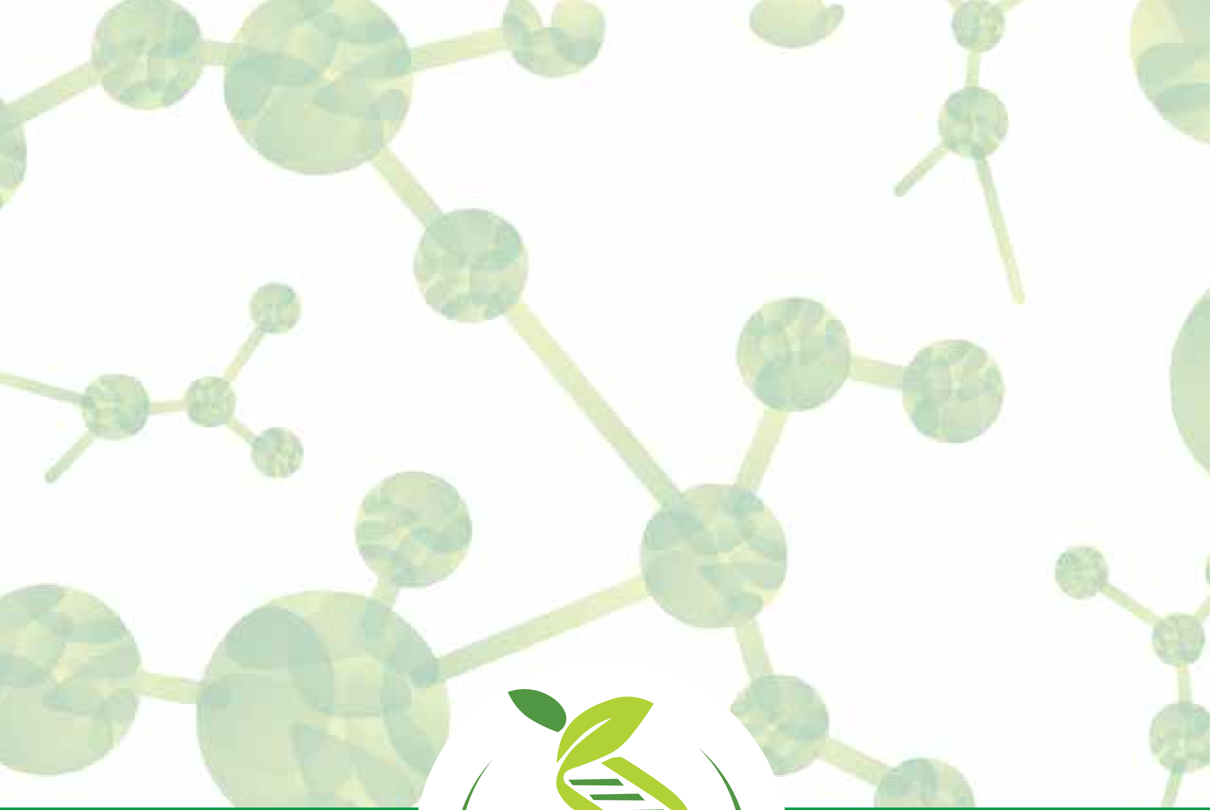

# ABSTRACT BOOK

# II. INTERNATIONAL PLANT BREEDING CONGRESS
# AND
# EUCARPIA – OIL AND PROTEIN CROPS SECTION CONFERENCE

**1-5 NOVEMBER 2015**
**WOW Kremlin Palace Hotel, Antalya, TURKEY**
www.intpbc2015.org

# ABSTRACT BOOK
# II. INTERNATIONAL PLANT BREEDING CONGRESS
# AND
# EUCARPIA – OIL AND PROTEIN CROPS SECTION CONFERENCE

**Edited By**

**Prof. Bülent UZUN[1]**

**Assoc. Prof. Yalçın KAYA[2]**

**Dr. Vehbi ESER[3]**

**Prof. S. Ahmet BAĞCI[4]**

1. Akdeniz University, Turkey
2. Trakya University, Turkey
3. Plant Breeders Union of Turkey
4. Selçuk University, Turkey

**1-5 NOVEMBER 2015**
**ANTALYA, TURKEY**

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| International Center for Agricultural Research in the Dry Areas (ICARDA) |
| European Association for Research on Plant Breeding (EUCARPIA) |
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| Zhang, Xiurong | Oil Crops Research Institute | China |

## INVITED SPEAKERS

| SPEAKERS | INSTITUTION | SUBJECT |
|---|---|---|
| Evgeny Zuev | N.I. Vavilov Institute of Plant Genetic Resources (VIR) | Genetic Resources |
| Hans Braun | CIMMYT | Wheat Breeding |
| Hisashi Tsujimoto | Arid Land Research Center | Chromosome Engineering |
| Javier Betran | SYNGENTA | Artesian Approach in Maize Breeding |
| Nebahat Sarı | Cukurova University | Watermelon Breeding |
| Peter Hanson | AVRDC | Tomato Breeding |
| Richard Visser | Wageningen University | Tomato Breeding |
| Rishi K. Behl | CCS Haryana Agricultural University | Abiotic Stresses |
| Vehbi Eser | BISAB | Genetic Resources |
| Wybe Van Der Schaar | RIJK ZWAAN | Cucumber Breeding |
| Zetian Hua | China National Rice R&D Center | Hybrid Rice Breeding |

# GENERAL SESSION

| SUNDAY, NOVEMBER 1th, 2015 | |
|---|---|
| 14:00 - 18:30 | Registration |
| 17:00 - 18:30 | Welcome Cocktail |
| 14:00 - 18:30 | Side Events and Stands |

| MONDAY, NOVEMBER 2nd 2015 | |
|---|---|
| 08:00 - 09:00 | Registration |
| 09:00 - 10:15 | Opening Ceremony |
| 10:15 - 10:45 | Coffee break |
| 10:45 - 12:30 | **OPENING SESSION:**<br>Session Chair: ASSOC PROF DR MASUM BURAK GDARP - Food, Agriculture and Livestock of Turkey |
| 10:45 - 11:15 | Invited Speaker *Dr. Hans J. BRAUN* and *Dr. Alexey MORGUNOV* "Plant Breeding for Future" |
| 11:15 - 11:45 | Invited Speaker *Dr. Peter HANSON* "Practical Plant Breeding" |
| 11:45 - 12:15 | Invited Speaker *Dr. Vehbi ESER* "Genetic Resources for Plant Breeding" |
| 12:15 - 12:30 | DISCUSSION |
| 12:30 - 13:30 | LUNCH |

# IPBC-I ( Meeting Room)

| 2.11.2015 MONDAY | |
|---|---|
| 13:30 - 15:30 | **1st Session Chair: PROF. DR. S. AHMET BAGCI** |
| 13:30 - 13:45 | Invited Speaker<br>*ZETIAN HUA*<br>HYBRID RICE BREEDING |
| 13:45 - 14:00 | |
| 14:00 - 14:15 | GENOME-WIDE ASSOCIATION MAPPING USING A BAYESIAN MIXTURE MODEL FOR PLANT HEIGHT IN *ORYZA SATIVA - B. KARACAÖREN* |
| 14:15 - 14:30 | RICE BREEDING AND SEED PRODUCTION STUDIES IN EUROPE – *N. BEŞER* |
| 14:30 - 14:45 | ESTIMATION OF SPECIFIC COMBINING ABILITY (SCA), GENE ACTION AND PER-SE PERFORMANCES IN SOME MORPHO REPRODUCTIVE TRAITS OF RICE (*ORYZA SATIVA* L.) - *M. D. ARIFUL ISLAM, , M. A. KHALEQUE MIAN, GOLAM RASUL, Q. A. KHALIQ F.T JOHORA* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **2nd Session Chair: ASST. PROF. DR. NECMI BESER** |
| 15:30 - 15:45 | DEVELOPMENT OF BLAST RESISTANT RICE VARIETY THROUGH MARKER ASSISTED BACKCROSS BREEDING - *MOHD Y. RAFII, FATAH A. TANWEER, HARUN A. RAHIM* |
| 15:45 - 16:00 | CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS OF SOFT RICES (*ORYZA SATIVA* L.) – *S. KOTA* |
| 16:00 - 16:15 | YIELD PERFORMANCES OF SOME RICE VARIETIES ACCORDING TO LAND SUITABILITY CLASSES– *M. ŞAHIN* |
| 16:15 - 16:30 | ARTIFICIAL MUTAGENESIS AS A VALUABLE TOOL FOR FUNCTIONAL GENOMICS AND MOLECULAR BREEDING TOWARDS HIGH SALINITY AND DROUGHT TOLERANCE IN RICE – *S. JIANG, S. RAMACHANDRAN* |
| 16:30 - 16:45 | THE RESULTS OF RUSSIAN RICE BREEDING ACHIEVED WITH THE USE OF MAS - *ZH. MUKHINA, I.I. SUPRUN, E.V. DUBINA, S.V. TOKMAKOV, S.A. VOLKOVA, E.G. SAVENKO, V.A. GLAZYRINA, L.A. SHUNDRINA, V.S. KOVALYOV, S.V. GARKUSHA* |
| 16:45 - 17:15 | Discussion |
| 17:00 - 17:30 | Poster Session 1 |
| 17:30 - 18:00 | Poster Session 2 |
| 18:00 - 18:30 | Poster Session 3 |
| 08:30 - 18:30 | Side Events and Stands |
| 19:00 - | Dinner |

## 3.11.2015 TUESDAY

| | |
|---|---|
| 09:00 - 10:30 | **3rd Session Chair: DR. ALİ OSMAN SARI** |
| 09:00 - 09:15 | Invited Speaker<br>*DR. JAVIER BETRAN*<br>“DEVELOPMENT AND LAUNCH ARTESIAN MAIZE HYBRIDS” |
| 09:15 - 09:30 | |
| 09:30 - 09:45 | MAIZE CYTOPLASMIC MALE STERILITY AND RESTORER OF FERTILITY-ASSOCIATED LOCI ANALYSIS - *SLISCHUK G., VOLKOVA N., SOKOLOV V.* |
| 09:45 - 10:00 | ISSR ANALYSIS OF HYBRID MAIZE GENETIC RESOURCES IN A VARIETY DEVELOPMENT PROGRAM FOR CENTRAL ANATOLIAN CONDITIONS - *F. AKIN* |
| 10:00 - 10:15 | SNP-ANALYSIS APPLICATION IN CORN BREEDING IN UKRAINE - *V. BORISOVA, TATIANA N. SATAROVA, VLADYSLAV YU. CHERCHEL, BORYS V. DZIUBETSKYI* |
| 10:15 - 10:30 | Discussion |
| 10:30 - 11:00 | Coffee break |
| 11:00 - 12:30 | **4th Session Chair: DR. JAVIER BETRAN** |
| 11:00 - 11:15 | COMPARATIVE NUTRITIONAL ANALYSIS OF BARLEY GENOTYPES - *A. VASAN, M. MANI, R. K. BEHL* |
| 11:15 - 11:30 | VARIABILITY FOR AGRO-MORPHOLOGICAL TRAITS OF MAIZE (*ZEA MAYS* L.) INBRED LINES DIFFERING IN DROUGHT TOLERANCE – *I. ANDJELKOVIC, N. KRAVIC, D. RISTIC, V. BABIC, S. MLADENOVIC DRINIC* |
| 11:30 - 11:45 | THE STUDY OF THE SUM OF ACTIVE TEMPERATURES AFFECTING AUTUMN BREAD (*TRITICUM AESTIVUM* L.) WHEAT UNDER RAINFED CONDITIONS - *A. CAHANGIROV, A. CAHANGIROV, H. HAMIDOV* |
| 11:45 - 12:00 | MAIZE RESEARCH OF PUBLIC SECTOR IN TURKEY - *R. CENGIZ* |
| 12:00 - 12:15 | DETERMINATION OF INHERITANCE PATTERN IN LOW TEMPERATURE STRESS TOLERANCE RELATED TRAITS IN MAIZE (*ZEA MAYS* L.) BY FOLLOWING GENERATION MEAN ANALYSIS – *S. BANO* |
| 12:15 - 12:30 | Discussion |
| 12:30 - 13:30 | Lunch |
| 13:30 - 15:30 | **5th Session Chair: ASSOC. PROF. DR. TANER AKAR** |
| 13:30 - 13:45 | Invited Speaker<br>*PROF. DR. RISHI K. BEHL*<br>“INTERACTIVE EFFECTS OF HIGH TEMPERATURE AND DROUGHT STRESS ON THE GRAIN GROWTH OF WHEAT GENOTYPES” |
| 13:45 - 14:00 | |

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|---|---|
| 14:00 - 14:15 | GENETICS OF SALT TOLERANCE IN MAIZE (*ZEA MAYS* L) – *K. AHMAD* |
| 14:15 - 14:30 | INVESTMENT OF BIOCHEMICAL ADAPTIVE PLANT RESPONSES IN THE FORMATION OF CEREAL CROPS RESISTANCE TO BIOTIC AND ABIOTIC FACTORS OF ENVIRONMENT - *O.O. MOLODCHENKOVA, V.G.ADAMOVSKAYA, L.Y.CISELSKAYA, P.S. TIHONOV* |
| 14:30 - 14:45 | ASSOCIATION MAPPING OF ROOT TRAITS FOR DROUGHT TOLERANCE IN BREAD WHEAT – *I. AHMAD* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **6th Session Chair: DR. ALEXEY MORGOUNOV** |
| 15:30 - 15:45 | DEVELOPMENT AND VALIDATION OF HIGH-THROUGHPUT AND COST-EFFECTIVE SNP ASSAY FOR FUNCTIONAL GENES IN WHEAT – *A. RASHEED, X. XIA, S. DREISIGACKER, Z. HE* |
| 15:45 - 16:00 | MOLECULAR SCREENING OF RUST RESISTANCE FOR BREEDING WHEAT AND SECURING FOOD- *H.M.CHEEMA, A. A. KHAN, M. HUSSAIN, M. HUSSAIN, Z. ALI, I. KARIM* |
| 16:00 - 16:15 | DETECTION OF FIVE RESISTANCE GENES (BT-5, BT-8, BT-10, BT-11 AND BT-12) DETERMINED WITH MOLECULAR MARKERS AGAINST COMMON BUNT IN EIGHTEEN WHEAT VARIETIES NAMED AS DIFFERENTIAL SET - *A. UMAY* |
| 16:15 - 16:30 | EXPANDING GENETIC DIVERSITY OF WINTER WHEAT THROUGH UTILIZATION OF GLOBAL GERMPLASM, LANDRACES AND SYNTHETIC WHEAT - *A. MORGUNOV, F. OZDEMIR, M. KESER* |
| 16:30 - 16:45 | SYNTHETIC WHEAT: AN INDISPENSABLE PRE-BREEDING SOURCE FOR HIGH YIELD AND RESISTANCE TO BIOTIC AND ABIOTIC STRESSES IN WHEAT IMPROVEMENT - *M. YILDIRIM, V. ESER, Z. BEDŐ, S. A. BAĞCI, M. MOLNÁR-LÁNG, L. LÁNG* |
| 16:45 - 17:15 | Discussion |
| 17:00 - 17:30 | Poster Session 4 |
| 17:30 - 18:00 | Poster Session 5 |
| 18:00 - 18:30 | Poster Session 6 |
| 08:00 - 18:30 | Side Events and Stands |
| 19:00 - | Dinner |

| **4.11.2015 WEDNESDAY** | |
|---|---|
| 09:00 - 10:30 | **7th Session Chair: PROF. DR. IOANNIS TOKATLIDIS** |
| 09:00 - 09:15 | EVALUTION OF WHEAT CULTIVARS AND LINES FOR SENSITIVITY TO YELLOW LEAF SPOT DISEASES IN DIFFERENT AGROCLIMATIC REGIONS OF AZERBAIJAN - *J. ALIYEV* |

