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ORAL PRESENTATIONS

KEYNOTE

THE NEXT GENERATION OF BERRY CROP BREEDING: GENOMIC VS CONVENTIONAL APPROACHES

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The next generation of berry crop breeding: Genomic vs conventional approaches New technologies are allowing the mass sequencing of crop genomes. These sequences have proven useful for the genome-wide discovery of markers amenable for high-throughput genotyping platforms, like SSRs and SNPs, and the construction of high density genetic maps. These tools and resources have facilitated the discovery of useful genetic diversity, which has proven important for germplasm management and use, and they allow the identification of markers linked to individual genes and quantitative trait loci (QTLs). These markers can then be used for marker-assisted and genomic selection. Fruit breeders have generally lagged well behind agronomic breeders in the use of genomic technologies in crop improvement. To a large part this reluctance traces to the size of their respective industries and the amount of support available to conduct expensive foundation studies. In this talk, the status of genomic work in the small fruit crops will be reviewed, along with the potential benefits of such information.

SESSION I

OS 1-1:

COMPARATIVE RNA-SEQ ANALYSIS ON THE REGULATION OF CUCUMBER SEX DIFFERENTIATION UNDER DIFFERENT RATIOS OF BLUE AND RED LIGHT

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Cucumber (*Cucumis sativus* L.) is an economically important crop. light is one of the most important environmental stimuli, which control the timing of the transition from vegetative growth to reproductive development. To unravel the mechanism of light regulating cucumber sexual development, we performed high-throughput RNA-Seq analyses, which compared the transcriptomes of shoot apices between R2B1(Red light: Blue light = 2:1)-treated and R4B1(Red light: Blue light = 4:1)-treated cucumber seedlings. Results showed that the higher proportion of blue light in the R2B1 treatment markedly induced the formation of female flowers and accelerated flowering time. The genes related to flowering time, such as flowering locus T (FT) and SUPPRESSOR OF OVEREXPRESSION OF CO1 (SOC1), were up-regulated after R2B1 treatment. Furthermore, the transcriptome analysis showed that up-regulation and down-regulation of specific DEGs were primarily the result of plant hormone signal transduction after treatments with different types of light. The specific differentially expressed genes (DEGs) related with auxin (IAA) formed the highest percentage of DEGs in the plant hormone signal transduction, which was followed by the specific DEGs related with cytokine (CTK), abscisic acid (ABA), ethylene (ETH), brassinolide (BR), jasmonic acid (JA) and salicylic acid (SA). IAA might play a key role in the influence of light quality on sex differentiation in cucumber seedlings. In addition, the expression levels of transcription factors MYBs (MYB factors represent a family of proteins that include the conserved MYB DNA-binding domain, WRKY (transcription factors with WRKYGQK peptide), bHLH (basic helix-loop-helix) and MADS-box (The MADS box encodes the DNA-binding MADS domain) also changed after R2B1 treatment. Thus, sex differentiation affected by light quality might be induced by plant hormone signal transduction and transcription factors. These results suggest a novel model for light-mediated sex differentiation and provide a theoretical basis for further dissection of the regulatory mechanism of female flower formation under different light qualities in cucumber seedlings.

Keywords: RNA-seq; light quality; auxin; cucumber; flower; sex differentiation



OS 1-2:

PEACH GENOMICS AND BREEDING PROGRAMS AT ZHENGZHOU FRUIT RESEARCH INSTITUTE

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Zhengzhou Fruit Research Institute (ZFRI), Chinese Academy of Agricultural Sciences (CAAS) has acquired some advances in genetic resources, genomics and breeding programs over recent decades. To date, we have collected more than 1200 peach accessions from around the world, including wild relatives, landrace, and improvement varieties. The book PEACH GENETIC RESOURCES in China was published in 2002, which describes the diversity and evolution of peach and important agronomic traits for each accession. A total of 1000 accessions have been re-sequenced, comparative population genomics reveals the domestication history of the peach, and human influences on the evolution of perennial fruit crops. Genome-wide association studies (GWAS) of 12 agronomic traits in peach identify candidate markers and genes that contribute to the large-scale characterization of genes controlling important agronomic traits in peach. In the past 20 years, ZFRI has released more than 40 new peach varieties, including 11 peach, 17 nectarine, 2 flat peach and 10 ornamental, some of these varieties are planted widely in China now.

Keywords: peach; breedings; genomics; GWAS; genetic resources

OS 1-3:

WHOLE GENOME SEQUENCING OF 480 ACCESSIONS PROVIDES INSIGHTS INTO BREEDING HISTORY OF PEACH

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Understanding genome-wide breeding footprints during domestication and improvement is important to further improvement for peach that supplies one of the world's major resource of fruits. We detect 142 domestication sweeps and 104 improvement sweeps by analysis of 480 resequenced wild relatives, landrace and improvement accessions at $> 5 \times$ depth. A total of 5 fruit-weight-related quantitative trait loci (QTLs) and 36 fruit-edible-quality-related QTLs were identified in selective sweeps that may underlie fruit size and fruit edible quality changes during domestication and improvement. The different number of these QTLs in selective sweeps support that fruit size was mainly selected by domestication, while fruit edible quality was successively selected by both domestication and improvement, but stronger during improvement. Using genome-wide association studies, we identify associations between several candidate loci and six agronomically important traits. We discover genomic regions underlying local selection for Eastern and Western cultivars. Furthermore, by sequencing of nine accessions with known genetic relationships, we reconstruct the history of modern breeding over recent 100 years. Our results provide new resources and insights for genomics-guided improvements in peach breeding.

Keywords: breeding history; peach; genome sequencing; domestication; improvement

OS 2-1:

POLYEMBRYONY IN THE INTER-SPECIFIC HYBRIDS BETWEEN APRICOT AND ALMOND

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Seed polyembryony, referring to as the phenomenon that multiple embryos existed in the same seed coat, widely occurred in such fruit crops as mango, citrus and *Fragaria* species and so on. It is a useful trait in breeding and



propagation of them. However, polyembryony has not previously been reported in apricot (*Prunus armeniaca*) until we recently obtained the inter-specific hybrids between apricot and almond (*P. amygdalus*). The apricot we crossed in the distant hybridization was kernel-using apricot, a special apricot resource native to north China with thin, little juicy, astringent flesh but large-size sweet kernel within the stone. The objective of the inter-specific hybridization program was to widen the genetic basis of the kernel-using apricot cultivars by the introduction of valuable genes from almond. Among the hybrids, we found that some specific individuals had seeds with multiple embryos. And such individuals showed different frequencies of polyembryony (FP) ranged from 3.3% to 40%. The hybrids numbered 'P26-99', which obtained by the cross between *P. armeniaca* cv. 'Longwangmao' and *P. amygdalus* cv. 'Italian 1' had the highest FP of 40 percent, 'P56-89' crossed between 'Longwangmao' and *P. amygdalus* cv. 'Italian 2' with FP of 25 percent, 'P46-4' cross between 'Longwangmao' and *P. amygdalus* cv. 'Nonpareil' with FP of 6.7 percent and 'P7-45' cross between 'Longwangmao' and *P. amygdalus* cv. 'Italian 1' with FP of 3.3 percent. The plant materials with high FP might have great potential value in apricot breeding program in the future.

Keywords: Polyembryony, distant hybrid, apricot, almond

OS 2-2:

COMPARATIVE STUDY OF THE CONTENT OF PHENOLIC COMPOUNDS IN OLIVE FRUITS AND LEAVES FOR POSSIBLE USE IN BREEDING PROGRAMS FOR THE FUNCTIONAL SELECTION OF OLIVE CULTIVARS

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Olive breeding has traditionally focused on the agronomic traits but the growing number of scientific proofs supporting the positive impact of virgin olive oil (VOO) consumption on human health has made the functional quality of this product to be considered as an olive breeding target, particularly regarding the phenolic fraction of VOO. The presence of phenolic compounds in VOO is based mainly on the content of phenolic glucosides initially present in the olive fruit tissues and on the activity of hydrolytic and oxidative enzymes acting on these glucosides during the VOO extraction process. Thus, data on olive fruit phenolic composition would be of interest in olive breeding programs with the aim of obtaining new cultivars with improved functional quality. Taking into account that the main phenolics in olive fruits are essentially similar to those found in olive leaves, the objective of the present work was to carry out a comparative study of the phenolic fraction of fruits and leaves in selected cultivars characterized by having different contents of phenolic compounds in the oils to find out if the early selection of olive seedlings could be possible through an analysis of the phenolic compounds of their leaves. Results showed that there is no correlation between the level of the fruit and leaf phenolics for the different olive cultivars under study. In addition, no significant correlation was found between the content of tyrosol and hydroxytyrosol derivatives in the leaves of the different olive cultivars over time as it does in the case of the fruits during the ripening process. These preliminary data point out that although the biosynthesis of the major olive phenolics is carried out through similar biochemical pathways, they seem to be regulated differently in the different organs of the plant.

Keywords: *Olea europaea* L., leaf, fruit, phenolics, breeding

OS 2-3:

GENETIC EVALUATION OF APPLE NEOTETRAPLOIDS CV. 'REDCHIEF' OBTAINED BY IN VITRO METHOD AND PRELIMINARY PHENOTYPIC OBSERVATIONS

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Apple (*Malus x domestica* Borkh.) is the most important fruit species cultivated in Poland. The large production of apple is due to the implementation of technological and biological progress, especially with new and valuable cultivars. One of the breeding methods applied is the induction of variation via mitotic polyploidisation, which causes gene duplication and additionally, functional and/or structural changes in DNA. Variation within tetraploid clones may have an epigenetic (changes in DNA methylation) or genetic (DNA mutations, aneuploidy, deletion) nature. The aim of the presented studies was to determine changes in genomes of the newly formed apple tetraploids in relation to their diploid counterparts (standards). Four tetraploid clones obtained for the cultivar 'Redchief' and diploid standard were used for this study. To evaluate genetic changes in tetraploid plants, the AFLP (amplified fragment length polymorphism) analysis was performed. To determine epigenetic changes resulting from DNA methylation, the MSAP (methylation-sensitive amplification polymorphism) analysis was carried out. Analysis of AFLP markers showed that the degree of genetic diversity of the two tetraploid clones, No. 8 and No. 20, was on average 10% compared to diploid. The MSAP analysis revealed that the genomic DNA methylation levels in tetraploids were 28.0% and 21.7% for clones No. 11 and No. 13, respectively. In the tetraploid clones, no methylation was found for 83.9% of genomic DNA and full methylation for 6.4% of DNA. The external cytosine residues were methylated on average in 0.9%, while the internal cytosine residues were methylated in 8.8% of genomic DNA. Based on MSAP analysis, a preliminary DNA methylation pattern for apple trees was presented; it was generally similar in diploid and tetraploid plants. The newly obtained seven-month-old tetraploid plants differed from their diploid counterparts. Compared to diploids, tetraploids were shorter, had larger shoot diameter and significantly lower leaf numbers, their leaves were more round and chlorophyll indexes were higher. Plants of some tetraploid clones differed in photosynthetic activity from their diploid counterparts; one of the clones showed significantly higher photosynthetic activity and another one lower. The tetraploid clones also differed in resistance level to apple scab disease caused by *Venturia inaequalis*. All the tetraploid clones were more susceptible to this pathogen compared to their diploid counterpart.

Keywords: *Malus x domestica*, chromosome doubling, tetraploid, polyploidisation, AFLP, DNA methylation, *Venturia inaequalis*

Acknowledgements. This work was supported by the Ministry of Agriculture and Rural Development, a project No. HOR hn – 801 – 6/16_70.

OS 2-4:

SELECTION OF SERVICE TREE (*Sorbus domestica* L.) GENOTYPES NATURALLY GROWN IN TOKAT REGION

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This study was carried out during 2008-2011 years in order to determine genetic population of Service tree genotypes naturally grown in Tokat region, and also, to select genotypes from the resources in terms of selection criteria, adopted for the study. During the surveys, 304 genotypes out of 2275 genotypes recorded in the region were pre-selected for further detailed characterization. According to detailed characterization, 10 genotypes were selected as candidate for cultivars. Among the 10 candidate genotypes, 2 genotypes were very weak, 4 genotypes were weak, 1 genotype was medium growth and 3 genotypes were strong growth according plant growth strength. All candidate genotypes showed periodicity and the yields of all candidates categorized as high. According to years and genotypes, the average fruit weights were in the range of 9.69-36.28 g and the total amount of dry matter also ranged from 30.10% to 41.48%. Soluble solid content was ranged from 17.65% to 35.40% at maturation period, and from 18.05% to 29.70% at ripening period according to the years and genotypes. While total phenolic contents in fruits were in the range of 105.10-206.85 mg/100 g at maturation period, those ranged from 84.08 to 137.51 mg/100 g, respectively.

Keywords: Selection, Service tree, Population, Pomological, Phenological, Characterization



OS 2-5:

APRICOT BREEDING FOR LATE FLOWERING IN NIKITA BOTANICAL GARDENS

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Adaptation to environmental conditions is one of the main reasons limiting apricot plants introduction into various climatic zones. Cultivars characterized with later flowering most often avoid damages by spring frosts. The aim of the presented research was to study flowering dates of the apricot genotypes and to select promising ones for their cultivation in areas with changeable weather conditions and further breeding. The plants of 32 cultivars and breeding forms were studied during 2015-2017 years. Phenological observations were carried out in accordance with a well-known technique (Sedov, Ogoltsova, 1999). The control cultivar was Kryimskij Amur. The most late-flowering were genotypes created with the participation of *Prunus brigantiaca* Vill. (8103, 8134, Briol 38, Briol 98, Brigmas 2). Their blossom started 12-23 days later than in the plants of Kryimskij Amur cultivar. However, *Prunus brigantiaca* transmitted the traits of small fruits and poor fruit quality to its offspring, along with the late flowering. Saturating crossings had been carried out and new hybrids Brig and Fregat were obtained. In those hybrids the quality of fruits was improved, but the flowering dates shifted towards the control cultivar. The genotype Brig was characterized by large (56 g), tasty (4 points on a 5-point scale) orange fruits. The genotype Fregat was characterized with cream-yellow fruits, 43 g weight of good taste (4.5 points). Five promising late-flowering genotypes were selected (Boyarin, Lyubimec Richtera, Romeo, Samaritanin, Fiolent). They were characterized by large fruits (50-74 g), good taste (4.1-4.7 points), 5-7 days later bloom and are promising for growing in areas with changeable climatic conditions. The genotypes Dzentelmen Udachi and Zapozdalyij, with fruits 30-38 g weight and good taste (4.1-4.5 points), bloom later than the control for 10 days. They are valuable for breeding as sources of late flowering trait.

Keywords: apricot, cultivars, breeding forms, late flowering, fruit characteristics

OS 2-6:

CLONAL SELECTION OF SATSUMA MANDARIN IN RIZE PROVINCE, TURKEY

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In this study, Satsuma (Rize) Mandarin clone selection was made in Rize province and new candidate varieties were determined. The study was carried out by Recep Tayyip Erdoğan University Faculty of Agriculture and Natural Sciences between 2013 and 2016. Firstly, the areas having Rize Mandarin germplasm were searched and 51 genotypes with superior characteristics were determined. Tree development, productivity and maturation times were observed for these 51 genotypes for 2 years. Also, fruit properties (fruit weight (g), fruit length (mm), fruit diameter (mm), index (diameter /length), peel thickness (mm), number of slice, number of seeds per fruit, fruit juice content (%), total acidity (%), total soluble solids content (%), TSSC / total acidity, fruit outer appearance, fruit skin structure, and fruit skin color) of 50 fruit obtained from each of these 51 genotypes were examined. At the end of these studies, 11 Satsuma clones with superior characteristics were selected.

Keywords: Selection, breeding, genotype, mandarin, satsuma

This project was funded by Recep Tayyip Erdogan University, Scientific Research Projects Unit (BAP) Project number: 2013.112.01.1

OS 2-7:

IMPROVEMENT OF HUMAN NUTRITIONAL VALUE IN *B. rapa* (CHINESE CABBAGE) THROUGH MOLECULAR BREEDING

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The *Brassica rapa* ($2n = 20$, AA) is one among the six economically important cultivated *Brassica* species of U's triangle. The *B. rapa* subspecies has wide genetic and morphological diversity which grown as leafy vegetables, vegetable oils, turnip greens, turnip roots, turnip tops and as a fodder crop. Among *Brassica* species *B. rapa* is the smallest genome (529Mbp) and an ideal candidate genome as a reference, compared to *B. nigra* (BB, 632Mbp) and *B. oleracea* (CC, 696Mbp). In general plant secondary metabolites plays vital roles during different stages of growth and development. These functional compounds add high nutritional value to humans so the enrichment of these nutritional supplements in Chinese Cabbage cultivars is one of the important objectives. We have generated double haploid (DH) lines through micro spore culture from the collected germplasm accessions with high functional compounds like glucosinolites, vitamin C, total sugars and calcium. For glucosinolates through molecular markers approach we have performed a conventional QTL analysis using F2/3 mapping population of *B. rapa* combined with candidate gene association approach by using natural population in order to identify the genomic region and genes regulating glucosinolates biosynthesis in *B. rapa* crops. Recently we have re-sequenced 145 Chinese cabbage accessions and identified ~1.7 million high quality SNPs for the association studies. Results suggest several alleles with very high association for important compounds like gluconapin, neoglucobrassicin, sinigrin and glucobrassicinapin. Additionally, the comparative analyses of several association results were completely matching with previous analyzed QTL maps. The further analysis will be done to study the identified candidate genes related to glucosinolates enhancement.

Keywords: *B. rapa*, Vitamin C, Total sugars, glucosinolates

OS 3-1:

Resistance to *Tomato mosaic virus* (ToMV) in Sweet Pepper (*Capsicum annuum*)

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Pepper (*Capsicum* spp.) is an increasingly important crop worldwide, and commonly is used as a vegetable, spice, and food colorant. Tobamoviruses are the most important pepper-infecting viruses that are not transmitted by an insect vector. External seed contamination, internal seed infection, and contact are the primary modes of transmission for tobamoviruses. Resistance to the different species and pathotypes of tobamoviruses in pepper is conferred by different alleles of the *L*-locus on chromosome 11. *Tomato mosaic virus* (ToMV) is one of the most widespread tobamoviruses in Southeast Asia and Southern Europe. Little is known about the *L* gene alleles in sweet pepper involved in resistance to ToMV strain in Taiwan. The objective of this study was to identify novel resistance sources against ToMV from available sweet pepper germplasm accessions and to determine the possible genetic basis of these resistant lines. In total, 47 advanced sweet pepper breeding lines were screened for resistance to ToMV. Susceptible symptoms included leaf mosaic, yellowing, abscission and necrotic lesions, stem lesions, and plant death. Lines were considered resistant if necrotic lesions occurred only on inoculated leaves. Eight lines from three different genetic backgrounds were identified as resistant. Accumulation of ToMV coat protein was not detected in the systemic leaves of the resistant lines, but was detected in the systemic leaves of susceptible lines. Using previously published molecular markers, we found that all of the resistant lines possessed *L*² allele, and two of the resistant lines also contained *L*⁴ gene. The resistant sweet pepper lines identified in this study displayed good horticultural traits and can serve as sources of ToMV resistance in breeding programs. Additionally, these lines may serve as potential sources of resistance to other pathotypes and species of tobamoviruses.

Keywords: disease resistance, *L*², tobamovirus



OS 3-2:

SEARCH FOR RESISTANCE TO TOMATO SPOTTED WILT VIRUS (TSWV) IN PEPPER (*Capsicum annuum* L.)

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Pepper is widely grown vegetable crops in the world. Many pests and pathogens cause yield losses in pepper. One of the most important diseases in the pepper production is spotted wilt disease caused by Tomato spotted wilt virus (TSWV). The best way for the control of this disease is to use resistant varieties. In this study, it was aimed to determine resistance gene transferred to long pepper by using TSWV resistant pepper lines and cultivars. Hybrid cultivars resistant to TSWV were crossed with susceptible Serademre 8. The resistance tests were performed by both mechanical inoculation and molecular methods. Virulent strain isolated from infected pepper plants was used as a disease material in the mechanical inoculations. Resistance test was performed for 72 lines in F6 generations. A total of 1065 plants from 72 lines were tested and determined 1017 plants as homozygote resistance.

Keywords: Pepper, TSWV, Molecular, Biological screening

OS 3-3:

CHARACTERIZATION AND MAPPING OF A VIRESCENT-YELLOW LEAF GENE IN CUCUMBER (*Cucumis sativus* L.)

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Leaf color mutants in higher plants are ideal materials for investigating the structure and function of photosynthetic system. In this study, we identified a cucumber vyl (virescent-yellow leaf) mutant in the mutant library, which exhibited reduced pigment contents and delayed chloroplast development process. F2 and BC1 populations were constructed from the cross between vyl mutant and cucumber inbred line 'Hazerd' to identify that the vyl trait is controlled by a simply recessive gene designated as CsVYL. The CsVYL gene was mapped to a 3.8 cM interval on chromosome 4 using these 80 F2 individuals and BSA (bulked segregation analysis) approach. Fine genetic map was conducted with 1542 F2 plants and narrowed down the vyl locus to an 86.3 kb genomic region, which contains a total of 11 genes. Sequence alignment between the wild type (WT) and vyl only identified one single nucleotide mutation (C→A) in the first exon of gene Csa4G637110, which encodes a DnaJ-like zinc finger protein. Gene Expression analysis confirmed the differences in transcription level of Csa4G637110 between wild type and mutant plants. Map-based cloning of the vyl gene could accelerate the study of chloroplast development and chlorophyll synthesis of cucumber.

Keywords: *Cucumis sativus* L.; leaf color mutant; virescent; chloroplast function; DnaJ proteins.

OS 3-4:

TOLERANCE AND RESISTANCE OF ONION TO STEM AND BULB NEMATODE (*Ditylenchus dipsaci*)

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Resistance is known as a defense mechanism of plant, while tolerance is ability to give good yield where pathogen is found. Both mechanisms provide advantage to plant under unfavorable conditions. Onion is economically important plant species grown in the world for human nutrition and one of the important constraints is stem and bulb nematode (*Ditylenchus dipsaci*). Both tolerance and resistance of onion cultivars were investigated under greenhouse conditions to *D. dipsaci*. Totally 28 onion cultivar were evaluated for resistance



and tolerance reactions to *D. dipsaci* under growth room and greenhouse conditions, respectively. Valenciana cultivar had the lowest nematode multiplication in growth room resistance experiment (MR: 0,5). Plant height and plant diameter of cultivars statistically significantly changed with nematode treatment in greenhouse tolerance experiment. Plant weight of cv. Biotek Boran and plant height, diameter and weight of cv. Taraz had statistically significant positive correlations with nematode multiplication. It is recommended growing cv. Valenciana for lower nematode multiplication, and cvs Biotek Boran and Taraz for better plant development under nematode multiplication in stem and bulb nematode infested onion growing areas.

Keywords: *Ditylenchus dipsaci*, onion; resistance; stem and bulb nematode; tolerance

OS 3-5:

MAPPING OF RESISTANCE GENES TO RACES 1, 2 AND 5 OF *Podosphaera xanthii* IN PMR6 USING RIL POPULATION AND DEVELOPMENT OF NEW RESISTANT MELON VARIETIES IN TURKEY

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Genetic diversity of melon in Turkey is very high. The common pathogen in Turkey is *Podosphaera xanthii* race 5 (Ünlü et al. 2010) restrict melon cultivation. The chemicals used against to pathogen causes negative effects on environment and human health and additionally increase expenses. One of the best solution to disease is improve resistant cultivars. Because there are no national melon varieties resistant to mildew. All these problems can be solve by using molecular markers in a short time and easily. QTL mapping will be use to quantitative trait locus (QTL) that control resistance of powdery mildew have been identified *Pm-5* by using RIL population obtained from TKÜ3 (susceptible ♀) and PMR-6 (resistance ♂) hybridisation. For the mapping study, SRAP, SSR, ISSR, TRAP, CAPS, SCAR molecular markers will be used to QTL mapping. However, molecular marker will be achieved tightly linked to gene. Additionally, the results of this project will provide significant information to future works. The new resistant hybrid variety from this population that one of the parents is Turkish melon landraces will be developed.

