plants were transferred to the soil to determine pollen fertility. Progenies of the first and the second generation were obtained. No differences were observed among phenotypes and most somatic hybrids similar to *B. oleracea*. AFLP analysis was also carried out to determine genetic diversity of the first progenies obtained from somatic hybrids. (www.potatokorea.com)

1340-1440

S17-P-85

**INTRODUCTION OF NEW CYTOPLASMIC MALE STERILITY (CMS) OF WILD *B. RAPA* INTO *B. JUNCEA* (MUSTARD) USING CELL FUSION METHOD**

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Somatic hybrids with new types of 'Anand' cytoplasmic male sterility (CMS) were produced between a wild accession of *B. rapa* and an inbred line of *B. juncea*. Protoplast fusion was performed by PEG mediated method. Fused protoplasts were cultured in a modified K8p medium supplemented with 2.5 $\mu$ g I $\beta$ S gene in conjunction with restriction site analysis. Mitosis in two hybrid plants showed the chromosome number to be 2n = 56, and 2n = 54, similar to the sum of *B. juncea* (2n = 36) and *B. rapa* (2n = 20). These regenerated plants were morphologically similar to the wild types of *B. rapa* having similar petioles and leaf color. Flowers of somatic hybrids displayed a range of variation. For example, there were plants with normal flowers, but no pollen, and there were other plants with crinkled petal like stamens. (www.potatokorea.com)

1340-1440

S17-P-86

**PRODUCTION AND CHARACTERIZATION OF SOMATIC HYBRIDS AMONG *B. CAMPESTRIS*, *B. OLERACEA* AND *B. JUNCEA* BY MULTIPLE PROTOPLAST FUSION**

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Cytoplasmic male sterile (CMS) mustards were produced by the multiple protoplast fusion method. Protoplasts were isolated from hypocotyls and cotyledons of Chinese cabbage, broccoli, and mustard. Mustard and CMS lines of Chinese cabbage and broccoli were fused to combine different sources of the CMS trait. Ninety-six plants were regenerated from 24 calli, and they were successfully transferred to pots. Eighty-one of them were characterized as somatic hybrids based on analysis of morphological characteristics. PCR using primers for an Ogura CMS-specific mitochondrial DNA sequence permitted the identification of hybrids likely to be CMS. More than 90 regenerated plants with the CMS-specific band at 0.5 Kb were obtained. Mitochondrial DNA analyses were also performed using PCR amplification of the V7 region of the mitochondrial small ribosomal RNA (srRNA) gene in conjunction with restriction site analysis. Thirty-five plants

out of 96 regenerated plants were conclusively verified as somatic hybrids using AFLP DNA analysis. The somatic hybrids were grown in pots for five months and at least five of them flowered. The plants identified as CMS by PCR produced male sterile flowers. From the comparisons of leaf color and flower size, regenerated plants showed great variation.

1340-1440

S17-P-87

**EXPRESSION AND TRANSFORMATION OF CMVSCFV (CUCUMBER MOSAIC VIRUS SINGLE CHAIN VARIABLE FRAGMENT) GENE INTO WATERMELON (*CITRULLUS VULGARIS* SHRAD.) WITH *AGROBACTERIUM TUMEFACIENS***

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This study was carried out to establish efficient transformation of cotyledon explants in watermelon (*Citrullus vulgaris* shrad.). Cotyledon explants were used from 5-6 day old seedlings of four F1 hybrid watermelon (*Citrullus vulgaris* shrad.) cultivars, Wang-Jang<sup>®</sup>, Gum-Cheon<sup>®</sup>, Bitna<sup>®</sup>, and Rabbit<sup>®</sup>. The CMVscFv gene with ER leader sequence of the KDEL was introduced into cotyledon segments of four F1 hybrid watermelon using *Agrobacterium tumefaciens* (strain AGL1), which harbored pGA748 binary vector with the CaMV 35S promoter and the NPT II gene. Regenerated shoots were selected on MS medium containing 5.0 mg-L<sup>-1</sup> BAP, 1.0 mg-L<sup>-1</sup> IAA, 300 mg-L<sup>-1</sup> cefotaxim and 100 mg-L<sup>-1</sup> kanamycin. After eight weeks of culture on selection medium, the shoots were transferred to hormone free MS medium for root induction. The presence and integration of the CMVscFv gene was confirmed by PCR. PCR analysis using the NPTII gene primer and CMVscFv gene primer revealed that two plantlets were transformed. Transgenic plants producing stable expression of the CMVscFv gene were confirmed by Southern blot, Northern blot, and ELISA analyses. (www.potatokorea.com)

1340-1440

S17-P-88

**STABLE PLANT REGENERATION OF WATERMELON (*CITRULLUS VULGARIS* SHRAD.)**

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This study was carried out to examine the effects of auxins on callus formation, and rooting and shooting of cotyledon explants from watermelon. Cotyledon explants from 5-6 day-old seedlings of four F1 hybrid watermelon cultivars were used. Various combinations of 5 mg-L<sup>-1</sup> cytokinin (BAP) and 0.5, 1.0, 2.0 mg-L<sup>-1</sup> auxins (IAA, NAA, 2,4-D) were tested on MS medium, respectively. After three weeks, almost all the cultivars formed multiple shoots when cultured on MS basal medium supplemented with 5.0 mg-L<sup>-1</sup> BAP and 1.0 mg-L<sup>-1</sup> IAA. Then after one week, they developed into multiple shoots. Multiple shoots were induced on the cut part of veins at the frequency of 98%. Multiple shoot buds were elongated on MS medium containing 3 mg-L<sup>-1</sup> BAP for 1 week and maintained by consecutive subculture on the hormone free MS medium. Regenerated plantlets were transplanted to pots. Roots were formed at frequencies of up to 98% in MS medium supplemented with 5.0 mg-L<sup>-1</sup> BAP and 2 mg-L<sup>-1</sup> 2,4-D. The combination of BAP and IAA was very effective in inducing callus formation in almost all the cultivars and also increased shooting ratio. (www.potatokorea.com)