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|---|---|
| 09:00 - 09:15 | EFFECTS OF DROUGHT CONSIST OF DIFFERENT PLANT GROWTH ON SOME PHYSIOLOGİCAL TRAITS IN BREAD WHEAT (*T. AESTIVUM* L.) GENOTYPES – *I. OZTURK, KAYIHAN KORKUT* |
| 09:15 - 09:30 | EFFECTIVE AGRONOMICAL AND MORPHO-PHYSIOLOGICAL TRAITS FOR SCREENING DROUGHT TOLERANT BREAD WHEAT GENOTYPES - *BENNANI, S, BIROUK A, NSARELLAH, N, TADESSE, W.* |
| 09:30 - 09:45 | HIGH THROUGHPUT NON DESTRUCTIVE WATER STRESS TOLERANCE INDICES DETERMINATION IN WHEAT UNDER ARID CONDITIONS - *S. ELHENDAWY, Y. REFAY* |
| 09:45 - 10:00 | PHENOTYPIC AND GENOTYPIC ANALYSIS OF TRAITS PROMOTING ADAPTATION TO AEROBIC CULTIVATION FOR DEVELOPMENT OF HIGH YIELDING AEROBIC RICE VARIETIES - *A. KHARB, R.K. JAIN* |
| 10:00 - 10:15 | Discussion |
| 10:15 - 10:30 | Coffee break |
| 11:00 - 12:30 | **8th Session Chair: PROF. DR. EVGENY ZUEV** |
| 11:00 - 11:15 | THE ROLE OF COMPETITION IN RESOURCE USE EFFICIENCY IN VARIOUS CROPPING SYSTEMS AND BREEDING IMPLICATIONS CROPPING SYSTEM - *I. TOKATLIDIS* |
| 11:15 - 11:30 | GENOTYPIC VARIATION FOR FROST TOLERANCE IN WINTER WHEAT – *S. RAM, A. AMANOV, Z. ZIYAEV, E. SADIKOV, M. BAUM* |
| 11:30 - 11:45 | WHEAT PRODUCTION INCREASE IN CENTRAL WEST ASIA AND NORTH AFRICA THROUGH PARTNERSHIP – *M. KESER, A. MORGOUNOV, F. OZDEMIR* |
| 11:45 - 12:00 | EXPANSION OF NARROWING THE GENE POOL AT WINTER DURUM WHEAT BREEDING BY USING WILD RELATIVES – *A. SALANTUR* |
| 12:00 - 12:15 | GENOME -WIDE IDENTIFICATION OF THE MILDEW RESISTANCE LOCUS O (MLO) GENE FAMILY IN NOVEL CEREAL MODEL SPECIES BRACHYPODIUM DISTACHYON – *A. ABLAZOV* |
| 12:15 - 12:30 | Discussion |
| 12:30 - 13:30 | Lunch |
| 13:30 - 15:30 | **9th Session Chair: DR NEZHA SAIDI** |
| 13:30 - 13:45<br>13:45 - 14:00 | Invited Speaker<br>*PROF. DR. EVGENY ZUEV*<br>“THE VIR’S SPRING BREAD WHEAT COLLECTION AND ITS IMPORTANCE FOR BREEDING PROGRAMS IN RUSSIA AND IN THE WORLD” |
| 14:00 - 14:15 | AN ALTERNATIVE APPROACH TO IMPROVING NUTRITIONAL OUTCOMES FROM WHEAT: INCREASING NUTRIENT BIOAVAILABILITY – *I. AZIZ* |

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|---|---|
| 14 15 - 14 30 | IDENTIFICATION OF GENOTYPES UNDER VERY LATE SOWN CONDITION IN WHEAT (*TRITICUM AESTIVUM* L. EM. THELL) – *O. P. BISHNOI* |
| 14:30 - 14:45 | RANCIDITY: AN OBSTRUCTION FOR PEARL MILLET END PRODUCT QUALITY - *J. SINGH, A.K CHHABRA, A.U. ISLAM* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **10th Session Chair: DR. MESUT KESER** |
| 15:30 - 15:45 | Invited Speaker<br>*PROF DR HISASHI TSUJIMOTO*<br>“WHEAT PREBREEDING TO ENHANCE THE GERMPLASM FOR THE NEXT GENERATION” |
| 15:45 - 16:00 | |
| 16:00 - 16:15 | OPTIMIZATION OF EMBRYO RESCUE METHODS IN INTERSPECIFIC WHEAT HYBRIDIZATION – *C. KARAOĞLU* |
| 16:15 - 16:30 | MORPHOLOGIC AND MOLECULAR CHARACTERIZATION OF HULLED WHEAT POPULATIONS OF TURKEY – *F. DEMIREL,T. AKAR, K. GÜRCAN, M. KAPLAN* |
| 16:30 - 16:45 | Discussion |
| 16:45 - 17:15 | Poster Session 7 |
| 17:15 - 17:45 | Poster Session 8 |
| 17:45 - 18:15 | Poster Session 9 |
| 18:15 - 18:45 | Poster Session 10 |
| 18:45 - 19:00 | Closing Ceremony |
| 19:00 - | Gala Dinner |

## IPBC-II ( Meeting Room)

| 2.11.2015 MONDAY | |
|---|---|
| 13:30 - 15:30 | **1st Session Chair: PROF. DR. RISHI BEHL** |
| 13:30 - 13:45 | Invited Speaker<br>*PROF DR NEBAHAT SARI*<br>“WATERMELON BREEDING” |
| 13:45 - 14:00 | |
| 14:00 - 14:15 | DETERMINATION OF PERFORMANCE OF IMPROVED SUMMER SQUASH (*CUCURBITA PEPO*) HYBRIDS VARIETIES CANDIDATE OBTAINED FROM F1 HYBRID BREEDING WITH HYBRIDIZATION - *Ç. NACAR* |
| 14:15 - 14:30 | TY13- THE BRIDGE BETWEEN TY1 TO TY3 MARKERS – *E. ASSAF* |
| 14:30 - 14:45 | SOMACLONAL VARIATION ASSESSMENT AMONG IN VITRO PROPAGATED POTATO (*SOLANUM TUBEROSUM* L.) CULTIVARS BY METHYLATION SENSITIVE AMPLIFIED POLYMORPHISM (MSAP) MARKER – *F. N. FIROUZABADI, M. HOSSEINI, M. OTROSHI, A. ISMAILI* |
| 14:45 - 15:00 | Discussion |
| 15 00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **2nd Session Chair: PROF. DR. AHMET BALKAYA** |
| 15:30 - 15:45 | EST-SSR MARKERS-BASED DISSECTION OF DROUGHT-RESPONSIVE QTLS IN SEGREGATING POPULATION OF *GOSSYPIUM HIRSUTUM – R. M. ATİF* |
| 15:45 - 16:00 | VARIABILITY AND INHERITANCE OF CLEYSTOGAME FLOWER TYPE AND AGRONOMIC-VALUABLE ATTRIBUTES AT G. BARBADENSE L. COTTON HYBRIDS - *K. O. KHUDARGANOV, U. S. ANVAROVICH* |
| 16:00 - 16:15 | DEVELOPING OF AN INITIAL MATERIAL FOR PRACTICAL BREEDING ON THE BASE OF HIGH GENERATION OF G. BARBADENSE L. HYBRIDS - *U. S. ANVAROVICH, A. F. RASHIDOVICH, K. K. OMONBOYEVICH* |
| 16:15 - 16:30 | SCREENING OF POTATO GENOTYPES FOR PROCESSING QUALITY WITH MOLECULAR MARKERS – *C. YAVUZ* |
| 16:30 - 16:45 | ESTIMATING PARENTAL EFFICIENCY OF POTATO GENOTYPES – *A. K. TÜRKMEN* |
| 16:45 - 17:00 | Discussion |
| 17:00 - 17:30 | Poster Session 1 |
| 17:30 - 18:00 | Poster Session 2 |
| 18:00 - 18:30 | Poster Session 3 |
| 08:30 - 18:30 | Side Events and Stands |
| 19:00 - | Dinner |

| 3.11.2015 TUESDAY | |
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| 09:00 - 10:30 | **3rd Session Chair: PROF. DR NEBAHAT SARI** |
| 09:00 - 09:15 | EXPLORING TOMATO CHLOROSIS VIRUS-TOMATO INTERACTION FOR UNDERSTANDING THE MECHANISMS OF DISEASE AND SYMPTOM DEVELOPMENT - *B. ÇEVIK* |
| 09:15 - 09:30 | INVESTIGATION OF THE EFFECTS OF TOXIC BORON WITH DROUGHT STRESS ON TOMATO – *M. AYDIN* |
| 09:30 - 09:45 | USE OF MARKER ASSISTED SELECTION METHODS IN TOMATO BREEDING IN BELARUS – *A. KILCHEVSKY* |
| 09:45 - 10:00 | PHENOTYPIC DIVERSITY BASED ON AGRONOMIC AND FRUIT QUALITY TRAITS IN GBOMA EGGPLANT (*SOLANUM MACROCARPON* L.) - *O.T. ADENIJI* |
| 10:00 - 10:15 | QUALITY TRAITS AND SHELF LIFE ASSESMENT OF IRANIAN CUCUMBER GENOTYPES – *S. AZIZINIA, M. ALIZADEH* |
| 10:15 - 10:30 | Discussion |
| 10:30 - 11:00 | Coffee break |
| 11:00 - 12:30 | **4th Session Chair: DR. PETER HANSON** |
| 11:00 - 11:15 | Invited Speaker<br>*WYBE VAN DER SCHAAR*<br>“VEGETABLE BREEDING” |
| 11:15 - 11:30 | |
| 11:30 - 11:45 | METABOLITE DIVERSITY AND CANDIDATE GENE EXPRESSION ANALYSIS IN BHUT JOLOKIA IN COMPARISON TO OTHER CAPSICUM SPECIES – *R. GAUR, M. SARPRAS, M. NITIN, J. DAS, V. KUMAR, S. CHHAPEKAR, A. KUMAR, N. RAMCHIARY* |
| 11:45 - 12:00 | NUTRITIONAL PROPERTIES OF DIFFERENT KINDS OF ARTICHOKE INTRODUCED TO CHUI VALLEY – *A. DOLOTBAKOV* |
| 12:00 - 12:15 | EMASCULATION, POLLINATION, FRUIT SET AND SEED QUALITY IN EARLIER SWEET CHERRY VARIETY BREEDING – *H. C. SARISU* |
| 12:15 - 12:30 | Discussion |
| 12:30 - 13:30 | Lunch |
| 13:30 - 15:30 | **5th Session Chair: DR. IRINA MITROFANOVA** |
| 13:30 - 13:45 | AN EXAMPLE TO THE USE OF GENETIC RESOURCES FOR IMPROVEMENT THE RESISTANCE: THE DEVELOPMENT OF NEW POWDERY MILDEW TOLERANT GRAPE VARIETIES – *C. OZER* |
| 13:45 - 14:00 | EVALUATION OF GENETIC DIVERSITY AND STRUCTURE OF LEONURUS SPP. POPULATIONS BASED ON INTER - PRIMER BINDING SITE (IPBS) MARKERS - *F. BORNA, N. M. AHMAD, S. V. NAZERI, M. SHOKRPOUR* |

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| 14 00 - 14:15 | TOWARDS THE IDENTIFICATION OF SSR MARKER LINKED TO VIGOR IN OLIVE TREE (*OLEA EUROPEA* L.) – *Z. HAYAT* |
| 14 15 - 14:30 | IMPORTANCE OF SEXUAL AND ASEXUAL VARIATIONS IN THE DIVERSIFICATION PROCESS OF CULTIVATED OLIVES TREES IN THE MEDITERRANEAN BASIN – *M. ABDELMAJID* |
| 14 30 - 14:45 | IDENTIFICATION OF OLIVE VARIETIES USING MICROSATELLITE MARKERS DATABASEPUNJAB, PAKISTAN – *M. Z. IQBAL, A. MEHMOOD* |
| 14 45 - 15:00 | Discussion |
| 15 00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **6th Session Chair: PROF. DR. METIN TUNA** |
| 15:30 - 15:45 | Invited Speaker<br>*DR. RICHARD G. F. VISSER*<br>“TYLCD (PROBLEMS) IN TOMATO: UPDATE ON RESISTANCE RESEARCH AND IMPLICATIONS FOR BREEDING” |
| 15:45 - 16:00 | |
| 16:00 - 16:15 | A NEW OLIVE VARIETY HAYAT – *F. SEFER, U. GÜLOĞLU, H. KAYA , N. ULUÇAY, N. METE, Ö. ÇETİN, M. ŞAHİN* |
| 16:15 - 16:30 | POMOLOGICAL CHARACTERISTICS OF MEMECIKXUSLU HYBRID (F1) OLIVE GENOTYPES – *Ö. ÇETİN, N. METE, M. ŞAHİN, H. KAYA, F. SEFER, U. GÜLOĞLU, M. HAKAN, N. ULUÇAY* |
| 16:30 - 16:45 | GENETIC CHARACTERIZATION OF CAMU-CAMU (*MYRCIARIA DUBIA*) BY MOLECULAR MARKERS – *M. PASQUAL, NUNES C.F, SANTOS D.N, SETOTAW T.A, FERREIRA, J.L, CHAGAS E.C AND CANÇADO, G.M.A* |
| 16:45 - 17:00 | Discussion |
| 17:00 - 17:30 | Poster Session 4 |
| 17:30 - 18:00 | Poster Session 5 |
| 18:00 - 18:30 | Poster Session 6 |
| 08:00 - 18:30 | Side Events and Stands |
| 19:00 - | Dinner |

## 4.11.2015 WEDNESDAY

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|---|---|
| 09:00 - 10:30 | **7th Session Chair: DR HISASHI TSUJIMOTO** |
| 09:00 - 09:15 | *PROF DR. HULYA ILBI*<br>EU-2020 PROJECT<br>“EUROPEAN PLANT BREEDING COLLEGE |
| 09:15 - 09:30 | MOLECULAR CHARACTERIZATION OF TURKISH HAZELNUT (*CORYLUS AVELLANA* L.) GERMPLASMS – *S. C. ÖZTÜRK* |
| 09:30 - 09:45 | IDENTIFICATION OF DIFFERENT COBALT-60 IRRADIATED NAGAMI KUMQUAT GENOTYPES WITH RAPD MARKERS – *C. KARA, Z. DALKILIÇ* |
| 09:45 - 10:00 | ROLE OF BIOAGENTS AGAINST FUNGI CAUSING GUAVA DECLINE DISEASE AND ENHANCEMENT OF THE GROWTH OF GUAVA TREES – *Y. HAMAD* |

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| 10:00 - 10:15 | SOME RESULTS OF APRICOT BREEDING IN REP. MOLDOVA – *M. PINTEA* |
| 10:15 - 10:30 | Discussion |
| 10:30 - 11:00 | Coffee break |
| 11:00 - 12:30 | **8th Session Chair: PROF. DR. A. NACI ONUS** |
| 11:00 - 11:15 | PARTICIPATORY SELECTION AND AGRONOMIC EVALUATION OF AFRICAN EGGPLANT AND ROSELLE VARIETIES FOR FRUIT, LEAF AND CALYX PRODUCTION IN MALI - *D. MEISSA, G. MATHIEU, S.P. IBRA, G. MATHIEU* |
| 11:15 - 11:30 | EVALUATION OF PRODUCTION TECHNOLOGIES FOR SEED YIELD OF IRON WEED- *H. AHMAD* |
| 11:30 - 11:45 | FARMER-SCIENTIST INTERFACE FOR DEVELOPMENT OF VARIETIES AND THEIR PROTECTION-*M. NAQBAL* |
| 11:45 - 12:00 | ANALYSIS OF THE RELATION BETWEEN THE PLOIDY LEVELS OF HYPERICUM PERFORATUM L. AND THE AMOUNT OF HYPERICIN PRODUCED – *G. SAVAŞ TUNA, G. DUYU, K. UZUN, G. YÜCEL, A. YILMAZ, M. TUNA* |
| 12:00 - 12:15 | IN VITRO MASS MULTIPLICATION AND VARIABILITY IN STEVIA (STEVIA REBAUDIANA BERTONI) - *A. YADAV, I.S. YADAV* |
| 12:15 - 12:30 | Discussion |
| 12:30 - 13:30 | Lunch |
| 12:30 - 15:00 | **9th Session Chair: PROF DR. HÜLYA İLBİ** |
| 12:30 - 13:30 | ISSR CHARACTERIZATION OF DAHLIA (DAHLIA CAV.) GENOTYPES COLLECTED FROM THE REGION OF KONYA – *B. B. BATI* |
| 13:30 - 15:30 | COMPATIBILITY EVALUATION OF VARIOUS SCENTED ROSA SPECIES THROUGH CROSS – *A. FAROOQ, M. A. KHAN, A. RIAZ, A. YOUNIS, S. J. BUTT, M. NADEEM* |
| 14:00 - 14:15 | SYRINGA BREEDING IN NIKITSKY BOTANICAL GARDENS – *V. ZYKOVA, Y. PLUGATAR, Z. KLIMENKO* |
| 14:15 - 14:30 | GENOFOND FOUNDATION OF GARDEN ROSE DOMESTIC CULTIVARS IN NIKITSKY BOTANICAL GARDENS - *Y PLUGATAR, Z. KLIMENKO* |
| 14:30 - 14:45 | PHENOLIC COMPOUNDS IN THE INFLORESCENCES OF LAVANDIN (LAVANDULA X INTERMEDIA EMERIC EX LOISEL) – *A. PALIY* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |

| 15:30 - 17:30 | **10th Session Chair: ASSOC. PROF. DR. ZEYNEL DALKILIC** |
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| 15:30 - 15:45 | GENETIC RESOURCES OF WILD USEFUL AND MEDICINAL PLANTS OF KYRGYZSTAN: EVER-LIVING SOURCE FOR SEED BREEDING AND PLANT SELECTION – *K. SHALPYKOV* |
| 15:45 - 16:00 | PLANT GENETIC RESOURCES, CRYOPRESERVATION, PLANT BIOTECHNOLOGY – *M. DZHUNUSOVA* |
| 16:00 - 16:15 | WILD TETRAPLOID OAT SPECIES: A NEW CHALLENGE TO IMPROVE OAT CULTIVATION IN MOROCCO – *N. SAIDI* |
| 16:15 - 16:30 | GENETIC DIVERSITY IN NIGERIAN KENAF (*HIBISCUS CANNABINUS* L.) GENOTYPES AS ASSESSED BY AGROMORPHOLOGICAL TRAITS AND SEED PROTEIN MARKERS – *M. A. AYOVAUGHAN, C O. ALAKE,* |
| 16:30 - 16:45 | Discussion |
| 16:45 - 17:15 | Poster Session 7 |
| 17:15 - 17:45 | Poster Session 8 |
| 17:45 - 18:15 | Poster Session 9 |
| 18:15 - 18:45 | Poster Session 10 |
| 18:45 - 19:00 | Closing Ceremony |
| 19:00 - | Gala Dinner |