Keywords: *P. xanthii*, resistance, breeding, QTL mapping, MAS

OS 3-6:

EVALUATION OF TURKEY QUINCE GENE BANK FOR RESISTANCE BREEDING TO FIRE BLIGHT DISEASE

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Turkey, which is one of the major quince producer countries in the world, also has an important part in terms of export. In our country that is among the centers of origin of quince, studies on the protection of quince genetic resources are being conducted in Institutes, located in Izmir, Isparta and Erzincan locations, within the scope of GDAR (General Directorate of Agricultural Researches and Politics). The Aegean Agricultural Research Institute (AARI) is the first responsible institute for the conservation of quince genetic resources and 61 genotypes are protected in the field gene bank at Menemen / Izmir location. Fire blight is the leading cause of disease that restricting production and causing significant economic losses. Quince is described as one of the most susceptible hosts to the disease, the extensive breeding studies; the world was launched for the first time with the project of "Fire Blight Resistant Quince Breeding" funded by GDAR in 2016 under the leadership of AARI. In this context, genetic resources and cultivars (total 56) are tested with a mixture of 3 virulent strains in 3 different periods for the evaluation of disease tolerance. In addition, selection breeding studies carried out Manisa, Sakarya, Bursa, İzmir and Denizli locations for determining the tolerant genotypes under natural



epidemic conditions in two consecutive years. As a result of the artificial inoculations, 50 genotypes took place in medium susceptible group, whereas susceptible group included 6 genotypes. Under natural infection conditions 15 genotypes were selected as tolerant to the disease with the range of 0-12 % disease index. The possibility of using as a variety or genitor in the breeding studies and the importance of Turkey quince genetic resources in terms of tolerance to disease were determined.

Keywords: *Erwinia amylovora*, *Cydonia oblonga*, resistance breeding, selection breeding, plant genetic resources

OS 4-1:

EFFECTS OF DIFFERENT ROOTSTOCKS ON SEED YIELD AND QUALITY OF TRIPLOID WATERMELON GROWN IN GREENHOUSE

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This study was carried out at the experimental greenhouse and laboratory of the Department of Horticulture, Faculty of Agriculture, Cukurova University during the growing season of 2017. Nun-9075 from *Cucurbita maxima* × *Cucurbita moschata* group, Argentario from Lagenaria group and watermelon - *Citrullus lanatus* var. citroides coded PI296341 were used as rootstocks. In control, the seedlings from these plants were grown without grafting (non-grafted plants). Tetraploid ST 101 and diploid WL 92 lines were used as scions and two parents were grafted onto each rootstocks. The aim of this study was to investigate the effects of different rootstocks on fruit/seed yield and quality of tetraploid female parent pollinated with diploid male parent. In the study plant height, main stem diameter, number of nodes, total fruit yield, average fruit weight, average fruit height, average fruit diameter, fruit rind thickness, total soluble solids (TSS), seed yield, weight of 1000 seeds, seed coat/embryo ratio, seed germination and seed emergence tests were examined. According to the results of this research, plant growth, the total fruit/seed yield and the other fruit parameters of the ST 101 tetraploid female line observed to be higher in NUN-9075, Argentario and PI296341 rootstocks respectively, and TSS value was found to be higher in control (non grafted) plants. In terms of seed germination and emergence ratio and duration, there was no significant differences between rootstocks.

Key words: Plant growth, tetraploid, fruit/seed yield and quality

OS 4-2:

EVALUATION OF HETEROSIS ON YIELD AND FRUIT NUMBER OF HYBRID BELL PEPPER (*Capsicum annuum* L.) IN UNHEATED GREENHOUSE CONDITION

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Diallel analysis supplies important information about populations for parameters of interest in breeding programs. The objective of the present study was to determine the most promising bell pepper hybrid varieties and to study the effects of heterosis for fruit yield and fruit number in 15 hybrids (F1) with respect to the mean of the parents, mean of the superior parent and commercial hybrids used as checks. Six parents belonging to Batı Akdeniz Agricultural Research Institute (BATEM) were crossed in a half diallel scheme. The performance of 15 hybrids and pure lines were tested in randomized complete block design (RCBD) with three replications in a single crop season in unheated greenhouse. Data obtained were submitted to analysis of variance. The magnitude of heterosis ranged from -16.34 to 48.69 % for fruit yield per plant and -23.28 to 55.82 % for number of fruits per plant in total yield whereas the magnitude of heterobeltiosis varied from -21.09 to 41.51% for fruit yield per plant and -28.76 to 45.48 % for number of fruits per plant in total yield. The most promising hybrid combinations with the greatest heterosis were P1xP3, P1xP4, P3xP4, P3xP5 and P4xP6 and their parents are thought to be important in the breeding studies of new varieties.



Keywords: Pepper (*Capsicum annuum* L.), diallel, hybridization, heterosis, heterobeltiosis

OS 4-3:

EFFECT OF DIFFERENT VERNALIZATION DURATION TO SEED YIELD IN WHITE HEAD CABBAGE

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Cabbage seed production have longer periods compared to the other vegetables. Controlling of flowering duration and shorten the period required for seed production are important for cabbage cultivar breeding. There are many factors affecting bolting and flowering for the cabbage seed production. Vernalization duration is the most important factor affected bolting and flowering. This study was carried out in Black Sea Agricultural Research Institute in 2016-2017 to determine seed yield affecting different vernalization duration in terms of hybrid combination synchronization. 3 CMS-female and 15 male parents was used as material in the study. Vernalization duration determined as 0, 6, 9 and 12 week at 5°C±1 for each genotypes. P62-1 genotype applied 6 week vernalization had higher seed production amount (31.93 g/plant) compared to the female genotypes and W13 genotype non-vernalized had higher seed production amount (96.10 g/plant) compared to the male genotypes. The highest seed yield were obtained from CMS-P62-1 X W13 (69.37 g/plant), CMS145 X P92 (67.55 g/plant) and CMS-P62-1 X MANF4 (65.50 g/plant) combination independently vernalization duration.

Key Words: cabbage, seed yield, vernalization, flowering

OS 4-4:

SCREENING OF SOMATIC HYBRIDS OF CELERY AND CARROT WITH THE CHLOROPLAST MARKER DcMP

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In celery (*Apium graveolens* L.) breeding somatic hybridization might be used to induce male sterility, to introgress disease resistance, new variation in colour and or size, or to increase yield. Therefore, we have developed protocols for protoplast isolation and established conditions that allow plant regeneration from isolated protoplasts. With the aim to induce cytoplasmic male sterility (CMS) an asymmetric protoplasts electrofusion was performed between IOA treated celery suspension derived protoplasts and UV treated carrot (*Daucus carota*) mesophyll protoplasts. In total 55 independent plants and 6 Weck-jars of micro-plants were recovered 8 months after the asymmetric protoplast fusion. Screening of these regenerants with the chloroplast specific marker DcMP (*Daucus carota* Mitochondrial Plastid sequence) showed that none of the 55 independent plants contained carrot specific chloroplasts. However, one of the 6 micro-plants samples amplified for both celery and carrot DcMP, confirming the true asymmetric hybridity. Further screening with mitochondrial specific markers will be performed in order to validate the potential of the fusion for the development of CMS in celery.

Keywords: protoplasts, asymmetric protoplasts fusions, electrofusion, celeriac

OS 4-5:

MARKER-FREE APPLE PLANTS EXPRESSED THE SUPERSWEET PROTEIN THAUMATIN II GENE DRIVEN BY PLANT PROMOTER

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Using the pMF1 vector, which combines inducible site-specific recombinase and bifunctional selectable gene, we have obtained marker-free apple plants with the supersweet thaumatin II protein under the control of tomato genetic regulatory elements. Exploitation of this gene in our laboratory allowed enhancing of sweetness, as well as improving the taste characteristics of fruits and vegetables of plants such as strawberry, carrot, tomato, pear and apple. In the early works we used a constitutive virus 35S promoter. GM plants with viral and bacterial genes are adopted by consumers with concerns; in addition, constitutive promoters have a number of disadvantages in the industrial cultivation of agricultures. In this paper, we used a plant mainly fruit-specific promoter, along with a selective gene removal system, which prevented the presence of any foreign DNA in the apple genome. And we were faced with the task of evaluating the of transferred gene expression level in 39 derived apple sublines. Despite the predominant fruit specificity of the promoter, the mRNA of the thaumatin II gene was detected in the leaves. Two methods for analyzing the expression of thauII at the RNA level were used - semiquantitative RT-PCR and real-time PCR. Six sets of primers were designed - 3 for the housekeeping genes and 3 for the thaumatin II gene. Both methods showed high repeatability and close results, but one highly productive line was identified only by real-time PCR. All apple sublines were divided into groups according to the level of thaumatin II gene expression, the plants with the highest level were chosen for further experiments.

Keywords: marker-free plant, apple, *Malus x domestica*, supersweet protein, thaumatin II, semiquantitative RT-PCR, real-time PCR

OS 4-6:

TRANSFER OF *RolABCD* GENES IN SOME CITRUS ROOTSTOCK THROUGH *Agrobacterium rhizogenes*

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Gene transferring is an important experimental tool in plant genetics. *Agrobacterium*-mediated transformation an effective and universal tool for transferring of target gene to plant species. To improve dwarf rootstock is one of the most important subject in plant breeding. It is among the most important breeding objectives to make dwarf citrus rootstock. In the present study, non-recombinant wild-type *A. rhizogenes* strain ATCC15834 was used to get dwarf citrus rootstock in *in vitro* conditions. Tuzcu 3131 Sour Orange (*Citrus aurantium* L.), Carrizo citrange (*Poncirus trifoliata* Raf. X *Citrus sinensis* Osb. var. "Carrizo"), Gou Tou Sour Orange (*Citrus aurantium* L.), Swingle citrumelo (*Citrus paradisi* Macf. × *Poncirus trifoliata* [L.] Raf.) and Troyer citrange (*Citrus sinensis* 'Washington' sweet orange X *Poncirus trifoliata*) were used as plant materials. Internodal stem and leaf explants were used from germinated seeds of *Citrus* rootstocks. Two different methods were applied for transformation. In the first treatment, explants were excised and inoculated with *A. rhizogenes* suspension and shaken at 80 rpm for 30 min, and explants were transferred on MS for 2 days in darkness at 24 °C. After co-cultivation, the explants were cultured on MS containing 500 mg/l Cefotaxime. In the second treatment over night bacterial cells were pelleted by centrifugation at 5000 rpm for 10 min, resuspended and diluted in bacterial suspension medium. The explants were immersed for 15 min in bacterial suspension and transferred in petri dishes containing cocultivation medium (MS, 2 mg/l IAA, 1 mg/l 2IP, 2 mg/l 2,4-D) for 3 days at darkness. Then the explants were transferred onto shoot regeneration medium (MS supplemented with 500 mg/l of Cefotaxime and 1 mg/l of BAP). Shoots and roots formation were scored at 4-8th weeks after transformation. The presence of *rol* genes in the putative transformed plants was confirmed by PCR analysis. According to molecular analysis, 13 clons containing *rol* genes were determined in Troyer citrange and they were rooted in *in vitro* conditions.

Keywords: Callus, transformation, MS, BAP, PCR



OS 4-7:

COMPREHENSIVE INSIGHTS ON GENES REGULATION ON PLANT ARCHITECTURE OF LAGERSTROEMIA

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Study on plant architecture is always one of the hotspots. Although different growth habits of trees are in great demands by orchards and nurseries, the molecular mechanism in plant architecture of woody perennial plants is still poorly understood because of the complex phenotypic analysis and regulatory system. In our research, traits related to plant architecture had been analyzed in F1 population derived from *L. fauriei* (non-dwarf) × *L. indica* 'Pocomoke' (dwarf), and internode length (IL) trait was positively correlated with the plant height. Additionally, two markers highly correlated with the IL trait were validated in the F1 and B1 populations. Further analyzation in six generations (P1, P2, F1, B1, B2 and F2) using a gene inheritance model suggested that IL trait was mainly controlled by genetic factors with a low effect of environmental factors and should be selected in early generations. Subsequently, we combined the morphophysiological measurements with transcriptional profiling identifying putative regulator genes of Lagerstroemia plant architecture. The results indicated that IAA was an important hormone regulating cell number in shoot apical meristems and cell elongation in internodes. The interaction between the two cell processes determined the internode length of Lagerstroemia, which contributed to the final branch length. The branch length together with branch number were two dominances defining the Lagerstroemia plant architecture. Differentially expressed genes (DEGs) involved in IAA biosynthesis, homeostasis, transport and signaling were dug. Exogenous IAA and gibberellin A4 treatments further indicated that the short branches and dense branching of the dwarf progenies were caused by defects on the IAA transport and signaling. In addition, the DEGs regulating cell-cycle and cell elongation progressions were also uncovered. These potential candidates will lay a foundation for further functional genomic studies to improve woody plant architecture.

Keywords: Genetic inheritance; histogenesis; IAA; Lagerstroemia; plant architecture; RNA-seq; SNP markers.

OS 4-8:

TRANSFORMATION OF KALANCHOË AND OILSEED RAPE WITH ORFS 11-15 FROM *Agrobacterium rhizogenes*

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Infection by naturally occurring *Agrobacterium rhizogenes* gives rise to hairy roots in many host plants. Moreover, plants transformed with this bacterium exhibit compact growth and frequently wrinkled leaves that often are reduced in size. The phenotypes are caused by the bacterial T-DNA integration in the plant host genome. The T-DNA includes many genes and the best characterized are the *root oncogenic loci* (*rol*) genes: *rolA*, *rolB*, *rolC* and *rolD*, which correspond to open reading frames (ORFs) 10, 11, 12 and 15, respectively. Understanding how the *rol*-genes confer compact growth traits in plants is relevant given the potential to reduce the use of chemical growth retardants, thus providing environmentally friendly produced plants. Few studies have investigated the association of genotypes with phenotypic traits caused by the individual *rol*-genes and selected ORFs from *A. rhizogenes*. The current study aims to investigate this association in *Kalanchoë* spp. and oilseed rape by producing plant lines with a selection of single gene constructs comprising *rol*-genes and ORFs. Hence, transformation and tissue culture methods are currently being developed. The aim is implementing a transformation platform to facilitate the regeneration of transgenic lines to study the individual genes. Callus formation of 100% and 80-100% was observed in *K. blossfeldiana* 'Molly' and *K. pinnata* leaf explants, respectively. Whereas in *Brassica napus* 'Elan' cotyledons, the callus formation ranged from 50 to 75% a month after inoculation. Shoot formation in the studied *Kalanchoë* species was between 0 to 10% of the initial number of inoculated explants; whereas in *B. napus* 'Elan' it ranged from 2 to 9%.



Keywords: biotechnology, compact plants, natural transformation, *root oncogenic loci* genes, tissue culture

OS 5-1:

IDENTIFICATION OF TRADITIONAL EGGPLANT HEIRLOOMS FOR CONSERVATION AND SUSTAINABLE COMMERCIAL PRODUCTION

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Eggplant is one of the important Solanaceous crops consumed for human nutrition. Thanks to its highly adaptable capability giving growing possibility in different zones and altitudes in the world. Because of its ability to adopt changing global environments, it will still keep signification in the future. Traditional heirlooms still cultivated in regions of crop domestication attract attention of the breeders. This paper presents origins, some morphological observations and breeding potentials of some heirlooms which are maintenances by the farmers who meet local market demands. Totally, 40 eggplant genotypes collected from different regions and altitudes ranging from 40 to 1200 meters in Turkey identified morphologically. The number of days from planting to flowering changed in between 27 and 41. The number of days from planting to % 50 flowering ranged from 30 to 47, average fruit width (cm) from 2.4 to 7, average fruit length (cm) 10-32.5, average fruit weight (g) from 108 to 221, brix from 4.3 to 5.4 and average total fruit yield per parcel (g) from 1,398 to 7,025 in the greenhouse conditions. There was a wide variation between the fruit color (L*, a* and b* values) and shape. The horizontal dendrogram was created by using UPGMA with morphologic data. The genetic similarity rates ranged from 0.30 to 0.97. These results showed that there is a great genetic diversity among the heirlooms showing a potential for breeding which could be used as sources of variation for F1 eggplant breeding programmes. Furthermore, some genotypes belong to the open field conditions which could be used for commercial production under greenhouse conditions in different growing periods were also determined in this study.

Keywords: diversity, selection, observation, quality, breeding, resistance, growing, greenhouse

OS 5-2:

EFFECT OF BUDDING ON MORPHOLOGY OF HYBRIDS OF *Solanum melongena* AND *Solanum torvum* Sw.

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Solanum melongena is susceptible to numerous diseases and parasites, particularly the bacterial, *Fusarium* and *Verticillium* wilts, nematodes and some insects. *Solanum torvum* is resistant to *Verticillium* and some bacterial wilts, root-knot nematode and some mycoplasmas. It is known that the interspecific hybrid plants resulted from cross hybridization of these species were sterile. It was reported that due to rootstock used, the response of scion to photoperiod and sex expression were affected in cucurbits, and some fruit characteristics of scions were changed in pepper and eggplant. The objective of this study is to investigate the effect of budding on the morphology of interspecific diploid and tetraploid hybrid (*Solanum melongena* x *Solanum torvum*) plants. The plants of two interspecific hybrid genotypes (AU2/I-6, AU4/I-10) were obtained by in vitro germination of seeds produced by crossing *Solanum torvum* and eggplant cultivar, Faselis F1. The buds of these 2 interspecific diploids and 2 tetraploids (autotetraploid Kol53, amphidiploid U4/IV-I-4) genotypes that have obtained by colchicine application were budded on Pala and Faselis F1 rootstocks. Then the budded plants were grown in a glasshouse and the morphological characteristics were studied. In diploid genotypes, budding significantly affected some properties of the plant; such as brunch number, leaf blade width, and length, leaf lobing, petiole length, leaf hair, inflorescence type, flower or bud number per inflorescence, calyx length, corolla number and width. However, the effect of budding was not significant in tetraploid genotypes.



Keywords: Interspecific hybrids, diploid, tetraploid, morphological characteristics, budding

OS 5-3:

COLLECTION, IDENTIFICATION AND CONSERVATION FOR SUSTAINABILITY OF TRADITIONAL LOCAL PEPPER GENOTYPES

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Traditional peppers (*Capsicum annuum* L.) are grown in different types and shapes in different local regions in Turkey. They have significant genetic richness with different forms of processing and consumption. The development and certified seed production of pepper varieties from local populations are necessary for different aims and regions. This study was carried out for collection, morphological characterization and conservation of traditional local pepper genotypes. A total of 50 domestical traditional pepper genotypes was collected from several regions ranging in altitudes from 2 to 1210 meters in Turkey. Morphological characterizations of fifty genotypes were evaluated in the spring season in greenhouse in Bati Akdeniz Agricultural Research Institute (BATEM). First flowering time ranged from 26 to 41 days, average fruit length from 2.7 to 24.9 cm, average fruit diameter from 15.4 to 103 mm, average fruit thickness from 1.99 to 6.85 mm, average fruit weight from 6.3 to 246 g, average total fruit yield per parcel from 2615 to 14430 g, average total fruit number per parcel from 50 to 903, total solids content of water from %3.2 to 5.48 and fruit texture from 6.11 to 13.1 mm/s in greenhouse conditions. Fruit color at immature stage was measured L*, a* and b* values. In terms of traits examined, wide diversity was found between pepper genotypes. The horizontal dendrogram was created by using UPGMA with morphologic data. The genetic similarity rates ranged from 0.31 to 0.96. It is understood that these traditional peppers grown in different regions were important as genetic sources in the development of new varieties for open fields and protected cultivation.

Keywords: pepper, traditional genotypes, collection, identification, diversity, conservation and sustainability

OS 5-4:

DEVELOPMENT OF DOUBLE-HAPLOID LINES IN GALIA-TYPE MELONS USING IN VITRO COLCHICINE TREATMENTS

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Melon is an important vegetable crop in the world. Cantaloupe type of melons (*Cucumis melo* var. *cantalupensis* L.) ripen early and are aromatic however they have a short shelf life, which limits transport and export opportunities. In this research, we used 84 BC3 populations to developed 100% homozygous haploid lines by using irradiated pollen (300 Grays of Cobalt60) technique for breeding cantaloupe melons having a long shelf life. A total of 600 haploid melon lines were obtained with irradiated pollen technique. The haploid plants of these lines were propagated by *in vitro* micro-cuttings. *In vitro* colchicine (0.5%) was applied to 15 micro-cuttings of each haploid line for 2 hours to double chromosome number. After rinsing 3 times with sterile distilled water micro-cuttings were dried and transferred into test tubes containing MS medium. Then they were placed in growth chamber having 24°C temperature and 16/8 h day/night photoperiod conditions. After 1 month plants were acclimatized to greenhouse. The ploidy level was identified by morphological observations, pollen presence and chloroplast/stoma countings. Among the 600 *in vitro* colchicine applied haploid lines, 152 were found to be diploid and the success of *in vitro* duplication was obtained as 25.33 %.

Keywords: Melon, irradiated pollen, ploidy level, micro-cutting



OS 5-5:

THE SOUTH AFRICAN MANGO BREEDING PROGRAMME: GAINING MOMENTUM TOWARDS THE RELEASE OF PROMISING NEW CULTIVARS

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It is common knowledge, and extensively documented that classical breeding of mango cultivars is a time-consuming exercise, taking many years for a new cultivar to be released to the Industry. The Agricultural Research Council - Tropical and Subtropical Crops' (ARC-TSC) mango breeding programme started 28 years ago, in 1990. From inception, only 5 cultivars were registered and released to the Industry. This situation is now starting to change mainly due to the more scientific approach of using seed from polycross nurseries as a source of natural crosses (open pollination), establishing these as Phase I seedlings. A high percentage of promising selections are derived from these orchards. This can be attributed to the concentration of superior genotypes in the polycross nursery. In addition, relocation of the mango breeding programme had the unexpected advantage of shortening the juvenile stage, as well as increasing the uniformity of the seedling plant material. During 2013 and 2014, 831 Phase I selections, 120 Phase I extension selections and 16 Phase II selections, using 5 600 grafts, were top worked at the new site. The first evaluations at the new site were carried out during the 2015/2016 season, when 168 trees were evaluated. From 35 selections that will advance, 7 selections of exceptional quality will bypass Phase I extension, and will proceed directly to Phase II. During the 2016/2017 season, 462 trees were evaluated, of which a further 37 promising selections were identified. Eighteen of these selections were deemed good enough to enter Phase II directly. Working with only 831 Phase I seedlings, and being able to identify 90 selections with potential, shows the momentum gained during the last few years of the programme.

Keywords: *Mangifera indica* L., breeding, cultivar, selection, evaluation.

OS 5-6:

MORPHOLOGICAL AND PHENOLOGICAL CHARACTERISTICS OF 'LIKYA KAYA' CARNATION

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It is thought that the development of domestic varieties of carnations that can meet consumer demands and can be preferred on the market, will provide a significant contributions to the economy of the country as well as the cut flower sector. This study was carried out at the Bati Akdeniz Agricultural Research Institute between 2012 and 2015 with the aim of developing new varieties of carnation to be used in ornamental plant sector. In this study, standard and spray genotypes obtained by cloning selection method were evaluated. According to the obtained results, 50 individuals with standard and spray type characteristics were selected. In the present study, some morphological and phenological characteristics of 'Likya Kaya' carnation that was applied for registration was given.

Keywords: Carnation, Clonal selection, Variety development, Likya Kaya

OS 6-1:

BREEDING *Leucospermum* HYBRIDS FOR POTTED FLOWERING PLANT PRODUCTION, LANDSCAPE USES AND FOR CUTFLOWER PRODUCTION IN THE TROPICS; GENETIC FACTORS CONTRIBUTING TO PLANT ARCHITECTURE

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Protea research at the University of Hawaii has produced over 100 cultivars primarily for cutflower cropping at both temperate elevations, up to 1500 m, and tropical climates near sea level in Hawaii. Some hybrids have been identified for suitability as landscape specimens and more recently cultivars have been evaluated for suitability as potted flowering plants. Some hybrids were simple primary crosses, while others were complex hybrids with up to 11 species in their genealogy, sometimes representing 4 taxonomic sections. Data linking the composition of taxonomic sections in the genealogy of hybrids with their market suitability for potted flowering plants, landscape plants and cutflower stock for tropical climates will be presented.

Keywords: *Leucospermum*, pincushion protea, breeding, Principal Component Analysis

OS 6-2:

GENOPARFUM, BRIDGING THE GAP BETWEEN MOLECULAR TOOLS AND BREEDING PROGRAM IN LAVENDER (*Lavandula angustifolia* Mill.)