1340-1440

S17-P-89

**MUTATION SPECTRUM OF TOMATO INDUCED BY SEED RADIATION WITH CARBON AND HELIUM ION-BEAM**

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Ion beam, a recently innovated technique has been shown to produce a wide mutation spectrum in biological systems of *Arabidopsis thaliana*. However, no attempts have been made to expand the genetic diversity of the less

variable cultivated tomato using this new mutagenic procedure. It was therefore the objective of this study to investigate the effects of ion beams on mutation in M1 and M2 seedlings as a fundamental basis for tomato genetic advancement. Future development in the tomato industry following successful generation of mutants would involve selection for suitable agriculturally important characteristics. Tomato seeds were irradiated with carbon (C) and helium (He) ion beams and thereafter, the performance of the irradiation on survival ratio, and seedling and plant characters was monitored. Biologically visible effects of ion beam were noted via a reduced radicle elongation in both C and He irradiation dosages. The radicle is a suitable organ for the detection of irradiation effects even where germination would not offer precise indication. C ion beam irradiation severely affected the 50% survival rate of the seedlings with a dosage of 60 Gy compared to He-240 Gy. In M1 seedlings, stunted growth, parthenocarpic fruit, failure of pollen production, and failure to complete plant life cycle were detected. In the M2 seedlings, chlorophyll mutants such as albino, viridis, xantha, and short internode, self-topping and broad leaf-shape were observed. Based on the radiation-dosage experiments, C-50 Gy and 150A '200 Gy are likely to be optimum levels for irradiating tomato seeds, allowing for the possibility of generating tomato mutants without causing excessive injury to the embryo. In general, He ion beam was more effective with a wide range of mutation spectrum than C ion beam.

**1340-1440**

**S17-P-90**

**SEQUENCING AND ANALYSIS OF RAPD FRAGMENTS POLYMORPHIC AMONG CLONES OF THE SWEETPOTATO (*IPOMOEA BATATAS*) CULTIVAR JEWEL**

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Sweetpotato is asexually propagated and theoretically clones should be genotypically identical. Phenotypic variation was observed among orange fleshed Jewel clones collected from seven state foundation seed programs as well as one clone that produced white fleshed roots. Phenotypic variation is expected due to genotype x environmental interaction, but cannot account for all observed variation. In order to determine whether this phenotypic variation had any genetic basis, RAPD profiles were generated using 17 primers. Ten primers yielded clear, repeatable, polymorphic fragments. These fragments were cloned, sequenced and compared with known sequence in the NCBI database. Fragment sizes ranged from 300 to 750 bp and showed little homology with each other. Sequences were also screened for the presence of open reading frames (ORF) and the majority of fragments showed numerous ORFs.

**1340-1440**

**S17-P-91**

**DETERMINATION OF CULTIVAR IDENTITY IN *BRASSICA OLERACEA* BASED ON POLYMORPHISMS BETWEEN SSRs DERIVED FROM SEQUENCE DATABASES**

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Sequence databases were screened to identify simple sequence repeats (SSRs) within known sequences of *Brassica oleracea*. A total of 512 *B. oleracea* DNA sequences were screened using SSRIT program and 43 SSRs were detected. PRIMER 3.0 software was used to design 36 primer pairs flanking the SSR regions. DNAs from 26 cabbage, 14 cauliflower and 14 broccoli cultivars were extracted to determine allelic polymorphisms at the SSR locations. Of the 36 primer pairs, 5 failed to amplify fragments of expected size and 15 primer pairs failed to generate polymorphisms when separated on metaphor agarose and/or polyacrylamide gels. PCR annealing conditions were optimized for each primer pair using a gradient thermocycler and polymorphisms were scored for the 54 *B. oleracea* cultivars using the primer pairs generating polymorphisms. Primer pairs derived from sequences flanking SSR regions in the genes CAL, PLD1, PLD2, PC15 and DEL9 showed the highest rate of polymorphisms between the cultivars tested. The polymorphisms at these loci can potentially be used to determine the pedigree of *B. oleracea* breeding lines, to determine seed purity and to confirm cultivar identity.

**1340-1440**

**S17-P-92**

**MAPPING GENES FOR BROWN SPOT RESISTANCE IN A SNAP BEAN POPULATION**

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Bacterial Brown Spot (BBS) incited by *Pseudomonas syringae* pv. *syringae* (Pss) is an important disease of snap beans (*Phaseolus vulgaris* L.) in Wisconsin, USA. BBS reduces pod quality. To understand the nature of the resistance to this disease, a study was carried out during three years on the F8 recombinant inbred line population Eagle x Puebla 152 (EP). Our objective was to identify QTL associated with BBS resistance. This was done by using a framework map developed for EP, field data from two years and leaf freezing data from 3 years, the latter as a surrogate indicator of the Pss population size. Up to the year 2000, a QTL for leaf freezing was consistently associated over years to variation in bacterial population using composite interval mapping, and the leaf freezing assay data better explained the differences due to variable bacterial population across genotypes than the field evaluation. Consistency of these findings with data from 2001 is presented.

**1340-1440**

**S17-P-93**

**COMPARISON OF MORPHOLOGICAL AND MOLECULAR VARIATION IN SEEDS AND SEEDLINGS OF RADISH CULTIVARS**

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Radish (*Raphanus sativus* L.) is an important vegetable crop around the world and it is very popular in Asian countries. It is the most important seed crop in Nepal. Variation during production reduces profitability for seed producers and farmers and variation in seed quality may be the cause. Variation will be due to genetic and environmental factors. The main aims of this research were to determine the relationship between individual seed weight and germination and seedling vigor, to assess the degree of phenotypic and genetic variability within and between radish cultivars, to correlate morphological characters with genetic data and to develop a method of fingerprinting the most popular radish varieties. Seed purity analysis, moisture determination, germination and vigor tests were carried out for seven radish cultivars from Nepal and Australia. Seedlings were transplanted into pots in the glasshouse and height and leaf number were observed weekly to determine the relationships between seed weight and growth characters. Seedlings were harvested at four weeks, growth parameters were measured and seedlings were stored at -80 °C for genetic analysis. Individual seed weight was correlated with seedling length, fresh weight, plant height and leaves/plant in all seven cultivars. RAPD analysis was used to study the genetic variation within and between the seven cultivars of radish. Fourteen primers were examined and 10 yielded polymorphisms within and between varieties. Some polymorphisms were consistent within varieties while others differed between genotypes, and so RAPDs could be used to fingerprint genotypes and distinguish varieties. The morphological and genetic data were correlated using multivariate analysis. DNA markers are associated with morphological traits, which would be helpful in seedling selection of interesting traits. Seed grading and improving genetic purity might be helpful to reduce morphological variation and hence increase uniformity.