# EUCARPIA (Meeting Room)

| 2.11.2015 MONDAY | |
|---|---|
| 13:30 - 15:30 | **1st Session Chair: PROF. DR. RICHARD G.F. VISSER** |
| 13:30 - 13:45 | USING THE NEW INTRODUCED SPECIES - SAFFLOWER IN THE CONDITIONS THE CENTRAL REGION OF THE RUSSIAN FEDERATION – *S.TEMIRBEKOVA* |
| 13:45 - 14:00 | GENETIC DIVERSITY ANALYSIS OF VARIOUS SAFFLOWER (*CARTHAMUS TINCTORIUS* L.) ACCESSIONS USING ISSR MARKERS - *K. HOUMANAT, J. CHARAFI, H. MAZOUZ, M. EL FECHTALI, A. NABLOUSSI* |
| 14:00 - 14:15 | POTENTIAL LINE DEVELOPMENT WITH HIGH SEED YIELD, OIL YIELD AND OLEIC ACID BY HYBRIDIZATION BREEDING IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.) - *S. ERBAŞ* |
| 14:15 - 14:30 | VALIDATION OF FIELD RESISTANCE TO LATE LEAF SPOT BY USING A MOLECULAR MARKER IN GROUNDNUT- *E. YOL* |
| 14:30 - 14:45 | EVALUATION OF GRAIN YIELD AND QUALITY CHARACTERISTICS OF SOME SAFFLOWER (*CARTHAMUS TINCTORIUS* L.) GENOTYPES WITH BIPLOT ANALYSES - *H. KEYVANOGLU* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **2nd Session Chair: DR. MARIA JOITA PACUREANU** |
| 15:30 - 15 45 | CHARACTER ASSOCIATION AND PATH ANALYSIS FOR SEED YIELD AND COMPONENT TRAITS IN INDIAN MUSTARD (*BRASSICA JUNCEA* L.) - *B. Singhbeniwal, S. Singhsivia* |
| 15:45 - 16:00 | RESYNTHESIS OF NEW R LINES IN BRASSICA NAPUS L.- *M.A.M ALAMGIR, M.G. RASUL, M.A.K. MIAN* |
| 16:00 - 16:15 | YİELD PERFORMANCES OF SOME RICE VARIETIES ACCORDING TO LAND SUITABILITY CLASSES– *M. ŞAHİN* |
| 16:15 - 16:30 | DISCOVERING DEFENSE PROTEINS AND PEPTIDES FROM RAPE (*BRASSICA NAPUS* L.) SEEDS TO DETECT BREED RESISTANCES TO ENVIRONMENTAL BIOTIC STRESS FACTORS- *E. ROGOZHIN, A.A. MURAVLEV, V.V.KARPACHEV* |
| 16:30 - 16:45 | A NOVEL CHEMOMETRIC STRATEGY FOR THE ESTIMATION OF SESAME (*SESAMUM INDICUM*) OIL ADULTERATION WITH EDIBLE OILS – *H. RIZKI, F.KZAIBER, W.TEROUZZI, M. EL HARFI, A.OUSSAMA, H.HANINE* |
| 16:45 - 17:15 | Discussion |
| 17:00 - 17:30 | Poster Session 1 |

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| 17:30 - 18:00 | Poster Session 2 |
| 18:00 - 18:30 | Poster Session 3 |
| 08:30 - 18:30 | Side Events and Stands |
| 19:00 - | Dinner |

| **3.11.2015 TUESDAY** | |
|---|---|
| 09:00 - 10:30 | **3rd Session Chair: PROF. DR. MARIA DUCA** |
| 09:00 - 09:15 | GENETIC VARIATION IN CARBON ISOTOPE DISCRIMINATION AND ESTIMATED-WATER USE EFFICIENCY IN SUNFLOWER (*H. ANNUUS* L.) – *A. A. LATİF* |
| 09:15 - 09:30 | DEVELOPMENT OF HIGH YIELDING AND HIGH QUALITY SUNFLOWER GENOTYPES – *M. MUHAMMAD* |
| 09:30 - 09:45 | EFFECTS OF DROUGHT ON MORPHOLOGICAL TRAITS OF SOME SUNFLOWER LINES – *V. PEKCAN,G. EVCI,M. I. YILMAZ, A. S. BALKAN NALCAIYI,Ş. ÇULHA ERDAL,N. CICEK,Y. EKMEKCI, Y. KAYA* |
| 09:45 - 10:00 | SUNFLOWER BREEDING – *M. JOITA PACUREANU* |
| 10:00 - 10:15 | THE EFFECTS OF IRRIGATION, NITROGEN LEVELS AND PLANT POPULATION ON YIELD AND QUALITY CHARACTERISTICS IN CONFECTIONARY SUNFLOWER (*HELIANTHUS ANNUUS* L.) – *V. PEKCAN* |
| 10:15 - 10:30 | Discussion |
| 10:30 - 11:00 | Coffee break |
| 11:00 - 12:30 | **4th Session Chair: PROF. DR. FATIH SEYIS** |
| 11:00 - 11:15 | CONFECTIONERY SUNFLOWER UNDER CONVENTIONAL AND ORGANIC PRODUCTION SYSTEMS – *N. HLADNI* |
| 11:15 - 11:30 | GENOME-WIDE SNP DISCOVERY AND IDENTIFICATION OF QTL FOR AGRONOMIC TRAITS IN SUNFLOWER (*HELIANTHUS ANNUUS* L.) USING A GENOTYPING BY SEQUENCING (GBS) APPROACH – *I. CELIK* |
| 11:30 - 11:45 | CHARACTERIZATION OF MICRNAS HAVING ROLE IN OLIVE OIL BIOSYNTHESIS MECHANISM – *H. TOMBULOGLU* |
| 11:45 - 12:00 | DEVELOPMENT OF MALE SPECIFIC SCAR MARKERS IN DATEPALM - *F. S. AWAN,* |
| 12:00 - 12:15 | RAPD AND ISSR ANALYSIS OF DNA POLYMORPHISM OF GRAIN AMARANTH SPECIES – *S.V. LYMANSKA, T.A. GOPTSIY, L.A. MIROSHNICHENKO* |
| 12:15 - 12:30 | Discussion |
| 12:30 - 13:30 | Lunch |

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| 13:30 - 15:30 | **5th Session Chair: DR. NADA HLADNI** |
| 13:30 - 13:45 | UTILIZATION LOCAL GERMPLASM OF COCOA (*THEOBROMA CACAO* L.) TO SELECT HIGH YIELDING CLONAL PLANTING MATERIAL IN SULAWESI INDONESIA – *A. W . SUSILO, H. PURUNG, I. ANITA-SARI, I. IMRAN* |
| 13:45 - 14:00 | GENETIC VARIATION OF OLEIC ACID CONTENT IN IOPRI'S OIL PALM BREEDING POPULATIONS – *E. SUPRIANTO, H. A. SIREGA, H. Y. RAHMADI, N. SUPENA, A. PURBA* |
| 14:00 - 14:15 | MOLECULAR MARKERS FOR DROUGHT TOLERANCE IN CHICKPEA (*CICER ARIETINUM* L.)- A REVIEW WITH A CASE STUDY - *G. Mehta* |
| 14:15 - 14:30 | SELECTION OF STABLE GENOTYPES FOR GENETIC AMELIORATION OF SEED YIELD WITH DROUGHT AND HEAT TOLERANT TRAITS IN CHICKPEA (*CICER ARIETINUM* L.) – *H. S. YADAVA, A. L. BAGHMARE, N. C. SHARMA* |
| 14:30 - 14:45 | HIGH YIELDING AND DROUGHT TOLERANT GENOTYPES DEVELOPED THROUGH MARKER-ASSISTED BACK CROSSING (MABC) IN CHICKPEA - *S. SAMINENI* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |
| 15:30 - 17:30 | **6th Session Chair: PROF. DR. CENGIZ TOKER** |
| 15:30 - 15:45 | CHICKPEA BREEDING FOR MAJOR BIOTIC CONSTRAINTS IN TUNISIA – *M. AMR, Z. ABBES, M. BOUHADIDA,I. HALILA, A. NAJAR, S. KUMARI, N. OMRI, A. OUJI, W. JENDOUBI, F. SRARFI BEN AYED, I. TRABELSI, D. SFAYHI, R. SAYAR, B. SIFI, H. BEN SALEH, M. IMTIAZ, A. HAMWIEH, H. MOHAMED* |
| 15:45 - 16:00 | RESISTANCE TO STRESS AND CALCIUM BINDING PROTEIN TYPE IN PLANTS – *S. KARBOU* |
| 16:00 - 16:15 | EFFECT OF POST-EMERGENCE HERBICIDE IMAZETHAPYR ON PHENOLOGICAL AND AGRONOMIC TRAITS IN CHICKPEA BREEDING LINES – *S. SAJJA* |
| 16:15 - 16:30 | GENETIC VARIABILITY IN CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES FOR TOLERANCE TO HERBICIDE IMEZATHPYR - *A. G VIJAYAKUMAR* |
| 16:30 - 16:45 | SUPPLEMENTARY ANALYSIS OF PHOSPHOENOLX PYRUVATE CARBOXYKINASE GENE EXPRESSION IN DEVELOPING SEEDS OF CHICKPEA- *M. BEIHAGHI, BAHRAMI A.R, BAGHERI,A.R, MIRSHAMSI, A AND ZARE MEHRJERDI, M* |
| 16:45 - 17:15 | Discussion |
| 17:00 - 17:30 | Poster Session 4 |
| 17:30 - 18:00 | Poster Session 5 |
| 18:00 - 18:30 | Poster Session 6 |
| 08:00 - 18:30 | Side Events and Stands |
| 19:00 - | Dinner |

| 4.11.2015 WEDNESDAY | |
|---|---|
| 09:00 - 10:30 | **7th Session Chair: PROF. DR. AIGUL ABUGALIEVA** |
| 09:00 - 09:15 | DETERMINATION OF EFFECT OF CHEMICAL MUTAGEN EMS ON MORPHOLOGICAL CHARACTERISTICS OF TAEK A-3 AND TAEK C-10 MUTANT SOYBEAN VARIETIES IN M1 GENERATION – *Z. SAĞEL, M. İ. TUTLUER, H. PEŞKİRCİOĞLU, Y. KANTOĞLU, B. KUNTER* |
| 09:15 - 09:30 | BIOCHEMICAL MARKERS IN THE SOYBEAN BREEDING OF FOOD DIRECTION – *O. MOLODCHENKOVA, ADAMOVSKAYA V.G., SICHKAR V.I., KARTUZOVA T.V., BEZKROVNAYA L.YA* |
| 09:30 - 09:45 | COMPARATIVE ANALYSIS OF SEED STORAGE PROTEIN PROFILES AND AGRONOMIC TRAITS TO EVALUATE GENETIC DIVERSITY AMONG THE SOYBEAN [*GLYCINE MAX* (L.) MERR.] GENOTYPES – *Ö. DURSUN* |
| 09:45 - 10:00 | THE DEPENDENCE OF THE SOYBEAN POD SHATTERING RESISTANCE FROM THE SCLERENCHYMAS STRUCTURE OF PODS VALVES – *S. ZELENTSOV, E. V. MOSHNENKO* |
| 10:00 - 10:15 | IS AUSTRALIAN FABA BEAN INDUSTRY VULNERABLE TO RUST (*UROMYCES VICIAE-FABAE*) - *K. N. ADHIKARI, P. ZHANG, A. SADEQUE, S. HOXHA, R. TRETHOWAN* |
| 10:15 - 10:30 | Discussion |
| 10:30 - 11:00 | Coffee break |
| 11:00 - 12:30 | **8th Session Chair: PROF. DR. SALEM S. ALGHAMDI** |
| 11:00 - 11:15 | GENETIC MANIPULATION OF LENTIL (*LENS CULINARIS MEDIK.*) FOR HERBICIDE RESISTANCE THROUGH INDUCED MUTATIONS – *M. ASLAMASLAM* |
| 11:15 - 11:30 | ON FARM CONSERVATION OF A LENTIL LANDRACES IN MOROCCO WITH AN AD-VALUE ON ADAPTABILITY AND QUALITY – *N. BENIBRAHIM, F. GABOUN, M. TAGHOUTI* |
| 11:30 - 11:45 | EVALUATION OF PEA (*PISUM SATIVUM* L.) GERMPLASM FOR WINTERHARDINESS IN CENTRAL ANATOLIA, TURKEY- *A. HOMER* |
| 11:45 - 12:00 | RELIABLE HOUSEKEEPING GENES FOR QRT-PCR OF PEA GENOTYPES GROWN UNDER DIFFERENT BORON TREATMENTS – *H. CAN* |
| 12:00 - 12:15 | SCREENING OF COMMON BEAN SAMPLES (*PHASEOLUS VULGARIS* L.) FROM VIR COLLECTION FOR BREEDING HIGH PROTEIN CONTENT VARIETIES – *T. V. BURAVTSEVA, M.O. BURLYAEVA, G. P. EGOROVA, A. E. SOLOVYEVA* |
| 12:15 - 12:30 | Discussion |
| 12:30 - 13:30 | Lunch |

| 12:30 - 15:00 | **9th Session Chair: PROF. DR. HASAN BAYDAR** |
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| 12:30 - 13:30 | SALICYLIC ACID ROLE IN THE REGULATION OF OXIDATIVE STRESS OF *VICIA FABA* (L.) UNDER SALT STRESS - *F. ANAYA* |
| 13:30 - 15:30 | ASSESSMENT OF SUMMER DROUGHT TOLERANCE IN 154 HALF-SIB FAMILIES OF AFALFA (*MEDICAGO SATIVA* L.) UNDER MOROCCAN FIELD CONDITIONS – *A. BOUIZGAREN, Y. LAHRIZI, I. T. ALAMI, P. ANNICCHIARICO* |
| 14:00 - 14:15 | IMPROVEMENT OF NEW SAINFOIN (*ONOBRYCHIS VICIIFOLIA SCOP.*) LINES VIA IN VITRO MUTAGENESIS TECHNIQUE - *R. BEYAZ* |
| 14:15 - 14:30 | COMBINING ABILITY ANALYSIS OF FORAGE SORGHUM HYBRIDS FOR YIELD, QUALITY AND THEIR RELATED TRAIT – *S. PAHUJA* |
| 14:30 - 14:45 | GENOME SIZE AND CHROMOSOMAL DIVERSITY IN THE GRASS GENUS DACTYLIS L. – *M. TUNA* |
| 14:45 - 15:00 | Discussion |
| 15:00 - 15:30 | Coffee break |
| 15 30 - 17:30 | **10th Session Chair: DR. HAFIZ MUMINJANOV** |
| 15:30 - 15:45 | THE VARIATION OF CRUDE PROTEIN AND TOTAL FAT OF THE MAIN GRASSLAND PLANTS, IN VARIOUS STAGES OF GROWTH, IN “KOSTILATA” SUBALPINE GRASSLAND IN THEODORIANA, ARTA, GREECE – *CH. KOUTSOUKIS, K. AKRIDA-DEMERTZI, P. G. DEMERTZIS, CH. ROUKOS, CH. VOIDAROU, S. KANDRELIS* |
| 15:45 - 16:00 | BIOCHEMICAL CHARACTERIZATION OF THE CHUFA (*CYPERUS ESCULENTUS* L.) COLLECTION OF N.I.VAVILOV INSTITUTE (VIR) - *N. KONKOVA, L.A. MIROSHNICHENKO* |
| 16:00 - 16:15 | HYBRID PIGEONPEA: RESEARCH TO REALITY – *C.V.S. KUMAR* |
| 16:15 - 16:30 | INHERITANCE AND STABILITY OF SOME AGRONOMIC TRAITS OF AFRICAN YAM BEAN (SPHENOSTYLIS STENOCARPA (HOCHST EX. A. RICH) HARMS) - *ADEWALE, B. D., KEHINDE, O.B* |
| 16:30 - 16:45 | Discussion |
| 16:45 - 17:15 | Poster Session 7 |
| 17:15 - 17:45 | Poster Session 8 |
| 17:45 - 18:15 | Poster Session 9 |
| 18:15 - 18:45 | Poster Session 10 |
| 18:45 - 19:00 | Closing Ceremony |
| 19:00 - | Gala Dinner |

# INVITED PAPERS

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|---|---|
| 1 | DEVELOPMENT AND LAUNCH OF ARTESIAN MAIZE HYBRIDS |
| 2 | GENETIC IMPROVEMENT OF TOMATO (*SOLANUM LYCOPERSICUM* L.) FOR PHYTONUTRIENT CONTENT AT AVRDC – THE WORLD VEGETABLE CENTER |
| 3 | INTERACTIVE EFFECTS OF HIGH TEMPERATURE AND DROUGHT STRESS ON THE GRAIN GROWTH OF WHEAT GENOTYPES |
| 4 | THE HISTORY AND CHALLENGE OF CHINESE HYBRID RICE |
| 5 | THE VIR'S SPRING BREAD WHEAT COLLECTION AND ITS IMPORTANCE FOR BREEDING PROGRAMS IN RUSSIA AND IN THE WORLD |
| 6 | TYLCD (PROBLEMS) IN TOMATO: UPDATE ON RESISTANCE RESEARCH AND IMPLICATIONS FOR BREEDING |
| 7 | WATERMELON BREEDING |
| 8 | WHEAT PREBREEDING TO ENHANCE THE GERMPLASM FOR THE NEXT GENERATION |
| 9 | WHAT A WONDERFUL WORLD, PLANT BREEDING! |

# THE HISTORY AND CHALLENGE OF CHINESE HYBRID RICE

Zetian HUA

Tianjin Tianlong Agricultural S & T Co., Ltd., Tianjin, China

Email: fanxiaoman819@163.com

The planting area of rice in China is about 30 million Ha and hybrid rice occupied about 60% of total area. The planting area of hybrid rice reach 5.2 million Ha in 2012. In 1964 Yuan Longping published the first paper of MALE STERILITY OF RICE, which start the research of Chinese indica hybrid rice.Then came up with the new strategy of CROSSING WILD RICE WITH CULTIVATED RICE and found the wild rice with pollen abortion in Hainan in 1970, In 1973, Chinese indica hybrid rice successfully realized THREE LINES matching and widespread popularization in 1976. In 1986, Yuan Longping published THE STRATEGIC VISION OF HYRIDE RICE BREEDING and came up with the strategic vision of hybrid rice breeding from THREE LINES to TWO LINES, then to ONE LINE. In heterosis utilization, outbreeding from intervarietal to intersubspecific, then to other species.