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The French lavender industry is facing significant challenges both in terms of plant health and international competition. One of the key factors that is necessary to successfully resolve these issues, and therefore meet growers' needs, is the creation of new varieties that combine high yield of good quality essential oil with tolerance to the phytoplasma Stolbur. The need for new varieties is currently all the more important due to the fact that the genetic base of the French plantations is relatively narrow due to the recurrent use of a small number of varieties. The work carried out during this project allowed for the sequencing of parts of the genome (creation of a Unigene and subsequently a Genespace) of lavender Maillette and Diva and lavandin Grosso and the identification of more than 200 000 SNPs in 8 000 genes whose function has been validated by crossreferencing sequences with those present in a public database. These data were then used to genotype individuals from a collection of lavender. The SNPs identified in this study thus constitute a reservoir allowing for a dense marking of the genome. In total, 45 to 468 "private" SNPs were detected per accession, that can now be used to identify specific accessions helping to distinguish them easily from each other. These markers were also used as the basis for a study of the genetic diversity of several lavender clones and reference populations.

Keywords: *Lavandula angustifolia* Mill., molecular markers, breeding

OS 6-3:

MOLECULAR CYTOGENETIC CHARACTERIZATION OF SOME COMMON BEAN (*Phaseolus vulgaris* L.) GENE BANK ACCESSIONS

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Common bean (*Phaseolus vulgaris* L) which is a member of the genus *Phaseolus*, is one of the major protein source used as food with approximately 25 million annual production in the world. However, the number of



studies carried out on *P. vulgaris* is quite limited although it has a high economic importance. Until today, the genome of *P. vulgaris* was not analyzed by new molecular cytogenetic techniques except only a few accessions. The objective of this study was to analyze genomes of the 154 accessions included in a *P. vulgaris* genetic resource collection created to use in *P. vulgaris* breeding programs by using new molecular cytogenetic methods as flow cytometer and in situ hybridization. Based on the results of flow cytometric analysis, the mean nuclear DNA content of the accessions varied from 1.28 pg/2C to 1.55 pg/2C (mean 1.35 pg/2C) and the differences among the accessions were found to be statistically significant ($P < 0.01$). The mitotic chromosome number of all of the accessions that were counted in the study by using microscope was $2n=22$ indicating that the number was stable within the species. Fish analysis carried out on five different accessions with varying DNA content between 1.30 and 1.55 pg/2C by using 5S ve 25S rDNA genes as probes. According to the results of FISH analysis, *P. vulgaris* genome had 4 5S rDNA locus, and the number and location of the locus were stable among the 5 accessions investigated in the study. However, the number of the 25S rDNA locus was determined as 6 in two accessions with 1.55 pg/2C DNA content and 14 in other three accessions which had varying DNA content between 1.30 and 1.35 pg/2C. Location of the 25S signals were generally similar. In conclusion; there was an important nuclear DNA content difference among the *P. vulgaris* accessions investigated in study although the chromosome number is stable as $2n=22$ and it look like the organization of the genom is effected by DNA amount in nucleus.

Keywords: *P. vulgaris*, nuclear DNA content, FISH, flow cytometer, cytogenetics

Acknowledgments: This study was supported by the Scientific and Technological Research Council of Turkey (Proje No: 116O057).

OS 6-4:

AEGEAN AGRICULTURAL RESEARCH INSTITUTE PROCESSING TOMATO BREEDING STUDIES

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Tomato is the most common vegetable species of the *Solanaceae* family both the World and Turkey. The Aegean Agricultural Research Institute's tomato breeding program is carried out for developing new processing tomato varieties. Resistant to some diseases and pests processing tomato breeding lines have been obtained by taking into account the demands of tomato processing companies, farmers of regions where processing tomato is grown intensely. Crossing have been conducted to determine the specific combining ability (SCA) of the tomato breeding lines that identified as a result of the general combining ability (GCA) test. In this study, 80 hybrid candidate processing tomato varieties, which were selected in preceding experiment that was formed 500 hybrid candidate processing tomato varieties in 2016 by taking into account yields and some fruit characteristics were determined yields, some fruit characteristics and the genes of diseases-pests resistance (*I2*, *Ve*, *Mi* and *Sw5*).

Keywords: Processing tomato (*Solanum lycopersicum* L.), yield, fruit quality, breeding

OS 6-5:

CABBAGE NUCLEAR MALE STERILE (NMS) MATERIAL AND ITS APPLICATION IN RECURRENT SELECTION OF CABBAGE BREEDING

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The cabbage nuclear male sterile (NMS) material is discovered in China. It is controlled by a dominant NMS gene. The proportion of sterile plants to fertile ones is 1:1 in the first generation (F₁) after crossing sterile plant with fertile one. The fecundity of fertile plants does not separate after self-cross. Acting as female parent, the



NMS material hybridized respectively with 10 normal cabbage varieties with target characteristics. The 10 crosses seeds were mixed together at equal quantity and were planted in an isolated greenhouse with bees for open pollination. Thus the recurrent selection basis group was built up. Among the basis group, sterile plants were conducted the phenotypic mixed selection according to breeding goal so as to produce the next round recurrent group, fertile plants which were separated from sterile plant line were conducted the individual plant selection in order to gain breeding materials with excellent characters. Especially through bagging identification on fertile plants, we obtain materials with strong self pollination ability. After several years of self purification, inbred lines with high incompatibility index were bred, such as 'Hugan 399', 'Hugan266' etc. It has been proved that the nuclear sterile recurrent selection in cabbage is an effective way to create new breeding materials. Every year we can get all kinds of new materials and enrich the gene bank of cabbage effectively. In particular, the high affinity inbred lines of 'Hugan 399', 'Hugan266' have changed the traditional way of cabbage artificial pollination, and only need to grow in isolated greenhouse, it can self- fruitful and save a lot of manpower and material resources.

Keywords: Cabbage, Nuclear male sterile, Recurrent selection, Breeding

OS 6-6:

CHROMOSOME DOUBLING OF *Cichorium intybus* L. HAPLOIDS THROUGH PROTOPLAST REGENERATION

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Industrial chicory (*Cichorium intybus* L.) is mainly grown for inulin production. To enhance production and uniformity, hybrid cultivars are preferred. Therefore, a controlled pollination system and homozygous parental lines are needed. The most desirable pollination control system is cytoplasmic male sterility (CMS). A new, naturally induced CMS has been reported by Van der Veken et al. (2018). To regenerate homozygous parental lines of modern industrial chicory cultivars, different haploid inducing techniques have been compared and evaluated. The only successful method was intergeneric hybridization with *Cicerbita alpina* (Doré et al., 1996), yielding haploid plants. Here we show that protoplast regeneration is an efficient tool for chromosome doubling of these haploids. The presented method can be used for chromosome doubling of slowly developing haploids.

Key words: *Cichorium intybus* L., protoplasts, doubled haploids, chromosome doubling

OS 6-7:

INNOVATIVE F1 HYBRID METHOD ENABLES TESTING OF LARGE NUMBER OF LINE TO LINE CROSSINGS FOR COMBINING ABILITY

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Hybrid vigor has been demonstrated in the early 20th century after hybrid corn was invented. This discovery led to high yield increases in all major crops tested. Hybrids are preferred varietal forms since they can provide better yield, greater uniformity and faster identification of desired combinations of characters. Hybrid varieties are also preferred by breeding companies since the progeny of the next F2 generation from those F1 hybrids will segregate and therefore not consistently express the desired characteristics. Procedures to breed hybrid cultivar are more complex than breeding open-pollinated varieties or pure lines. Hybrid varieties are most often based on the crossing of two true breeding lines that should genetically complement each other. This complementarity of genotypes of genetically different parental lines in the F1 hybrid often results in a



considerable improvement of e.g. growth characteristics, yield or adaptation to environmental stresses as compared to the individual parental lines and non-hybrid cultivars. Numerous methods have been proposed, the most common is based on development of large numbers of inbred lines originated from heterozygous parents by either self pollination or doubled haploid induction. Inbred lines are then tested for hybrid vigor often in two steps, by which first »general combining ability« and then »specific combining ability« is tested to identify a pair that expresses optimal characteristics. This standard procedure allows only a very limited number of line to line crosses since it is laborious and long lasting. Here we are proposing a new method that allows much higher number of line to line crosses as previously known. Our invention relates to innovative method of testing combining ability of inbred lines, which is based on genotyping of each genetically diverse inbred line followed by allowing the plants of the donor lines to intercross to obtain F1 hybrid progeny. In the next season progeny is phenotyped on individual basis. For superior individuals parental lines are revealed by paternity testing, which due to homozygosity of lines and previous genotyping allows identifying both parental lines. By this method a much larger number of line to line testing can be achieved thus overcoming major bottleneck in breeding hybrid varieties. Details of the protocol and its utilization will be discussed.

Key words: F1 hybrid breeding; paternity testing; haploidy induction; genotypization

OS 6-8:

CLONAL SELECTION OF KABAASI APRICOT VARIETY IN MALATYA ECOLOGY

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This study was carried out to determine fertile clone candidates of Kabaasi apricot cultivars in Malatya ecology in 2009-2013. For this aim; selection studies began in 2009. Fertility status, pomological and chemical features of clone candidates were determined at the end of selection. When the clone candidates were evaluated in terms of fertility and attractiveness the clone candidates took the score between 5,33-8,67 and 5,33-8,33 respectively. Fruit weight varied between 38,06-54,04 g and fruit firmness varied between 17,7-21,9%. After five years selection study; 7 clone candidates acquiring highest score from 17 clone candidates as result of "Modified Weighted Rating Method " by considering fruit weight, fertility, fruit attractiveness, fruit firmness and solid soluble were selected.

Keywords: Kabaasi, Apricot, Clonal Selection

OS 7-1:

SELECTION OF MEDLAR (*Mespilus germanica* L.) GENOTYPES NATURALLY GROWN IN TOKAT REGION

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The study was conducted in the centre, districts and villages of Tokat during 2010-2012 years. In the study, 2605 medlar genotypes which is grown naturally in Tokat flora were established. Finally, 11 genotypes species candidate with high characteristics were determined as a result of the evaluations in the population. The flowering of 11 genotypes began between 26 April/6May and lasted 10-12 days. Fruit harvesting took place between 22 October and 10 November. The weights of fruit were identified as between 15,99 and 37,20 g, the ratio of the Seed weight and Fruit weight between 6.12 % and 15.63 %, respectively, and the amount of total solid substance between 27,34 % and 44.11 %. The amount of total soluble solid were identified as 14,10 % - 27,30 % during maturing and 13,80 % - 20,50 % during



consumption time. Total acidic were ranged between 4,25 g/L - 8,94 g/L at maturing and 2,80g/L - 7,24g/L during consumption time. The amount of Vitamin C at maturing varied between 30,00-8,00 mg/100g; whereas between 26,67-6,40 mg/100g during consumption time. The total phenolic substance of genotypes were also between 92,05-10,64 mg/100 g at maturing and between 45,30-10,35 mg/100 g during consumption time.

Keywords: Selection, Medlar tree (*Mespilus germanica* L.), Pomological characteristics, Tokat province.

OS 7-2:

THE MOST VALUABLE FEATURES OF FLOWERING ORNAMENTAL PLANTS FOR BREEDING UNDER THE CONDITIONS OF THE SOUTH OF RUSSIA

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In the Nikitsky Botanical Gardens there have been collected 2456 species, cultivars and forms of 8 flowering ornamental crops: garden roses, lilacs, tulips, irises, chrysanthemums, clematis, cannes. As a result of long-term complex varietal studies, the main valuable features of cultivars under the conditions of the South of Russia have been revealed, as well as the cultivar sources of these traits for breeding. Six features are common to all studied cultures: abundant flowering, long-term flowering, pure and original color of the flower, resistance to fading color under sunlight, low incidence of disease, high ability to vegetative reproduction. Also the specific features valuable for each culture have been identified: early-flowering of chrysanthemums and lilacs, late flowering of tulips and irises, shape constancy of the flower and presence of more than one flower per stem of tulips, large size of the flowers and inflorescences of lilacs, original form of the flower of lilies, tulips and clematis, original color of cannes leaves, frost-resistance of chrysanthemum and drought-resistance and dropping the faded flowers of cannes. For garden roses the most valuable trait is the strong aroma of flowers, because its presence allows to use rose cultivars for aromatherapy rosaries in recreational areas. As a result of the study in the floral ornamental collections of the Nikitsky Botanical Gardens, about 500 cultivars were identified as potential sources of valuable features for selection under the conditions of the South of Russia. The research was supported by the grant of the Russian Science Foundation (№14-50-00079).

Key words: garden roses, lilac, tulip, iris, lily, chrysanthemum, clematis, canna.

OS 7-3:

BREEDING AND PRESERVATION OF GENETIC RESOURCES OF CARROTS (*Daucus sativus* Rohl.)

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Breeding of carrots in Lithuania involved the creating competitive hybrids by utilizing local genetic resources. Four hybrids of carrots distinguishing by rich biochemical content have been developed at the Institute of Horticulture, Lithuanian Research Centre for Agriculture and Forestry. They are included in the National Plant Variety List and in the EC Common Catalogue of Varieties of Vegetable Species. The effect of heterosis was used in carrot breeding. Lithuanian CMS lines of carrots were crossed with the constant lines and cultivars. The breeding of cultivars was focused on the productivity, quality traits, and resistance to biotic and abiotic factors. New carrot hybrids ‘Svalia’, ‘Ieva’, ‘Rokita’ and ‘Jola’ have good properties for storage and maintenance of biochemical components. More than 200 samples of carrots are preserved at collection of genetic resources at the Institute and differ according their individual properties are used for breeding purposes. Evaluation of productivity, quality and morphobiological parameters of preserved cultivars and breeding lines will be presented.



Key words: breeding, carrot, heterosis, genetic resources

OS 7-4:

DETERMINATION OF SOME MORPHOLOGICAL AND QUALITY TRAITS OF TURKISH LOCAL TOMATO GENOTYPES

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Tomato is considered as one of the most widely grown vegetable crop in the world. One of the most important challenges in tomato production is pests and diseases reducing yield and quality of the crop. Also tomato adapted to the different geography of world has shown a high biodiversity. In this research, 50 local genotypes which were collected from different province areas of Turkey to assess yield, morphological variations and some quality traits. These genotypes were planted in a greenhouse at the Bati Akdeniz Agricultural Research Institute, during the spring and autumn growing seasons. Fifty local tomato genotypes were evaluated on the basis of plant growth type, flowering earliness, fruit width, fruit length, fruit shape, fruit fasciation, color of mature and immature fruit, number of locules, puffiness, Brix value, fruit color L, a*, b*, c*, h and yield per plant. Twenty cultivars had a greater adaptation and were found yield per plant 225-1887 (g), fruit weight (at maturity) 15-418 (g), brix 2,55-5,45, semi and indeterminate growth type and different fruit shape.

Key words: tomato, local genotype, genetic diversity

OS 7-5:

STUDY ON COMBINING ABILITY AND HETEROTIC PATTERN IN CUCUMBER (*Cucumis sativus* L.)

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This research was carried out to determine general combining ability (GCA) and heterotic pattern by using a line x tester mating design in cucumber. General combining ability (GCA) and specific combining ability (SCA) were evaluated for total yield and number of fruit per plant of cucumber in a line x tester mating design comprising 41 inbred lines and 2 testers. Forty-one cucumber female lines were crossed to two male testers and two heterotic groups obtained. The 82 F1 hybrids were planted in a randomized complete block design with two replications in a greenhouse at the Bati Akdeniz Agricultural Research Institute, Antalya, during the spring growing season. The results revealed that line x tester interaction and differences among the inbred lines were high and significant for total yield per plant. The highest effect on GCA among lines had TH-44, TH-62 and TH-76 for yield per plant. On the other hand, TH-33, TH-192 and TH-281 were found high GCA effects for number of fruits. Considering SCA effects, 10 out of the 41 inbred lines tested were classified into two heterotic groups for yield and number of fruit per plant. Seven and three inbred lines were placed into A and B group respectively. Finally, 10 diverse inbred (7 maternal and 3 paternal) lines can be recommended as potential parental lines in order to develop new hybrid varieties in cucumber hybrid breeding studies.

Key words: Cucumber, combining ability, heterotic pattern, line x tester, yield

OS 7-6:

HYBRIDIZATION BREEDING PROGRAM FOR RESISTANCE TO MONILINIA (*Monilinia laxa*) ON APRICOT

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Turkey is the leading country in production and export of apricots in the world, besides, there are fluctuations in yield, depending on years. In this situation, many factors are effective, pests and diseases also play an important role. Monilinia, which is one of the fungal diseases that appeared especially in the years when climatic conditions suitable leads to serious product loss in apricot production areas. Due to the importance of human and environmental health, intensive breeding programs are carried out in order to obtain genotypes resistant to diseases and having favorable fruit characteristics. In this context, a long term hybridization breeding project is carried out in order to gain resistance Hacıhaliloğlu variety, which is one of the most important export products of our country and world famous, having superior drying properties but sensitive to monilinia. In this circumstance, genotypes obtained from different hybridization combinations between Hacıhaliloğlu variety and resistant varieties were tested artificial inoculation against disease and transferred to the land. The phonological observations, plant and fruit characteristics in the bearing genotypes were examined. As a result of the evaluations, promising genotypes have been determined and studies are going on.

Keywords: apricot, monilinia, hybridization, inoculation, fruit characteristics.

OS 7-7:

FRUIT CHARACTERISTICS OF FIRE BLIGHT RESISTANT F₁ PEAR POPULATION

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Fire blight, caused by *Erwinia amylovora* is the most devastating bacterial disease of pear. Disease effects all upper and under organs of host plants and kills whole plant. There is no certain management practice against this disease and chemicals used for fire blight are harmful to environment, animal and human health. The lack of effective solution to the disease and the shift of the consuming tendency towards organic products lead to the usage of resistant rootstocks and cultivars in controlling the disease. The cultivar number, which has high-resistance to fire blight and superior fruit quality parameters of pear, is inadequate in the World. For this purpose, breeding projects TOVAG 106O719 and TOVAG 110O938 (TUBITAK) initiated in order to develop new pear cultivars which are resistant to fire blight and have superior fruit characteristics. In scope of that, different hybridization combinations were carried out. F₁ hybrid population was artificially inoculated with different strains of *Erwinia amylovora*. Hybrids that bear fruit belong to group “A” (Very low susceptibility) were analyzed. Superior hybrids were detected via weighted ranking method by evaluating some characters as eating quality, fruit attractiveness, size, soluble solids content, firmness and rustiness, using two years data. Three genotypes were found superior. As a conclusion of the study, registration of the genotypes which are found to be superior is thought to contribute to fire blight disease management and pear cultivation.

Keywords: *Erwinia amylovora*, Hybrid, *Pyrus communis*, Resistance breeding, Weighted ranking method

OS 8-1:

DEVELOPMENT OF DIAMONDBACK MOTH RESISTANT TRANSGENIC CABBAGE AND CAULIFLOWER BY STACKING CRY1B & CRY1C BT GENES

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Cabbage and cauliflower are extensively cultivated Cole vegetables the world over. These are highly prone to the most notorious insect pest *Plutella xylostella* (Diamondback moth), which cause severe damage to these crops resulting in huge yield losses to the growers. Conventional breeding for host plant resistance against this insect pest could not be possible due to lack of resistance source in the available germplasm. The chemical control measures are cumbersome, costly, health hazardous and environment unfriendly. Therefore, using quarterly gene pool for incorporation of genes for resistance from unrelated sources such as bacterial derived insecticidal Bt toxins through genetic engineering is a viable option. Genetic manipulation of plants through *Agrobacterium*-mediated transformation is limited by a multitude of factors resulting in poor transformation efficiency. Hence, optimization of plant transformation method suitable for a particular crop is highly essential. Here in we report the optimization of plant transformation protocol for cabbage and cauliflower by the manipulation of various key parameters, including the type of explants, *Agrobacterium* strains, bacterial cell density, age of the explant, preculture period, media formulations etc. The binary vector pPIPRA560 containing stacked Bt genes (*cry1b/cry1c*) and *npt II/Basta* as selectable marker was chosen for plant transformation. As a proof of concept, initially the effectiveness of the Bt genes against diamondback moth was validated in transgenic *Arabidopsis*. Insect bioassay revealed 100% mortality within 48 hours of feeding. Based on the exciting results, the same construct was used for transforming Indian popular varieties of cabbage (Golden Acre) and cauliflower (Pusa Meghna & Pusa Snowball K1). We confirmed the presence of the Bt genes in the transgenic cabbage and cauliflower by PCR and expression through RT-qPCR. Insect bioassay revealed 100% mortality in some of the plants tested so far. Further molecular analyses including Southern blotting to check for the transgene copy number and ELISA for determining the Bt protein concentration in the independent transgenic plants are under way and will be presented.

Keywords: Cole crop, *Plutella Xylostella*, plant transformation, Bt genes, Genetic Engineering

OS 8-2:

OR GENE LED B-CAROTENE ENRICHING OF INDIAN CAULIFLOWER TO TACKLE MALNUTRITION

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Vitamin A micronutrient deficiency is one of the major causes of malnutrition amongst larger population especially children and women in India. Since cauliflower is an extensively grown and widely consumed vegetable lacking vitamin A precursor betacarotene, therefore the present study was undertaken to enhance betacarotene content in commercial varieties of Indian cauliflower by introgressing a spontaneous dominant mutant Or gene. The donor source of Or gene EC625883 and the recipient parents DC 41-5, Pusa Meghna and CC14 from early maturity group and Pusa Sharad, DC 18-19 and CC35 from mid maturity group were involved in hybridization programme of marker assisted backcross breeding. The AFLP based SCAR marker SA4 was validated and functional SSR marker was developed for foreground selection of Or gene containing plants at seedling stage. Besides, for background selection, 400 SSR markers spanning across 9 chromosomes were utilized for polymorphic survey. Of these, thirty-five polymorphic markers were identified and utilized for background selection in selected BC2 plants for recurrent parent genome recovery. The Or gene led biofortification of β -carotene in Indian cauliflower will be sustainable and cost effective strategy which will play a significant role in alleviation of vitamin A deficiency led malnutrition in developing world. This paper reports about the integration and β -carotene increase due to Or gene in Indian cauliflower background using marker assisted selection.

Keywords: *Brassica oleracea* var. botrytis L., Vitamin A, marker assisted selection



OS 8-3:

AGRONOMIC AND NUTRITIONAL CHARACTERIZATION OF OKRA (*ABELMOSCHUS ESCULENTUS*) GENOTYPES AND TRAIT ASSOCIATIONS IN SOUTH AFRICA

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Okra, *Abelmoschus esculentus* L. (Moench) is an important fruit vegetable crop belongs to family Malvaceae. It is a highly nutritious fruit vegetable and produced in some parts of the provinces in South Africa. The study was carried out to assess the genetic diversity using agronomic and nutritional traits in the fruits of okra for use in the breeding programme. The experiment was conducted at the Roodeplaat research farm of the ARC in a randomized complete block design replicated three times. Agronomic data was recorded on the field. The fresh immature fruits of the okra genotypes were harvested and analyzed for total protein content and selected mineral elements (calcium, copper, iron, potassium, magnesium, manganese, sodium, phosphorus, aluminum, boron and zinc) at the analytical laboratory of the Agricultural Research Council in Pretoria, South Africa. Multivariate analysis (NCSS, 2004) was done using principal component analysis (PCA). The phenotypic and nutritional data were subjected to analysis of variance (ANOVA) using Agronomix computer software (Agronomix, 2008). The correlation coefficients were also computed to determine the degree of trait association (NCSS, 2004). The ANOVA for agronomic and nutritional traits showed highly significant differences for most traits recorded. The multivariate analysis showed wide genetic diversity among the okra genotypes, which could be exploited in selecting suitable and potential parents when breeding for high yield and nutritional qualities. The present study revealed the genetic potential of the genotypes studied and their importance for use in the breeding programme aimed towards addressing malnutrition, food security and poverty alleviation by breeding for increased yields, and nutritional contents in South Africa.