**1340-1440**

**S17-P-94**

**AFLP ANALYSIS IN TOMATO GENOTYPES THAT DIFFER IN FRUIT SHELF LIFE**

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IBR-Suipacha 531, Genetica-Fac. Cs. Agrarias CC 14, CONICET-UNR, Rosario, Santa Fe, Argentina, 2000

Though *Lycopersicon pimpinellifolium* has been generally used in tomato breeding programs as a source of genetic resistances, recent reports suggest that some accessions carry valuable genes for prolonging fruit shelf life (SL). Seventeen F6 families were derived after agonistic selection for both SL and fruit weight (W) from an interspecific cross among the cultivar 'Caimanta' (C, mean W = 105.2 g, mean SL = 13.9 days) of *L. esculentum* and LA722 (P, mean W = 1.0 g, mean SL = 19.7 days) of *L. pimpinellifolium*. With the aim of identifying molecular markers associ-

ated with SL, genomic DNA was obtained from one plant per family. Two bulks of plants having similar values of SL were assembled by mixing 0.2 µg of the extracted DNA. Phenotypic differences among bulks were significant for SL (26.4 vs. 13.0 days;  $t = 3.6$ ,  $P < 0.05$ ) but not for W (15.1 vs. 10.8 g;  $t = 0.8$ , n.s.). Samples of DNA from the bulks, C, P and the F1 were analyzed by the AFLP standard protocol. Fourteen combinations of EcoRI and MseI primers were assayed. All of them produced polymorphic fragments among the parents, but only three were efficient for differentiating the bulks. Most of these polymorphic fragments were present in P, the F1, and the bulk of long SL plants. Some fragments were detected in C, the F1 and the bulk of long SL plants. These results verify that P carries genes that prolong tomato fruit SL. In addition, also C appeared to contribute to the expression of a longer SL. This finding would account for the transgressive variation recovered for SL at the early segregant generations and fixed through selection.

**1340-1440**

**S17-P-95**

**GENETIC MAPPING IN *CITRULLUS LANATUS* POPULATIONS SEGREGATING FOR RESISTANCE TO GUMMY STEM BLIGHT**

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*Didymella bryoniae* is the causal agent of gummy stem blight and black rot in cucurbits. Losses to gummy stem blight have increased as resistance to other diseases has been incorporated into cucurbits. An F2 population segregating for resistance to gummy stem blight is being used to develop a genome map of *Citrullus lanatus*. AFLP (amplified fragment length polymorphism) and ISSR (inter-simple sequence repeats) markers are used to supplement the current RAPD marker-based genome map. Disease resistance gene homologues will be mapped using primers specifically designed from conserved motifs of resistance genes isolated and identified in other plant species.

**1340-1440**

**S17-P-96**

**ANALYSIS OF GENETIC RELATIONSHIPS OF WATERMELON [*CITRULLUS LANATUS* (THUNB.) MANSFELD] GERMPLASM USING RAPD AND AFLP**

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Random Amplified Polymorphic DNA (RAPD) and Amplified Fragment Length Polymorphism (AFLP) analysis was applied in assessing genetic relationships among 30 accessions of watermelon *Citrullus lanatus* (Thunb.) Matsum. & Nakai. which represent a wide range of breeding lines, cultivars and wild accessions. Fifteen primers (2.08%) were screened from 720 arbitrary 10-mer primers, and a total of 104 DNA bands were amplified, 43 of which (41.35%) were polymorphic. The average number of DNA bands amplified by each primer was 7.0. Among bands generated by eight selected AFLP primer combinations (among 24 primer combinations, 13.0%-31.9% were polymorphic within the cultivars; while 45.3%-64.2% were polymorphic among all the germplasm. DNA fingerprinting based on 15 bands amplified with four primer combinations E-AT/M-CTA, E-AG/M-CAT, E-AT/M-CAT, E-AA/M-CAA was performed and utilized in watermelon genotype identification. A tree diagram was constructed by using complete linkage method. The 30 accessions were assigned to 6 groups, which were East-Asia group, American group, two medial groups, and two African wild groups. Each ecological group exhibited specific bands, which were useful in discriminating other groups. Results of cluster analysis based on the RAPD and AFLP data were consistent with and verified previous classification of the germplasm.

**1340-1440**

**S17-P-97**

**IDENTIFICATION OF A RAPD MAKER TIGHTLY LINKED TO A SELF-INCOMPATIBILITY GENE IN NON-HEADING CHINESE CABBAGE**

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Self-incompatibility, the physiological mechanism that prevents self-fertiliza-

tion and insures cross-pollination, provides a useful model for studying gene evolution, expression control, and intercellular signaling in flowering plants. These factors are important in the switch to sexual reproduction in plants, but are also utilized in the formation of hybrids and the exploitation of heterosis. Bulk segregant analysis (BSA) and random amplified polymorphic DNA (RAPD) were employed to identify molecular markers linked to a self-incompatibility gene in a segregating population of non-heading Chinese cabbage (*B. campestris* L. ssp. *chinensis* Makino var. *communis* Tsen et Lee) developed by crossing self-incompatible and self-compatible near-isogenic lines. Primer S1107 produced a 900 base pair (bp) reproducible fragment only in the self-incompatible line. Using the F2 mapping population from the cross (SC-104-1 X SI-13-2), S1107-900 was shown to be closely linked to the self-incompatibility gene at a genetic distance of  $7.54 \pm 0.11$  cM. This work has provided a solid basis for molecular marker-assisted selection for self-incompatibility, and made location and cloning of the self-incompatibility gene possible.