In the breeding of THREE LINES, Yan Longan bred sterile line JENXIAN 97A in 1972, Xie Huaan used restorer MINGHUI 63 crossing with JENXIAN 97A in 1981,and breed the combination XIANYOU 63, and its popularized area occupied 45% of total planting area in China. In 1974, Zhu Yingguo used redhead wide rice crossing with Liantang Rice and bred the new sterile line HL-CMS, HL-CMA, WA-CMA and BT - CMA is the international recognized cytoplasm male sterile line of three lines. Zhou Kaida bred sterile line Gang and D type and series of hybrid rice. And came up with THE HIGH YIELD BREEDING STRATEGE BY CROSSING HEAVY PANICLE BETWEEN INTERSUBSPECIFIC.

Chinese two line hybrid rice research started in 1973, Shi Mingsong from Mianyang Hubei found PTGMS and bred japonica type NONGKEN 58S. In 1986, TWO LINES research list in China National High Technology Research And Development Program, which laid a solid foundation for TWO LINES development.

At present, the development of Chinese hybrid rice especially hybrid japonica faced series of challenge and the key to promoting hybrid japonica development is how to solve low seeds production and unconspicuous heterosis. The Chinese breeders have done a lot of work,such as bred a batches of parents with high stigma exerted rate and study the flower time of hybrid japonica rice, so that to solve the yield problem of hybrid japonica rice. Using the matching mode of heterosis utilization between indica and japonica, complementary form of male and female parent, which solved the yield problem basically, at the same time came up with the heterosis utilization of more genotype group and solved the problem of large quantity seeds using in directsowing rice's, we also have done a lot of work in simplification, high efficiency and machanization of seeds production.

# TYLCD (PROBLEMS) IN TOMATO: UPDATE ON RESISTANCE RESEARCH AND IMPLICATIONS FOR BREEDING

RGF Visser, M Caro Rios, MG Verlaan, Y Zhe, AMA Wolters, Y Bai

Wageningen UR Plant Breeding, Wageningen University & Research Centre, Droevendaalsesteeg 1, 6708 PB Wageningen, the Netherlands

Email: richard.visser@wur.nl

Tomato yellow leaf curl disease, a devastating disease of tomato, is caused by a complex of begomoviruses generally referred to as Tomato yellow leaf curl virus (TYLCV). Almost all breeding for TYLCV resistance has been based on the introgression of the Ty-1 resistance gene derived from Solanum chilense LA1969. We reported previously the fine mapping and cloning of Ty-1 located on chromosome 6 of tomato and encoding a novel RNA-dependent RNA polymerase. Next to this Ty-1 resistance which is allelic to Ty-3  there have other resistance genes been identified (in total six resistance genes (Ty-1–Ty-6) to this disease in wild tomato relatives including S. chilense, S. habrochaites, and S. peruvianum.

In many cases breeding for the resistance proved to be difficult because often inversions are observed which result in suppression of recombination. Such inversions hamper the transfer of important traits from a related species to the crop by introgression breeding. Suppression of recombination was reported for the TYLCV resistance genes Ty-1 and Ty-2.

This presentation will report on the progress and status of the identification and mapping of the other TYLCD resistance genes and their potential use in breeding.

Keywords: TYLCD, tomato, resistance, chromosomal rearrangements

# THE VIR'S SPRING BREAD WHEAT COLLECTION AND ITS IMPORTANCE FOR BREEDING PROGRAMS IN RUSSIA AND IN THE WORLD

Evgeny ZUEV

All-Russian Institute of Plant Genetic Resources named N.I. Vavilov (VIR)

e.zuev@vir.nw.ru

The spring bread wheat collection conserved at the Wheat Department of the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) currently includes 14536 accessions and allows solving various scientific and practical tasks. The Wheat Department has cooperation agreements with 20 Breeding Centers of Russia, where it annually sends an average of 1400 accessions of spring bread wheat.

In order to optimize the work with the collection and cooperation with breeding institutions, creation of the "VIR Spring Bread Wheat" information system was initiated in 2000. This work is aimed at collecting and computerizing all the available information about the collection including the passport data, the results of field and laboratory tests, etc.

Firstly, the passport database was expanded for 5493 accessions by adding the collecting site geographical details. With this information, the Wheat Department takes part in the FIGS (Focused Identification of Germplasm Strategy) international project. Secondly, hard copies of research materials on the VIR spring bread wheat collection were computerized. The created database included information on 433 various traits of about 8891 accessions studied at 69 different locations.

Finally, the field book records from VIR experiment stations and breeding centers for the period from1961 through 2013 were computerized. The total of 209 947 records from 23 locations has been processed so far. On the basis of these data, working collections were created for different regions of Russia. The limits of the main breeding traits variation in the studied locations were determined. The regional working collections will be offered to the appropriate breeding institutions of Russia.

Keywords: Spring bread wheat, collection, accessions, Breeding Center

# WATERMELON BREEDING

Nebahat SARI

Çukurova University Faculty of Agriculture Department of Horticulture 01330
Adana-TURKEY

nesari@cu.edu.tr

Watermelon is an important vegetable species in terms of production amount and commercial value in Turkey and in the World. Major objectives for watermelon breeding include proper fruit type, high fruit quality such as high total soluble solids, fructose, proper sugar to acid ratio, excellent flavor and crispness, high nutritional value (vitamins and lycopene), firmness of flesh and non-fibrous texture, less seed amound or seedless fruits, resistance or tolerance to some important biotic and abiotic stress conditions.

Preperation of the objectives of the breeding program and the choice of parental materials are the most important factors for a breeding program. Recurrent selection, backcross breeding, F1 hybrid breeding and ploidy breeding methods for seeded and seedless watermelon variety development will be discuss during this key note speech.

Keywords: Genetic resources, breeding methods, seedless and seeded variety development

# WHEAT PREBREEDING TO ENHANCE THE GERMPLASM FOR THE NEXT GENERATION

Hisashi TSUJIMOTO

Arid Land Research Center, Tottori University, Japan

tsujimot@yokohama-cu.ac.jp

In the mid of this century, the world population will become more than 9 billion, and therefore we must prepare basic agricultural techniques from now to produce food to support the life of these peoples. One of the possible techniques is to explore useful genes from crop-related wild plants and to utilize the genes extensively in the breeding programs. If the wild species have an intensive qualitative gene expressing in any genetic background or if the gene has been well documented in molecular level, we may find out a promising wild species form the germplasm kept in a gene bank or in the natural habitat. The trait of the gene could be transferred to the crop species through interspecific hybrids. However, the traits as yield potential and abiotic stress tolerance are quantitative, and therefore their performance are largely affected by the genetic background. Thus, observation of only the nature of the wild species is not enough to discover useful genes hidden in the genome. To overcome this difficulty, we should first transfer the genetic materials, i. e., genes or chromosomes, to the genetic backgrounds of crop cultivars and then evaluate the performance in genetic condition with less 'noise'. We have transferred the chromosomes of wheat-related wild species to wheat and found out the traits of high bread-making quality, heat-stress tolerance, high phosphorus uptake and biological nitrification inhibition. The materials must be useful for the wheat breeding for the next generation. Recently, we produced wheat populations (MSD populations) including the intraspecific variation of a bread wheat ancestor, Aegilops tauschii, in some bread wheat cultivars and cultivated the populations under harsh environments. We could successfully select plants with heat stress tolerance from a population. The MSD populations will be further evaluated in the other conditions. I discuss here the significance of 'prebreeding' in the breeding procedures for the next generation.

# INTERACTIVE EFFECTS OF HIGH TEMPERATURE AND DROUGHT STRESS ON THE GRAIN GROWTH OF WHEAT GENOTYPES

Vikender Kaur[1], R.K. Behl[2]

1. National Bureau of Plant Genetic Resources, Pusa Campus,
New Delhi – 110012, India.

2. Department of Genetics and Plant Breeding, CCS Haryana Agricultural
University, Hisar-125004, India.

rkbehlprof@googlemail.com

Heat in conjugation with coincident drought is an increasing constraint for the productivity of wheat. Keeping in view the trends in global climate change, there is a growing need to quantify the effects of heat and drought on wheat yield in different agro-ecologies and agri-production environments. Two contrastingwheat (*Triticum aestivum* L.) cultivars WH730 (thermo-tolerant) and UP2565 (thermo-sensitive) were tested for differential response to combined and individually applied high temperature (HT) and drought (D) stress at three growth stages (Booting stage, post-anthesis stage and booting+post-anthesis stage). All the stress treatments decreased functioning of various physiological parameters of the plants such as photosynthesis and associated pigments (54-72%), stomatal conductance (34%), transpiration (48%), plant water status parameters such as relative water content and excised leaf weight loss and increase in membrane injury. Interaction of high temperature and drought resulted in more decline in grain yield in UP2565 (33%) than WH730 (13%). Anatomical studies through the longitudinal sections of grain revealed that stress treatments resulted in more decline in thickness of pericarp as well as average endosperm length and breadth in UP2565. Peptide profiling through SDS-PAGE of leaf extracts revealed that some of the bands that appeared in stress treated seedlings were also present after revival indicating their protective role, while some new peptides synthesized after stress but disappeared after revival period may be designated true stress proteins associated with better stress tolerance potential of WH730. The effects of high temperature and drought were additive and post-anthesis stage was the most sensitive one for stress induced damage. The interactive effect was much more severe than those of each individual treatment as high temperature increased the degree of water stress.

Keywords: Wheat, high temperature, drought, tolerance, interaction, grain, stress, yield

# DEVELOPMENT AND LAUNCH OF ARTESIAN MAIZE HYBRIDS

Giovanni Della Porta, Raffaele Capitanio, Tommaso Lombardi, Jean Yves Lecoq,

Sebastian Moureau, Benoit Petiard, Javier Betran

Syngenta Seeds S.A.S. 12 Chemin de L’Hobit, 31790 Saint-Saveur, France.

With water becoming an increasing limiting resource in agriculture, the existing trend of higher global temperatures and potential greater regional and seasonal climatic changes, the development of corn hybrids with better drought tolerance and water use efficiency becomes an important goal in breeding programs. A multidisciplinary approach involving breeding, physiology and molecular genetics can synergistically bring more understanding to the response of corn plants to water deficits and enable the development of more tolerant hybrids. Using molecular tools targeting metabolic pathways that are related with response to stress conditions, the search for key genes involved in these pathways is underway through functional genomics, reverse and forward genetics. With better understanding of the physiological mechanisms associated with the response of corn plant to drought and their genetic dissection it is possible to identify, transfer and select key genes and alleles within these genes that provide better stress tolerance. Syngenta Seeds has developed and launched Agrisure Artesian™ technology, the new brand name for its range of water optimized hybrids. Agrisure Artesian technology enables corn plants to use available moisture more efficiently, resulting in higher yields on drought-stressed acres including dryland and limited-irrigation farms in the western US Corn Belt and more stable yields in years of inconsistent rainfall or fields with variable soil types and moisture-holding capacity in central, southern, and eastern U.S. Corn Belt. In years of ideal rainfall, hybrids with Agrisure Artesian technology have demonstrated no yield penalty compared with hybrids without the technology. Syngenta created Agrisure Artesian technology through years of advanced molecular breeding to begin identifying and mining the many genes from the corn genome responsible for managing water use in corn. Syngenta‘s water-optimized hybrids combine multiple genes from this pool, all of which were identified as helping corn plants produce higher yields when available water  is limited.

# GENETIC IMPROVEMENT OF TOMATO (*SOLANUM LYCOPERSICUM* L.) FOR PHYTONUTRIENT CONTENT AT AVRDC – THE WORLD VEGETABLE CENTER

Peter M. Hanson and Ray-Yu Yang

AVRDC – The World Vegetable Center, P.O. Box 42, Shanhua, Tainan, Taiwan peter.

hanson@worldveg.org

Tomato is a widely consumed global vegetable and a major source of the phytonutrients vitamin C, beta-carotene (provitamin A), lycopene, and flavonoids. Tomato cultivars with increased fruit phytonutrient density could help overcome micronutrient malnutrition and contribute to better human health. It is important for plant breeders to understand the genetic diversity and genetic control of targeted phytonutrients, the extent to which environmental factors such as temperature or light intensity affect phytonutrient content, and whether altered phytonutrient content significantly affects yield and horticultural or fruit quality traits. Tomato breeding at AVRDC – The World Vegetable Center has included phytonutrient objectives in its breeding programs and has developed tropically adapted, high yielding and multiple disease resistant lines with increased content of beta-carotene, lycopene, flavonoids, or anthocyanin in different fruit types. Increased content of some phytonutrients such as lycopene is associated with better fruit quality. On the other hand, high beta-carotene content results in orange-fleshed fruit, which is not readily accepted by many consumers. AVRDC seeks to popularize high phytonutrient tomato cultivars through linkages with organizations promoting nutrition and health.

Keywords: Nutrition, beta-carotene, lycopene, flavonoids.

# GENETIC RESOURCES FOR PLANT BREEDING

Vehbi ESER

Plant Breeders Sub-Union of Turkey, Ankara, Turkey

vehbieser@gmail.com

In this presentation, ex-situ management of genetic resources of plant species in general and cereal species in particular will be overviewed in Turkey. Moreover, large historical experience of cereal cultivation and enormous variation among wheat landraces studied by Mirza Gokgol, leading wheat scientist and breeder in Turkey, and contribution of these studies to reshape gene centre theory of wheat by prominent scientist Vavilov are going to be discussed. Finally, this work also aims to illustrate some of other contributions of Mirza Gokgol to plant breeding and science.

# WHAT A WONDERFUL WORLD, PLANT BREEDING!

Wybe van der Schaar

RIJK ZWAAN, Antalya, Turkey

wybe.van.der.schaar@rijkzwaan.com.tr

It has never been a greater period to be a plant breeder than in the year 2015. The discipline itself is very much enriched due to advances in molecular biology by providing genetic markers. Bioinformatics providesgenomic sequences which can subsequently be used for mapping phenotypes to genes in quantitative genetics. Programmes can be sped up by making use of doubled haploids. Taste and fragrances can be further explored biochemistry and new resistances added by collaboration with phytopathology. Seed technology can advise on new traits to deliver excellent quality seeds to the growers/nurseries. In my presentation I will provide examples,by focussing on the crop cucumber, how all these disciplines work together in a modern breeding company.