Keywords: fruit, genetic diversity, yield

OS 8-4:

CHARACTERISTICS OF ONION (*Allium cepa* L.) DOUBLED-HAPLOID LINES GENERATED FROM IMMATURE FLOWER BUD CULTURE

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Onion, because it is biennial crop, it takes long time to make purebred line. However, doubled-haploid lines take shorter time to make purebred line than practice breeding, also mass proliferation is possible. Tissue cultured onion show very low regeneration rate, even though uses qualified method like anther culture and immature embryo culture which other plants can make high regeneration rate. To make onion doubled-haploid lines, effective method is needed. 404,275 immature flower buds cultured, 24 lines were used. 667 doubled haploid lines generated from immature flower bud culture, regeneration rate was 0.17%, but it show different results between lines. The lowest line, regeneration rate was 0.01%, on the other hand, the highest line show 0.61% regeneration rate. To improve regenerate rate, investigation on optimal immature onion flower bud picking time was carried out, but onion lines had variety bolting and flowering time, so there wasn't constant tendency. Polyploidy level of plant which generated from doubled-haploid line was analyzed by flow cytometry, most of plants were haploid, and di-, tri-, tetra-, and pentaploids were observed. 14 male sterility lines and 8 pollen parents (purebred line) lines used at immature flower bud culture, 78 lines generated from male sterility lines, and harvested 630 plants, also 24 lines generated from pollen parent lines, and harvested 121 plants. Part of them corrupted during storage, so 267 plants generated from male sterility lines and 34 plants generated from pollen parents were planted at seed production greenhouse. Weighted harvested lines, bulb weight more than 40~50g which can used for seed production was 83 bulbs, and most of them were under 40g.

Keywords: onion, doubled haploid line, immature flower bud culture, polyploidy



OS 8-5:

BLACK PERSIMMON: A VERY UNIQUE AND VALUABLE GERMPLASM IN CHINA

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There are more than 1000 persimmon (*Diospyros kaki* Thumb) varieties in the world. However, almost all varieties known have orange or orange red pericarp when mature, due to the accumulation of carotenoid. Surprisingly, there are some accessions in China with black pericarp color during mature, named black persimmon. It is a unique and valuable germplasm. Nevertheless, the information about black persimmon is scarce. We analyzed the black pigments by ultraviolet and visible spectrophotometer. Compared with 'Mopanshi' (orange pericarp), black persimmon showed an additional absorption peak around 540nm, which corresponded to anthocyanins accumulation. Determination of pigment content resulted in abundant accumulation of anthocyanin in its pericarp rather than carotenoid. We collected 15 black persimmon accessions around China. We studied the morphology and molecular markers to determine its taxonomic status. There were no spines on its branches, no glands or spots below the leaf, and no hair on the fruit. At the same time, black persimmon has large leaves (>7cm), the length of fruit stalk was over 6mm, and the fruit diameter was about 4.5-5.5cm. All morphology characteristic manifested it belong to the *D. kaki*, rather than a new species. Its taxonomic status was further identified by 12 IRAP (Inter-retrotransposon amplified polymorphism) markers and 15 SCoT (start codon targeted polymorphism) markers. Results suggested black persimmon belongs to *D. kaki* species and had a closer relationship with pollination constant and astringent type persimmon native to China. Meanwhile, there were high genetic variations between black persimmons. It was more likely to find black persimmon germplasm with better fruit quality. In conclusion, black persimmon was a *D. kaki* germplasm resource with black pericarp due to the accumulation of anthocyanin. It was a very unique and valuable germplasm for breeding persimmon with different pericarp color and anthocyanin content.

Keywords: *Diospyros kaki*, black persimmon, germplasm resources, anthocyanin, taxonomic status, morphology, molecular marker

OS 8-6:

DEVELOPMENT OF EARLY MATURING, HIGH YIELDING, LONG DURATION OF HARVESTING, AND CHOANEPHORA TOLERANT *Amaranthus* FOR RELEASE IN NIGERIA.

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Production of *Amaranthus* is affected by wet rot of leaves and stems caused by the fungal organism *Choanephora cucurbitarum* which can cover completely the entire plant thereby causes significant yield losses (70%). The objective of this work is to develop and release early mature, high yielding improved varieties tolerant to the fungi disease *Choanephora* blight. One hundred *Amaranthus* germplasm was collected and screened in order to identify desired genotypes with high yielding and *Choanephora* tolerant traits. Twenty accessions of *Amaranthus* seedlings were planted in the National Horticultural Research Experimental field infected with *Choanephora* spores. The spacing between plants within rows was 40cm and between rows was 90cm. Data were taken on growth traits: 50% Days to flowering, included average number of inflorescence with branches, maturity fruit length and weight. The F1 plant derived from the crosses from divergent parents was self-pollinated to produce F2 plants. The selected populations were advanced to derive F6 Recombinant inbred lines (RILs). Purelines of F6 was evaluated and confirmed in the controlled screen house and on the field. The improved variety NHAMOLA5 was tested across the country. The On farm trials were carried out with five farmers per location. The improved variety NHAMOLA5 outperformed the farmer local (check). The seed weight for the improved variety was 2.5t per hectare while the farmer's local check gave 0.9t per hectare. The on-farm trial confirmed the superiority of the crop and the acceptance by the farmers.

Keywords: Genetic improvement, Hybridization, Multilocal, Breeder seed



POSTER PRESENTATIONS

S20-P1:

GENETIC DIVERSITY OF GERMPLASM RESOURCES OF WALNUT IN HEBEI REVEALED BY SSR ANALYSIS

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【Objective】 The genetic diversity and phylogenetic relationship of walnut germplasm resources in Hebei were discussed at the molecular level, thus providing a scientific basis for more effective protection and use of these resources. 【Method】 The genetic diversity and relationship of 115 walnut germplasms were analyzed by SSR (sequence tagged microsatellite site). The specific bands were counted and analyzed by NTSYSpc2.11a software. 【Result】 SSR fingerprinting of 115 walnut germplasms with sixteen pairs of primers revealed a total number of 87 polymorphic bands and 5.5 polymorphic bands were detected by each pair of primer on average. The polymorphism frequency was 98.9%. This result showed the abundant diversities of enzyme digestion sites among walnut germplasm resources in Hebei. As analyzed by NTSYSpc2.11a, the similarity coefficient of 115 walnut germplasms ranged from 0.66 to 0.94. These walnut germplasm resources were divided into six groups by UPGMA (unweighted pair group method with arithmetic average) based on similarity coefficient. The genetic relationship of 115 walnut germplasms was analyzed according to the similarity coefficient.

【Conclusion】 There are rich genetic diversity and complex genetic background in walnut germplasm resources in Hebei.

Keywords: Walnut; Germplasms, SSR; genetic diversity, relationship

S20-P2:

COMPARISON OF DNA EXTRACTION METHODS FROM MATURE LEAVES OF WALNUT

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Using the leaves of mature walnut as the experimental materials, four extraction methods of walnut genomic DNA including the two kinds of CTAB method, high salt and low pH, kit extraction were compared. The DNA samples were tested by agarose gel electrophoresis and ultraviolet spectrophotometer. The results showed there is a great difference in purity and yield. The high salt and low pH was the optimal method by comparing yield and quality of the DNA. It is not suitable for Kit Extraction to extract DNA of mature walnut leaf.

Keywords: walnut, mature leaf, DNA extraction, method, comparison

S20-P3:

THE EVALUATION OF SOME ROOTSTOCK CHARACTERISTICS OF SELECTED ALMOND GENOTYPES

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The main purpose of this research was to develop the new rootstocks for almond. For this purpose, in the study, the seedling growth characteristics for 42 almond genotypes selected by Yildirim (2007) from Isparta region (Turkey) as a result of previous breeding study were investigated. The mature seeds with endocarp of selected genotypes were stratified at 4 °C for 60 days. At the end of stratification, seeds were sown into plastic pots in outdoor conditions. The results indicated genetic variabilities among genotypes. The germination percentage



changed from 4.8% (Genotype 183) to 100% (Genotypes 57 and 143), rate of emergence from 41% (Genotype 9) to 88% (Genotype 231), seedling diameter from 4.56 mm (Genotype 57) to 7.46 mm (Genotype 123), seedling height from 16.64 cm (Genotype 42) to 41.27 cm (Genotype 78), primary root length from 16.63 cm (Genotype 42) to 41.28 cm (Genotype 78), primary root diameter from 5.35 mm (Genotype 42) to 9.74 mm (Genotype 29) secondary root length from 19.94 cm (Genotypes 241 and 228) to 35.45 cm (Genotype 78) total secondary root number from 11.51 (Genotype 57) to 36.87 (Genotype 228) and lateral branch length from 8.18 cm (Genotype 52) to 28.30 cm (Genotype 161). In the study, the lowest CVs for seedling diameter was observed in genotypes 33, 57 and 196 (respectively 0.57%, 0.95% and 0.97%), while the lowest CVs for seedling height was found in genotypes 176, 183 and 5 (respectively 0.87%, 0.96% and 1.61%).

Keywords: Almond, Seedling Growing, Stratification, Germination, Genetic Variability

S20-P4:

SIMPLE SUGARS PERFORM BETTER THAN SUCROSE FOR *IN VITRO* AND *IN VIVO* GERMINATION OF BANANA POLLEN

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Poor stigma receptivity is one of the limitations to seed set in East African Highland Bananas (EAHBs) that constrains their improvement through conventional breeding. This study was aimed at identifying a suitable pollen germination media (PGM) for faster germination of banana pollen both *in vitro* and *in vivo*. PGM was prepared by dissolving 0.01g H₃BO₃, 0.25g MgSO₄·7H₂O, 0.25g KNO₃ and 0.4g Ca(NO₃)₂ in 1 litre along with different sugars. Sucrose, glucose, fructose, glucose + fructose, and glucose + fructose + sucrose at six concentration levels of 1%, 3%, 5%, 10%, 15% and 20% were tested. Pollen from Calcutta 4 and TMB2x 8075-7 diploid bananas was dusted on a cover slip and slowly lowered over four drops of PGM on a glass slide. The set up was incubated in a humid chamber for 3 hours and germinated pollen counted using a light microscope at X40 magnification. Results revealed that glucose at 1% and 3% concentration performed best with the latter having the higher pollen germination percentage. Results from comparison of 3% glucose PGM with diluted nectar from Tereza and TMB2x 8075-7 showed that 3% glucose PGM generated highest pollen germination. It is suggested that glucose being a simple sugar is more readily available energy source for pollen. When 3% glucose PGM was applied on stigmas after pollination, stigma receptivity was enhanced.

Key words: stigma receptivity, seed set, EAHBs

S20-P5:

POPULATION STRUCTURE, PARENTAGES, PLOIDY LEVELS AND GWAS IN AN APPLE GENE BANK

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We used more than 15,000 genome-wide SNPs to explore the genetic diversity in a diverse apple collection. The study included 350 apple accessions kept in The Pometum gene bank collection (University of Copenhagen, Denmark) and covers local Danish and world-wide important cultivars. The level of heterozygosity in the SNP



markers generated by genotyping-by-sequencing (GBS) allowed estimation of ploidy levels and was in accordance with flow cytometry results. We found 119 accessions sharing a clonal relationship with at least one other accession, thereby identifying 272 (78%) unique accessions in the collection. Out of the unique accessions identified, more than half (52%) share a first-degree relationship with at least one other accession. It demonstrates a high degree of both clonal and family relationships in the gene bank. The results show genetic differentiation between *Malus domestica* and its supposed primary ancestor, *M. sieversii*. Among the *M. domestica* cultivars, there were genetic differentiation between accessions of Danish origin and all other accessions. Finally, we combined the genotypes with about 100 phenotypes in a genome-wide association study (GWAS). Here we used data for 49 fruit volatiles created by Dynamic Headspace Sampling/Gas Chromatography-Mass Spectrometry analysis of apple juice samples. We also performed a GWAS for individual sugar and acid quantities in addition to several fruit quality traits and found significant association for e.g. fruit colour, harvest time and sucrose level. The findings provide important information for future breeding of apple cultivars for North European climate conditions.

Keywords: Genotyping-by-sequencing, ploidy levels, clonal relationships, parent-offspring relations, GWAS, fruit quality traits, pre-breeding, apple gene bank resources

S20-P6:

FROST RESISTANCE OF PEACH HYBRIDS IN THE SOUTHERN STEPPE OF RUSSIA

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The climatic conditions of the southern zone of industrial Russian horticulture are rather unstable. Here, from time to time, extreme winters and spring recurrent frosts occur. In the assortment of fruit crops there are few peach cultivars, well adapted to such environmental factors. Therefore, research of peach frost-resistance and the problems of creating very winter-hardy cultivars are important and urgent tasks. Assessment of hybrid peach seedlings was performed in the steppe zone of the Crimea on the basis of the Steppe Branch of the Nikita Botanical Gardens near Simferopol. The aim of studies was to identify the most frost-resistant hybrids, which had the least damage to generative buds, and also to determine best hybrid combinations for further peach selection on winter hardiness. 272 peach seedlings of 26 F₁ hybrid families were studied. In January 9, 2002, the negative air temperature dropped to -23.2°C. This year was the most indicative for studying the frost resistance of generative peach buds. Evaluation of damaged flower buds was carried out according to methods developed in the Nikitsky Botanical Garden, processing of the obtained data was carried out by standard statistical methods. As a result, it was found that the damage degree of peach buds varied from 0 to 91%, depending on the origin of hybrids. A total of 35 very frost-resistant seedlings (1-10% of damage to the buds) and 108 – frost-resistant (11-30%) were detected. 100 hybrids proved to be moderate frost-resistant (31-60%), 28 – poor resistant (61-90%) and one – not resistant (more than 90%). Most frost-resistant hybrids were obtained in combinations ‘Valiant’ x ‘Krimskiy Feyerverk’, ‘Start’ x ‘Arm Gold’ and ‘Start’ x ‘Ognennyiy’. It were recommended too to use elite forms ‘Tovarishch’, ‘F₁26-76’ and ‘F₁2130’ as parental forms in further breeding for peach winter-hardiness.

Key words: cultivar, peach, hybrid families, seedlings, winter resistance

S20-P7:

THE STUDY OF ORNAMENTAL PEACHES WINTER HARDINESS IN THE CRIMEAN STEPPE ZONE

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Twenty ornamental peach cultivars have been studied in the southern steppe zone of the Crimea. The aim of the studies was to assess the adaptability of cultivars to the conditions of the winter and early spring period in this region and to identify high resistant genotypes with excellent ornamental characteristics. The climate of the Crimean steppe part is characterized by unstable weather in the winter-spring period, low temperatures at final



stages of the microsporogenesis, and spring recurrent frosts during the flowering period of fruit trees. The researches were conducted from 2007 to 2017 according to the generally accepted methods for cultivar investigation. The most critical weather conditions were in 2007 and 2012. A field assessment of the peach's generative buds resistance to frost -23.6

highly winter hardy cultivars 'Ave Maria', 'Vesennij Ogon' and 'Ophelia'. Damage to generative buds in them was 60-70%, the flowering intensity and yield reached 3-4 points. In assessing frost damage at the end of February 2007, after -19.1

the plants were not affected. Cultivars 'Dyujmovochka' and 'Malenkij Prince' always suffered the greatest damage due to lower frost resistance and earlier flowering. As a result, ornamental peach cultivars, well adapted to the conditions of the steppe Crimea and with excellent ornamental characteristics, were identified. These include 'Ave Mariya', 'Vesenniy Ogon', 'Ofeliya', etc., which characterized by medium and early-middle flowering periods and semi-double flowers of various shades of pink. These genotypes were recommended for landscape gardening in the southern regions of the European part of Russia and for use in breeding as sources of high winter hardiness. This study was funded by a research grant №14-50-00079 of the Russian Science Foundation.

Key words: cultivar, winter resistance, flowering period, ornamental characteristics

S20-P8:

GENETIC PREDISPOSITION OF SOME APPLE PROGENIES TO BURRKNOT

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Burrknots are one of the undesirable characteristics of rootstock and cultivar due to increase disease and insect sensitivities, reduce cold resistance and cause differences in tree development. Despite the climatic factors that promote burrknot formation, such as temperature and humidity, the genetic susceptibility has a great influence on it. In this study, the tendency, location, size and density of burrknot in some apple genotypes obtained from controlled crosses have been analyzed. The assessments were made on a total 1112 genotypes of four cross combinations composed of Golden Delicious, Braeburn, Jersey mac, Priscilla and William's Pride cultivars. Burrknot number, intensity and size varied to the combinations. Burrknot severity was higher in Golden Delicious x Priscilla (24.20%) and Braeburn x William's Pride (19.20%) hybrids than Golden Delicious x William's Pride and Jersey mac x William's Pride. It was not observation in 84.93% of the Jersey mac x William's Pride hybrids.

Keywords: hybridization, *Malus*, burrknot, physiological disorder, rootstock, *Synanthedon scitula*

S20-P9:

MAPPING THE FRUIT MAJOR TRAITS OF APPLE GERMPLASM IN A GENOME-WIDE ASSOCIATION STUDY

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Apple (*Malus x domestica*) is one of the most variously and economically important fruit crops in the world. Apple breeding needs a long-term endeavour and it is imperative that new cultivars are selected to have outstanding consumer appeal. The goal of the breeding was to identify genomic associations which is useful for apple breeding and can improve fruit quality. Using Genotyping by sequencing data of NGS technology generated from 308 apple germplasm, here we perform a comprehensive genome-wide association study to identify SNPs associated with 6 target major fruit traits. A genome wide association analysis suggested significant genomic associations for several target traits including acidity and skin color. As a result of association analysis, high association level SNPs were confirmed on chromosome 9 about skin color and were identified on chromosome 16 about acidity. According to RosBreed information, Ma gene, is known for involved in acidity is located chromosome 16. Also, Md-MYB10 gene and Md-MYB1 gene for skin color are



located at chromosome 9. These results will can be proposed candidate gene and marker including SNP and based data for apple breeding.

Keywords: genotyping by sequencing, genome-wide association study, fruit trait, acidity

S20-P10:

ASSOCIATION BETWEEN BLUE MOLD RESISTANCE AND QPCR-BASED MOLECULAR MARKERS IN APPLE

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Apple cultivars vary in their susceptibility to *Penicillium expansum*, the causal agent of blue mold, which is one of the most devastating storage diseases in this crop. The genetic background to susceptibility/resistance has not yet been fully clarified, but significant associations have been detected between (1) the size of lesions caused by blue mold after artificial inoculation of harvested fruit, and (2) various fruit texture-related traits (e.g. fruit firmness at harvest and rate of fruit softening during storage) as well as (3) fruit biochemical contents (e.g. polyphenols). In the present study, 82 apple cultivars were phenotyped for fruit firmness, fruit softening rate and size of blue mold lesions after wound inoculation of newly harvested fruit with *P. expansum* spores. These cultivars were screened using 15 qPCR-based molecular markers targeting loci linked to fruit texture and chemical composition on apple linkage groups (LG) 10 and 16. The results revealed significant phenotype-genotype associations between two loci on LG 16 (ss475881696 and ss475882555) and lesion decay ($p=0.047$ and 0.037 , respectively). In addition, a non-significant relationship ($p=0.08$) between softening rate and two fruit acidity-related loci on LG 16, ss475876558 and Ma1-SNP1455, was indicated. These results will be useful in further investigations of key genes for blue mold resistance, and for developing markers that can be applied in apple breeding programs.

Keywords: Breeding, Fruit quality, *Malus x domestica*, *Penicillium expansum*, QTL, Storage rot, Taqman assay

S20-P11:

DIFFERENTIAL GENE EXPRESSION ANALYSIS ASSOCIATED WITH SKIN COLOR IN SOMATIC MUTANT OF 'FUJI' APPLE (*Malus X domestica*)

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'Fuji' is one of the popular apple fruit around the world. Although it has high quality, genetic weakness causes pale coloration. To overcome this problem, somatic variation has been an important source to discover that are superior to the parent and skin color sport is the most captured. 'Fuji' and its enhanced somatic mutant, 'Kiku8' also have attractive pattern. In this study, 'Fuji' and 'Kiku8' were characterized at six developmental stages. RNA was extracted from fruit skin samples and cDNA was synthesized immediately. They were used for quantitative real time PCR to identify how 8 genes related to the anthocyanin accumulation and 3 genes related to the carotenoid accumulation may be expressed in diverse apple skin color phenotype. As a result of the analysis, it was confirmed that the expression level of most genes was increased during maturity stages. In case of anthocyanin related genes, MdWD40, MdCHS, MdF3'H, MdUFGT and MdGST and about carotenoid genes, MdZISO and MdCRTISO were expressed higher than 'Fuji'. They were significant in predicting final anthocyanin and carotenoid accumulation in mature 'Kiku8' apple fruit.



Keywords: Apple, Somatic variation, Coloration, Quantitative real time PCR

S20-P12:

THE TOLERANCE TO CRACKING OF EARLY RIPENING SWEET CHERRY HYBRIDS

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"Breeding of new sweet cherry varieties" named project has been begun at Fruit Research Station in 2007. Currently, breeding programmes focus on generating progeny from controlled hybridization. In this study also as method has been followed classical breeding method. Celeste, Sunburst, Lapins, 0900 Ziraat, Stella, P. Bernard and E. Burlat were used as parents. The aim of Project is to improve new cultivars with high yield, large, and firm fruit, self-fertile, resistant to cracking, early and late harvest time. Rain-induced cracking is a major problem in many cherry growing regions of the world. Even in drier growing areas, it can be a major problem in occasional years. The rain induced fruit cracking is a big, serious and costly problem for cherry growers. 2000 hybrid genotypes from different crosses were obtained and investigated cracking index of the early ripening genotypes. Testing of fruit cracking was done using index by Christensen (1996).

Key words: Breeding, *Prunus avium* L., early ripening, cracking

S20-P13:

PARTICULARITIES OF INHERITANCE OF RIPENING TIME, YIELD CAPACITY AND VULNERABILITY TO POWDERY MILDEW BY THE PEACH

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The research comprised hybridological analysis of inheritance of such important quantitative traits as ripening time, yield capacity and vulnerability to powdery mildew (*Sphaerotheca pannosa* Lev.var. *percicae* Woronich.) in the hybrid peach progeny. As a result of research on particularities of segregation of ripening time in the hybrid progeny, it was detected that it is being inherited neutrally or with inclination towards one of the parents, according to their donor characteristics. The cultivar Favorita Morettini was detected as the donor of early ripening time. Gamma-irradiation of seeds at doses of 40, 60 and 80 Gy increased the variability of ripening time in the hybrid progeny ($V = 37.9-66.7\%$) compared to control (25.7 %). The number of mid and early-mid season seedlings has increased at all dose levels, especially of 60 and 80 Gy. Inheritance of yield capacity was of a neutral nature or with inclination towards one of parents, according to their donor characteristics. The cultivars Chekhov, Tovarishch, Favorita Morettini, Sochniy were selected as donors of yield capacity. Hybridological analysis for resistance to powdery mildew allowed us to detect following donors of low vulnerability to this disease: the forms Baby Gold-5 x Stoyka 81-1211, Nektadiana I₁ 26-76 and the cultivar Stoyka.

Keywords: peach, hybridological analysis, inheritance, quantitative characteristics, donors

S20-P14:

GENOME-WIDE ASSOCIATION STUDIES OF IMPORTANT AGRONOMIC TRAITS IN PEACH

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Peach (*Prunus persica* L.) is a highly valuable crop species and is recognized by molecular researchers as a model fruit for the Rosaceae family. Using whole-genome sequencing data generated from 129 peach accessions, here we perform a comprehensive genome-wide association study for 12 key agronomic traits. We



show that among the 10 qualitative traits investigated, nine exhibit consistent and more precise association signals than previously identified by linkage analysis. For two of the qualitative traits, we describe candidate genes, one potentially involved in cell death and another predicted to encode an auxin-efflux carrier, that are highly associated with fruit shape and non-acidity, respectively. Furthermore, we find that several genomic regions harbouring association signals for fruit weight and soluble solid content overlapped with predicted selective sweeps that occurred during peach domestication and improvement. Our findings contribute to the large-scale characterization of genes controlling agronomic traits in peach. Among these associations, several have been verified to be with high accuracy in hybridization population and used to early selection in seedling period. Now, we are conducting GWASs on peach fruit quality related traits, such as sugar content, acid content, and fruit size.