**1340-1440**

**S17-P-98**

**NEW WATERMELON SSR LOCI FROM SEQUENCE DATA BASES**

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Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakay) is a very important crop in the Almería province of Spain with more than 50% of the Spanish watermelon production harvested there every year. Watermelon belongs to the genus *Citrullus*, which has at least three more species, two being annual (*C. lanatus* and *C. rhemi*) and two perennial (*C. ecirrhosus* and *C. colocynthis*). The only cultivated species is *C. lanatus*. It has been suggested that many resistance genes for viral and fungal diseases of watermelon can be found in the wild species, which might be crossed with *C. lanatus*. Recent reports have identified seven loci for watermelon SSRs, but to be able to apply a marker-assisted selection approach to watermelon breeding, it would be very convenient to have more loci to work with. A search was carried out in public DNA sequence databases, and from this information, 20 primer pairs were designed to amplify targets in the watermelon genome. This new set of microsatellite loci has been studied and published recently (Guerra-Sanz, in press) in several watermelon varieties and local landraces, *C. colocynthis* and interspecific hybrids. We will present here some results from those new microsatellite loci which could be used for further variety identification and in marker-assisted selection.

**1340-1440**

**S17-P-99**

**PISTIL RECEPTIVITY, POLLEN TUBE GROWTH AND GENE EXPRESSION DURING EARLY FRUIT DEVELOPMENT IN SWEET PEPPER (*CAPSICUM ANNUM*)**

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Fruit and seed development are initiated after successful pollination and fertilization. The absence of fertilization results in either senescence of the entire flower or cessation of carpel development. The growth of pollen tubes was observed in sweet pepper variety Golden Bell, using fluorescence microscopy. At two days after pollination, almost all the tips of the pollen tubes had reached the ovules in the ovary. This result indicates that fertilization in sweet pepper takes place two days after pollination. Pistil receptivity, taken as the growth of pollen tube through the style into the ovary, was also studied. It was observed that the pistil of sweet pepper remains receptive until two days after anthesis and may indicate the failure of pollen hydration and hence germination. In this study, naphthalene acetic acid (NAA), at a concentration of 5-10 M, stimulated the growth of emasculated flowers and resulted in the production of parthenocarpic fruit. Morphologically, fruit developed from hand pollination had a bell shape while that from NAA treated flowers had three locules/lobes and was smaller in size. Unpollinated emasculated flowers failed to set fruit. Genes that are specifically expressed after fertilization in sweet pepper have been isolated and will be discussed.

**1340-1440**

**S17-P-100**

**GENETIC IDENTIFICATION AND PURITY ASSESSMENTS OF GARLIC USING RAPD PRIMERS**

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One hundred five random RAPD primers were screened for useful primers with which to study genetic identification and purity assessments. Twelve useful primers were selected and used to assess 80 garlic cultivars and lines collected from 17 provinces and regions of China, and abroad. The optimum reaction system and program of temperature adjustment for PCR was determined. RAPD banding patterns of the garlic germplasm showed good polymorphism. Differences in the garlic based on the banding patterns were similar to that based on agronomic characters. Confusion from one garlic cultivar with different names, or by one name given to several garlic cultivars has been made clear. Purity of several garlic cultivars were tested. It is anticipated that the RAPD technique will be one of the useful tools in genetic identification and purity assessments of garlic.

**1340-1440**

**S17-P-101**

**TOWARD AN INTEGRATED LINKAGE MAP OF WATERMELON**

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An integrated linkage map is being assembled by merging three maps constructed for watermelon. Among these is a recent map derived from a testcross population [Plant Accession Griffin 14113 (*C. lanatus* var. *citroides*) x New Hampshire Midget (NHM); *Citrullus lanatus* var. *lanatus*] x U.S. Plant Introduction (PI) 386015 (*C. colocynthis*). The map contains over 141 randomly amplified polymorphic DNA (RAPD) markers, 27 inter simple sequence repeat (ISSR) markers, and 12 sequence characterized amplified region (SCAR) markers. Among them a SCAR marker linked (1.6 cM) to race 1 Fusarium wilt resistance in watermelon. The map consists of 25 linkage groups covering a total distance of 1166.2 cM, with an average distance of 8.1 cM between two markers. Among the linkage groups is a large group of 22 markers covering a mapping distance of 225.6 cM. Also, six large groups each with 10–20 markers that cover a mapping distance of 68.8–110.8 cM, five linkage groups each with three to seven markers that cover a mapping distance of 36.5–57.2 cM, and thirteen small linkage groups each containing two to 11 markers that cover a mapping distance of 3.5–29.9 cM. The integrated map is used for further development of markers linked to disease resistance and fruit qualities in watermelon.

**1440-1500**

**S17-O-102**

**LINKING QUANTITATIVE TRAITS WITH AFLP MARKERS IN SWEETPOTATOES USING DISCRIMINANT ANALYSIS**

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We evaluated a discriminant analysis technique to link molecular markers with root dry matter in sweetpotatoes. This technique does not require a priori segregation data or controlled populations in order to identify putative trait linked markers. Thirty-eight sweetpotato varieties were sampled on the basis of their root dry matter content from an original USDA population of 394 clones. Sixteen of the 38 clones had a high dry matter ranging from 36.67% to 43.48%. The second group of 22 clones had a low dry matter content ranging from 12.20% to 21.99%. DNA samples from the 38 clones were analyzed using AFLP. AMOVA found significant ( $P < 0.001$ ) differences between the two groups. Stepwise discriminant analysis (SAS, 2001) was used to select markers that discriminate between the two phenotypic groups. Twenty-five molecular markers were selected from 222 markers generated using 1 AFLP primer combination. Using the 25 selected markers, discriminant analysis (SAS, 2001) validated the phenotypic grouping with a zero error rate. AMOVA also found significant differences ( $P < 0.001$ ) between the two phenotypic groups using the 25 selected markers.