Keywords: Company, technology, plant breeding

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# IPBC MEETING
# ROOM-I

# GENOME-WIDE ASSOCIATION MAPPING USING A BAYESIAN MIXTURE MODEL FOR PLANT HEIGHT IN ORYZA SATIVA

Burak KARACAÖREN

Faculty of Agriculture, Akdeniz University, 07059, Antalya, TÜRKİYE

burakkaracaoeren@yahoo.com

Genotypic and phenotypic data could be used to predict complex traits for plant breeding in genome wide association mapping studies (GWAS). In GWAS using a single marker model may leads to suboptimal use of genotypic datasets. Alternatively, using whole genome, a Bayesian mixture model may cluster markers into predefined classes. We used 413 diverse accessions of Oryza sativa with 36900 Single Nucleotide Markers (SNPs) for plant height. We assumed different genetic architectures for the phenotype. We estimated heritability as 0.61. Bayesian mixture model detected 144, 446, 54 SNPs with explanatory levels of 0.0001, 0.001 and 0.01 respectively. Chromosome 1 (n=109), and 3 (n=85) had the highest explanatory genetic variances as 23% and 19% respectively. All SNPs explained %65 of the total variance. Correlation between genomic predicted observations and actual observations found to be 0.94. Since GWAS are mostly based on only one replication (as was also the case in this study); results needs to be confirmed by independent validation experiments.

Keywords: Genome wide association mapping studies, Bayesian mixture model, Single Nucleotide Markers, Oryza sativa

# RICE BREEDING AND SEED PRODUCTION STUDIES IN EUROPE

Necmi Beşer

Trakya University, Engineering Faculty, Department of Genetic and Bioengineering, Edirne – TURKEY

necmibeser@trakya.edu.tr

Rice was introduced Europe during fifteenth century and it is grown in 8 of E.U countries (Bulgaria, France, Greece, Hungary, Italy, Portugal, Romania, Spain) Russia, Ukraine, Macedonia and Turkey in Europe. It is not main energy source for Europe people. Rice is seeded from mid-April to the end of May and harvested from mid-September to the end of October. About 80 percent of the rice cultivated area is planted with japonica varieties, and rest is cultivated with indica varieties in EU countries. On the other hand the other Europian countries Turkey, Russia, Ukrain and Macedonia are produced only japonica rice. In EU and other European countries generally governmental organization and cooperatives are carrying out research on rice breeding, but in Italy, main rice producer country in Europe, private sector is most active for rice breeding than the other all European countries. Generally certified rice seed production is done by private companies. In this paper rice breeding and seed production activities in Europe were discussed.

Keywords: Breeding, Europe, rice, seed production

# DEVELOPMENT OF BLAST RESISTANT RICE VARIETY THROUGH MARKER ASSISTED BACKCROSS BREEDING

Mohd Y. Rafii[1], Fatah A.[2], Tanweer[3], Harun A. Rahim[3]

1. Institute Of Tropical Agriculture, Universiti Putra Malaysia, 43400 Serdang, Selangor, Malaysia
2. Department Of Crop Science, Faculty of Agriculture, Universiti Putra Malaysia, 43400 Serdang, Selangor, Malaysia
3. Agrotechnology & Biosciences Division, Malaysia

Rice Blast caused by fungal pathogen, Magnaporthe oryzae is the most common and highly affecting biotic stress of rice around the world including Malaysia. Developing blast resistant rice varieties is most economical, effective and suitable approach for reducing the yield loses and sustaining the rice production. In this study, two major blast resistance genes (Putative Pi-b and Pi-kh) were introgressed from local Malaysian blast resistant rice variety Pongsu Seribu 2 into a high-yielding blast susceptible rice variety MR219 through marker-assisted backcross breeding. Therefore crosses were made between the MR219 used as recurrent parent and Pongsu Seribu 2 as donor parent to transfer blast resistance genes into MR219 without losing their actual quality and yield sustainability. PCR-based tightly linked SSR markers were used for monitoring the blast resistance genes in each backcross population. 72 polymorphic SSR markers were used in each backcross population for estimating the genome recovery of recurrent parent MR219. The recovery of recurrent parent genome i.e. MR219 was more than 95% in selected advanced blast resistant rice lines. The each backcross population was also challenged with most virulent Malaysian fungal pathotype P7.2 for selecting the true blast resistant line. At final stage, from BC2F2 population 15 blast resistant homozygous lines were identified with similar genome background of MR219 along with additional blast resistance genes. The developed blast resistant rice lines will contribute an important role in sustaining the rice production in Malaysia.

# YIELD PERFORMANCES OF SOME RICE VARIETIES ACCORDING TO LAND SUITABILITY CLASSES

Mevlüt ŞAHİN[1], İsmail SEZER[2], Orhan DENGİZ3, Hasan AKAY[4],
Abdulveli SİRAT[5]

1. Tarla Bitkileri Merkez Araştırma Enstitüsü, Ankara
2. Ondokuz Mayıs Üniversitesi Ziraat Fakültesi Tarla Bitkileri Bölümü, Samsun
3. Ondokuz Mayıs Üniversitesi Ziraat Fakültesi Toprak Bölümü, Samsun
4. Ondokuz Mayıs Üniversitesi Ziraat Fakültesi Tarla Bitkileri Bölümü, Samsun
5. Gümüşhane Üniversitesi Şiran Mustafa Beyaz Meslek Yüksek Okulu, Gümüşhane

mevluts@yahoo.com

This study was conducted in order to determine the yield performanses and qualities of 12 rice varieties (Osmancık 97, Neğiş, Aromatik-1, Beşer, 7721, Halilbey, Gönen, Karadeniz, Kızılırmak, Koral, Durağan ve Şumnu) in areas of Kızılırmak town having suitable (S2) and less suitable(S3) classes for two years (2009 and 2010). Experiments were established in RCB design with 3 blocks. The highest yield in S1 class was 0.8469 t/ha and obtained from Kızılırmakvariety .This was followed by Halilbey variety with 0.8069 t/ha. As the highest yield was obtained from Halilbey variety with 0.8407 t/ha in the area of S2 class, it was 0.5808 t/ha with 7721 variety in S3 land suitability class. The average yields of S1, S2 and S3 land suitability classes were 0.7056, 0.6930 and 0.4461 t/ha, respectively. During the study, grain yield, plant height, bunch length, seed number per bunch, thousand kernel weight and lodging and unbroken kernel rate were investigated separately.

Keywords: Rice, yield, unbroken kernel, land suitability classes

# ARTIFICIAL MUTAGENESIS AS A VALUABLE TOOL FOR FUNCTIONAL GENOMICS AND MOLECULAR BREEDING TOWARDS HIGH SALINITY AND DROUGHT TOLERANCE IN RICE

Shuye Jiang and Srinivasan Ramachandran

Temasek Life Sciences Laboratory, 1 Research Link, National University of
Singapore, Singapore 117604

shuye@tll.org.sg

High salinity and drought stresses severely diminish rice production. To better understand the stress mechanism and to further improve rice varieties in their tolerance, we have carried out studies on artificial mutagenesis as a tool for functional genomics and molecular improvement of these two stresses. We have developed an efficient two element maize Ac/Ds gene trapped system and have generated more than ten thousand Ds insertion rice lines. We subjected these lines to drought and high salinity stress screens. We then evaluated these lines and functionally annotated their tagged genes. Our data show that random Ds insertions into the rice genome have led to various genetic variations in response to these stresses. Although hundreds of genes might contribute to abiotic stress tolerance, knock-out of single gene could significantly increase or decrease rice tolerance. Thus, rice has the genetic potential to survive under abiotic stresses by silencing or suppressing appropriate endogenous genes. The Ds insertion lines that exhibit higher tolerance to abiotic stresses have been used for rice breeding by conventional backcrossing combining with molecular marker-assisted selection. On the other hand, we have genome-widely identified genes with differential expression under drought and high salinity stresses between tolerant and sensitive rice lines. Some of these regulated genes have been employed to improve rice tolerance to these abiotic stresses by over- or down-expression of these genes through transgenic technology. We have also explored a new strategy to further improve rice abiotic stresses by overexpressing artificially synthesized genes, which combined functional domains from multiple genes.

# THE RESULTS OF RUSSIAN RICE BREEDING ACHIEVED WITH THE USE OF MAS

Mukhina Zh.M, Suprun I.I., Dubina E.V., Tokmakov S.V., Volkova S.A.,
Savenko E.G., Glazyrina.V.A., Shundrina L.A., Kovalyov V.S., Garkusha S.V.

Federal State Budgetary Scientific Institution All-Russian Rice Research Institute
Belozerny, 3, Krasnodar, Russia

agroplazma@gmail.com

ARRRI, Krasnodar, Russia, actively conducts programs of marker assisted selection for resistance to rice blast disease, improving the quality of grain, resistance to cold and other agronomically important traits. Breeding and seed production schemes are accompanied by marker control of target genes (genes of resistance to the fungal pathogens: Pib, Pita, Piz, Pi9, Pi40, etc.; genes determining cooking quality of grain: Waxy, etc.; genes of red coloring of caryopsis: Rc, etc.; OTLs of resistance to cold) on all stages of development of breeding samples with specified traits.

In the course of these programs valuable breeding resources of rice are developed.

In particular, the breeding nursery of the Institute currently evaluates hundreds of lines with 3-5 introduced - including piramyded ones - genes of resistance to blast. Some of them are already passing State trials for being registered as varieties. In the report we observe breeding material obtained with MAS method.

In the primary seed production molecular genetic approach is also used for quality control of produced rice seeds. Thus, control of genetic purity of reproduced varieties and of absence of red-grain dockage is carried out using methods of DNA - marking. For marking the above traits we use markers well-known from the literature as well as our own ones, developed by ARRRI's biotechnology laboratory.

The institute is also using cell engineering methods (experimental haploidy) for many years to accelerate breeding schemes. Each year we develop many dihaploid lines of rice and pass them to the breeders.

Keywords: Marker-assisted backcrossing, pyramiding of blast resistance genes, double haploid rice line, genetic purity control of seeds

# ISSR ANALYSIS OF HYBRID MAIZE GENETIC RESOURCES IN A VARIETY DEVELOPMENT PROGRAM FOR CENTRAL ANATOLIAN CONDITIONS

Ahmet Tamkoc[1], Fatma Akin[2], Noyan Eken[2], Saliha Mutaf[2], Hasan Can[2],
Ahmet Konuk[3], Erdogan Esref Hakki[4]

1. Selcuk University, Department of Field Crops, Konya/Turkey
2. Selcuk University, Soil Science and Plant Nutrition Department, Konya/Turkey
3. Taspinar Tarim, Konya/Turkey
4. Selcuk University, Soil Science and Plant Nutrition Department, Konya/Turkey

eehakki@selcuk.edu.tr

Maize is among the major staple crops consumed extensively worldwide. Numerous hybrid maize genotypes have been developed since George Shull presented hybrid vigor issue in maize at the beginning of the 20th century. Maize production in Central Anatolia of Turkey, known also as cereal storehouse of Turkey, recently increased extensively, trend followed also by the Southern Anatolian region of the country. Annual yield of maize production became 726 and 907 kg/da, respectively, in 2010 and 2014 in Turkey. In this study, we aimed to determine the genetic relationships between 57 inbred maize lines, belong to Taspinar Tarim. This material is used in a hybrid maize development program. Molecular characterization of inbred lines were conducted using ISSR, a PCR based dominant marker system. From a larger set of ISSR primers tested in a preliminary trial, 9 were found to present adequate level of polymorphism in a repeated manner. Five individual DNA samples of each genotype were pooled in equal amounts in order to make a bulk group for every genotype. The polymorphic bands were scored according to the presence and absence of fragments and simple matching coefficient was used for the matrix generation to be used in NTSYS PC 2.1 software while generating dendrogram and Principle Coordinate Analyses. In total, 78 DNA fragments were scored, 71 of which were polymorphic. According to the results obtained, the total polymorphism between the bulk groups were found to be 91.03% and the genetic distances were in between 0.57 and 0.90.

Keywords: Hybrid maize, issr, plant breeding, molecular marker

# COMPARATIVE NUTRITIONAL ANALYSIS OF BARLEY GENOTYPES

Alka Vasan[1], Manisha Mani[2], R. K. Behl[3]

1. Department of Foods and Nutrition, CCS Haryana Agricultural University, Hisar
2. Department of Management, Chaudhary Bansi Lal University, Bhiwani
3. CCS Haryana Agricultural University, Hisar

alkavasan@yahoo.com

Barley has been a vital food crop in many parts of the world after wheat and rice. The present investigation was carried out to assess the nutritional composition of four barley genotypes viz. BH- 942, BH- 952, BH-933 and BH-946. Nutritional composition of the selected genotypes indicated that BH-942 was found to have maximum amount of crude protein, crude fiber and ash content among all the barley genotypes. Value of crude fat was found to be higher in BH-946 genotype. Likewise, total soluble sugar and non-reducing sugar content were also observed to be higher in BH-946 genotype when compared to other barley genotypes. However, starch content was maximum in BH-952 genotype and minimum in BH-946. Maximum amount of total, soluble and insoluble dietary fiber content was observed in BH-933 genotype followed by BH-946, BH-952 and BH-942. These results suggest that these barley genotypes can be used as functional ingredient to develop low cost heath promoting food products.

Keywords: Barley, proximate composition, nutritional evaluation, crude protein, crude fiber

# VARIABILITY FOR AGRO-MORPHOLOGICAL TRAITS OF MAIZE (*ZEA MAYS* L.) INBRED LINES DIFFERING IN DROUGHT TOLERANCE

Loleta Andjelkovic, Natalija Kravic, Danijela Ristic, Vojka Babic,
Snezana Mladenovic Drinic

Maize Research Institute Zemun Polje, 11185, Belgrade, Serbia

msnezana@mrizp.rs

Drought tolerant genotypes have high yield in optimal conditions and lower, but stable yield in dry environments. Gene bank collection (6000 accessions) of Maize Research Institute was tested under controlled drought in Egypt, and in temperate climate. The mini-core collection of 15 inbreds and 26 populations was created. Inbreds together with lines B73, A632, Mo17 and few commercial inbreds with different tolerance to drought, were evaluated for agro-morphological traits (plant and ear height, total number of leaves, number of leaves above ear, ear leaf length and width), grain yield, number of rows per ear and number of kernels per row, under optimal and increased density in the field in 2014. Since optimal precipitation for maize growing in Serbia is 425mm, total precipitation of 873.2 mm along with the average temperature of 18.8˚C were exceptionally good for maize production. According to Principal Component Analysis, traits that contributed to the differentiation and were in common for both densities were: number of kernels per row, grain yield and leaf width. Obtained results indicate that inbreds T4 and T8 performed the highest stability, together with commercial T1 and T2 lines, in both experimental conditions. Cluster analysis based on grain yield and morphological traits, grouped them together with the other drought tolerant lines, apart of B73 and lines that showed sensitivity to drought in previous studies. Higher density conditions, simulating mild stress, contributed to more accurate separation of lines from mini-core collection, which could be used as a source for drought tolerance in breeding programs.

Keywords: Drought, inbred lines, gene bank, maize, grain yield.

# MAIZE RESEARCH OF PUBLIC SECTOR IN TURKEY

Rahime Cengiz

Mısır Araştırma Enstitüsü, Turkey

rcengiz24@gmail.com

Maize plant is still among the six cereals that feed the world's population. It is the most widely produced cereal in the world thanks to its versatile use, adaptation capability and yield. Despite the fact that 5.95 million tons of maize was produced in Turkey in 2014, consumption coverage was 90%. Hybrid maize breeding in Turkey started in 1950. Through breeding programs carried out to present have been developed valuable populations, a large number of varieties and inbred lines. Seed production rights of varieties were transferred to the private sector with the aim to reach more farmers. Various maize research projects of public institutes engaged in maize improvement were consolidated under a single project and National Maize Integrated Product Management Project (NMIPMP) was initiated. NMIPMP covers the subjects of breeding, abiotic and biotic stress tolerance breeding, biotechnology, agronomy, plant health, registration, seed, industry and agricultural economics and enhancemen- et of germplasm in Turkey. Collaborative variety development has been put into prac- tice by means of active exchange of inbred lines developed by various public research institutes. Inoculation work is also carried out for identifying inbred lines and varieties with resistance to Fusarium moniliforme, Maize dwarf mosaic potyvirus (MDMV) and Sugarcane mosaic potyvirus (SCMV). Determination of high temperature and drought tolerance inbred lines of work are carried out. Genetic distance detection, purity analysis and marker-asisted selection are being conducted using SSR markers in recent years.

Keywords: Maize, breeding, biotechnology, abiotic stress, biotic stress

# DETECTION OF FIVE RESISTANCE GENES (BT-5, BT-8, BT-10, BT-11 AND BT-12) DETERMINED WITH MOLECULAR MARKERS AGAINST COMMON BUNT IN EIGHTEEN WHEAT VARIETIES NAMED AS DIFFERENTIAL SET

Ahmet Umay, İsmail Poyraz

Department of Molecular Biology and Genetic, Faculty of Art & Science,
Bilecik Seyh Edebali University, 11210 Bilecik, Turkey.

ahmetumays@hotmail.com

Common bunt (*Tilletia* sp.) is an important seed borne disease posing a threat to wheat production and may cause serious economic losses. The alternative fight method instead of chemical fungicides against common bunt disease is use of wheat cultivars including resistance genes. These resistance genes in wheat are called as bt genes. Until today, a little number of bt genes in wheat has been detected by some molecular markers based SSR and RAPD-PCR. There aren't yet developed molecular markers for detection of all bt genes in wheat. In this study, detection of five bt genes (bt-5, bt-8, bt-10, bt-11 and bt-12) was carried with molecular markers (microsatellite and RAPD) in eighteen wheat varieties named as differential set (Heines VII, SEL 2092, SEL1102, Ridit, Turkey 1558, Hohenheimer, Rio, SEL 50077, M82-2161, M82-2098, R63-6968, M82-2102, M82-2123, P.I.178383, M73-2154, P.I.173438, P.I.119333 (M82-2141) BW, ThuleIII; P.I. 181463 BW). PCR-amplified fragments were separated on 1.3 % agarose gel containing ethidium bromide (0.5 µg/ml). Gels were visualized under UV light and digitally photographed. Using amplified band sizes of each molecular marker determined according to literature data, the obtained DNA bands were scored as present or absent for detection of bt genes. It was obtained the analysis results for five bt genes in eighteen wheat varieties named as differential set and compared with data of molecular markers mentioned in scientific literatures.