Keywords: peach, GWAS, resequencing, genomics, breeding

S20-P15:

ESTIMATION OF INTRODUCED APRICOT CULTIVARS DROUGHT RESISTANCE BY THE INTENSITY OF LEAF CHLOROPHYLL FLUORESCENCE

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In the conditions of the south of Russia in July-August, there is often a lack of moisture, which negatively affects important physiological processes that provide formation of the apricot fruit crop. The aim of the research was to study the fluorescence intensity of apricot leaf chlorophyll in the process of dehydration and to select the cultivars characterized with high drought resistance. In the experiment, leaves of four apricot cultivars were included: Krymskij Amur (control), Budapest, Mindalnij and Hong Iu. Chlorophyll fluorescence was measured by a portable fluorometer "Floratest". The studies were carried out in the second decade of August 2015-2016. Initial fluorescence levels after irradiation (F_0), maximum (F_m) and stationary (F_{st}) values after the light adaptation were recorded (Stirber, 2011). Short dehydration (4 hours) resulted in an increase of the fluorescence parameters. Long-term dehydration (24 hours) caused a significant decrease of all the studied indexes. The lowest values were observed in the cultivar Krymskij Amur (control) that demonstrated its lowest drought resistance in comparison with other studied cultivars. After a long wilting, leaf turgor in this cultivar restored poorly (7.5-64.5%). It was revealed a correlation (0.4-0.8) between the calculated fluorescence parameters and the total water content in the leaves. The cultivar Budapest was characterized by a slow loss of moisture and due to this high (32-81.4%) restoration of leaf turgor after 24 hours wilting. However, indexes of leaf chlorophyll fluorescence hardly regenerated after a long wilting. In the cultivar Mindalnij leaf turgor was restored more slowly after a long wilting (7-62.4%), but it was characterized with high photosynthetic activity at low water content. The cultivar Hong Iu demonstrated high values of fluorescence process regeneration, as well as leaf turgor restoration. It was characterized with a high potential and is promising for the regions with insufficient water supply, as well as for use in breeding for drought resistance.

Keywords: apricot, cultivars, introduced plants, drought resistance, fluorescence parameters, experiment, floratest

S20-P16:

CONTENT OF BIOLOGICALLY ACTIVE SUBSTANCES IN FRUITS OF HYBRID PEACH PLANTS FROM BREEDING POOL OF NIKITA BOTANICAL GARDENS

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For several decades, Nikita Botanical Gardens has been working on breeding new promising peach cultivars. New cultivars must exhibit better characteristics than the existing ones. Modern horticulture needs peach cultivars with such properties as good commercial qualities of fruits, early bearing age, resistance to diseases, high and stable yields. High-quality fruits must have an attractive appearance, excellent taste properties, ensure ease of



transport and have a high content of biologically active substances. The solution of these problems makes possible the obtaining of economically high efficient cultivars for implementation into industrial horticulture. The breeding process included several researches on detecting biologically active substances in mesocarp of peach plants studied, which were obtained through purposeful hybridization. The analysis showed that the solids content in fruits of researched hybrid plants varied between 13.30 % (in the seedling 7/43) to 19.70 % (7/43). The fruit flesh showed a low content of ascorbic acid (6.60 to 13.20 mg/100 g). Its maximum content emerged in fruits of the hybrid form 2/18. The total number of organic acids in fruits varied from 0.43 % (7/73) to 0.57 % (7/43). The total concentration of phenolic compounds in fruits varied from 150 mg/100 g (4/43) to 465 mg/100 g (7/43). Maximum concentration of leucoanthocyanins in fruits showed the peach seedling 7/43 (456 mg/100g) and of flavons - the seedling 4/43 (144 mg/100 g). The seedling 7/43 proved to be promising re its further investigation and involving in the breeding, thanks to maximum complex content of biologically active substances in fruits. Acknowledgements: This study was funded by the research grant no. 14-50-00079 of the Russian Science Foundation.

Keywords: peach, hybrids, biologically active substances

S20-P17:

VARIATION IN THE HALF-SIB FAMILIES OF KERNEL-USING APRICOT

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Kernel-using apricot breeding is especially concerned by apricot breeders in China for its economic importance and large-scale growing in this country. In a breeding program, we obtained more than 2000 progenies with 'Longwangmao' (*Prunus armeniaca* L. cv 'longwangmao') as female parent, a predominant cultivar of kernel-using apricot. 14 traits of fruit and kernel of these progenies were analyzed. The results showed that in the breeding population, the characteristics such as average dry kernel weight, unshelled kernel weight, single fruit weight varied dramatically with the variation coefficient of 16%, 16% and 42% respectively. The maximum weight of dry kernel is more than 1.1g, which is 0.3g heavier than the dry kernel weight of 'Longwangmao' (generally 0.7- 0.8 g). The average dry weight of the hybrid progeny population has normal distribution, and the distribution was concentrated between 0.55g and 0.74g. Therefore, it is possible to select a hybrid with increased and improved kernel weight in these half-sib families.

Keywords: Variation, kernel-using apricot, progeny

S20-P18:

Agrobacterium-MEDIATED GENETIC TRANSFORMATION OF 146-2 RUSSIAN APRICOT AND PLUM ROOTSTOCK WITH THE *GFP* GENE.

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A protocol for *Agrobacterium*-mediated genetic transformation was developed for 146-2 Russian apricot rootstock. Whole leaves from *in vitro* cultured shoots were used as explants for transformation by *A. tumefaciens* CBE21 strain containing binary vector pBINmGFP5ER. It has the *nptII* gene coding for neomycin phosphotransferase II as a plant-selectable marker under the control of the NOS (nopaline synthase) promoter and *gfp* reporter gene coding the green fluorescent protein under the control of the Cauliflower Mosaic Virus (CaMV) 35S promoter. Integration of the *nptII* and *gfp* into transgenes was confirmed by PCR. The expression of the green fluorescent protein was observed by fluorescence microscopy. Transformation efficiency based on PCR analysis of kanamycin resistant independent lines was 0.41-0.83 %. All transgenic lines showed kanamycin resistance at concentration 40 mg L⁻¹. They were rooted and acclimatized to greenhouse conditions.



Keywords: leaf explants, CBE21, *A. tumefaciens*, *nptII*, GFP

S20-P19:

EVALUATION OF DISTANT HYBRIDS OF ALMOND WITH PEACH AND NECTARINE

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Almond, peach and nectarine are among the most wide-spread fruit-bearing crops in the world. The almond is characterized with high taste qualities of seeds, for peach and nectarine juicy and taste pericarp is a typical feature. Combination of these crops properties is possible applying method of distant hybridization. The researches were being conducted in 2004-2016 in Nikita Botanical Gardens, Russian Federation. The following species were chosen for breeding work: *Prunus amygdalus* Batsch., *Prunus persica* (L.) Bastch., *Prunus persica* (L.) Bastch. var. *nucipersica* (Suckow) Schneid., *Prunus mira* Koehne., *Prunus davidiana* (Carr.) Franch. It was revealed among new hybrids there are genotypes with late blossoming terms, dwarf plant size and male sterility. Hybrids with semidouble flower are classified here as well. A high variability of fruit ripening terms is typical for the hybrids: from the beginning of August to the end of September. Taste quality and fruit weight of these hybrids are mainly worse than control nectarine cultivar has. Good taste quality of these hybrids, close to Stark Sunglo parameter was fixed only for some genotypes by F₄-F₅. Saturated crossing with nectarine let increase fruit weight up to level of the control cultivar by F₄-F₅ as well.

Keywords: almond, peach, nectarine, distant hybrids, cultivar evaluation, pomology

S20-P20:

MOLECULAR CLONING AND EXPRESSION ANALYSIS OF THE TRANSCRIPTION FACTOR GENE *ChCBF* FROM HAZELNUT (*Corylus heterophylla* Fischer)

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The *CBF* (C-repeat binding factor) genes are an important family of transcription factors in plants, encoding transcriptional regulators with a variety of functions involved in developmental and physiological processes. In this study, the conserved domain of the *CBF* gene in *Corylus heterophylla* Fischer. was cloned using two degenerate primers, and the 5'terminal and 3'terminal of the gene were amplified by using rapid amplification of cDNA ends (RACE) methods. The complete cDNA sequence termed as *ChCBF1* was obtained and the sequence was submitted to GenBank (GenBank accession number HQ639413). Sequence analysis showed that the nucleotide sequence of *ChCBF1* was 1053 bp, containing an open reading frame (ORF) of 684 bp and encoding a protein with 227 amino acids. The alignment analysis indicated that the predicted protein sequence contained a typical AP2/EREBP DNA-binding domain. Homology analysis showed that the *ChCBF1* protein had high homology with CBF from *Citrus trifoliata* and *Malus x domestica*, respectively. *ChCBF1* gene showed that its transcripts were abundant in floral bud. And its hydrophobicity/hydrophilic, physico-chemical properties, phylogenetic tree, and main functional domains were predicted. Real-time quantitative polymerase chain reaction (Real-Time PCR) analysis was performed for *ChCBF1* treated with a low-temperature of 4 °C. The results showed that *ChCBF1* gene expression was increased 2 h after being cold induced and reached a peak after 4 h, and then decreased. *ChCBF1* might play a key role during the development of cold resistant molecular mechanisms in *Corylus heterophylla* Fischer.

Keywords: *CBF* gene, *Corylus heterophylla*, RACE, Real-Time PCR



S20-P21:

ANALYSIS OF THE GENETIC DIVERSITY FOR THE JUGLANS HOPEIENSIS HU CULTIVARS BY FISH-AFLP MARKERS

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The *Juglans hopeiensis* Hu cultivars were used to study the genetic diversity and parentage relationship in molecular level, providing scientific basis to protect and utilize these germplasm effectively. FISH-AFLP markers were conducted, with 8 primers to analyse the genetic diversity and parentage relationship among 28 *Juglans hopeiensis* Hu cultivars at genomic DNA level. Totally 1009 AFLP fragments were obtained, in which there were 837 polymorphic bands and 202 characteristic bands. The average percentage of polymorphic bands (ppb) was 82.95% and the genetic similarity coefficient distributed among 0.4446~0.744. The value of effective number of alleles (N_e) ranged from 1.00 to 1.99 with an average of 0.36 ± 0.01 ; Nei's gene diversity (H) ranged from 0.00 to 0.39 with an average of 0.23 ± 0.01 and Shannon's information index (I) ranged from 0.00 to 0.59 with an average of 0.44 ± 0.02 . The *Juglans hopeiensis* Hu germplasm had abundant genetic diversity and complex genetic background. Dendrogram of walnut materials origins based on AFLP data showed that 'shanxiguanmao' was different, maybe a new taxa.

Keywords: AFLP, *Juglans hopeiensis* Hu, Genetic diversity

S20-P22:

IN VITRO TESTING OF APPLE TETRAPLOIDS FOR RESISTANCE TO FIRE BLIGHT

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The most severe bacterial disease of the apple tree is the fire blight caused by *Erwinia amylovora*. Due to the lack of effective disease control methods, it is extremely important to introduce into production apple cultivars with reduced susceptibility to this disease. In our previous studies, several neotetraploids for 6 apple cultivars ('Free Redstar', 'Gala Must', 'Co-op 32', 'Pinova', 'Redchief' and 'Sander' have been obtained using *in vitro* method. Most of the cultivars used for polyploidisation characterized with the high or moderate resistance level to *E. amylovora*. We suppose that due to the resistance gene duplication, some tetraploids could be characterized with enhanced resistance to *E. amylovora*. The aim of the study was to evaluate the level of *E. amylovora* resistance in the apple tetraploids compared to their diploid counterparts using *in vitro* assay. In the first stage of research, an *in vitro* method for apple resistance to fire blight assessment was developed. Eight apple cultivars including those used for polyploidisation and the reference cultivars highly susceptible to *E. amylovora* ('Idared' and 'Lobo') were used for experiments. Shoots from *in vitro* cultures were inoculated with pathogen (isolate 659) inoculum at various concentrations with different inoculation methods. The best correlated results of *in vitro* test with the assessments performed in natural conditions were obtained using the pathogen inoculation on the cut surface of shoot apex with a scalpel immersed in a bacterial inoculum of 10^4 cfu/ml. This method was selected for evaluation of resistance level to *E. amylovora* of the neotetraploid compared to their diploid counterparts. Two to five tetraploid clones of five cultivars were tested. The individual tetraploid clones within the cultivar differed in the resistance level. Most of the tetraploid clones showed similar resistance level to their diploid counterparts and some of tetraploids revealed a significantly greater or lower resistance to the pathogen.

Keywords: fire blight, *Malus x hybrida*, susceptibility, *in vitro* assay, inoculation

S20-P23:

DYNAMICS OF POLYSACCHARIDES DURING POLLEN DEVELOPMENT IN *Pyrus pyrifolia*: A COMPARATIVE STUDY BETWEEN POLLENIZER AND POLLENLESS ANTHER

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Pear cultivars are self-sterile and require pollenizer cultivars for cross-pollination and fruit set. Effective pollenizers for self-incompatible and pollenless *Pyrus pyrifolia* 'Niitaka' have been known as *P. pyrifolia* cultivars, 'Chuwangbae' and 'Wonwhang' in Korea. Unfortunately, structural events involved with pollen abortion in pollenless cultivar are still clearly unknown. In the current study, the pollen development of above-mentioned pollenizers and pollenless cultivar was compared to define the onset point and structural manifestations of pollen abortion, with particular attention to the distribution of polysaccharides, which may function as structural carbohydrates, as metabolic reserves, or as a role in determining pollen longevity in anther development. Semi-thin sections of both pollenizer and pollenless anthers at different developmental stages were stained using a Periodic Acid-Schiff's reaction to detect cytochemical changes that may occur in the distribution of insoluble polysaccharide. Ontogenetic differences between pollenizer and pollenless anthers have occurred since generative cell moved towards the center of the microgametophyte at a bicellular pollen stage. During pollen grain maturation, pollen grains of pollenizer cultivars showed cytoplasmic polysaccharides in cells, while those of pollenless cultivar presented accumulation of many starch grains in cells, suggesting defects in amylolysis processes. Although it is necessary to study the pollen development of more cultivars and to examine more precisely in amylogenesis-amylolysis processes, we hope that the results of this study contribute to investigate the relationship between reserves metabolism and pollen abnormality and offer a basis for further complementary molecular studies.

Keywords: *Pyrus pyrifolia*, pollen abortion, cytochemistry, polysaccharide, starch

S20-P24:

PERFORMANCES OF GENOTYPES SELECTED FROM TOKAT NATURAL SERVICE TREE (*Sorbus domestica*) POPULATION (SELECTION II)

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This study was carried out in order to determine the performances of some high quality service tree genotypes selected and protected from Tokat region. The study was carried out between 2015-2016, in conservation parcel, at Gaziosmanpaşa University, horticulture research and practice garden. Phenological, morphological and some chemical observations and analyzes were carried out with six genotypes. Phenologically, all genotypes bloomed earlier than those of their own ecologies, and with lower rates of fruiting. While TSS and pH amounts was similar values, titratable acidity values are lower than those of their own ecologies. In general, all genotypes had a lower crown volume. Fruit weights were average; 5.58-12.28 g. The average number of seeds in the genotypes was determined as 1.61-2.59.

Keywords: Selection II, service tree, phenological properties, morphological properties, chemical properties

S20-P25:

ANALYSIS OF THE GENETIC DIVERSITY FOR THE *Juglans hopeiensis* CULTIVARS BY FISH-AFLP MARKERS

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The *Juglans hopeiensis* cultivars were used to study the genetic diversity and parentage relationship in molecular level, providing scientific basis to protect and utilize the germplasm effectively. FISH-AFLP markers were conducted, with 8 primers to analyse the genetic diversity and parentage relationship among 28 *Juglans* cultivars at genomic DNA level. Totally 1009 AFLP fragments were obtained, in which there were 837 polymorphic bands and 202 characteristic bands. The average percentage of polymorphic bands (PPB) was 82.95% and the



genetic similarity coefficient distributed among 0.4446~0.744. The value of effective number of alleles (N_e) ranged from 1.00 to 1.99 with an average of 0.36 ± 0.01 ; Nei's gene diversity (H) ranged from 0.00 to 0.39 with an average of 0.23 ± 0.01 and Shannon's information index (I) ranged from 0.00 to 0.59 with an average of 0.44 ± 0.02 . The *Juglans hopeiensis* germplasm had abundant genetic diversity and complex genetic background. Dendrogram of walnut materials origins based on AFLP data showed that 'shaanxiguanmao' was different, maybe new taxa.

Keywords: AFLP, *Juglans hopeiensis*, Genetic diversity

S20-P26:

OBTENTION OF TETRAPLOIDS IN BOTTLE GOURD (*Lagenaria siceraria*) AND CITRON (*Citrullus lanatus* var. *citroides*) BY SHOOT IMMERSION METHOD USING DIFFERENT COLCHICINE DOSES AND APPLICATION TIME

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The study to obtain tetraploid plants from bottle gourd (*Lagenaria siceraria*) and citron (*Citrullus lanatus* var. *citroides*.) by using shoot immersion colchicine application method in *in vivo* condition was conducted at Experimental area of the Department of Horticulture, University of Cukurova in Turkey. The aim was to determine the best colchicine dose and time in obtaining tetraploids that can be used as rootstocks in watermelon grafting. Colchicine was applied 7 weeks after transplanting to all genotypes. For both two genotypes, plants were treated with 2 doses of colchicine (0.5% and 1.0%) at three different times (1h, 2h and 4h). Colchicine dose of 0.5% resulted in high induction rate of tetraploids at 1h and 2h in '*Lagenaria*'. Immersing bottle gourd plant shoot tips into 1% colchicine resulted in burning of the growing shoot in all times. Colchicine application induced higher rate of tetraploids in citron than in bottle gourd. Immersing the tip of citron shoot into 0.5% colchicine for 1h resulted in highest induction rate of tetraploids. Immersing growing shoots of citron into 1% colchicine dose resulted into induction rate of 33.33% for 1h and 50.00% for 2h. Citron has high resistance to 1% colchicine dose when immersed into solution for up to 2h. Immersing the growing shoot tip into colchicine for 4h caused burning. Based on the results of our study, colchicine application by shoot immersion method is best when applied at low dose in a short time in bottle gourd and at high dose in a short time in citron.

Key words: Chloroplast, double chromosomes, grafting, *in vivo*, rootstock, stomata

S20-P27:

MORPHOLOGICAL CHARACTERIZATION, PLANT GROWTH, YIELD AND POD PROPERTIES OF SOME WINGED BEAN [*Psophocarpus tetragonolobus*] GENOTYPES

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Winged bean [*Psophocarpus tetragonolobus* (L.) DC] is an important vegetable with high nutritional value. As a tropical vegetable, it contains high protein, fat, unsaturated fatty acids and vitamins. This vegetable, being an important source of protein, is a well-known pulses and also called the soybean jelly or green gold of the tropics. Winged beans are grown in approximately 80 countries around the World, however it is an unknown vegetable in Turkey. The aim of this study was to grow winged bean [*Psophocarpus tetragonolobus* (L.) DC] in Turkey condition, morphological characterization and determination of some plant growth, yield and pod characteristics. In the study, 8 winged bean genotypes brought from AVRDC (Asian Vegetable Research and Development Center) were used as plant material and morphologically characterized for 25 traits and also seed measurements, plant measurements, yield, pod characteristics, protein and fatty acids analysis were conducted. According to the research results, the seed average weight was changed between 0.24 - 0.34 g, the seed width was between 7.66 - 9.23 mm, the seed length was 7.08-8.16 mm and the seed thickness was 6.01 - 7.05 mm in the 8 genotypes. Seed emergence rates were 58.50 - 86.00 % and emergence time was between 18.58 - 31.91 days. The best plant



growth was observed at 4WBE-001 in the measurements carried out in 3 different dates in the plant. The weakest developed genotype was in the genotype PT-016. Yields were obtained from only 4 genotypes that flowered under Adana conditions and yield ranged from 0.19 to 0.40 kg plot⁻¹. Generally, the genotype 4WBE-001 gave the highest results in pod measurements. The highest protein content was obtained in 4WBE-001 (49.66 %) and the lowest in Pong-Chawa (23.47 %). It has been noted that the most abundant fatty acids were palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid and behenic acids in the winged bean pods and seeds. In the morphological characterization, the Purple Winged Bean genotype was found to be the most distant from the others. PT-003 and PT-029 genotypes were 83.57% similar to each other.

Key Words: Winged bean, legume, palmitic acid, pod length, pod characteristics

S20-P28:

NEW HYBRIDS OF EGGPLANTS OBTAINED AT VRDS BUZAU AND THE EVALUATION OF THEIR PRODUCTION POTENTIAL IN OPEN FIELD AND PROTECTED SPACES

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The crop area cultivated with eggplants grew significantly in Romania from one year to another since twenty years ago. However, most of the cultivars used in crop production are of import. It was found that the imported hybrid seed is very expensive and do not always correspond to our climatic conditions. Therefore, at the beginning of 1996, breeding researches for this species were highly intense at VRDS Buzau. Debuting with the achievement of a valuable germplasm collection, continuing with its evaluation and, the accessions that proved descendent genetic stability and useful traits for the breeding program, had been tested for the general and specific combining ability. Between the selected genitors was carried out a large number of hybrid combinations, and after a careful assessment was found that two of these combinations manifested visibly the heterosis phenomenon in F1. The results obtained for this two hybrid combination in open field and protected spaces are presented in this paper. The two new obtained cultivars were registered in the Romania Official Catalogue of Crop Plants as Rebeca and H2Bz. For highlighting their production and quality potential in protected spaces and open field cultivation the hybrid Aragon produced by Hazera Company was used as a control variant. During the vegetation period were made biological and phonological measurements, with a special emphasis on their quality and production potential in comparison with the control variant. In terms of earliness, high values were observed at H2Bz and in what concerns the fruit size and plant productivity Rebeca registered the highest values. The accessions used in this experience recorded lower values in what concerns the plant vigor as well as crop production in open field cultivation by comparison with the ones recorded in the protected spaces. Even so, they are recommended to be cultivated in both culture environments.

Keywords: Romania, aubergine, *Solanum melongena*, crop, Rebeca

S20-P29:

EFFECT OF GENOTYPE ON MICROSPORE CULTURE OF EGGPLANT (*Solanum melongena* L.)

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Microspore embryogenesis is promising method for obtaining androgenic haploid and doubled haploid (DH) plants. This research aimed to examine genotype effect, which is one of factors influencing microspore embryogenesis, in three eggplant F₁ cultivars. For this purpose, the microspores were firstly isolated from the anthers containing mostly vacuolate microspores and young bicellular pollen and subjected to pre-treatment at 35°C for 3 days in dark conditions. After pre-treatment, the microspores were cultured in liquid NLN culture medium supplemented with 2 % sucrose, 0.5 mg/l naphthaleneacetic acid (NAA), and 0.5 mg/l,6-benzylaminopurine (BAP), pH 5.9, and kept in the dark at 25°C for one month. Immediately after induction, before the microspores develop into callus, they were induced to divide



symmetrically and form multinucleated structures, and then microspores did not form direct embryos but formed callus. At the end of one month, only callus formation occurred from microspores and total callus number per petri, therefore, was analyzed. The cultivars showed differences in calli formation. The average calli was 31.44 calli/petri dish for Amadeo, was 10.22 calli/petri dish for Faselis while Anamur did not exhibit any microspore-derived structures or callus formation.

Keywords: *Solanum melongena* L., microspore embryogenesis, haploid, DH, microspore culture

S20-P30:

BREEDING OF INBRED LINE "HUGAN-399" WITH HIGH COMPATIBLE INDEX IN CABBAGE

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Materials with high compatible index were discovered from the fertile offspring of crosses between one dominant nuclear male sterile individual and other cabbage varieties. The "Hugan-399" is obtained from one of the individuals with high compatible index by directional selection. In spring 2009, the dominant nuclear male sterile individual was crossed with ten cabbage varieties, respectively. In autumn 2009, equal number of seeds derived from the ten crosses were mixed together and planted in an isolated greenhouse. In spring 2010, the mixed pollination using bees was conducted for the individuals in greenhouse at flowering period. Thus, the basic population for recurrent selection had been established. In order to generate the next population for recurrent selection, the offspring of infertile individuals was chosen according to the breeding target. The recurrent selection was conducted three times in this way. In the process of recurrent selection, some fertile individuals with high rate of self-fertility were found. For the compatible index measurement of these individuals, bagging and without artificial pollination were carried out in 2013. The individuals with compatible index over 4.0 were chosen for homozygous selection in the same year. After five generations of strict selection, one inbred line exhibited stable and high compatible index more than 7.0. We named this inbred line as "Hugan-399". The "Hugan-399" displayed medium maturity, yellow-green leaves with less wax powder, round and green heads, head weight about 1000g and the ratio of the core length to the head vertical diameter less than 0.4. And it is suitable for cultivating in the middle and lower reaches of Yangtze River in autumn. In conclusion, the "Hugan-399" exhibits good uniformity and high compatible index. A lot of seeds of the "Hugan-399" could be harvested without artificial pollination, so the cost should be reduced drastically in seed production.