**1500-1520**

**S17-O-103**

**TRANSGENIC CARROTS EXPRESSING ENHANCED TOLERANCE TO HERBICIDE AND FUNGAL PATHOGEN INFECTION**

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Transgenic carrot (*Daucus carota* L.) plants expressing a thaumatin-like protein (TLP) from rice with potential antifungal activity were obtained by *Agrobacterium tumefaciens*-mediated genetic transformation. Two genes encoding phosphinothricin (PPT) acetyltransferase (*bar*) and hygromycin (*hyg*) phosphotransferase (*hpt*) were used as selectable markers. Petiole and hypocotyl explants of three carrot cultivars (Danvers Half Long, Nanco and Nantes Coreless) from 3–4 week-old seedlings were used for infection. Selection was initiated after three days of coculture, using Murashige and Skoog medium containing 1 mg·L<sup>-1</sup> 2,4-D and 1 mg·L<sup>-1</sup> PPT, or 25 mg·L<sup>-1</sup> hygromycin. After two weeks, selection was increased to 10 mg·L<sup>-1</sup> PPT and 100 mg·L<sup>-1</sup> *hyg*. The presence of the *tip* and *bar* transgenes was detected by polymerase chain reaction and confirmed by Southern analysis. The expression of the TLP was demonstrated by Western analysis. From 45 primary transformed lines, 13 were selected for assessment of enhanced herbicide and/or disease tolerance. The transgenic lines showed varying levels of tolerance to phosphinothricin, the active ingredient in several commercially available herbicides. Four of the transgenic lines also showed significantly enhanced tolerance to the fungal pathogens *Sclerotinia sclerotiorum* or *Botrytis cinerea* when detached petioles and leaflets were inoculated under controlled environment conditions. Two carrot lines had significantly enhanced tolerance to the herbicide as well as to both pathogens (lesion development reduced by 30–50%). The results from this study demonstrate the feasibility of introducing two potentially useful agronomic traits into carrot through genetic engineering.

**1520-1540**

**S17-O-104**

**EMBRYO RESCUE AND BRIDGE CROSSING FOR INTROGRESSION OF ANTHRACNOSE RESISTANCE FROM *CAPSICUM BACCATUM* TO *CAPSICUM ANNUUM***

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Chile pepper (*Capsicum annuum* L.) is one of the most important vegetable crops in many Asian countries. The pepper yield, however, has severely been reduced due to fruit anthracnose caused by *Colletotrichum gloeosporioides* Penz. In Korea alone, the damage by this disease has been estimated at more than US \$100 million annually. Attempts to find usable resistance sources to the disease within *C. annuum* germplasm have failed. Recently, AVRDC phytopathologists have reported that two lines of *Capsicum baccatum* are resistant to this disease. Interspecific hybridization between *C. annuum* and *C. baccatum* was attempted to transfer resistance to *C. annuum*. Fertilization occurred normally, but all embryos aborted within 15 days after pollination. Embryo rescue and tri-species bridge crosses were then done to overcome the interspecific incompatibility. Interspecific hybrid plants of *C. annuum* x *C. baccatum* were obtained via embryo rescue, but significant differences in success were observed among *C. annuum* cultivars. *Capsicum chinense* was used as a bridge parent between *C. annuum* and *C. baccatum* was possible. Interspecific hybrids obtained using either embryo rescue or tri-species bridge crossing were completely male-sterile. Backcrossing of the interspecific hybrids to *C. annuum* resulted in partially male-fertile plants showing normal growth pattern. The interspecific hybrids of *C. annuum* x *C. baccatum*, and of *C. baccatum* x *C. chinense* showed resistance to anthracnose, thus the resistance appeared to be dominant. Consecutive backcrossing of the interspecific hybrids with *C. annuum* will be done to develop anthracnose-resistant cultivars.

**1540-1600**

**S17-O-105**

**INDUCTION MECHANISM OF CYTOPLASMIC MALE STERILITY BY ARTIFICIAL CHIMERA SYNTHESIS IN *BRASSICA***

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We have studied graft transformation in tomato, eggplant, tobacco and soybean and gene transfer in chimeral tissue in *Brassica*. In the progenies from *Brassica* interspecific chimeras between *Brassica campestris* and *B. oleracea*, cytoplasmic male sterility was obtained and stably inherited. We have analyzed the molecular natures of the CMS, indicating the origination of the Ogura radish mitochondrial genome in *Brassica campestris*. The CMS line has an Orf 138, indicator of radish Ogura CMS and the same RFLP patterns using 16 mt probes and cp full length probes as CMS radish. PCR and sequencing data showed that CMS-linked genome is dominated in the CMS line, but very few in normal type, clearly showing a heteroplasmic state at different copy numbers between CMS and normal. PCR cycle experiments using Orf138 specific primer supported this conclusion. It is a so-called "stoichiometric shift." These phenomena were observed also in CMS types derived from somatic cell hybrids between radish and cabbage. We are now investigating the complete genome map of CMS and normal mother materials, finally making clear the mechanism of CMS induction and control. In parallel, we are trying to establish stable and useful CMS material for leaf *Brassica campestris* hybrid breeding.

**1600-1620**

**S17-0-106**

**DETECTING MOLECULAR MARKERS ASSOCIATED WITH HEAT TOLERANCE OF CHINESE CABBAGE**

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Chinese cabbage (*Brassica campestris* L. ssp. *pekinensis*) is one of the most popular vegetables cultivated widely in China. For balanced production throughout the year, the heat tolerance trait has been considered an important breeding objective for Chinese cabbage. This study was conducted to identify molecular markers linked to quantitative trait loci (QTL) influencing heat tolerance of Chinese cabbage. A genetically stable population of recombinant inbred lines was derived from five cycles of single seed descent (SSD) from a cross between a heat tolerance line 177 with a heat sensitive line 276. A segregating population of 105 S5 families was analyzed using isozyme, RAPD and AFLP techniques and 2, 36 and 110 polymorphic isozyme, RAPD and AFLP markers spaced throughout the Chinese cabbage genome were scored in the SSD population. The results of variance analysis of single factors and multiple linear regression analysis indicate that 9 markers on four chromosomal arms are significantly associated with heat tolerance QTLs, they are five AFLP markers, three RAPD markers and one PGM isozyme marker. Six of them are localized in the same chromosomal region. The total genetic contribution rate of these markers for heat tolerance is 46.7%. The detection of relatively few markers associated with genomic regions controlling heat tolerance suggests that development of heat tolerant germplasm of Chinese cabbage via isozyme, RAPD and AFLP marker-assisted selection may be feasible.