Keywords: Wheat, Bt resistance genes, Common bunt, Molecular markers.

# EXPANDING GENETIC DIVERSITY OF WINTER WHEAT THROUGH UTILIZATION OF GLOBAL GERMPLASM, LANDRACES AND SYNTHETIC WHEAT

Alexey Morgunov[1], Fatih Özdemir[2], Mesut Keser[3]

1. CIMMYT, P.K. 39 Emek 06511 Ankara, Turkey
2. ICARDA, P.K. 39 Emek 06511 Ankara, Turkey
3. Bahri Dagdas International Agric. Research Institute, Konya, Turkey

a.morgounov@cgiar.org

International winter wheat improvement program (www.iwwip.org) is a partnership between Ministry of Food, Agriculture and Livestock of Turkey, CIMMYT and ICARDA to develop new winter wheat varieties for the region of Western and Central Asia. The main breeding priorities are broad adaptation, rust resistance and grain quality. Annually 800-1000 crosses are made which are subjected to conventional multi-locational breeding framework in Turkey. Around 500 new varieties and breeding lines are submitted to IWWIP by its collaborators for evaluation in Turkey and distribution through the international nurseries. The best advanced lines as well as the best introduced lines are annually distributed through FAWWON (Facultative and Winter Wheat Observation Nursery) to more than 100 cooperators in around 50 countries. Till now around 60 varieties were released in the region occupying more than 2 mln ha. Maintaining the genetic diversity in international wheat breeding program addressing variable environments and several biotic and abiotic stresses is highly important. Three main sources of genetic diversity for different traits are utilized by IWWIP: global germplasm shared by cooperators (primarily Eastern Europe, Central and West Asia and USA); wheat landraces recently collected from Turkey, Tajikistan and Uzbekistan; synthetic wheat developed at CIMMYT-Mexico by crossing east European durum varieties and Aegilopes taushii as well as Japan synthetics originating from crosses between durum wheat Langdon and collection of Ae. tauhsii. Each group of the germplasm has its advantages and drawbacks but jointly represent and excellent resource of genes to be utilized in the commercial breeding program.

Keywords: Wheat breeding, biotic and abiotic stresses, genetic resources

# SYNTHETIC WHEAT: AN INDISPENSABLE PRE-BREEDING SOURCE FOR HIGH YIELD AND RESISTANCE TO BIOTIC AND ABIOTIC STRESSES IN WHEAT IMPROVEMENT

M. Yildirim[1], V. Eser[2], Z. Bedo[3], S. A. Bağci[4], M. Molnár-Láng[5], L. Láng[5]

1. Kahramanmaraş Sütçü İmam University, Turkoğlu Vocational School, Kahramanmaraş, Turkey
2. Republic of Turkey Ministry of Food, Agriculture and Livestock, Ankara, Turkey
3. Centre for Agricultural Research, Hungarian Academy of Sciences, Martonvásár, Hungary
4. Selcuk University, Sarayönü Vocational School, Konya, Turkey
5. Centre for Agricultural Research, Hungarian Academy of Sciences, Martonvásár, Hungary

bagcia@hotmail.com

In addition to being the most widely cultivated crop, wheat is also the most ancient cultivated plant species. Today, as in the past, wheat continues to be a crop of strategic importance. Cultivated hexaploid bread wheat (2n=42) consists of three genome groups (AA, BB, and DD), with each genome group further comprising three diploid wild species. Over the past 70 years, the world population has been rapidly increasing, while the amount of agricultural lands have remained more or less constant. To be able to feed this continually increasing human population, scientists have begun to investigate the biological origins/roots of wheat, with the aim of achieving higher yield and greater resistance to biotic and abiotic stresses. This was because, based on the studies they performed, they determined that "reconstructing" wheat from its origins was a more effective solution than working with limited and currently available genetic resources. Bread wheat reconstructed by using diploid wild forms are called "synthetic wheat." Synthetic wheat receives certain characteristics from wild forms that render them superior to cultivated wheat. Diploid wild forms bearing the "D" genome (Ae. tauscii) are known to be particularly very resistant to biotic and abiotic stresses. Nowadays, it has become imperative to use synthetic wheat in order to increase genetic variation in breeding programs. To break the "yield per unit area" barrier, to ensure world peace, and to prevent the starvation of children around the world, wheat breeders must place greater emphasis on the production of synthetic wheat.

Keywords: Synthetic wheat, Aegilops, D genome, crossing

# EVALUTION OF WHEAT CULTIVARS AND LINES FOR SENSITIVITY TO YELLOW LEAF SPOT DISEASES IN DIFFERENT AGROCLIMATIC REGIONS OF AZERBAIJAN

Shahriyar Sadigov[1], Ehtibar Ibrahimov[1], Cavanshir Talai[1], Irada Huseynova[2]

1. Research Institute of Crop Husbandry, Ministry of Agriculture of Azerbaijan Republic
2. Institute of Botany, Azerbaijan National Academy of Sciences

aliyev-j@botany-az.org

Ascomycete fungus Pyrenophora tritici-repentis (Died.) Drechs causes a foliar disease of wheat known as tan spot or yellow leaf spot. The leaf spotting is one of the major destructive diseases worldwide that causes serious losses in quality and quantity of grain yield. The aim of the present study includes large scale screening of wheat cultivars/lines, ranging from highly susceptible to resistant for their reactions to this infection under field conditions and identification of new sources of resistance. A survey of wheat crops was conducted from early spring to the end of season in Ismayilli, Shaki (rainfed), Khachmaz (humid, irrigated) districts in 2015. In all regions plants were infected after the appearance of the third leaf (Zadoks-13), at the beginning of the tillering phase (Z-21), and necrotic and chlorotic spots were observed in the infected plants. Chlorotic spots were more observed in plants grown in Ismailli district, while necrotic spots prevailed in plants in Shaki and Khachmaz. Chlorotic spots surrounding necrosis were observed in some varieties and the pathogen development continued till the flag leaf. The disease degree increased in primarily infected varieties during the active vegetation period in Ismayilli. Yellow spot disease was observed in 159 samples from 180 (88.3%) grown at the experimental field of this region. From all infected plants 18.23% are very susceptible samples (VS), 19.47% susceptible (S), 32.07 % medium susceptible (MS) and 30.18% low susceptible (LS) samples. In Shaki 67 samples from 69 (97.1%) were infected, a high degree of the disease was observed in 56.7 % of them and a low degree in 43.28%. The ratio between necrosis and chlorosis was found to be 3/1.4/1 for the infected samples. In Khachmaz 9 samples from examined 17 (52.94%) were VS and 7 samples (41.17%) S. Only one sample (5.88%) appeared to be resistant. The Parvin variety was found to be resistant in all regions, and Fatima, Gyzyl Bugda, Agaly etc. appeared to be susceptible and very susceptible.

Keywords: Yellow leaf spot diseases, tan spot, sensitivity, wheat

# EFFECT OF DROUGHT CONSIST OF DIFFERENT PLANT GROWTH ON SOME PHYSIOLOGICAL TRAITS IN BREAD WHEAT (*TRITICUN AESTIVUM* L.) GENOTYPES

İrfan Öztürk[1], Korkut K. Z[2]

1. Trakya Tarımsal Araştırma Enstitüsü Müd. Edirne, Turkey

2. Namık Kemal Uni. Fac. of Agr. Dep. of Field Crops. Tekirdağ, Turkey

irfanozturk62@hotmail.com

Water stress is a severe abiotic stress and major constraint to wheat productivity. It was investigated yield and some physiological traits related to drought resistance and the relationships between physiological characters. Study was carried out in Edirne, during 2 growing seasons with totally 15 bread wheat genotypes in split block design with 3 replicated. Drought applications and genotypes were main plot and sub-plot, respectively. Drought was applied in stem elongation stage, heading and during grain filling stage. Also, it was included non-stress and there was no any treatment condition on main plots. Some physiological traits such as canopy temperature and chlorophyll content were investigated at booting, heading and grain filling stage. Also, days of heading and maturating, grain filling period and glaucousity and among these traits were investigated. Drought stress effected canopy temperature and CT increased at dry condition while non-stress was decreased. Highest temperature was determined from fully drought treatment and first main plots. It was determined between grain yield and canopy temperature at booting r= -0.779, heading stage r= -0.793 and grain filling stage r= -0.924*. Although, drought stress affected and reduced leaf chlorophyll content at three development stages, chlorophyll content on heading stage was higher than the others. The highest leaf chlorophyll was determined in non-stress treatment. It was determined between grain yield and chlorophyll content at booting r= 0.499, heading stage r= 0.498, and grain filling stage r=0.954*.

Keywords: Wheat, drought stress, genotype, canopy temperature, chlorophyll content

# THE ROLE OF COMPETITION IN RESOURCE USE EFFICIENCY IN VARIOUS CROPPING SYSTEMS AND BREEDING IMPLICATIONS

Ioannis Tokatlidis

Pantazidou 193, 68200 Orestiada, Greece

itokatl@agro.duth.gr

In densely grown plants unequal use of the limited growth sources is due to competitive advantages of some individuals over others. The intensity of inter-plant competition is reflected by the plant-to-plant differences, either genetically or environmentally induced. Therefore, competition comprises two main parts, the genetic part and the acquired one. Since inter-plant competition conditions the effectiveness in resource capture, appraising the kind of competition that prevails in different cropping systems is essential. The acquired part of competition is always present, the magnitude depending on genotype vulnerability to abiotic and biotic forces. The genetic competition stands on intra-specific and/or inter-specific genetic differences, by inference affecting the acquired competition as well. In terms of a sole crop of a mono-genotypic variety (pure line or single-cross hybrid of pure lines) only the acquired competition prevails, while intra-specific genetic competition is added in sole crop of a multi-genotypic variety (multi-line, landrace, open pollinated line of outbreeders, synthetic etc). In inter-cropping systems, the genetic competition is inter-specific on the premise that only mono-genotypic varieties are mixed, while both intra- and inter-specific competition will be present when multi-genotypic varieties are mixed. Competitive and yielding ability are distinct agronomic characters, commonly inversely connected. Thus, involvement of the appropriate variety(ies) in a particular kind of agricultural system is of prime importance to optimize resource use efficiency and production. From breeding perspective, the development of ‘specific’ varieties capable to satisfy the demands of the various cropping systems is a mandate.

Keywords: Breeding, competition, cropping system, resource capture

# GENOTYPIC VARIATION FOR FROST TOLERANCE IN WINTER WHEAT

Michael Baum[1], Esbosin Sadikov[2], Zafar Ziyaev[3], Amir Amanov[3], Sharma Ram[4]

1. Icarda, Rabat, Morocco
2. Karakalpakstan Research Institute of Crop Husbandry, Chimbay, Uzbekistan
3. Uzbek Research Institute of Plant Industry, Kibray, Uzbekistan
4. Icarda, Tashkent, Uzbekistan r.c.sharma@cgiar.org

Frost is a major constraint to winter wheat production in many parts of Central Asia. A set of 150 randomly selected commercial varieties and advanced breeding lines of winter wheat was field evaluated for frost tolerance in 2013-2014 (2014) and 2014-2015 (2015) wheat growing seasons in Chimbay, Uzbekistan. One hundred seeds of each genotype were planted in 1 m2 plots at 2-cm and 4-cm depths using 25-cm and 10-cm row and plant spacing, respectively. Winter temperatures were <-20°C for more than one week in the 3rd and 4th week of February 2014, and in the last week of March in 2015. Frost tolerance was estimated as percent of plants in a plot that survived the winter. In 2014, there were significant ($p<0.01$) genotypic variation for winter survival (0 to 100%). Planting depth significantly ($p<0.01$) affected winter survival. There was significant genotype-by-planting depth interaction for winter survival. The proportion of the genotypes with ≤20% frost kill were 25% and 65% at 2-cm and 4-cm planting depths, respectively. The lines with ≤20% frost kill in 2014 were further evaluated in 2015 at 2-cm and 4-cm planting depths. All lines survived winter in 2015. The five most frost tolerant lines were '20FAWWIR-144','15IWWYTSA-30', '20FAWWSA-296', 'Victoriya' and '15IWWYT-SA'. This study has identified frost tolerant winter wheat genotypes which could be further evaluated for varietal release or could be used in breeding program as parents for developing frost tolerant varieties. This study also underlines frost management strategy in winter wheat through planting depth.

Keywords: Frost tolerance, frost management, winter wheat, genotypic variation

# WHEAT PRODUCTION INCREASE IN CENTRAL WEST ASIA AND NORTH AFRICA THROUGH PARTNERSHIP

Mesut Keser[1], Alexey Morgunov[2], Fatih Ozdemir[3]

1. ICARDA, Ankara, Turkey

2. CIMMYT, Turkey

3. Bahri Dagdas Internation Agricultural Reserch Institute, Konya, Turkey

m.keser@cgiar.org

Wheat is staple crop in Central and West Asian countries. Except Turkey and Kazakhstan, most of the countries in this region are wheat importer. Climate change makes it worse for the region and they need sustainable wheat production increase in the region in order to feed their populations and not to damage their economies. International Winter Wheat Improvement Program (IWWIP) is a triparty program among Turkey, CIMMYT and ICARDA. It was established in 1986 between Turkey and CIMMYT and ICARDA joined program in 1990. This partnership develops winter wheat (WW) germplasm and distribute around 100 breeding programs in about 50 countries in the world though its main target area is Central West Asia and North Africa region (CWANA). Around 17 million ha winter wheat have been planted in CWANA. The countries in the region needs new, advanced germplasm either to release directly as variety or to use in their breeding programs. IWWIP is the only organization in the world who provides and facilitates the WW germplasm exchange globally with high yield potential, prevalent biotic and abiotic stress tolerance. The material development has been done in Turkey and Terbol, Lebanon and the developed germplasm is distributed to the collaborators of IWWIP. Up to now, there are more than 60 cultivars released in 11 countries in the region originating from IWWIP and the planting area of those cultivars reached close to 2.5 ha in those countries. In this study, it will be highlighted how biotic and abiotic tolerant germplasm has been developed and what their performances in the target regions are will be given.

Keywords: Winter Wheat, Breeding, Yield increase, Central West Asia

# EXPANSION OF NARROWING THE GENE POOL AT WINTER DURUM WHEAT BREEDING BY USING WILD RELATIVES

Ayten Salantur, Selami Yazar, Bayram Özdemir, M. Emin Alyamaç

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd.
No. 9-11, Yenimahalle, Ankara, Turkey

asalantur@mynet.com

The main purpose of breeding activities are, by creating variations evaluating the progenies and selecting the bests, to get better genotypes in case of resistance to biotic and abiotic stresses, quality and yield. As the consequence of gradually increased se- lection pressure on yield and quality characteristics of durum wheat narrowed genetic variation became imminent in case of said traits within the present gene pool. One of the ways of broadening the gene pool is to transfer desired traits from other gene pools, including wild relatives. Thus, to achieve widened durum wheat gene pool *T. dicoccoides, T. araraticum* and *T. dicoccon* have been included in our durum wheat crossing program. Above mentioned species have been crossed with widely grown durum wheat varieties. In total, 20 crosses between wild relatives and durum wheat varieties have been done. Crosses made in 2008 and F5s have been had in 2013. Between F2 and F4 stages genotypes having shattered spikes have been discarded. In F5 800 single spike rows planted in 2013 and 500 spike rows were selected according to observation made on plant and spike height, spike color, awn color, grain color, anthocyanin formation between upper node and spike, spike hairiness, and greasiness and earliness. As a result of this study, it can be concluded that T. dicoccoides, T. araraticum and T. dicoccon can be off value to be used to increase variation within gene pools of durum wheat in case of studied characters.