Keywords: cabbage, high compatible index, recurrent selection, breeding

S20-P31:

SELECTION OF USEFUL PURPLE SPROUTING BROCCOLI (*Brassica oleracea* L. Italica Group) VARIETIES FOR CULTIVATION IN JAPAN WITH ITS WARM AND WET CLIMATE BASED ON THEIR YIELDS AND CHARACTERISTICS OF THE BEARING BUDS

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Purple sprouting broccoli ("PSB") is a vegetable cultivated for commercial purposes primarily in Britain along the west coast with its marine climate, and the lateral branches are harvested. The results of a preliminary examination suggested the problem of it taking too long for the buds of the "PSB" cultivated in Japan - a country with a warm and wet climate, to sprout. Therefore, in order to introduce "PSB" to Japan, it is necessary to select and cultivate appropriate varieties while taking the yields and characteristics of the bearing of buds into consideration. A survey was conducted to examine the yields of 'Santee', an early maturing variety, cultivated in fields of Japan, and the number of days for the plants to bear buds over two cropping seasons between 2014 and 2016. The yields of 'Santee' planted in August to September were equal to or higher than those of 'Pixel' (broccoli) and 'Stick Señor' (sprouting broccoli). However, the start of the harvest of 'Santee' planted in August



to September was later than that of 'Pixel' and 'Stick Señor' planted around the same period. To examine the budding characteristics of "PSB" varieties that can be harvested earlier than 'Santee', the morphological characteristics of nine "PSB" varieties and the number of days for them to bear buds were compared. The number of days required for 'Rioja' to bear buds was significantly shorter than the period required for other varieties. Regarding the morphological characteristics, the diameter of the stem of 'Mendocino' was significantly greater and its yield was higher compared with other varieties. When considered from the viewpoint of characteristics, 'Rioja', which requires only a short period of time to bear buds, and fertile 'Mendocino', with its thick stems, are favorable "PSB" varieties to be cultivated in the warm and wet climate of Japan.

Keywords: morphogenesis, accumulated temperature, vernalization, planting time, scape

S20-P32:

IMPROVING SALT TOLERANCE OF TOMATO THROUGH THE USE OF THE WILD TYPE *Solanum habrochaites*

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Plant breeding has been demonstrated as an important strategy for improving tolerance to biotic and abiotic stresses. In tomato, the availability of wild relatives offers an interesting gene pool that has been explored for improving crop performance. Here we compared the performance of the cultivar *Solanum lycopersicum* 'Moneymaker' (MM) with 9 selected introgression lines (ILs) from the LYC4 tomato population, which resulted from the cross of MM and *S. habrochaites* (a less studied wild type) and backcrossing to MM. Plantlets were transplanted to rockwool and further grown under standard (EC=3 dS.m⁻¹) and saline conditions (~50 mM NaCl added to the nutrient solution; EC=8 dS.m⁻¹) for 124 days. Plant growth and development, fruit quality and ion content in the leaves and stems were assessed. It was found that saline conditions resulted in a significant reduction in total dry weight (TDW) and fresh weight (less 11% and 21% on average, respectively), which were mainly owed to lower fruit dry weight (due to both lower fruit number and lower average fruit weight). Nevertheless, IL1-4 and IL2-3 showed a slightly higher TDW in EC8 than in EC3. Reduced marketable fruit dry weight (-22%) under EC8 was partly explained by higher blossom-end rot incidence, mainly in MM, IL2-3, IL6-1, IL6-2 and IL10-4. Salinity increased the fruit's total soluble solids (TSS) by 0.7 °Brix on average, and IL6-2, IL1-4, IL12-1 and IL2-3 showed significantly higher TSS than MM under salt stress. Despite that none of the ILs showed a clear higher salinity tolerance in a basis of TDW or in a total fruit yield as compared to MM, a significant genotypic difference was observed in IL2-3 which showed higher TDW than MM in global terms and was not affected by salinity relatively to this trait. Under EC8, genotype IL12-1 showed more favorable K:Na and Ca:Na ratios compared with MM, which can be considered good indicators of salt tolerance. It is concluded that the studied ILs have some potential to be used in breeding programs for salt tolerance improvement of tomato, by selecting specific characteristics of interest that can contribute to this goal.

S20-P33:

A NEW WATERMELON CULTIVAR SHANNONG NO.4

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With the increased earning and the changes in consumption conception, people have stronger demand for middle fruit type in watermelon with a high quality. 'ShanNong No.4' is a new watermelon cultivar developed by crossing J2M and J2F, whole growth period is 89 days, and fruit development period need 29 days. This variety is easy to bear fruits. Its fruit shape is oval and the shape index is 1.1. The fruit skin is dark green with thin stripes, and the pericarp thickness is about 1.1 cm. The fruit has strong skin toughness, and good shipping quality. The fruit flesh is red fine sandy and high quality. The center sugar content is 12 %, which is closed to the edge sugar content. It has an average single fruit of 6.3 kg and a yield of 63000 kg/hm². It also has a high disease-resistance as well as a strong adverse-resistance. It is suitable to cultivate in the open field and early spring protected area in the Shaanxi province of China.

Keywords: watermelon, cultivar, maturing

S20-P34:

QTL-SEQ IDENTIFIES A VERNALIZATION REQUIREMENT QTL LOCATED NEAR FLOWERING LOCUS T IN RADISH

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Radish (*Raphanus sativus* L., $2n = 18$), a member of the family Brassicaceae, is a vegetable worldwide. Flowering time is an important agronomic trait because bolting results in the failure of harvest while the root is converted from a nutrient sink to a source. On the other hand, flowering time is also important for economical seed production. Most of radish including daikon radish (*R. sativus* var. *hortensis*) and European small radish (*R. sativus* var. *sativus* L.) need a cold treatment, a process known as vernalization, to flower. While, rat-tail radish (*R. sativus* var. *caudatus*) and oil radish (*R. sativus* var. *oleiferus*) can flower without vernalization. The genetic dissection of vernalization requirement in the flowering is important for breeding of radish. A F₂ population including 516 individuals produced from a cross between a daikon radish and rat-tail radish was used for QTL mapping of vernalization requirement. We employed the bulk segregant approach coupled to whole genome sequencing (QTL-seq) to identify candidate QTL regions. For QTL-seq, two DNA pools, early pool and late pool were constructed, respectively, by mixing an equal amount of DNAs from 38 early flowering and 38 late flowering F₂ individuals. Pair-end sequencing libraries (read length 150 bp) were prepared for sequencing with Illumina HiSeq X Ten. The bioinformatics analysis were executed according to Takagi (2013). One genomic region on R07 (1.0 Mb) showing significant ($P < 0.05$) deviation from equal inheritance of the two parental genomes that harboured a Flowering Locus T (FT) homologous, which has a central position in mediating the onset of flowering. Semi-quantitation PCR shows that FT expressed in leaves in rat-tail radish, but not in daikon radish before vernalization. These data suggest that FT is involved in vernalization requirement in controlling flowering time in radish.

Keywords: Radish, Vernalization requirement, QTL, Flowering Locus T

S20-P35:

"AUTONOMOUS FRUIT SET" IN AN F1 HYBRID OF CAPSICUM CHINENSE

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In Capsicum production, a pollinator or hormonal treatment is necessary for fruits to set. When temperatures are high, Capsicum chinense 'Sy-2' and '51' seldom set fruits in the absence of pollinators or hormonal treatment. Nevertheless, the F₁ hybrid of 'Sy-2' and '51' (F₁) did set fruits even in the summer season, without pollinators or hormonal treatment. To evaluate the "autonomous fruit set", the term used here for the phenomenon of setting fruit without any pollinators, wind, or hormonal treatment, C. chinense 'Sy-2', '51' and 'Sy-2' × '51' (F₁) were cultivated in a greenhouse covered with mesh to prevent the incursion of pollinators. In August 2017, autonomous fruit set (%) relative to the total number of flowers in the F₁ was higher than that in the parent cultivars 'Sy-2' and '51'. To evaluate the pollen germination, 5–10 flowers were collected immediately upon



flowering at 9:00–10:00 a.m. and pollen collected from these flowers was put on a 1% agar gel containing 5% sucrose and 0.01% boric acid. After 24 h, pollen germination (%) of the F1 was higher than those of 'Sy-2' and '51'. In addition, also in F2 population, pollen germination was revealed to be slightly to moderately correlated to the autonomous fruit set ($n = 155$, $R = 0.358$). In conclusion, the autonomous fruit set observed in the F1 under high temperature conditions is partly due to the improved germination of their pollen.

Keywords: heterosis, high temperature stress, pollen germination, fruit set, pollination

S20-P36:

APPLICATIONS OF PLANT RAPID GENERATION TECHNOLOGY IN BRASSICACEAE PLANTS

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The studies of modern plant breeding are seeking method to shorten the generation cycle in producing pure line populations for genetic studies and selecting new varieties. The plant rapid generation technology is a fast and efficient way to significantly shorten the generation cycles and increase breeding efficiency. Six or seven generations per annum were achieved in canola and flowering Chinese cabbage using the 'embryo culture plus soil' procedure based on plant growth in soil under conditions of high temperature, water stress, long lighting hours and young embryo culture on special media to bypass seed maturation. In order to increase the value of the rapid generation technology, application research must be conducted for standardization and large scale production. Combined with molecular markers assistant selection, the rapid generation technology will be widely adopted in plant breeding and genetic improvement.

Keywords: Rapid generation technology, Breeding, Embryo culture, Stress environment, Genetic improvement

S20-P37:

CREATION OF PURPLE HEADING CHINESE CABBAGE AND ITS CHARACTERISTICS

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Heading Chinese cabbage (*Brassica campestris* syn *rapa* L. ssp. *pekinensis* (Lour) Olsson) is a significant vegetable crop for its edible heading leaves in Asia countries. Breeding new varieties of Chinese Cabbage with high quality are always goals for breeders, but the germplasm resources of purple heading Chinese Cabbage had not been found until. Here, a common heading Chinese Cabbage and purple flowering Chinese Cabbage were used as parents, via crossing, single plant selfing for three generations, then crossing with an orange heading Chinese Cabbage, continuing single plant selfing for five generations, a new purple heading Chinese Cabbage line with green outer leaves was successfully bred, which will make the basis for purple heading Chinese Cabbage hybrid. Genetic analysis shows that the purple inner leaves trait is controlled by a single dominant gene BrPur, which was mapped on linkage group A07 based on the sequence of two linked markers flanking BrPur. Leaf cross-section observation showed that the anthocyanin distribution is non-uniform in the purple heading leaf, specially enriched in the epidermis and its adjacent mesophyll cells. Comparing with the negligible amount of anthocyanin in the non-purple parent, the anthocyanin amount in purple inner heading leaves of purple line is up to $0.79 \text{ mg} \cdot \text{g}^{-1} \text{ FW}$. Q-PCR analysis indicated that the EBGs (Early Biosynthesis Genes), such as CHS, CHI, F3H, F3'H, and LBGs (Late Biosynthesis Genes), ANS and GST, as well as the regulatory gene MYB2, MYB4 were up-regulated in the inner leaves of purple heading

Keywords: Chinese cabbage, purple leaf-head, Genetic analysis, anthocyanin, Q-PCR



S20-P38:

ORYZALIN APPLICATION TIMES AND DOSES ON TETRAPLODIZATION IN CITRON (*Citrullus lanatus* var. *citroides*)

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The interest in tetraploid plant production recently has been developed in vegetable grafting especially in cucurbits. In this study oryzalin doses of 0 μ M (Control), 30 μ M, 60 μ M, 90 μ M and 120 μ M were applied to the shoot tips of Citron (*Citrullus lanatus* var. *citroides*) genotype 'PI 296341' at 24h, 48h and 72h to determine the obtention of tetraploids from citron. The experiment was conducted at the experimental field of the Department of Horticulture, Cukurova University in Turkey with the objective of determining the best oryzalin application time and dose in obtaining tetraploid plants. There was no tetraploid plant obtained in all application doses at 48h. Oryzalin doses of 30 μ M, 60 μ M and 120 μ M resulted in obtention of 25% tetraploid plants each at 24h. After 72h of plants treatment with oryzalin, 30 μ M and 120 μ M doses resulted in 25% and 90 μ M dose resulted in 50% tetraploids. According to the results of this study, Citron responds well in tetraploid induction at 90 μ M and 120 μ M oryzalin concentrations when applied for 72h.

Keywords: Chromosome doubling, chloroplasts, guard cells, shoot tip

S20-P39:

GERMINATION AND SEED VIGOR IN HUSK TOMATO (*Physalis ixocarpa* Brot. ex Horm.)

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In order to evaluate the physiological seed quality of husk tomato through the time, under the effect of two storage conditions, seeds from four varieties produced in 2013 were stored for three years at the Laboratory of Seed Analysis under room conditions (23.43 ± 0.64 °C; R.H. 23 %), and at the Gene Bank (-20 °C; R.H. 13 %) at Chapingo Autonomous University, Mexico. Sampling was performed every year from October 2013 to November 2016. For each sample, germination and vigor tests were carried out under a completely randomized experimental design, with six replications. Percentage of germination was tested placing the seeds in a germination chamber at 30° C for 21 days. Seed vigor was assessed through speed of germination index (SGI), seedling length (SL), dry weight of seedling (DWS) and percentage of normal seedling (NS). After three year storage period, germination decreased 4.3 %, with the highest percentages obtained in Diamante and Tecozautla 04 varieties. The four varieties presented values of germination above 90 %, which are over the certifications standards. The storage environments had no effect on germination. However, the storage under Gene Bank conditions showed the highest values in SGI and NS. The variety Diamante showed the highest values of percentage of germination and SGI. The vigor variables (SGI, SL, DWS) showed a negative effect caused by storage time.

Keywords: Germination, vigor, seed quality, deterioration, conservation

S20-P40:

HETEROSIS IN FOUR POPULATIONS OF HUSK TOMATO (*Physalis ixocarpa* Brot. ex Horm.)

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Currently do not exist breeding by hybridization in husk tomato (*Physalis ixocarpa* Brot. ex Horm.), thereby it is important to study heterosis in this crop to implement a hybridization strategy. In this research, the heterotic effects among 11 maternal half-sib families from four populations were studied. Under greenhouse conditions, interfamilial diallelic crosses were made. Later, the on field evaluation of crosses and progenitors was carried out. It was measured yield per plant (kg) in two harvests (RPC1 and RPC2) and total yield (RTP), as well as, the weight of ten fruits (g) in each harvest (P10FC1 and P10FC2) and the average of harvests (PP10F). To compare progenitors by their progeny, analysis of variance and tests of comparison of means were performed (Tukey, 0.05). It was estimated midparent heterosis. To determine if estimation of heterosis was significant, it was performed contrast analysis. In those crosses whose midparent heterosis was positive and significant, it was made the estimation of better-parent heterosis, which was also tested by contrasts. Significant positive better-parent heterosis was shown in the hybrid 1x10 to yield per plant in the first harvest, and crosses 6x9 and 10x6 for yield per plant in second harvest, even though no hybrid expressed significant better-parent heterosis for total yield per plant. The best female progenitors for total yield per plant were the families 2, 3 and 4, whereas there were no differences between male progenitors. Therefore, such families could be used in breeding programs by selection and hybridization.

Keywords: Diallelic crosses, half-sib families, hybridization

S20-P41:

A CANDIDATE MECHANISM FOR NON-VERNALIZATION FLOWERING OF CABBAGE BY GRAFTING ON RADISH STOCKS

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Cabbage (*Brassica oleracea* var. capitata) is a plant-vernalization-responsive type plant, which can respond to low temperature only after several true leaves are formed. Its strong vernalization requirement hampers a rapid cycle of breeding and seed production, especially in warmer areas with unsuccessful flowering under natural conditions. Thus, a non-vernalization flowering (NVF) method has long been sought. In this study, we examined the flowering response of several cabbage cultivars grafted on Rat's Tail radish (*Raphanus sativus* var. caudatus) without vernalization, and also discussed the candidate mechanisms for NVF by examining the expression level of genes related to flowering. Seeds of the cabbage cultivars 'Watanabe-seiko No. 1', 'Red cabbage', and 'Kinkei No. 201' were sown and grown for 3–6 weeks in a growth room maintained at $21 \pm 2^\circ\text{C}$ under long-day (16L:8D) conditions at a light intensity of $80 \mu\text{mol m}^{-2} \text{s}^{-1}$ (PPFD) provided by fluorescent lamps. Another cultivar, 'nfc', which had been vegetatively propagated in vitro, was also grown in the same conditions. The terminal shoots with 2–3 leaves of cultivars that had never experienced vernalization were grafted onto stems of bolting Rat's Tail radish grown in the same conditions for 1–2 months. Flower bud formation in the grafted cabbage was continuously checked for 70 days after grafting. Successful NVF was observed in all cultivars, except for 'Kinkei No. 201', while none of the control plants (non-grafted) flowered. The earliest flowering was observed within 50 days after grafting. Viable pollen and germinable seeds were obtained from the NVF plants. In the leaves of 'Watanabe-seiko No. 1', high expression of the floral repressor gene FLOWERING LOCUS C (FLC) and very low expression of the florigen gene FT were observed. These results indicate NVF could be induced by a graft-transmissible agent, possibly FT protein, provided by the radish stock.

Keywords: *Brassica oleracea* var. capitata, vernalization, *Raphanus sativus*, grafting, seed production

S20-P42:

BREEDING AND VARIETY IMPROVEMENT OF SNAP BEAN (*Phaseolus vulgaris*) FOR PRODUCTIVITY AND RESILIENCE UNDER DROUGHT STRESS

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Effective breeding and genetic improvement of beans (*Phaseolus* spp) aims to harness their tremendous genetic diversity to match location-specific growing conditions and the needs of households and local markets in response to climate change. Development of improved cultivars involves evaluation of genetic resources (e.g. genotyping, phenotyping) for identification of sources of desired traits, gene discovery, and knowledge-based breeding for genetic enhancement. This paper presents the screening process as part of the developing regionally adapted snap bean cultivars for growing under water deficiency conditions. Different screening approaches have been applied, including: plant growth and yield parameters (Biomass, plant height, pod and grain yield, seed germination, flower abortion); and physiological responses (chlorophyll fluorescence induction parameters). Results from field trails with Bulgarian snap bean varieties are presented and discussion on physiological mechanisms used by plants to cope with this abiotic stress factor, as well as approaches for screening and their relation with yield in the tolerant genotypes are encompassed in the context of plant breeding methods. Two bean cultivars 'Tangra' and 'Zaria' with different water efficiency, post-drought recovering capacity and heat tolerance were identified and their incorporation into the regional industry may expand the range of conditions suitable for bean production while reducing growers' costs and risks.

Keywords: common bean, selection methods, abiotic stress, productivity, drought tolerance

S20-P43:

SALT TOLERANCE DURING GERMINATION, SEEDLING AND ADULT PLANT OF WILD TOMATO

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Salt tolerance in commercial varieties of tomatoes is low, reason why the study of wild materials in search of salt resistance is of great importance for breeding. The aim of this research was to identify native tomato collections of Mexico tolerant to salt during the stages of germination, seedling and adult plant. Seeds of 96 collections of native tomato were germinated in a chamber (25°C and 80% of relative humidity) in two concentrations of NaCl (0 and 70 mM). Germination percentage, germination rate index and dry matter production were determined. The salt tolerance evaluation in seedling stage included the 29 best material which were sown in polypropylene trays filled with peat moss and irrigated with nutritive solution with 0 and 70 mM of NaCl. Thirty days after sowing, the number of seedling and their length, dry matter accumulation, and visual scale of damage were assessed. The test in adult stage, carried out under greenhouse conditions with a hydroponic system, included 13 tolerant collections cultivated under two saline concentrations (0 and 80 mM) from 20 days after transplant. In the three initial clusters, total soluble solids, intensity of leaf green color, plant height, fruit yield, number of fruits, and concentrations of the aerial part of N, Ca, Mg and K, were quantified. By means of multivariate analyses 12 out of the evaluated collections showed tolerance to salt. Of these, four showed good performance in the three phenological stages (germination, seedling and adult plant) since showed higher germination, emergence, dry matter production; as well as in adult plant, major concentration of N, K, Mg and Ca under the saline condition. This situation is possible since during the processes of adaptation or domestication, the plants were exposed to the salinity conditions in the soil.

Keywords: *Solanum lycopersicum* L., Selection, nutritional content

S20-P44:

THE MORPHOLOGIC AND PHENOLOGICAL CHARACTERISTICS OF SOME CARNATION (*Dianthus* L.) TAXONS NATURALLY FOUND IN TURKEY

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The cultivation of the species located in natural vegetation of Turkey and researching the usage opportunities in ornamental plants sector are very important for both conservation of the natural plant biodiversity and contribution to the economy of the country. In this study, it was given information about the phenological and morphological properties of the *Dianthus* species collected within the “Variety Development Studies of Some Cephalaria (*Cephalaria* Schrad. ex Roem. & Schult.), Sage (*Salvia* L.) and Carnation (*Dianthus* L.) Taxons Naturally Found in Turkey for Using as Outdoor Ornamental Plant” named TAGEM Research and Development Project. In this study, plant length, branching, flowering time, flower size, petal shape and petal colour of the carnation (*Dianthus* sp.) species were observed.

Keywords: Ornamental plants, Natural species, *Dianthus* sp., Carnation

S20-P45:

SELECTION OF HEAT-TOLERANT INTERSPECIFIC DIANTHUS FOR BEDDING PLANTS

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The genus *Dianthus* L. is widely used as bedding plants, potted flowering plants, or cut flowers. Bedding plant dianthus does not tolerate heat and humid environments. Taiwan indigenous *D. longicalyx* Miq. (Maxim.) Will. can flower all year round and thus might serve as breeding parents for desirable characteristics. We crossed *D. chinensis* L. ‘Super Parfait Strawberry’ with *D. longicalyx* to obtain interspecific seedlings. Following hybridization, four single plants CsLtp1, CsLmz1, CsLmz2, and CsLmz3 were selected, and cutting-propagated for further evaluation. The leaf disc relative injury (RI) values of these four selected lines were 4.5%, 2.8%, 0.4%, and 48.9%, respectively after a test for cell membrane thermostability at 54 °C water bath for 20-30 min. Since CsLmz3 could be heat-intolerant as shown by a high RI value and CsLmz2 was tall and poor-branched, these two lines were discarded thereafter. The selected line CsLtp1 is dwarf with 6 cm diameter flowers in deep purple color (RHS N74B), and the selected line CsLmz1 has fragrant light purple flowers (RHS72B) and the flower diameter is 5 cm. Both selected lines exhibited high branching and flowered year-round in sub-tropical Taiwan climates.

S20-P46:

GENOMIC ASSESSMENT OF LILIUM HYBRIDS BY UTILIZING CYTOGENETIC METHODS

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In cytogenetic, genomic analysis of hybrids has been improved greatly over the past several decades. In situ hybridization technique is a primary and prominent method for chromosomal and breeding study. Due to large genome size, *Lilium* genus is an ideal for chromosomal analysis. Hybridity and genomic status of interspecific progeny must be analyzed in the initial growth stage. Therefore, genomic in situ hybridization (GISH) method has proved to be most accurate and active approach for parental contribution confirmation. Chromosome composition and genomic impact detection are significant applications of GISH in cytogenetic. In this experiment, intergenomic crosses were made to develop interspecific hybrids of *Lilium*. Chromosomal counting analysis of interspecific hybrids showed diploid ($2x=24$) ploidy status. GISH results showed that interspecific crosses (LM) between *L. longiflorum* and Martagon sections showed equal chromosomal contribution from each parent i.e. 12 longiflorum chromosomes & 12 martagon chromosomes were found in F1 hybrids without any recombination. LO hybrids also showed the similar results, inheriting 12 chromosomes from each parent (*L. longiflorum* and oriental). Furthermore, some of the F1 hybrids were genomically identified as unsuccessful cross due to absence of maternal chromosome in GISH results. In spite of that, in backcross LAA hybrid, GISH findings reported an increase in number of chromosomes of Asiatic parent than *L. longiflorum* parent. Therefore,



GISH analysis verified and screened out the *Lilium* hybrids genetically without consuming time for phenotypic analysis. It also revealed the genomic inheritance in the resulting hybrids.