**1620-1640**

**S17-0-106-A**

**TO BE ANNOUNCED**

**1640-1700**

**S17-0-106-B**

**TO BE ANNOUNCED**

**Friday · August 16**

**0800-0900**

**S17-P-107**

**PHYSICAL-CHEMICAL CHARACTERIZATION OF TOMATO FRUITS FOR INDUSTRIAL PROCESSING**

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The objective of the present work was to characterize fruits of 28 tomato cultivars for industrial processing. The experiment was carried out in Jaboticabal-

SP, Brasil at 21°15'22" South, 48°18'58" West, at an elevation of 575 m, in Haplorthox soil from June-December. Cultivars used in this study were: H 7155, Hypeel 108, Andino, U 573, H 9036, Ipa 6, H 9494, AG 33, Yuba, RPT 1294, AG 72, Peelmech, Curico, Hypeel 45, RPT 1478, H 9492, H 9498, H 2710, Hitech 45, Halley, Botu 13, H 9553, U 646, NK 1570, AG 45, RPT 1095, RPT 1570 and PSX 37511. To evaluate different cultivars for fruit characters, the experiment design consisted of randomized blocks replicated four times. Ten fruits per plot were analyzed, evaluating the following characteristics: shape (elongated or round); length and diameter (mm); external and internal coloration; presence of fissures; number of loculi; pulp thickness (mm); soluble solid content (oBrix) and total acidity. Cultivars Hypeel 108, AG 72, NK 1570, RPT 1570 had elongated fruit. Cultivars with values higher than 5.5 mm for pulp thickness, a characteristic which is directly related to fruit yield for industrial purposes were: Ipa 6, Andino, U 646, H 9553, RPT 1294 and Hypeel 108. Cultivars Ipa 6 and Andino also had high values for length, diameter and pulp thickness, identifying them as material of quality for industry and one alternative for fresh market. Among cultivars with better values for acidity (higher or equal to 0.3 g citric acid per 100 g) were RPT 1095, AG 45, H 9553 and Hypeel 45.

**0800-0900**

**S17-P-108**

**DEVELOPMENT OF TOMATO HYBRIDS SUITABLE FOR FRESH MARKET AND PROCESSING**

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Tomato is one of the most important vegetable crops of the world and is known for its versatile uses. Eleven F1 hybrids identified on the basis of superior performance during the preceding years were evaluated for various horticultural traits over two years viz. 1999-2000 and 2000-01. The two check hybrids included were TH 802 and Avinash-2. The ANOVA revealed that there existed significant differences among the hybrids for all the characters studied when analyzed for individual years and also when pooled over the years. The MS due to years were significant for TSS, fruit weight and total yield. The interaction between years x hybrids was significant for all the characters studied except for fruit shape index. TH-4 out-yielded Avinash-2, better of the two checks, by 35.8 per cent. TH-1 and TH-2 recorded identical yields and out-performed Avinash-2 by 27.1 per cent. TH-1 was significantly better than both the checks for number of locules and TSS. TH-2 was significantly better than both the checks for number of locules and pericarp thickness and was at par for TSS. Three hybrids viz. TH-1, TH-2 and TH-4, identified on the basis of superior performance in the field were evaluated for biochemical constituents important for processing. Based upon the field performance and the laboratory analysis, hybrid TH-1 was found suitable both for fresh fruit market and processing and hybrid TH-2 for processing.

**0800-0900**

**S17-P-109**

**'SUIOH': A NEW SWEETPOTATO CULTIVAR FOR GREENS UTILIZATION**

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Sweetpotato greens are rich sources of proteins, vitamins and minerals and are using as a vegetable in many parts of the world. In developing countries, sweetpotato greens are also a potential source of vitamin A and iron. In addition, our recent study indicated that the polyphenols content in sweetpotato greens, which are physiologically functional for health, was much higher than other commercial vegetables. A new sweetpotato cultivar, 'Suioh' was developed for tops utilization by Kyushu Okinawa National Agricultural Research Center, Japan. The new cultivar was a bushy type plant that was easy to harvest. We harvested greens from "Suioh" 6 times a year from April to October on nursery beds. Total greens yield was 4.16 kg per 1 kg of seed tubers. Sensory evaluation showed that the taste of cooked leaves and petioles was delicious and the hot water extract from greens could be substituted for green tea. The polyphenols content was 5-8 mg per 100 g dry powder. The content of potassium, calcium, iron, beta-carotene, total vitamin C, total vitamin E and vitamin K was 5.600 mg, 1.17 mg, 18 mg, 34.7 mg, 72 mg, 16 mg and 5.58 mg per 100 g DW of leaves, respectively. Utili-

zation of 'Suioh' for flour, paste and beverages is developing, and supplements for nutrition and medicine are expected.

**0800-0900**

**S17-P-110**

**CONSUMER DETECTION OF, AND PREFERENCES FOR, GREEN COLOR DIFFERENCES IN FRESH SNAP BEANS**

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Samples were hand-harvested from plants of five snap bean (*Phaseolus vulgaris* L.) cultivars in a yield trial at Bixby, Oklahoma. Five uniform, unblemished pods (sieve size 4) per cultivar were selected for evaluation by an untrained consumer panel of 7 males and 18 females. Panelists were asked to rank the samples from lightest to darkest green and from least to most desirable. Other replicated samples were analyzed in the laboratory for L-value and hue angle. Panelists could detect differences in snap bean pod greenness. However, these differences did not always correlate with the objective measures. For example, 'Jade' and 'Seville' were very similar in objective measurements of greenness, but 'Jade' was ranked darkest green by the panel, while 'Seville' was ranked lightest green. Both of these cultivars were rated intermediate in desirability. 'Brio' did not rate especially high for objective measurements of greenness and was perceived as intermediate in greenness by the panel, yet it was rated the most desirable cultivar. Greenness was only one factor determining pod desirability to consumers, and it could be outweighed by other appearance factors such as pod smoothness and uniformity.

**0800-0900**

**S17-P-111**

**RESPONSE OF SHALLOT TO MOISTURE STRESSES IN ETHIOPIA**

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Shallow rooted vegetables are known to be sensitive to water deficiency and require a frequent supply of moisture for better yield and quality. Responses of shallots (*Allium cepa* var. *ascalonicum* Baker) to moisture stresses were assessed under glasshouse and field conditions at Alemaya Univ., Ethiopia in 1999 and 2000. The experiments comprised of eight treatments: WWW, WWS, WSW, WSS, SWW, SWS, SSW and SSS; where plants received water at 40% depletion of available soil moisture (W) or at 100% depletion of available moisture (S) at early, mid- and late growth stages. (15-45, 45-75 and, 75-105 days after crop emergence, respectively). A complete randomized design with 20 plants per treatment was used for the pot experiment and RCBD with three replications was used for the field experiment. Early and mid-growth stage stresses reduced leaf number, bulb number and bulb weight. Mean bulb weight was reduced by 20–27% as a result of the early and mid-growth stage stresses. The yield reduction amounted to 20 and 25% in the pot and 30 and 46% in the field experiments due to early and mid-growth stage stresses, respectively. Stresses at all stages lowered the number of laterals produced per plant resulting in lower number of bulb splits. Moisture stresses 75 days after crop establishment did not significantly affect bulb weight and yield. There was no significant effect on bulb dry matter and total soluble solids contents due to the moisture stress treatments. Moisture conservation practices and supplemental irrigation are suggested to reduce moisture stress problems of rain-fed shallot cultivation in eastern Ethiopia.