Keywords: Durum wheat, breeding, variation, gene pool, wild relatives

# GENOME-WIDE IDENTIFICATION OF THE MILDEW RESISTANCE LOCUS O (MLO) GENE FAMILY IN NOVEL CEREAL MODEL SPECIES BRACHYPODIUM DISTACHYON

Abdugaffar Ablazov, Huseyin Tombuloglu

Department of Biology, Faculty of Arts and Science, Fatih University,
Buyukcek- mece, Istanbul, Turkey

ablazov3@gmail.com

Powdery mildew (PM) is an important plant fungal disease that adversely affects a broad range of angiosperm species, including grass families such as wheat and barley. The Mlo (powdery mildew locus O) protein acts as a negative regulator in PM-resistance. Loss-of-function mutation in Mlo shows complete resistance to PM disease. In this study, for the first time we reported Mlo gene family members in Brachypodium distachyon, model species for grass. 11 BdMlo genes were identified on all five chromosomes with a scattered occurrence rather than clustered. The subcellular localization and topology analyses confirmed that all BdMlo proteins anchored to plasma membrane. The seven trans-membrane (TM) and calmodulin-binding domain (CaMBD) sites were well conserved. Amino acid composition showed that BdMlo proteins were leucine-rich (9.9-13.1 %) except BdMlo5 and BdMlo8, which were alanine-rich (10.0%) and serine-rich (8.7%), respectively. In silico functional dissection of cis-acting elements revealed that BdMlos were associated with mainly hormonal, stress, light response and tissue-specific signaling pathways. Phylogenetic relations of BdMlos within distinct plant species (Arabidopsis, wheat, maize, and peach) were evaluated. Also, digital expressions of BdMlos in drought, cold and pathogen infection conditions revealed stress-responsive Mlo genes. Phylogenetic and expression analyses provided a preliminary evidence that BdMlo2 could be the best susceptible gene which may play important role in PM resistance. It was concluded that identification and characterization of Mlo gene members in Brachypodium will provide essential knowledge for studying full-scale functional analysis of these genes in grass species.

Keywords: Mlo gene; powdery mildew; Brachypodium distachyon; resistance

# AN ALTERNATIVE APPROACH TO IMPROVING NUTRITIONAL OUTCOMES FROM WHEAT: INCREASING NUTRIENT BIOAVAILABILITY

Irum Aziz

107 Cobbitty Road, cobbitty 2570 New Australia

iazi6734@uni.sydney.edu.au

Wheat cultivars that either load more Fe and Zn into the grain or improve the bioavailability of these nutrients in the human digestive system could contribute to the alleviation of malnutrition in many countries where wheat is a primary source of calories. Semi-dwarf wheat genotypes with enhanced Zn and Fe concentration and low levels of phytate and high fructan have been developed and their impact on animal nutrition, processing quality and P use-efficiency is being determined. Low grain phytate and high fructan are considered to be enhancers of micronutrient bioavailability. Preliminary results show that phytate and fructan are independent of yield, while micronutrient concentration is associated with the aleurone and therefore negatively correlated with yield. Evidence suggests that processing quality is not influenced by more extreme levels of phytate and fructan and low phytate wheat tends to be more P use-efficient. The nutritional value of different wheat genotypes is greatly influenced by the environment and the nutritional status of the soil. However, a significant genotype x environment interaction was observed indicating that cultivars with improved nutritional value adapted to specific environmental conditions can be developed.

Keywords: Breeding, wheat, Fe and Zn

# IDENTIFICATION OF GENOTYPES UNDER VERY LATE SOWN CONDITION IN WHEAT (*TRITICUM AESTIVUM* L. EM. THELL)

O. P. Bishnoi

Department of Genetics and Plant Breeding, CCS Haryana Agricultural University,
Hisar-125004

opbishnoi363@gmail.com

In Haryana several crop rotations are followed depending upon the agro-ecological condition. In cotton-wheat rotation several time the cotton picking is delayed due to which wheat sowing has to be delayed, in several niches the sowing is delayed till mid January. The normal genotypes for normal sown conditions show heavy reduction in yield when sown very late (mid January). Therefore, it is essential to identify genotypes which could complete their vegetative growth in cold winter season and set grain during the March-April by tolerating terminal heat stress. In view of this we selected genotypes MP 3091, Raj 4012, Raj3765, WH1021, WH1124, WH1105, Sonak, Halna and a mutant (Sushil -18) as a check known to be early maturing (110 days ) for sowing in mid January. A number of crosses among them were attempted some of them are Halna x WH1021, Halna x WH1124, Halna x WH1105, WH1124 x Sushil-18, WH 1105 x Sushil-18, WH1124 xWH1021, MP3091 x Raj4012, Raj3765 x Raj4012 to check allelism (complementary test). We could observe a number of genotypes flowered between 60-70 days as against Sushil-18 (58 days) and Halna (61 days). These genotypes yielded upto 35q/ha, this is because of faster grain growth rate and terminal heat stress tolerance. These genotypes can be used in areas where pearlmillet/carrot crop rotation is followed. The carrot crop is harvested in by mid January and field is vacant till 1st week of June, in between such genotypes can be sown to have successful wheat crop so that farmers can get additional income by fitting short duration wheat in Pearlmillet /Carrot/cotton-Wheat rotation.

Keywords: Terminal Heat Stress, Early Maturing Wheat, Crop Rotation

# OPTIMIZATION OF EMBRYO RESCUE METHODS IN INTERSPECIFIC WHEAT HYBRIDIZATION

Cuma Karaoglu, Ayten Salantur

Biotechnology Research Center, Central Research Institute for Field Crops
06220 Yenimahalle/Ankara/Turkey

cumakaraoglu@hotmail.com

Interspecific hybridization studies have been made to improve the genetic base of durum and bread wheat. However, cross-breeding among plants of different ploidy level usually ends up with incompatibility issues that results in failure to establish cross-bred embryos. Potentially this immature embryos could maintain normal growth if they are isolated as immature embryos and may be kept alive by culturing them on basal medium such that resulting hybrid plants can be achieved an important contribution to agriculture. This study reports embryo rescue among different crosses of wheat with varying ploidy level with aim to gather desired features. Twelve (12) different crosses were performed (Bezostaja×Kızıltan, YDF-28×Kızıltan, A. cransa×Bezostaja, Çavdar×Jaguar, Kamut×Quality, A. columnaris×KateA-1, A. columnaris×Pehlivan, Bayraktar-2000×Kızıltan-91, YDF-15×Bezostaja, YDF-25×Tosunbey, YDF-26× Tosunbey, T. Dicoccon×Eminbey). Experiments were performed related to selection of optimal number of days for selection of immature embryos after hybridization, the best conditions for sterilization of spikelets, and the appropriate basal media for growth of rescued embryos. It was determined that the immature embryos needed to be collected after 18 days of hybridization , there was need of 30% bleach concentration for sterilization and R9 regeneration medium was ideal for embryo culture. The plantlets were rooted and grown under in vitro conditions and vernalised at +4 oC for 4 weeks followed by transfer to greenhouse. Colchicine was applied to 50% plants for chromosome doubling. Seeds were collected from treated plants in the greenhouse.

Keywords: Wheat, interspecific hybridization, embryo rescue

# MORPHOLOGIC AND MOLECULAR CHARACTERIZATION OF HULLED WHEAT POPULATIONS OF TURKEY

Fatih Demirel[1], Taner Akar[2], Kahraman Gürcan[3], Mahmut Kaplan[4]

1. Iğdır University, Faculty of Agriculture, Department of Field Crops, Suveren/Iğdır/Turkey
2. Akdeniz University, Department of Field Crops, Antalya, Turkey
3. Erciyes University, Department of Agricultural Biotechnology, Kayseri, Turkey
4. Erciyes University, Department of Field Crops, Kayseri, Turkey

yezakar66@hotmail.com

23 hulled wheat populations collected from Kastamonu province of Turkey and 9 durum and bread wheat cultivars were characterized at morphological and molecular level, in this study. Based on the morphological data, 9 of them were distinguished as emmer wheat while the other 14 population as einkorn. The highest coefficient of variation and mean of these parameters for hulled wheat were 17.7% and 22.1;  14.1 % and 38.4 g; 9.03 % and 17.54 % for grain number per spike, 1000 kernel weight and protein ratio, respectively. Qualitatively, hairiness on leaves and glaucosity on the spike for emmer wheat and einkorn populations were 100 % and 22.2; and 88.8 % and 44.4, respectively. Molecular characterization based on ISSR markers showed that mean Dice similarity coefficient for all wheat genotypes including checks was 0.553. Additionally, mean polymorphic loci and polymorphism rate for 14 ISSR primers were 10.21 and 95.42 %, respectively. All genotypes were clustered two main groups and registered cultivars were close to emmer wheat and between einkorn and emmer wheat based on molecular data. 80.08 % total variation based on molecular data ex- plained by two main components. This study showed that some populations can be selected as parental material for further organic emmer and einkorn breeding program. Acknowledgment: This study was financially supported by Erciyes University, Department of Scientific Research Project.

Keywords: Emmer wheat, einkorn, genetic variation, pre-breeding, ISSR

# THE STUDY OF THE SUM OF ACTIVE TEMPERATURES AFFECTING AUTUMN BREAD (*TRITICUM AESTIVUM* L.) WHEAT UNDER RAINFED CONDITIONS

Atabey Cahangirov, Ali Cahangirov, Hamid Hamidov

Gobustan Experimental station of Research Institute of Crop Husbandry,
Azerbaijan National Academy of Sciences

i_guseinova@mail.ru

A more rapid formation of optimal surface sizes of leaf, which is the main assimilating organ, as well as its long-term functioning, during grain filling is necessary for achieving high productuvity. To study the sum of active temperatures (SAT) affecting wheat plants during grain filling, a chlorophyll amount decrease was determined in the 8th tier leaves of 21 autumn bread wheat varieties and lines with contrasting morphophysiological properties using SPAD meter. Then according to these parameters and using the mean square method the theoretical “0” point of chlorophyll was found and SAT corresponding to this day was estimated. SAT values were found to be lower in 2014, than in 2013 when it was rainier. During both years SAT values were higher in Murov 2 and Zirva 85 varieties and lower in Tale 38, Bezostaya 1, and 12 IWWYT 9 genotypes compared with other varieties. Productivity of the studied varieties/lines was higher in 2013 than in 2014. A strong correlation between productivity and SAT (R2=0.92 v R2=0.96), as well as between earing dates and SAT (R2=0.98) was observed for both years. Thus, the values of SAT, influencing on autumn bread wheat under rainfed conditions during the grain filling phase can be used as a criterion in breeding programs.

Keywords: Bead wheat, sum of active temperature, productivity

# IPBC MEETING ROOM-II

# SCREENING OF POTATO GENOTYPES FOR PROCESSING QUALITY WITH MOLECULAR MARKERS

Caner Yavuz, İlknur Tındaş, Ayten Kübra Türkmen, Ufuk Demirel, Sevgi Çalışkan, Mehmet Emin Çalışkan

Department of Agricultural Genetic Engineering, Faculty of Agricultural Sciences and Technologies, Niğde University, 51240 Niğde, Turkey

caneryavuzmbg@gmail.com

The selectivity of 3 different SSR markers which are related with chips quality and starch content in diferent types of processing cultivars will be discussed in 120 different varieties and breeding lines with processing and cooking quality. The markers that we used were Stp23-8b, AGPsS-9a and Pain1-8c. The markers were developed from invertase, ADP-glucose pyrophosphorylase gene and plastid starch phosphorylase in order from Pain1-8c, AGPsS-9a and Stp23-8b before in a recent study. The youngest leave parts of potatoes in greenhouse were taken to have DNA isolation during July and after required dilution measurements, unlike AGPsS-9a, touchdown PCR was applied for the rest to increase specifity. It was examined whether the results of experiment lead us to make a certain evaluation to distinguish processing cultivars from cooking cultivars and it will be investigated whether marker selection will provide an easier and quicker way to determine the processing cultivars beforehand.

Keywords: Potato, processing, molecular marker, chips

# ESTIMATING PARENTAL EFFICIENCY OF POTATO GENOTYPES

Ayten Kübra Türkmen, Caner Yavuz, Ramazan İlhan Aytekin, Ufuk Demirel, Sevgi Çalışkan, Mehmet Emin Çalışkan

Department of Agricultural Genetic Engineering, Faculty of Agricultural Sciences and Technologies, Niğde University, 51240 Niğde, Turkey

aytenkubraturkmen@gmail.com

This study was aimed to estimate the parental efficiency of 40 potato genotypes commonly grown in Turkey. The study was conducted in a nethouse in Nigde between May and September in 2015. Each genotype planted in two different dates (April 1st, May 1st) to extend flowering and crossing period. Seed tubers sprouted in 0,75 lt pots, and plants with mother tubers were transferred to larger pots (12 lt) when sprouts reach to approximately 15-20 cm in height. Mother tubers put on the soil surface in larger pots to facilitate stolon removing to promote flowering. Crossings were made early in the morning (between 0600 and 0830) and late afternoon (between 1800 and 2000), and fresh pollens were used in each time. A crossing label indicating the date and time of day, and number of flowers crossed were attached after crossing. The numbers of fertilized and dropped flowers on each inflorescence were determined at harvest of berries. The berries were collected approximately 2 months after pollination, and diameter, height and fresh weight of each berry were determined. The true seeds of each berry were extracted under running tap water in a mesh strainer, and seeds were dried for two days on a filter paper in room conditions. Then, number of seeds per berry, and weight of seeds per berry were determined. The parental efficiency of evaluated genotypes using fruit and seed set values were estimated, and relationships between fruit and seed traits were evaluated with correlation analysis.

Keywords: Breeding, crossing, male efficiency, female efficiency, fruit set, seed set

# DETERMINATION OF PERFORMANCE OF IMPROVED SUMMER SQUASH (*CUCURBITA PEPO*) HYBRIDS VARIATES CANDIDATE OBTAINED FROM F1 HYBRID BREEDING WITH HYBRIDIZATION

Çetin Nacar

Alata Bahçe Kültürleri Araştırma Enstitüsü Erdemli, Mersin, Turkey

cetinnacar@gmail.com

In order to improve suitable variety for squash growing, 92 pure lines which obtained after seven inbreeding, hybridized as male parent with two tester lines according to top-cross method. 25 pure line of sqash where those choosen among the hybridized diffirent commercial hybrid squash variety in Alata Horticultural Research Institute gen pool, then 14 F1 hybrid were selected in terms of their friut charecteristics and yield. Higher yield is one of the most important criteria in under protect growing. Moreover, smoothness of fruit shape, fruit color and tendency to branching were important criteria for selection. According to the those criteria, 3 hybrids varieties candidate (108*203, 365*203 ve 136*280-A) were chosen promising lines suitable for under protect growing.

Keywords: Summer squash, heterozis, yield

# TY13- THE BRIDGE BETWEEN TY1 TO TY3 MARKERS

Eybishtz Assaf

Tomatech R&D Ltd Oppenheimer 5, Park Rabin, Rehovot 76701, Israel

assaf@tomatrch.co.il

Tomato yellow leaf curl virus (TYLCV) is a whitefly-transmitted geminivirus which causes devastating loss of tomato crops worldwide.

This study is based on the known resistance alleles Ty-1, Ty-3 which mapped to different region on chromosome 6. Recent publication suggests they rather be alleles of the same gene (Verlaan et.al; 2013). we collaborated with Dr. Rotem Neta from the Hebrew University and DYN Diagnostics LTD aimed to identify Real Time PCR (RT-PCR) based marker linked to gene confer resistance, a new RT-PCR markers, TY-13 found more reliable in our tested lines. We tested plants from 9 Tomatech commercial hybrids and 34 different lines from F-3 till F-10 generation lines. TY1 match in 72.22 %, TY3 match in 77.77% and TY13 match in 81.11% to the symptom scoring. The added advantage was while TY1 and TY3 markers mismatch was false positive and negative, TY13 mismatch was only false positive, meaning no sensitive plant escaped from TY13 marker.

Further test was made on 376 plants, from 4 different commercial hybrids and 11 different F2 populations. In this analysis we identified four performances: full match between Ty1-Ty3-Ty13, match only between Ty1- Ty13, match only between Ty3- Ty13 and incompatibility between Ty1, Ty3, Ty13. The correlation between the markers was 80% for TY1, 73% for TY3 and 90% for TY13. TY3 marker didn’t respond on one of our F2 populations from the S. habrochaites source, while TY13 fits to TY1 and clearly identified with the symptom scoring.

These results confirmed the reliability and the advantage of using TY13 marker. TY13 identify resistance from several sources, reduces the need of using two different markers in parallel, and increasing the reliability of the decision in the breeding process.