Keywords: hybrid, progeny, genome, in situ, recombination

Acknowledgement

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S20-P47:

A POLYPLOID PINK AND WHITE SHOWER TREE, *Cassia javanica*, PRODUCES DIPLOID PROGENY

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A purported tetraploid ($2n = 4x = 56$) plant of the pink and white shower tree, *Cassia javanica*, confirmed by guard cell measurement and root-tip chromosome count, was crossed to a diploid ($2n = 2x = 28$) plant of the same species to produce triploid ($2n = 3x = 42$) progeny that were expected to be sterile. The progeny, however, from six crosses were $2x$. Flow cytometry was used to help determine that the purported $4x$ parent plant was in fact a mixoploid, consistent with a 4-2-4 periclinal cytochimera having $4x$ epidermal and cortex tissues with a $2x$ tissue layer between giving rise to haploid gametes.

Key Words: colchicine, tetraploid, flow cytometry, chimera

S20-P48:

FUNCTION OF FLAVONOID 3'5' HYDROLASE (F3'5'H) GENE ISOLATED FROM *Aquilegia buergeriana*

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We isolated homologues of a F3'5'H gene (named AbF3'5'H) from *Aquilegia buergeriana*, which is wild flower in Korea. We introduced the AbF3'5'H gene into *Petunia hybrida* 'Dream's Red' by Agrobacterium-mediated transformation technique. We analyzed the pseudo-transgenic plants regenerated from the selection medium by PCR and Southern. Northern and real-time PCR were executed to identify which the transgene expressed normally in the AbF3'5'H-transgenic petunia plants or not. We acclimatized the plants and transferred into greenhouse. When the plants flowered, flower color was observed and investigated by color chart (Royal Horticultural Society, fifth edition). Flowers of non-transgenic petunia plants was red group (46A or 46B), whereas that of the AbF3'5'H-transgenic petunia plants was red group (45B). Color of inside in corolla tube of non-transgenic petunia plants was purple group (77A or 79B), whereas that of the AbF3'5'H-transgenic petunia plants was red purple (59A). Color of stigma and style of non-transgenic petunia plants was purple group (77C or 77D or 79B or 79D), whereas that of the AbF3'5'H-transgenic petunia plants was white group (155C).

Keywords: Flavonoid 3'5' Hydrolase, Gene, *Aquilegia buergeriana*, flower color

S20-P49:

AtNDPK2 GENE ENHANCED REMOVAL ABILITY OF EXOGENOUS TOLUENE IN PETUNIA



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We initiated this study to identify which genes to make enhancement in resistance to abiotic stresses have function to remediate indoor air pollutions or not. We used only NDP kinase (NDPK) 2 gene- or both superoxide dismutase (SOD) 2- and NDPK2 genes-transgenic T5 petunia plants identified as plant material. The transgenic seeds were obtained in 2011, and their seedlings were identified by PCR analysis in 2015. We confirmed that the NDPK2 gene transgenic plants removed 1.5 times more toluene gas (1 ppm) than both SOD2- and NDPK2- genes transgenic plants, and 3 times more than non-transgenic petunia plants during a 12-h measurement period.

Keywords: abiotic stress, gene, enhancement, removal, toluene

S20-P50:

POSITIVE EFFECT OF LOW DOSE GAMMA ON MORPHOLOGICAL AND BIOCHEMICAL PROPERTIES OF HORTICULTURAL PLANTS

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The use of gamma rays in plant breeding is not a new technique, but there has been an increasing interest in this method in recent years. High doses of gamma rays increase the mutation frequency, but the number of survival plant is reduced. Studies show that gamma rays applied at low doses improve the morphological and biochemical properties of some plants. Gamma ray treatments in early stages of seed germination promote the synthesis of RNA and protein so enhances seedling growth and also increases the antioxidative ability of cells helps cell fight back daily stresses. Studies in many plants such as apricot, okra, rocket, tomato, banana, pepper, gerbera show that the use of low doses gamma rays has positive effects on some properties of these horticultural crops. It has been determined that low dose gamma treatment stimulates seed germination, vigor and seedling growth in okra and rocket. Besides it was detected that this treatment increased chlorophyll content of red pepper and the activities of peroxidase were enhanced by gamma irradiation in radish and also increased the nutritional quality of broad bean. In this review, the effects of low dose gamma applications on plant growth and biochemical contents of horticultural crops have been examined.

Keywords: biochemical properties, gamma ray, horticultural plants, low dose, morphological properties

S20-P51:

GENERAL AND EXACT INBREEDING COEFFICIENT OF SYNTHETICS DERIVED FROM THREE-WAY LINE HYBRIDS

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In México, some of the farmers who grow hybrids grow their advanced generations later on. Although the resulting population could be viewed as the synthetic derived from the lines (SynL) that are parents of the hybrids, there may be differences. The synthetic variety (SV) whose parents are t TWLHs (SynT) is interesting because the contributed gene frequencies of the three lines that are parents of a TWLH are not balanced and this may generate a difference between the inbreeding coefficients (ICs) of the two types of SV's. Since an exact and general IC of the SynT is unknown and since the IC of a SV is related with its performance, the main objective of this study was to derive a general (for any IC of the initial parental lines) and exact formula for the IC (FSynT). To form the t TWLHs, it was supposed that 3t unrelated lines whose IC was F ($0 \leq F \leq 1$) were



employed, and that each parent was represented by m plants. Exact and general formulae for $FSynT$ were derived: in particular, $FSynT = [3(1 + F)]/(16t)$. $FSynT$ was also expressed in terms of the contributions to inbreeding from selfpollinations and from intraparental crosses (r_0, w). In a previous study, restricted to the use of pure lines, it was found that the $SynT$ IC derived there was inexact since exceeded $FSynT$ due to an error in r_0, w . In addition, since the IC of the $SynL$ ($FSynL$) is $(1 + F)/(6t)$, then $FSynT > FSynL$. These findings imply that $SynL \neq SynT$ and suggest that the genotypic mean of the $SynL$ is larger than the $SynT$ 'S.

Keywords: *Allium cepa*, *Zea mays* L., genotypic mean, identity by descent, coancestry

S20-P52:

MUTATION BREEDING OF BUTTERFLY PEA BY LOW-ENERGY ION BEAM

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Low-energy nitrogen ion beam at 50 keV was used to induce mutation of butterfly pea (*Clitoria ternatea* L.) seeds. Ion fluences of 1×10^{16} to 12×10^{16} N-ions.cm⁻² did not affect the seed survival percentage. However, the 12×10^{16} N-ions.cm⁻² fluence caused variegated and deformed leaves on some plants in 'M1' (the 1st generation of mutation induction) population. The 'M1' population ($n=137$) also had lower average internode and leaflet lengths than the wild type population ($n=50$). All 'M1' plants were self-pollinated and their seeds were grown as 'M2' population following the pedigree method. Four dwarf mutant plants derived from one line were found among 516 'M2' plants, and coded 'M2S'. They were self-pollinated and their seeds were grown as 'M3S'. All seeds from the 'M2S' plants grown to be dwarf plants. Characteristics of the 'M3S' plants ($n=15$) were compared to the wild type plants ($n=6$) at 70 days after sowing in December 2017. The 'M3S' plants had significant shorter internodes, smaller leaflet, and smaller flower than the wild type plants (at $p<0.05$). The mutant plants drastically reduced their climbing habit. Thus, their average height was only 19.3 ± 3.4 cm. While the average plant height of wild type was 53.7 ± 33.6 cm. The dwarf mutants could be developed as a pot plant or used as a tool for molecular genetic study.

Keywords: Ionizing radiation, *Clitoria ternatea*, bluebell vine, Asian pigeonwing, dwarf, seed

S20-P53:

FRUIT QUALITY OF PROCESSING PEACH CULTIVARS IN THE COLLECTION OF NIKITA BOTANICAL GARDENS

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Gene pool of processing peach cultivars (with gristly flesh) in Nikita Botanical Gardens is presented by 101 units. Evaluation of gene pool resulted in selection of 27 cultivars with good fruit quality (4.0 to 4.5 points). Among them there were listed 3 early and early-mid (Dostoyniy, Usgor 1, Usgor 2), 17 mid, 5 mid-late, 2 late (Neznakomets, Voskya Ashun) and 1 extra late (Aydinovskiy Prodolgovaty) season cultivars. There were selected 6 large fruit cultivars; 17 cultivars with yellow flesh; 5 cultivars with coating coloration, covering 40-70 % of the fruit surface; 3 cultivars with excellent taste (Uspekh, Laureat, Zlatogor) and a cultivar with the best overall score (Uspekh). Most cultivars have round-shaped fruits (64 %) with red or dark red coating coloration (46.4 %). 19 cultivars belong to North-Chinese eco-geographical group (rose-shaped flower) and 8 - to Iranian group (bell-shaped flower). 19 cultivars of them present the European, 6 - the American and 2 - the Transcaucasian ecotype (Voskya Ashun and Aydinovskiy Prodolgovaty).

Keywords: Peach, fruit quality, ripening time, eco-geographical groups, ecotypes.



S20-P54:

MORPHOLOGICAL CHARACTERIZATION IN EARLY-FLOWERING TRIPLOID LOQUAT (*Eriobotrya japonica*)

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Loquat (*Eriobotrya japonica* Lindl.), an important sub-tropical fruit tree, belongs to the family Rosaceae, and is broadly cultivated in many countries. Flowering process of loquat is a continuous development that is not interrupted by winter dormancy, and almost all shoots on the loquat tree are flowering shoots. However, the flowering mechanisms of loquat are still unclear. Compared with diploid loquat, the triploid loquat is an available germplasm with a high edible fruit rate, reflecting the seedless in nature, and has thicker leaves, larger flowers, and different pollen morphology. The natural triploid of early-flowering loquat (Q11) were selected from the offsprings of 'Changbai' diploid loquat, and provides ideal material of floral initiation for evergreen perennials. Here we continuously observed the flowering process of Q11 for five years. Time of floral initiation in Q11 was one month earlier than that in 'Changbai' diploid loquat. Nine morphologically distinct stages were defined from the vegetative meristem to the full bloom during the flower development of Q11. Stage I was summer dormant bud; Stage II corresponded to floral meristems initiation. Stage III was floral swelling; Stage IV was the rapid panicle elongation; Stage V was the branches of a panicle elongation; Stage VI was floral buds visible; Stage VII was white corollas of floral buds; Stage VIII was full bloom; Stage IX was petals fall. These stages presented in our study is available for triploid loquat so far and will serve as a framework for investigating the genetic regulation of the flowering process.

Key words: triploid loquat, early-flowering, morphologically distinct stages, flowering process

S20-P55:

YELLOW PASSION FRUIT GENOTYPES REACTION TO WOODINESS DISEASE (COWPEA APHID-BORNE MOSAIC VIRUS - CABMV) IN FIELD CONDITIONS

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Passionfruit woodiness disease (PWD) is the most important viral disease of yellow passionfruit (*Passiflora edulis* f. *flavicarpa*) and has caused serious damage to passionfruit growers. This disease causes decrease and deformation of the fruits and is associated with the occurrence of mosaic symptoms, accompanied by leaf malformation, blisters, a marked reduction in plant development, and woodiness in a variable percentage of fruits. The present work has the objective of evaluating genotypes of yellow passion fruit, in terms of resistance to CABMV, under field conditions. The experiment was carried out at Fazenda Água Limpa (FAL), belonging to the University of Brasilia (UnB), located in Federal District, Brazil. The experiment was deployed at the end of August 2016. The experimental design used was a randomized complete block design. The plots were of four seasons and the subplots were composed of 32 genotypes, four replications and six useful plants per plot. No pesticide application has been carried out to control diseases and pests. The evaluations of incidence and severity of the PWD were realized monthly, evaluating adult plants in full fruiting stage. The experimental data were submitted to analysis of variance and the averages grouped by the Scott Knott averages test, at 5% probability. There was a statistical difference between the evaluated genotypes. The genotypes RC3, MAR20 # 15R3, hybrid MAR20 # 100R2 x MAR20 # 21R2, hybrid RUBI G4 P3 R3 x MAR 20 # 15R2, hybrid MAR20 # 19P4R3 x MAR 20 # 2005 and hybrid MAR20 # 44 x ECL7P2R4 presented the lowest values of severity of the disease in the evaluation periods in the summer and fall of 2017, and were considered medium susceptible (MS) in the field conditions while the other genotypes were considered susceptible (S), including the control treatment BRS Giant Yellow.



Keywords: passionfruit, passiflora, plant breeding, cowpea aphid-borne mosaic virus

S20-P56:

SELECTION OF OKRA COLLECTIONS BASED ON SEED MINERALS AND PHENOLIC CONCENTRATIONS

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Okra is one of traditional and underutilized fruit vegetables grown in South Africa. It is an important source of vitamins, minerals, proteins, polyphenols, antioxidants, and other bioactive compounds. Besides its nutritional benefit, different parts of okra plants are used extensively in traditional medicine (as antidiabetic, antipyretic, diuretic, antispasmodic) around the world. The immature fruits of okra are consumed as vegetables in the form of salad, soups, and stews, fresh or dried, fried or boiled (Habtamu et al., 2014). This species is under-exploited and have potential for contributing towards food and nutritional security for alarmly growing population, plays a vital role in income generation and poverty alleviation. Okra provides dietary fibers and distinct seed protein balanced in both lysine and tryptophan amino acids it provides to diet. Being a less-researched and undermined crop in South Africa, there is no information on breeding and utilization for enhanced breeding for yield, nutritional, phytochemical and antioxidant properties of okra in the South Africa. The experiment focused on the selection of candidate okra genotypes based on mineral elements and phenolic contents in the seeds of 46 okra genotypes. The experiment was conducted at the Roodeplaat site in South Africa in 2016/2017 cropping season. The seeds of 46 okra genotypes were harvested and used to extract the selected mineral elements (Fe, Zn, Mn, Mg, P, K, Cu, Na, Al, B) and phenolic contents. The seed samples were analyzed at the Analatical laboratory of the Agricultural Research Council in Pretoria, South Africa. The mineral elements and phenolic data was subjected to analysis of variance (ANOVA) and multivariate analysis was performed using the GenStat computer software (Payne et al. 2016). The correlation coefficient was also carried out using the Genstate computer software. The anova for mineral elements and phenolic compounds revealed highly significant differences among the tested genotypes. The multivarriate analysis similarly showed a wide genetic divergence among the genotypes, which would be used in selecting candidate parental lines for population development in the future okra breeding improvement programme for nutritional quality in South Africa and beyond. The existence of genetic divergence in the tested genotypes interms of mineral lelements and phenolic contents would help in effective and efficient selection of candidate and desirable parental lines for the effective and efficient improvement of nutritional quality in okra in South Sfrica. Results of this study, therefore, will contribute to food and nutritional security in the counrty. Therefore, improving the genetic potential of indigenous vegetables like okra species is of paramount importance for nutritional quality, phytochemical and antioxidant properties.

Keywords: Mineral element, diversity, multivariate, variability

S20-P57:

CHOICE OF PARENTS AND USE OF DWARFISM GENE IN POPULATION OF INDUSTRIAL TOMATO

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warfism can model the plant architecture and be used for a compact and upright plant, which will help to minimize damage to harvesters and maximizing yield of processing tomato (*Solanum lycopersicum*). The objective was to select parents able to reduce processing tomato size, and generate a population where it is possible to make selection of promising plants. Four accesses of the Vegetable Genebank of Federal University of Viçosa have dwarf phenotype, and were used in a partial diallel cross with eight commercial hybrids of



processing tomato, that evaluated them and the F2 generation for the canopy diameter, total soluble solids of the fruits and yield per plant. The BGH-2006 (dwarf) and the hybrid H-9889 (Heinz) had the highest general combining ability values, which suggests that they can be used as parents to create a segregating population. Therefore, in order to increase a proportion of favorable genes in the population, a backcrossing was performed using the commercial hybrid as a recurrence, followed by self-fertilization of the BC1F1 plants, generating the dwarf individuals (homozygous recessive) in BC1F2 population, that were self-fertilized again, originating 150 BC1F2:3 families that were evaluated for canopy diameter and yield. The means of the canopy diameter was 82.0, 52.5 and 57.8 cm for the H-9889 and BGH2006 parents and the 150 F2 families, respectively, demonstrating that the families had average close to the dwarf-sized access. The yields average was 3.72 and 2.76 kg for the H-9889 and BGH2006, respectively. Ten families had higher means than the commercial hybrid, which is very interesting from the breeding point of view because it enables to continue the program using these promising materials. We can conclude that using the access we obtained good results and this dwarfing gene was helpful in overall increase in production with the reduction in the plant canopy.

Keywords: genetic resources, partial diallel, backcross, yield, *Solanum lycopersicum*, dwarf phenotype

S20-P58:

GENETIC DETERMINATION OF CROSS ABILITY, AS WELL AS INHERITANCE IN GENERATIVE HYBRIDIZATION

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At present, despite the methods of genetic engineering and bioengineering development, the main method of breeding new varieties of horticulture crops and in particular grapes is generative hybridization. For a long time, the main attention in the formation of scientific bases for breeding varieties was assigned to the establishment of genetically determined principles of inheritance of individual characteristics. Despite the fact that the researchers noted that in the case of generative hybridization with different crosses, the amount of seed that was formed, including full-fledged ones, and subsequently seedlings, differed, this was not emphasized, as on genetically determined signs. Analysis of the extensive experimental material accumulated in the "Magarach" Institute for crossing varieties and forms of grapes of various eco-geographical origins, related to various botanical taxons and various genealogies, allows us to conclude that not only inheritance but also cross ability are genetically determined signs. It has been established that the formation of seeds, including full-fledged ones, and seedlings depends on the biological specificity of the initial forms, in particular, the maturation period of the maternal form used in hybridization. There is no significant effect on the effectiveness of hybridization, to which species within the subgenus *Euvitis* are the initial forms. However, the cross ability of varieties of *Vitis vinifera* with varieties of *Vitis Labrusca* is better than that of *Vitis vinifera* with varieties of *Vitis amurensis*. When crossing varieties of *Vitis vinifera* with complex interspecies varieties, the hybridization efficiency is higher when complex interspecies varieties were used as the maternal initial form. A wide spectrum of hybrid populations was analyzed from the point of view of relations of the initial forms. It is established that with closely related crosses, a smaller number of full-fledged seeds and seedlings are formed, which is determined by the viability of the emerging embryo.

Keywords: plant breeding, generative hybridization, embryo, seed, seedling, grapes

S20-P59:

IDENTIFICATION OF CANDIDATE GENES ASSOCIATED WITH SOLUBLE SOLIDS CONTENT USING WHOLE GENOME SEQUENCING AND RNA-SEQ ANALYSIS IN *Prunus persica*

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Prunus persica is one of the most important fruit crops in the world considering production and cultivated area. For this reason, the Chilean peach exporter industry carry out several peach breeding programs to develop new varieties to satisfy the consumer's needs. The soluble solids content (SSC) is one of the most important fruit quality traits for the consumer, and this character determine the fruit sweetness. We constructed a genetic linkage map using a genotyping by sequencing strategy and we performed a QTL analysis with the phenotypic data of three evaluation seasons from F1 population (n=182). A saturated linkage map with 498 markers and a marker density of 1.4 cM/marker was built and one consistent QTL of 5Mbp was identified on the chromosome 5 of the peach genome. Using a whole genome sequencing of contrasting siblings for this trait, we identified 7,301 genetic variations on the QTL region. We performed an RNA-Seq analysis to determine the differential expression of the genes between contrasting siblings for SSC, and we identified 239 DEG on detected QTL for this trait. Finally, 17 genes are postulated as SSC master regulators using the combination among genetic (QTL analysis), genomic (DNA-Seq) and transcriptomic (RNA-Seq) approaches. As second step, it is necessary to validate these candidate genes in other peach populations and commercial cultivars. This work was supported by Genoma 4 G13i1005, FONDECYT 1160584, Consorcio Biofrutales 13CTI-21520-SP03 and 13CTI-21520-SP04.

Keywords: Peach, SSC, QTL, RNA-seq

S20-P60:

INFLUENCE OF CLIMATIC CONDITIONS OF CRIMEAN SOUTHERN COAST ON YIELD CAPACITY OF INTRODUCED PEACH CULTIVARS 'AMBERGOLD' AND 'GOLDEN'

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In Russian Federation the peach is cultivated intensively in Southern regions, where it is the most important industrial stone fruit. In Crimea it covers an area of 2.6 thousand ha, which amounts to 56.0% of the total area of stone fruit crops. Peach yield capacity depends not only on specific cultivar traits, but also on soil and climatic cultivation conditions. Global climate change caused decrease and deterioration in the state of fruit plants. The purpose of researches was to study the influence of climatic environmental factors on the formation of yield capacity in different peach cultivars. The research has been conducted in 2015 - 2017 under conditions of the Crimean Southern Coast by using collection plantings of Nikita Botanical Gardens. Meteorological data during the periods of peach blossom, infestation with leaf curl and powdery mildew over a wide time span from 1990 to 2017, were collected and analyzed. Correlation analysis showed a sound negative correlation between the yield capacity of the cultivar Golden and the degree of its infestation with powdery mildew ($r = -0.53$), i.e. the higher the intensity of fungus disease manifestation the lower the yield. The cultivar 'Golden' displays a positive correlation of the yield capacity on the maximum air temperature during the blossom ($r = 0.56$). In both cultivars, 'Ambergold' and 'Golden', was detected a positive tendency of influence of flower buds setting ($r = 0.30$ и $r = 0.25$ respectively) as well as of the massive blossom date ($r = 0.32$ и $r = 0.37$ respectively) on the yield capacity. The cultivar 'Golden' demonstrated a negative correlation between the yield capacity and the relative humidity during the blossom ($r = -0.48$), the precipitation value during the blossom ($r = -0.35$), the average daily air temperature in July ($r = -0.33$) as well as the maximum air temperature in July ($r = -0.41$).

Keywords: peach, hybridological analysis, inheritance, quantitative fruits traits, donors of traits, ecogeographical groups, ecotypes

S20-P61:

OBSERVATION ON FERTILITY OF ALLOTETRAPLOID FROM *Citrus Grandis* 'Shatianyou' × *Citrus Ichangensis*

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Tetraploids could be used for the parents of seedless triploid citrus. For the study of fertility of allotetraploid hybrid of *C. grandis* 'Shatianyou' × *C. ichangensis*, the floral organs, meiotic chromosome behavior of PMCs (Pollen Mother Cells), pollen viability and seed number were observed. The results showed that the floral organs were no exception, only the diameter of flower bud of the allotetraploid was greater than parents, and the pollen viability and amount of the allotetraploid were lower than its parents. So pollens of the allotetraploid had some fertility, but lower than its parents. Compared with corresponding allodiploid, the pollen fertility of allotetraploid was partially restored. PMCs meiosis of *Citrus grandis* 'Shatianyou' and *Citrus ichangensis* were normal. However, abnormal rate of PMCs meiosis from the allotetraploid hybrid was about 30 percent, and there were many multivalent (about 40 percent) in metaphase. The laggard chromosomes, unequal separating of chromosomes, bridge of chromosomes and micronucleus were observed in anaphase and telophase. GISH (Genomic in situ hybridization) analysis revealed that the number of chromosomes of *Citrus ichangensis* divided into sub cells was different in the allotetraploid. The seeds of allotetraploid, allodiploid hybrid and their parents were monoembryo, the number of aborted seeds of the allodiploid was significantly higher than that of the allotetraploid and their parents. Therefore, the allotetraploid hybrid had certain fertility, but it just had lower fertility than their parents. The fertility of allotetraploid was partially restored after chromosome doubling. The phenomenon of abnormal meiotic chromosome behavior may lead to pollen abortion and seed abortion.