**0900-0940**

**S17-O-112**

**BACK TO THE FUTURE OF FOOD: PHYTONUTRIENTS AND QUALITY IN VEGETABLE CROPS FOR THE 21ST CENTURY**

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Plants are the foundation for a significant part of human medicine and for many of the most widely used drugs. Many vegetable crops were originally domesticated for medicinal purposes prior to their current use as food. Folkloric transmission of plant-based cures represents a formidable reservoir of information for most human cultures. While such remedies are still widely practiced

throughout the world, recent scientific developments ushered in a new era of synthetic medicine. During the 20th century, modern medical science introduced monomolecular drugs, many of which have achieved great success. However, along with this revolution has come a realization that many traditional plant-based remedies, which generally contain a wide variety of complex secondary compounds, have been forgotten or obscured. Beginning with the discovery of the vitamins in the early part of the 20th century, key elements of the health functionality of specific crop plants were elucidated. This led to a greater understanding of the importance of vegetable crops in the human diet. However, it was not until the 1950s that consumption patterns were tied to nutritional composition. Recently, strides have been made to improve our understanding of how plant secondary compounds influence human health. This trend will likely continue as consumers continue to desire health functionality in traditional crops. During the 20th century, vegetable breeders made large improvements in vegetable quality traits such as maturity, processing characteristics, postharvest longevity, nutritional content, and culinary quality. As breeders focused on quality, yields increased because of improvements in production practices such as fertilization, pest control, and irrigation. Vegetable breeding during the 21st century will continue its focus on quality traits, and capitalize on the growing demand for the unique health functionality of vegetable crops. The future of vegetable crops is in their past.

**0940-1000**

**S17-O-113**

**LYCOPENE CONTENT OF SEVERAL TOMATO VARIETIES GROWN IN TUNISIA**

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Tomatoes are the main vegetable grown and consumed in Tunisia. This crop produces up to 930,000 tons annually and the average per capita consumption is among the highest in the world (nearly 38 kg). Recently, tomatoes have been reported to have beneficial effects in the prevention of cancer and heart disease and lycopene has been identified as being responsible for these effects. Tunisian growers, processors and consumers are therefore interested in the lycopene content of different tomato varieties. This study evaluates the lycopene content of several new and well-known commercial varieties grown in Tunisia. Significant differences among varieties concerning the lycopene content were recorded. Values for lycopene content ranged from 48 to 120 mg/kg fresh fruit, the highest being Chicago, RS 937535, Perfectpeel and Rio Grande. In all varieties tomato skin contains up to 6 times more lycopene than the whole tomato pulp.

**1000-1020**

**S17-O-114**

**NIRS (NEAR INFRARED REFLECTANCE SPECTROSCOPY) METHOD DEVELOPMENT AS A RAPID SCREENING TECHNIQUE FOR QUALITY COMPONENTS IN MELON**

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Oriental melon (*Cucumis melo* L.) which is one of the major vegetable crops in Korea, was cultivated on 10,412 ha in 1999. A number of melon varieties have been bred for yield enhancement, pathogen resistance and environmental adaptability by conventional breeding, but as national income increases gradually, the concern of vegetable quality becomes more important. Because the evaluation methods of vegetable quality are very complicated and require high cost and a long time, conventional breeders use mainly panel tests. More rapid and convenient evaluation methods need to be developed for improvement of quality of melon. In this research, the applicability of near infrared reflectance spectroscopy (NIRS) was examined to determinate sugar content in melon. For 3 years (1997–99), 503 melon samples were collected by Nongwoobio Seed Co. Transmittance absorbance data of melon juice were measured in the region of 1.1–2.5 by NIRS (NIR system 6500). HPLC (High Performance Liquid Chromatography) had been adapted as the standard analytical method, and sucrose, glucose and fructose were detected in melon by HPLC. The most accurate calibration was obtained

with a multiple linear regression (step-wise) analysis using the second derivative of the original spectrum. The determination coefficients ( $R^2$ ) between standard laboratory values by HPLC and prediction values by NIRS were 0.89 for sucrose, 0.64 for glucose, 0.86 for fructose and 0.95 for total sugar, respectively. Using routine analysis performed with 288 samples by developed calibration equations, the determination coefficients ( $R^2$ ) between standard laboratory values by HPLC and prediction values by NIRS for validation samples (20) were 0.85 for sucrose, 0.60 for glucose, 0.76 for fructose and 0.95 for total sugar, respectively. Most of deviations between values by HPLC and NIRS was within 0.5% for individual sugar content.

**1020-1020**  
**S17-0-114-A**  
**TO BE ANNOUNCED**

**1400-1420**  
**S17-0-115**  
**RELATIONSHIP BETWEEN THE NUTRITIONAL VALUE AND THE HEAD STRUCTURE OF LETTUCE**

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Crisphead lettuce has much lower vitamin A, vitamin C, calcium, and iron contents than leaf or romaine lettuce. This experiment was conducted to determine whether the low nutritional value is associated with the head structure. Heads of a crisphead lettuce cultivar 'Salinas' grown in the field were kept open by hand, while leaves of a romaine lettuce cultivar 'Lobjoits' were closed by tying with wire. These plants as well as the normal controls were analyzed for their nutritional contents. The content of vitamin A, Ca, and Fe was higher in the outer leaves than in the inner leaves of a normal lettuce head, while there was little difference in vitamin C content between the two classes of leaves. Artificially opening the lettuce head greatly increased its nutrient content to a level comparable to leaf or romaine lettuce. After the romaine lettuce leaves were closed, the levels of vitamin A and vitamin C dropped to a minimum and the contents of Ca and Fe were also largely reduced. These results suggest that the lower nutritional value of crisphead lettuce is due to the enclosure of its leaves in the head structure. The physiological basis of these findings and implications in genetic improvement of nutritional value of lettuce will be discussed.