Keywords: *Citrus grandis* 'Shatianyou'; *Citrus ichangensis*; Allotetraploid; Pollen fertility, Meiosis; Genomic in situ hybridization (GISH)

S20-P62:

A NEW EARLY-MIDDLE PEACH CULTIVAR PODAROK LIKE

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'Podarok Like' is a new peach cultivar, which originated from a cross between 'Redhaven' and 'Sochny' by Z.N. Perfilieva, V.K. Smykov, A.V. Smykov, O.F. Fedorova, T.A. Lacko at the "Nikita Botanical Gardens – National Scientific Centre RAS" (NBG-NSC). The seeds from controlled cross were stratified and grown in the field nursery. The trees were established at a spacing of 3 m × 5 m and trained as open vase. Seven grafted trees were evaluated for tree and fruit characteristics. The evaluation of this cultivar was done in the comparison with the control cultivars 'Redhaven' and 'Golden Jubilee' peaches. Tree vigor, bloom, maturity date and fruit size were monitored annually. Trees are moderately vigorous and the growth habit of the trees is semi-upright. It has showy flowers and blooms in mid-April at Yalta, the Crimea Republic. Fruits ripen in late July. This is a self-fertility cultivar. The average fruit weight is 130 g, the maximum – 180 g. Fruit are attractively colored with a dark-red blush that covers more than 50-100% of the skin surface. Flesh is yellow and firmness, soft-melting type. Fruit intended for the fresh fruit market. This cultivar showed middle susceptibility to powdery mildew (*Sphaerotheca pannosa* (Lév.) Woronich) than 'Radhaven' and 'Golden Jubilee'. A plant patent was filed for 'Podarok Like' nursery production in Russian Federation in 2015. Acknowledgements: This study was funded by a research grant № 14-50-00079 of the Russian Science Foundation.

Keywords: peach, new cultivar, cross, early-season, fruit

S20-P63:

INNOVATION RESEARCH ON GERMPLASM RESOURCES OF WATERMELON WITH RESISTANCE TO FUSARIUM WILT

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Watermelon Fusarium wilt disease caused by *Fusarium oxysporum* f. sp. *niveum* is a destructive soil-borne disease in watermelon production. Breeding for resistance is the most advocated strategy to circumvent this disease. Marker assisted backcross breeding was employed to incorporate the *Fusarium oxysporum* f. sp. *niveum* race 1 resistance gene *Fon-1* from donor parents 'Calhoun Gray', 'F211' and 'BW85' into nine cultivated



susceptible watermelon varieties (No.1 to No.9) used as recurrent parents. The molecular markers tightly linked to gene Fon-1, CAPS marker 7716_fon was published in 2013 by Beijing Vegetable Research Centre and Indel marker InDel1_fon1 was published in 2017 by Zhengzhou Fruit Research Institute. The markers are co-dominant marker, which can be used for the distinguishing of homozygous and heterozygous genotypes, can be used as an important tool for the molecular marker assisted selection of watermelon with resistance to wilt. Each backcross generation foreground selection was carried out by the molecular marker detection, and screening in natural disease nursery (population levels of *Fusarium* in soil samples were 2.52×10^4 CFU·g⁻¹ of soil). BC4F2 plants homozygous for the target gene were planted in natural disease nursery, eight lines were expressed as highly resistance with the diseased plant rate under 20 %, in which six lines without disease. Further, selected plants will advance till BC4F3 generation and best families with resistance to *Fusarium* wilt from each of the combinations will be identified.

Keywords: watermelon, *Fusarium* wilt, breeding for disease resistance, molecular marker assisted selection

S20-P64:

SCREENING OF LOW CADMIUM ACCUMULATION WATERMELON CULTIVARS

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To assess the security of watermelon cultivation in Cd contaminated soil effectively and efficiently, the variation of Cd content in 58 watermelon genotype materials and the effect of Cd concentration in Cd contaminated farmland soil on Cd content in watermelons were investigated through field experiments and long season cultivation experiment. In the hope to screening out Cd-pollution-safe watermelon cultivars. It was found that the content of Cd in watermelon fruit which grow in the soil Cd content below 0.973 mg·kg⁻¹ is lower than the current national standard GB 2762-2012, the Hei Meiniang is the lowest. The Cd content in watermelon fruit long season cultivation with the increase of recovery batches showed a trend of increase, the last of the Cd content in fruit of 25 μg·kg⁻¹. So watermelon production in moderate Cd pollution area is safe, recommended in planting low accumulation of watermelon varieties as Hei mei niang, Chao ji jing xin, Jin xin and Jin Fu.

Keywords: watermelon; cadmium; accumulated

S20-P65:

DEVELOPMENT OF BLACK ROT RESISTANT *B. oleracea* PLANTS POSSESSING RESISTANCE GENES FROM *B. carinata* AND *B. rapa* Genomes

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Black rot caused by *Xanthomonas campestris* pv. *campestris* (Pammel) Dowson (Xcc) is one of the most devastating diseases of Brassica vegetable crops worldwide. To date 9 races of Xcc pathogen are known and races 1 and 4 are predominating worldwide. There are a few known black rot resistance locus donors genotypes in *B. rapa*, *B. carinata*, *B. juncea*. The aim of the present study is the development of *B. oleracea* plants with introgressed R1 and R4 genes from A and B genomes. Reciprocal crosses between *B. oleracea* inbred lines (diploid Et2, Agr and tetraploid Bu) and Xcc resistance donor accessions *B. rapa* (JR, CC), *B. carinata* (Pi9) have been made using ovules culture. Four interspecific hybrids *B. oleracea*-*rapa* (Arg×JR), *B. oleracea*-*rapa* (Et2×CC), *B. oleracea*-*carinata* (Bu×Pi9) and *B. carinata*-*oleracea* (Pi9×Bu) have been produced. Interspecific hybrids had an intermediate morphology exhibiting black rot resistance similar to donor plants - hybrid Agr×JR was resistant to Xcc race 4, Et2×CC, Bu×Pi9 and Pi9×Bu to races 1, 3 and 4. Following backcrossing of this hybrids to *B. oleracea* and selection of resistant progenies will allow to develop black rot resistant *B. oleracea* and assess the inheritance mode of resistance in C genome.

Keywords: Interspecific hybridization, *B. rapa*, *B. carinata*, *B. oleracea*, resistance, black rot, *X. campestris*, race



S20-P66:

THE NEW GARLIC (*Allium sativum* for. *Pekinense* Kino) VARIETY 'DANYOUNG' WITH LARGE BULBLETS IMPROVED BY CHEMICAL MUTAGEN OF SODIUM AZIDE

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It is very difficult to improve garlic variety with large bulblets to replace seed of the cloves. This study was conducted to improve new garlic variety with good characteristics such as large bulblets, adaptability in southern area of South Korea and etc. The mutagen (soaking 10% sodium azide for 24hrs) was treated to cloves of local cultivar 'Goheung' and these cloves were sowed in upland after washing in 2002. The mutated plants were selected in 2003 and the populations of mutation were evaluated for their main characteristics from 2003 to 2009. The high quality line ('Jeonnam #26') was selected in 2010 and its production performance test was conducted between 2012 and 2014. This line was renamed as 'Danyoung' and registered to the Korea Seed & Variety Service in 2016. The new garlic variety 'Danyoung' has large bulblets, incomplete bolting property, shorter height, thicker leaf-sheath and good adaptability compared with control 'Namdo' in southern area in South Korea. A number of bulblets of 'Danyoung' are 10 per plant and the mean weight of bulblet is 0.7g. We harvested 1.1ton/ha from the large bulblets (0.5~1.0g) cultivation of 'Danyoung'. As a result of this experiment, the large bulblets of 'Danyoung' that is over 0.5g can be used as the same as its cloves for reproduction.

Keywords: garlic, variety, bulblet, reproduction

S20-P67:

STRATEGIES IN PEPPER (*Capsicum annuum* L.) HYBRID BREEDING

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The production of doubled haploid plants has become a key tool in advanced plant breeding. Plant breeders are increasingly using this system in their mainstream pure-line programs to reduce the number of years needed from crosses to commercial variety registration. In laboratory of Medimat Ltd. over the past fifteen years have been tested more than 3600 different genotypes originating from Hungarian sweet pepper types (Cecei, tomato-shaped, apple-shaped, white blocky, light green and dark green blocky, green spice), Hungarian spice pepper genotypes, Dutch blocky types, Spanish types (Dolce Italiano, Lamuyo, red blocky) and Turkish types (e.g. Dolma, Charleston) and produced new homozygote breeding lines using in vitro anther culture. When haploid method has been combined with marker-based pre-selection it provided an exceptionally efficient method for paprika resistance breeding (TMV, TSWV, powdery mildew, Xanthomonas, nematodes). Integrated haploid technology is provided an attractive solution for production huge amount of pure-lines and new hybrid paprika candidates for registration. In the past years we continually improved haploid method including isolated microspore culture to increase the production of homozygote lines (DHs).

Keywords: pepper breeding, doubled haploids, anther culture, microspore culture

S20-P68:

OVERVIEW AND PERSPECTIVES OF USDA BYRON PEACH BREEDING PROGRAM

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Conventional breeding has been a widely used and successful approach in many crop improvement programs. Success to develop new cultivars depends on optimal combination of parents to produce sufficient hybrids, and



comprehensive evaluation of the hybrids and superior selections inheriting desired traits. Established in 1937 and succeeded by several breeders, the USDA peach breeding program has released several dozens of cultivars for the Southeastern peach industry in the US. An overview was given to summarize peach releases, selection trends, and breeding perspectives in this program. Based on the accumulated evaluation data, a normal distribution was observed for fruit size and ripening date. Other traits, including fruit set, external blush, attractiveness, firmness, freeness, shape, pubescence, and overall eating quality, showed an uneven distribution toward the desired directions, which was expected since data was rarely taken on discarded hybrids. The median value of fruit set was 7 and the average 6.59 in a scale of 0-9, suggesting this trait had been maintained in a majority of selections. Blush and attractiveness showed a similar distribution where 7 was the median for both and 6.81 and 6.95 were the averages respectively on a 0-9 scale, indicating the selection tendencies were toward a higher blush coverage but with some classic yellow background to indicate the ripening stage. Statistical correlations were also found between some of the evaluated fruit traits.

Keywords: *Prunus persica*, sexual hybridization, inheritability

S20-P69:

BREEDING STRATEGIES TO IMPROVE MALAYSIAN PAPAYAS

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Papaya (*Carica papaya*) breeding at Malaysian Agricultural Research and Development Institute (MARDI) involved various breeding strategies. The strategies have been changed concurrent with the changing of the consumer demands and the industrial needs. It was started with papaya mass selection program in 1972-1975, followed by backcross breeding in 1972-1987, development of F1 hybrid in 1985-1991, and breeding for papaya ring spot virus (PRSV) in 1991-2005. Since 2001, emphasis was given for long shelf life by double cross technique and resistant against papaya dieback disease (PDD). PDD outbreak was first recorded in 2003 caused by the notorious pathogen (*Erwinia mallotivora*) and still remains as the main constraint in papaya industry. Three intensive research phases have been implemented to overcome PDD. The first phase was increased the gene-pool to obtain resistant gene, followed by glass house and hot spot screening, then finally conducting the proper breeding program. About 495 accessions from indigenous and non-indigenous were collected and screened. Among them, Viorica was found to be highly tolerant against PDD and have been used as a donor in the breeding program to improve Malaysian papaya varieties. The F1 hybrid between Viorica and Eksotika has combined desirable traits i.e. tolerant against PDD together with good yield and fruit quality. At hot spot, the disease severity level (DSL) of the 15-month-old F1 (Viorica X Eksotika) was much lower (DSL = 0.7) compared to Eksotika (DSL = 3.6). The yield of F1 hybrid was 32 kg plant⁻¹ year⁻¹ compared to Eksotika, 30 kg plant⁻¹ year⁻¹. The fruit weight of F1 hybrid was higher (980 g fruit⁻¹) compared to Eksotika (670 g fruit⁻¹). The total soluble solids content (TSS %) of F1 hybrid and Eksotika were 11.2% and 11.6% respectively.

Keywords: *Carica papaya*, breeding, hybrid, resistance, *Erwinia mallotivora*, papaya dieback disease

S20-P70:

DIFFERENT PUMPKIN ROOTSTOCKS ON THE GROWTH AND FRUIT QUALITY OF WATERMELON

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Watermelon (*Citrullus lanatus*) is one of the most popular fruit vegetable crops in the world. However, with the expansion of cultivated area, soil borne disease expands and threatens the production of watermelon. Grafting is an useful and efficient technique to solve this problem. For the production of grafted watermelon transplants, pumpkin is one of the most important rootstock, the species of *Cucurbita moschata*, *Cucurbita maxima* and their



intraspecific hybrids are the main rootstocks source of pumpkin. Here a total of 19 pumpkin inbred lines, including 9 lines from *Cucurbita moschata*, 7 lines from *Cucurbita maxima* and 3 hybrids lines, including two hybrids of *C. moschata* × *C. moschata*, one from *C. maxima* × *C. moschata* were selected as the rootstock of watermelon 'Zaojia 8424, and the commercial rootstock 'Qinyan1' and 'Jingxinzheng4' were used as control rootstocks. Through evaluation of survival percentage after grafting and in the field, analysis of plant growth, fruit weight and fruit quality, we selected 8 lines from *Cucurbita moschata*, and 2 lines from *Cucurbita maxima* as parents of hybridization combination, and then we constructed 47 hybrids by using these parents, including 36 *C. moschata* × *C. moschata* and 11 *C. maxima* × *C. moschata* interspecific combinations. The effects of seedling traits, grafting compatibility, and their effects on the growth, fruit quality and yield of watermelon were evaluated comprehensively. Finally we selected 4 hybrids, which can be used as rootstock for watermelon in future.

Keywords: watermelon, grafting, pumpkin, rootstock, fruit quality

S20-P71:

OPPORTUNITIES FOR DEVELOPMENT OF IMPROVED VEGETABLE VARIETIES AND HYBRIDS IN CENTRAL ASIA AND THE CAUCASUS

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In addition to providing the nutrients needed for healthier diets, vegetables offer producers in Central Asia and the Caucasus numerous opportunities for income generation. Demand for vegetables is on the rise as the region's population grows and agriculture diversifies into new crops and production methods. More than 40 vegetable crops encompassing global vegetables such as tomato and peppers and traditional species such a melon are grown throughout the region. The need for a diversity of vegetable genetic resources to improve these crops is increasing as climates change and demand expands. The World Vegetable Center's (WorldVeg) genebank collection, with more than 60,000 accessions of 440 species, and the advanced breeding lines developed by WorldVeg breeders are outstanding resources for variety improvement. Over the last decade, more than 65 improved varieties of 15 vegetable species have been developed and released across the region through WorldVeg collaboration with national agricultural research and extension agencies participating in the Central Asia and the Caucasus Regional Network for Vegetable Systems Research and Development (CACVEG). Some vegetables newly introduced into the region through the network include vegetable soybean, yard-long bean, asparagus, Chinese leafy cabbage, and cherry tomato. There is potential to tap the genebank for the genetic resources to breed for market-oriented variety improvement and to develop new salt-, drought-, and heat-tolerant hybrids.

Keywords: vegetable genetic resources, varieties, breeding

S20-P72:

DEVELOPING KIWIFRUIT (*Actinidia* spp.) PROTOPLAST CULTURE AS A VERSATILE CELL SYSTEM FOR CROP IMPROVEMENT

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Kiwifruit and kiwiberry (*Actinidia* spp.) are recently domesticated horticultural crops with a short history of breeding and a vast potential for genetic improvement. Current kiwifruit cultivars have been developed using traditional breeding techniques, with emerging biotechnologies increasingly being used to assist breeders in the development of novel cultivars. Protoplast culture provides single cells that can be used for genetic manipulation, somatic hybridization, gene transformation and genome editing and subsequently regenerated into whole plants. Callus of two kiwifruit species, *Actinidia chinensis* and *A. melanandra* was induced from in vitro cultures of young leaves and stem nodal sections. These calli appeared friable with creamy white surfaces, and



showed vigorous and rapid growth under dark conditions. Calli were used to establish cell suspension cultures which when transferred to hormone-free solid medium in dark conditions, developed somatic embryos in 4–5 weeks. Embryogenic calli generated from cell suspension culture were used for protoplast isolation and protoplast culture. The influence on protoplast yield, viability and plating efficiency of various factors including enzyme composition, digestion time and osmoticum used in the medium will be presented. Regeneration of these cells into plants may allow the use of CRISPR/Cas9 RNPs (ribonucleoproteins) DNA-free editing tools.

Keywords: Kiwifruit, protoplast culture

S20-P73:

COMPUTATIONAL POLYMORPHIC MICROSATELLITES AMONG PRUNUS NUCLEAR EXPRESSED SEQUENCE TAGS AND CHLOROPLAST GENOMES FOR PEACH GENOTYPING

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Mass sequences are deposited to databases but many are exploited insufficiently and worth further utilization. In this study available expressed sequence tags (EST) and chloroplast genomes from *Prunus* species were exploited to develop in silico polymorphic nuclear and chloroplast microsatellites, which are very useful in maternal lineage and phylogenetic analysis among *Prunus* materials. A computational mining process yielded 319 haplotype-based polymorphic microsatellites among EST from main *Prunus* species, including peach (*P. persica*), apricot (*P. armeniaca*), sweet cherry (*P. avium*), Japanese apricot (*P. mume*), almond (*P. dulcis*), and European plum (*P. domestica*), and 67 polymorphic chloroplast microsatellites among peach, Japanese apricot, and Gansu peach (*P. kansuensis*) chloroplast genomes. In comparison between the genotyping data of selected haplotype-based polymorphic and monomorphic microsatellites, the mean allele number, heterozygosity, polymorphic information content, and gene diversity value were all significantly higher in the haplotype-based polymorphic microsatellites than in the haplotype-based monomorphic microsatellites, suggesting utilization of haplotype-based polymorphic markers could substantially increase the likelihood of allele polymorphism. Based on the genotyping results of the selected chloroplast microsatellites, peach materials are categorized into eight unique maternal lineages.

Keywords: *Prunus persica*, genotyping variability, polymorphic information content, maternal pedigree

S20-P74:

BREEDING FOR SEEDLESS KINNOW MANDARIN IN PAKISTAN

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Kinnow mandarin is the major stay of Pakistan's citrus industry. It has good size, taste and color but has seeds, late maturity and alternate bearing. Kinnow is the major exportable citrus fruit but fetch low price in the international market because of high number of seeds per fruit. Keeping in view the issue, various institutes in Pakistan started work on Kinnow breeding for seedlessness. First attempt was made through irradiation of budwood which resulted in low seed Kinnow strains but had a problem of rind browsing at styler end of the fruit. Interploidal hybridization resulted in embryo abortion where diploids were treated as female parent. In vitro embryo rescue technique resulted in establishing several seedlings, which are present in progeny orchard. A vigorous survey for selection of natural mutants/bud sports was initiated in major Kinnow cultivated area and three strains were selected as low seeded Kinnow. Out of these one is released as seedless Kinnow cultivar. The seed content is 0-4 as compared to 20-30 per fruit. The seedless fruit is comparable in size, rind thickness, color, TSS and acidity with its seedy counterpart. The seedless Kinnow nursery plants have high demand and alternatively the growers are top working of existing seedy Kinnow orchards with seedless Kinnow budwood.

Keywords: Citrus, breeding, seed content, embryo rescue, TSS, bud mutation



S20-P75:

MULTIVARIATE STATISTICAL OF SEED TRAITS IN *Iris germanica*

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Iris germanica L. is one of the most important rhizomatous and it is a native plant to Iran. This study aims to produce new hybrids of German Iris through hybridization as well as determination of its new characterization. The characteristics of the capsules length, capsule width, the number of seeds per capsule, the number of days from the cross to harvest, seed weight, the weight of wet grain and weight of dry grain were evaluated. Statistical analysis included descriptive statistics, simple correlation coefficients to estimate of cluster analysis and varimax analysis. According to the analysis descriptive statistics the highest and lowest correlation coefficient were related to characteristics of hundred wet grain weight per unit harvest from the cross capsule respectively. High differences in progenies for all studied traits showed for all wide variety of characteristic in result. Correlation coefficient between the different result show that the most positive and significant correlation related to hundred wet grain weight with hundred dry grain ($r=+0.59$) and the lowest correlation was between the length of capsule with the number of days from the cross until harvest of capsule. The factor analysis showed that the results of four main factors were justified 77.04 % changes total data. The progenies were placed in four groups based on cluster analysis using ward method and G6 and G33 progenies with distinct traits were smallest subgroup. This research provides new finding to produce new business varieties in Iran.

Keywords: Genetic diversity, Iris, correlation coefficient, cluster analysis

S20-P76:

EVALUATION PROGENY OF CROSSES AMONG DIFFERENT CULTIVARS OF GLADIOLUS IN THE ONE GROWING PHASE

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Three cultivars in Amsterdam, White prosperity, Advance red and Rose supreme were chosen for hybridization. In a total of Progenies were evaluated in a randomized complete block design with three replications. The Research was conducted in Ornamental Plants Research Center (OPRC) in Mahallat from 2015 to 2016. Quantitative traits included leaf length, leaf width, stem diameter, number of leaf, days to germination, weight and diameter corolla were superior progenies compared to other corolla. The Statistical analysis was performed with SAS and Excel. In this Study statistical parameters such as coefficients of correlation, mean, standard deviation, coefficient of variability, principal component analysis and cluster analysis were estimated. Analysis of variance among progeny (hybrids) showed that the progeny has significant differences ($P \leq 0.01$) in all traits were conducted, that indicate the wide variation in progenies observed for all traits. NIOP9 progeny in leaf length, leaf width, stem diameter, number of leaf, days to germination, weight and diameter corolla was superior progenies compared to other corolla, also progeny NIOP4 with 2.49 per in a seed was superior to produce corolla. Correlation coefficients among the different progeny shows that the most positive and significant correlation between the number of leaves and crown diameter ($r=+0.93$) and the correlation between the number of days to germination and number corolla were lowest level ($r= -0.17$), respectively. The highest coefficient of phenotypic variation was obtained in the number of corolla to rate 57.17% and the lowest number of days to germination 11.15%. The highest heritability in traits was estimated 98.46 in the number of corolla and corolla diameter and the lowest for crown diameter to 12.90%. This research provides a new horizon of produce the new commercial varieties in the country.

Keywords: diversity, hybridization, hybrid



S20-P77:

ANTIOXIDANT AND SUGAR PROFILE OF 75 ACCESSIONS FROM THE APPLE GERMPLASM COLLECTION OF THE EXPERIMENTAL STATION OF AULA DEI-CSIC

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Apple (*Malus x domestica* Borkh) is one of the most consumed fruit in the world. The antioxidant compounds, known for their health benefits, are increasingly studied in the horticultural products. Consequently, a phenotypic evaluation based on pomological and fruit quality traits evaluation was carried out in this study. Seventy-five apple accessions were evaluated. Among them, 51 were native Spanish accessions and 24 were foreign. According to fruit type, 52 accessions were classified as red/bicolor, 16 green, 5 yellow and 2 brown, with brown corresponding to completely recovered of russetting. All cultivars were selected from the apple germplasm collection of the 'Experimental Station of Aula Dei' (CSIC) located in the Ebro Valley (northern Spain, Zaragoza), and grown under a Mediterranean climate. During two consecutive years (2015 and 2016), fruit quality traits, such as skin color, soluble solids content (SSC) and individual soluble sugars, titratable acidity (TA), ripening index (RI), as well as antioxidant compounds such as total phenols content, flavonoids, vitamin C and relative antioxidant capacity (RAC), were evaluated. The statistical analysis (ANOVA) showed significant differences ($p \leq 0.05$) among accessions for all traits evaluated and according to the different characteristics above mentioned. A significant year effect was also observed. In addition, significant and positive correlations between RAC and total phenols content ($r=0.69$), RAC and flavonoids ($r=0.46$), RAC and vitamin C ($r=0.33$) and total phenol content and flavonoids ($r=0.38$) were found. Significant and positive correlation between titratable acidity (TA) and flavonoids compounds was also found ($r=0.51$). Among the accessions studied, 'Bossost-2', 'Camuesa Fina de Aragón', 'Mañaga' and 'Transparente' could be highlighted. They showed the highest antioxidant compound values. This work shows the importance and the interest of using local accessions in future breeding programs. Indeed, the variability found in fruit quality and antioxidants could be used as a phenotypic source of valuable traits in further apple breeding programs.

Keywords: *Malus x domestica*, bioactive compounds, phenols, flavonoids, fructose, glucose, saccharose, breeding programs