**1420-1440**  
**S17-0-116**  
**GENETIC ANALYSIS OF PROCESSING TRAITS IN GREEN BEAN (*PHASEOLUS VULGARIS* L.)**

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A recombinant inbred population consisting of 80 lines was developed from the cross 'Minuette' x 'OSU 5630'. OSU 5630 is an Oregon bush blue lake standard-sieve green breeding line and Minuette is a small-sieve cultivar developed by Harris-Moran. The two cultivars exhibited contrasting traits for pod size and length, cross-section, color, and shininess, as well as for plant architecture. A cripple phenotype segregating in the progeny of the cross was also observed, indicating the the parents carry different alleles at the Lcr locus. A test of phaseolin seed storage protein type revealed that OSU 5630 possessed S-phaseolin and Minuette had T-phaseolin. This result was unexpected because most North American green beans have T-phaseolin. The lines with parents were grown in a randomized complete block replicated twice in the field in 2001. Plots were hand-picked at processing maturity, and evaluated for sieve size distribution, pod color, length, cross-section, smoothness, straightness, strings, and shininess. Pods were then blanched and frozen for additional characterization of processing traits. Pod shininess (conditioned by ace allele) segregated as expected for a single qualitative gene, while other traits showed quantitative inheritance. While both parents have a round pod cross-section and are stringless, the progeny segregated for flat and oval pod cross-section as well as strings, suggesting that different genes control those traits in these two lines. The plant architecture traits (plant height, internode length, branching, pod distribution, and main stem thickness) all exhibited quantitative inheritance. Efforts are underway to develop a molecular marker map using this population, and map QTL associated with processing and

plant architecture characters.

**1440-1500**  
**S17-0-117**  
**SELECTING FOR LOW FLAVOR IN BULB ONION USING FOLIAR TISSUE ANALYSES**

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Developing low flavor, sweet onions has several difficulties associated with the analyses of mature bulbs. Current methods of analysis use destructive tests for pyruvate, the LF and flavor precursors that, subsequently leave bulbs damaged going into storage. As a result, losses in a breeding program can be high before the bulb-to-seed cycle can be initiated. A Univ. of Georgia red-bulb breeding line that was segregating for bulb pungency was used to determine if early cycle leaf tissue analyzed for different flavor components could be used to predict mature bulb flavor characteristics. Single, uniform leaves from 89 plants were harvested prior to bulbing and analyzed for flavor precursors and precursor intermediates as well as total sulfur and sulfate. Plants were then allowed to develop and mature bulbs were harvested in early May. Bulbs were subjected to flavor analyses and the results were compared to the earlier leaf flavor analyses. Leaves had very different flavor profiles compared to their mature bulbs. No single leaf flavor component could be used to consistently predict bulb flavor characteristics. Step-wise regression of several of the leaf flavor components on mature bulb pungency, however, could be used with some success.

**1500-1520**  
**S17-0-118**  
**INTERACTION OF TERPENES WITH SWEET TASTE IN CARROTS (*DAUCUS CAROTA* L.)**

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Carrots were grown at 9, 12, 15, 18 and 21 °C and submitted to sensory and chemical analyses. Highest sugar content was found in roots grown at 21 °C, while those grown at 9 °C scored highest for sweet taste. The hypothesis of terpenes interacting in the perception of sweet taste was tested. Terpenes were analysed using dynamic headspace and an overview of the data by means of Principal Component Analysis (PCA) is presented. The highest content of terpenes was found in carrots grown at 21 °C. However, alpha-terpinolene, which is the most abundant terpene in carrots, showed the highest content in carrots grown at 9 °C. It is concluded that terpenes have different threshold values for bitter taste, and alpha-terpinolene does not contribute to the interaction of sweet taste.

Different morphological parts of the carrot root were analysed. The upper part of the root, containing the highest concentrations of sugar and terpenes, was negatively correlated with sweet taste. The lower part of the roots had a lower total concentration of sugars and terpenes, but scored higher for sweet taste than the upper part. However, the theory of terpenes blocking sweet taste in carrots was not supported when analysing the phloem and xylem of the roots. Attempts were made to remove terpenes from carrots by freezing and thawing the roots. Such carrots were much sweeter than untreated ones, though the sugar content remained unchanged. The terpene content in frozen carrots was reduced, but the reduction in the terpene concentration was not as large as one could expect according to the increase in sweetness. Though the experiments tend to support the hypothesis of terpenes being responsible for the interaction of sweet taste in carrots there is still a possibility that other compounds might be responsible for such interaction.

**1520-1540**  
**S17-0-119**  
**PLANT BREEDING: A STRATEGY FOR FRUIT QUALITY INTROGRESSION IN TOMATOES**

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Fruit quality is an extremely important tomato characteristic for both the con-

sumer and the processor. The objective of this study was to use the wild tomato variety Cherry, *Lycopersicon esculentum* var. *cerasiforme* in interspecific crosses with NR 44 and NR 46, both local cultivars, and NR 1 and NR 2, both introductions from Israel, to improve the quality of the cultivated types. Important agronomic and fruit quality characters were determined for the F1, F2, B1, B2, and the parentals. Cherry had higher mean values than the NR lines for all the characters except average fruit diameter: The hybrids were observed to have better fruit quality than either one or both parents. The major problem with the use of cherry tomato in these crosses was on the size of the fruits, which was below marketable size. However, the fruit size of the F1 was improved through the use of the NR lines as donor parents (males) in a back-cross to produce B2 progenies. Fresh fruits picked at colour break and stored in the laboratory to the fully ripened stage were analysed for pH, soluble solids content, citric acid, total sugars, vitamin C

and colour. Cherry had higher soluble solids content, total sugars, citric acids and vitamin C than the commercial cultivars and its colour was as good as the other genotypes. All these qualities were passed on to the progenies. Heritability (in narrow sense) estimates for the vegetative, yield and fruit quality traits were high, indicating that all these traits are influenced by additive genes and as such progress can be made through selection for such traits. In order to develop stable varieties with acceptable fruit size and good fruit quality, it is suggested that single plant selection followed by back-crossing, using the commercial varieties as recurrent parents may be followed.

**1650-1600**

**S17-0-119-A**

**TO BE ANNOUNCED**