Keywords: Tomato yellow leaf curl virus, markers, resistance, TY13

# EXPLORING TOMATO CHLOROSIS VIRUS-TOMATO INTERACTION FOR UNDERSTANDING THE MECHANISMS OF DISEASE AND SYMPTOM DEVELOPMENT

Bayram Çevik[1], Mehtap Şahin Çevik[2], Emine Doğuş Sivri[2]

1. Süleyman Demirel University, Faculty of Agriculture, Department of Plant Protection.Isparta, Turkey
2. Süleyman Demirel University, Faculty of Agriculture Department of Agricultural Biotechnology. Isparta, Turkey

bayramcevik@sdu.edu.tr

Tomato chlorosis virus (ToCV) causes chlorosis on tomato and it has been spreading and causing significant economical looses in tomato production regions of Turkey and the world in recent years. In the absence of natural resistance to ToCV, development of alternative resistance strategies are necessary. The development of these strategies requires a better understanding of ToCV infection and disease development processes. In this study, ToCV-tomato interaction was investigated at the molecular level by identifying virus-induced changes in the expression of tomato genes. First, an experimental system enabling efficient graft inoculationwas developed for monitoring ToCV infection in tomato. Then, two different cDNA libraries enriched with genes induced or repressed in response to ToCV infection were constructed using suppression subtractive hybridization (SSH) method. The expression of more than 200 genesby reverse northern blot hybridization using nylon macroarray revealed that the expression of 86 genes was induced and 130 genes were repressed by 1.5 fold or greater in response to ToCV infection. Although ToCV infection affected the expression of genes involved in transcription, defense response, metabolism and energy, signaling and protein fate, majority of genes identified were related with structural and functional proteins associated with chloroplast and mitochondria. The expression of more than 50 of these genes was analyzed quantitatively by real-time RT-PCR and the changes in the expression of more than 40 genes were confirmed. The genes identified in this study may be used for understanding the mechanisms of disease development and symptom induction processes of ToCV in tomato.

Keywords: ToCV, Tomato, host-pathogen interaction, gene expression, macroarray, real-time PCR

# INVESTIGATION OF THE EFFECTS OF TOXIC BORON WITH DROUGHT STRESS ON TOMATO

Mehtap Aydın, Hüseyin Tombuloğlu, Güzin Tombuloğlu

Fatih Üniversitesi, Turkey

mehtapaydin23@gmail.com

Boron (B) is an essential micronutrient for plant growth. However, it is toxic in high concentrations. Also, drought is an important abiotic stress factor effecting plant growth and development. In nature, especially in arid and semi-arid conditions, plants face to B-stress further additional stress caused by water deficit. In this study, we focused on how the mRNA levels for three stress-related genes GR1, MT2, and Hsp90 varied under stress conditions involving B stress, drought stress and B + drought stress in order to understand the stress response of plants to Boron (B) stress accompanied by drought. In addition, we performed enzyme activity (MDA SOD, APX, and GR) and chlorophyll content analysis. In accordance with the study objective, the quantitative real-time PCR method was used to analyze the mRNA levels in tomato leaves exposed to B and drought stress. The results indicated that mRNA levels for these three genes increased under B and drought stress. The highest increase was observed in the mRNA levels for GR1 (7-8 times higher compared to the control), which indicated that the oxidative stress enzyme was activated to raise tolerance against to B and drought stress. In this study, MDA levels were also determined in order to assess stress levels. According to the chlorophyll content test, B and drought stress led to an increase in the amount of chlorophyll. B and drought stress also had the effect of decreasing SOD enzyme activity, while increasing APX and GR enzyme activity. According to these results, through the activation of stress-related genes and tolerance mechanisms, drought stress may actually serve to remedy Boron toxicity in tomato plants.

Keywords: B toxicity, Drought, HSP (Heat-shock Protein), GR (glutathionereductase), MT2 (metallothionein), RT-PCR (Reverse Transcriptase Polymerase Chain Reaction), MDA (malondialdehyde).

# EMASCULATION, POLLINATION, FRUIT SET AND SEED QUALITY IN EARLIER SWEET CHERRY VARIETY BREEDING

Hasan Cumhur Sarısu, Ömer Faruk Karamürsel

Fruit Research Institute, Egirdir, Isparta, TURKEY

hcumhurs@hotmail.com

Early sweet cherry variety breeding have gained momentum in different countries. In this study, it was aimed to determine success of crossing in different varieties which had low chill requirement and early maturing. 0900 Ziraat, Prime Giant and Early Lory as female parent, Early Lory, Bernard and Sweet Heart, Davraz as male parent were used in 2015 blooming time. In female 0900 Ziraat combinations, average 23.68% fruit set and 20.5% quality seeds rate were determined, in Prime Giant female combinations, it was achieved by average 7% fruit set and 6.4% rate of seed quality. Average 5.13% fruit set was counted and quality seeds could not be obtained in Early Lory female combination. Therefore embryo rescue techniques should be integrated into earlier variety breeding programs.

Keywords: Sweet cherry, low chilling, crossing, emasculation, breeding

# AN EXAMPLE TO THE USE OF GENETIC RESOURCES FOR IMPROVEMENT THE RESISTANCE: THE DEVELOPMENT OF NEW POWDERY MILDEW TOLERANT GRAPE VARIETIES

Cengiz Ozer[1], Erhan Solak[1], Nuray Özer[2]

1. Viticultural Research Instıtute 59100 Tekirdağ - TURKEY
2. Namık Kemal University, The Agricultural Faculty of Tekirdağ, Plant Protection Department, Tekirdağ - TURKEY

ozercengiz@gthb.gov.tr

Powdery and downy mildew are the main threats for viticulture all over worlds and most V. vinifera varieties are susceptible to these diseases. The hybridization studies had been made with the use of disease resistant wild species or hybrid varieties as one of the parents. The native grape varieties to the very rainy Northeastern coastal area of Turkey are grown without any fungicide application. These varieties including some V. labrusca types had been collected at National Collection Vineyard and used for cross-breeding studies. Among the selected genotypes for further studies, Italia x Favli - 149 showed minimum average powdery mildew index (1,43) between 2010 and 2013. This genotype was registered as Özer Karası while Italia x Mercan-174 and Italia x 28/259 had been identified as promising candidates. Quality properties of these genotypes and tolerance data at in vitro and in vivo conditions are presented in this study.

Keywords: Grapevine, powdery mildew, tolerance, breeding

# EVALUATION OF GENETIC DIVERSITY AND STRUCTURE OF LEONURUS SPP. POPULATIONS BASED ON INTER-PRIMER BINDING SITE (iPBS) MARKERS

F. Borna[1,2*], S. Luo[2], N. M. Ahmad[2] , V. Nazeri[1], M. Shokrpour[1], R. Trethowan[2]

1. Department of Horticulture, Faculty of Agriculture, the University of Tehran, Iran.

2. Plant Breeding Institute, Faculty of Agriculture and Environment,
University of Sydney, 107 Cobbitty Road, Cobbitty, Nsw 2570, Australia

fatemehborna@gmail.com

The availability of genomic information for many medicinal plant species is limited. DNA markers do not require prior knowledge of DNA sequences are therefore appealing for assessing genetic diversity and relationships among species, accessions and breeding materials. Inter primer binding sites (iPBS) markers developed from conserved primer binding sites within retrotransposons, was used to study the genetic variation and relationships in Leonurus spp. 89 genotypes of *Leonurus cardiaca* (comprised 79 from Iran and 10 collected in Australia) and 15 additional accessions of two related species (*L. heterophylus* and *L. sibericus*) collected in Australia were also included. PCR of 7 iPBS primers (dominant markers) produced a total of 191 bands ranging from 180 to 4000 bp and the mean PIC value for each primer ranging from 0.2213 to 0.3206. Genetic variation calculated using Shannon's Information index (I) and Nei's gene diversity index (H) showed high genetic diversity in studied germplasm. Ordination and cluster analysis showed that the genetic relationships among all accessions could be separated into three major groups *L. cardiaca, L. heterophylus* and *L. sibericus*. However, among the 89 accessions of *L. cardiaca*, genotypes collected from the same geographic region tended to cluster together, thus indicating greater genetic similarity. The Motherwort accessions originating in Iran are highly divergent and possess abundant genetic diversity and clearly provide a basis for selection and breeding. The iPBS PCR-based genome fingerprinting technology in this study is low-cost and provides another effective alternative in differentiation of accessions in Motherwort (*Leonurus cardiaca*) and related species.

Keywords: Genetic diversity, Germplasm, Plant breeding, Motherwort, iPBS.

# TOWARDS THE IDENTIFICATION OF SSR MARKER LINKED TO VIGOR IN OLIVE TREE (*OLEA EUROPEA L.*)

Zaher H.[1], Boulouha B.[1], Baaziz M.[2], Gaboun F.[1]

1. INRA Marrakech, Morocco

2. Faculty of sciences Semlalia, Marrakech, Morocco

hayatzaher@yahoo.fr

In this study, a progeny resulting from a cross between “Menara” and “Arbequina” varieties was characterized by both morphological and SSR markers (microsatellites). The technique Bulk Segregant analysis (BSA) was used to establish linkage between molecular markers and vigor parameters (tree height, perimeter of trunk diameter and canopy circumference). Thirty SSR primers were used to compare the parents and bulks of individuals of different vigor. Eleven SSR primers were selected for their ability to detect polymorphism between the two parents and bulks. Results of morphological analysis showed highly significant genotypic differences for all measured parameters. Principal component analysis revealed highly significant phenotypic variation where the first two axes represented 85.32 % of the total variation. For association analysis, results obtained by the General Linear Model showed that some of the used SSR markers are significantly associated with the phenotypic traits studied. Two SSR markers, DCA9 ($p < 0.05$) and GPAU59 ($p < 0.05$), were found significantly associated with tree height. Also PA2 ($p < 0.05$) and GPAU59 ($p < 0.05$) were associated to the perimeter of trunk diameter. Finally GPAU59, DCA9 and DCA18 were linked with the canopy circumference. These results are of great importance and incite to use these primers association analysis in characterizing our olive progeny.

Keywords: Olea europea, morphological characterization, molecular marker, SSR, association analysis

# IMPORTANCE OF SEXUAL AND ASEXUAL VARIATIONS IN THE DIVERSIFICATION PROCESS OF CULTIVATED OLIVES TREES IN THE MEDITERRANEAN BASIN

Abdelmajid Moukhli[1,5*], Laïla Essalouh[2], Ahmed El Bakkali[3] , Melek Gurbuz-Veral[4], Cherkaoui El Modafar[5] Nurengin Mete[4] and Bouchaib Khadari[2]

1. INRA, CRRA de Marrakech, U.R. Amélioration génétique des Plantes et de la Qualité (URAPQ), BP 533 Menara, Guéliz, 40000 Marrakech, Maroc.
2. INRA-CBNMed-Montpellier SupAgro, UMR 1334 Amélioration Génétique et Adaptation des Plantes (AGAP), F-34070 Montpellier, France.
3. INRA, CRRA-Meknès, U.R. Amélioration des Plantes et Conservation des Ressources Phytogenétiques (APCRPG), BP 578 Meknès, Maroc.
4. Olive Research Institute (ORI), Universite Cad. No: 43 Bornova 35100 Izmir, Turkey.
5. Laboratoire de Biotechnologie, Valorisation et Protection des Agroressources, Faculté des sciences et techniques Guéliz, B.P. 618, 40 000 Marrakech, Maroc.

moukhli2000@yahoo.fr

The relative importance of seeds and pollen genes flow in olive's varieties diversifica- tion and the somatic mutations accumulated during the history of the vegetative spread of olive's varieties in the Mediterranean Basin are presented according to a parentage analysis approach. For cultivated olive trees, the new genotypes issued from cross be- tween known varieties are less represented in the analyzed samples. Sexual selection of wild or feral olives and asexual variation are equally represented in the Mediterranean Basin. The process of diversification of the cultivated olive trees combines asexual vari- ations caused by mutation in the vegetative propagation with sexual variations obtained by spontaneous sowing seeds. Pairwise comparisons show that varieties whose differ by less than three loci are important reflecting an asexual variation. Similarly, the num- ber of accessions whose relatives have not been revealed by parentage analysis is large, suggesting a selection of local seeding involving wild or feral olives trees. This study show that farmers combine the advantage offered by sexual reproduction in creating diversity and the benefits of fixing the desired characters offered by vegetative propa- gation to obtain new varieties with better adaptation to environmental changing condi- tions. Our results also show that farmers benefit from the immediate advantage offered by asexual mutation variability to maintain their best genotypes from recombination effect while offering their varieties new desired traits to their needs. Furthermore, our results show in the case of Morocco, genomes displacement and asexual variations are important in olive varietal diversification compared to France, Spain, where the seed selection appears more important in varietal diversification.

Keywords: Gene flow, diversification, mutation, Pedigree, pollen, seed,
Olea europaea L., Mediterranean Basin.

# A NEW OLIVE VARIETY HAYAT

Filiz SEFER, Uğur GÜLOĞLU, Hülya KAYA, Nurcan ULUÇAY, Nurengin METE, Öznur ÇETİN, Mustafa ŞAHİN

Olive Research Station, Üniversite Cad. No: 43 Bornova, İzmir Turkey

filiztengizsefer@hotmail.com

New varieties are required in olive growing because of developing new socio-economic conditions in the world. For this aim, the Project titled "Variety Development By Crossbreeding In Olive" has been carried out with the aim of obtaining new table and oil varieties at the Olive Research Station . In the on-going studies, Memecik, the most important olive variety in the Aegean Region, was crossbred with the various varieties selected by taking into consideration their different characteristics. Among eleven candidate varieties determined during the pre-selection period, a crossbred coded as MG5, from Memecik x Gemlik combination, has been determined as the first variety evaluating its characteristics such as suitability the new growing techniques and mechanization, high productivity and high table olive and oil quality, and early and homegen ripening. This new olive variety officially registered with the name of Hayat has superior characteristics especially from the standpoint of growing as green table olive. Besides, the superiorities in terms of high oil rate and positive sensorial oil charesteristics of Hayat (fruity smell, bitterness, pungency) also point out this variety to be suitable for dual purposed utilization.

Keywords: New variety, olive, hybridization

# MOLECULAR CHARACTERIZATION OF TURKISH HAZELNUT (*CORYLUS AVELLANA L.*) GERMPLASMS

Süleyman Can Öztürk[1], Gökhan Kızılcı[2], Ömür Duyar[2], Hüseyin İrfan Balık[2], Selda Balık[2], Ahmet Göğüs[2], Sami Doğanlar[1], Anne Frary[1]

1. İzmir Yüksek Teknoloji Enstitüsü
2. Giresun Fındık Araştırma İstasyon Müdürlüğü

suleymanozturk@iyte.edu.tr

Turkey is the important hazelnut producer in the world. Turkish hazelnut resources should be examined for their molecular genetic diversity and potential for improvement of hazelnut. For this reason, 407 Turkish hazelnut genotypes which are represent wide range of Turkish hazelnuts were screened with 30 pairs of SSR primers. 388 SSR alleles were found. Diversity analysis of the Turkish hazelnut genotypes indicated that they were classified to three clusters according to hoc statistics and Neighbor-joining algorithms (r= 0.98). A total of 40 individuals were selected for core collections of Turkish hazelnut genotypes with SSR data. This core collection represents a maximum of genetic diversity in a minimum number of individuals. Examination of Turkish hazelnut diversity is a first step toward identification and genetic mapping of agronomic and biochemical traits of interest.

Keywords: Hazelnut, Simple Sequence Repeat, Molecular Markers

# IDENTIFICATION OF DIFFERENT COBALT-60 IRRADIATED NAGAMI KUMQUAT GENOTYPES WITH RAPD MARKERS

Cennet Kara, Zeynel Dalkılıç*

Adnan Menderes University, Faculty of Agriculture, Department of Horticulture,
South Campus 09100 Aydın, Turkey

zdalkilic@adu.edu.tr

Nagami kumquat (*Fortunella margarita L.*) and trifoliate orange (*Poncirus trifoliata* (L.) Raf.) were used as scion and rootstock, respectively, in this study. Nagami kumquat budwoods were treated with 0, 15, 30, 45, 60 Gy cobalt-60 gamma irradiation in July 2013. Irradiated budwoods were T-budded on two-year-old trifoliate orange rootstocks grown in a high plastic tunnel. From total of 248 budded plants, only 48 plants were successful in bud take. Thus, M1V1 plants were obtained. However, only 30 plants survived until fruit setting time. Bud take ratio in plants grown in high plastic tunnel was between 18.8 % at 60 Gy and 43.8 % at 15 Gy. The mophological measurements were ranged as follows: stem height 20.98 cm at 45 Gy-39.02 cm at 0 Gy, diameter 4.78 cm at 30 Gy and 45 Gy-5.72 cm at 60 Gy, node number 26 at 30 Gy and 45 Gy-47 at 0 Gy, fruit number 2.40 at 60 Gy-5.50 at 45 Gy, and fruit diameter 16.20 mm at 60 Gy-18.99 mm at 0 Gy approximately 16 months after budding. Plant no: 12 (S-26-45) was determined as different from other plants using RAPD primers. PM2, PM3, PM4, PM5, PM7, and PM8 primers gave four polymorphic and 14 total bands. It was observed that Nagami kumquat budwood resist to 60 Gy cobalt-60 gamma irradiation. Therefore, it is recommended to apply higher doses of cobalt-60 to test susceptibility levels of kumquat.

Keywords: *Fortunella margarita, Poncirus trifoliata*, cobalt-60 irradiation, nursery tree characteristics, RAPD markers, PCR

# EVALUATION OF PRODUCTION TECHNOLOGIES FOR SEED YIELD OF IRON WEED

Habib Ahmad[1*], Ishtiaq Ahmad[2], Inamullah[1], Zulfiqar Malik[1], Waqar Ahmad[1], Niaz Ali[2], Haidar Ali[3], Noman Fazal[1], Malika Khatoon[2]

1. Department of Genetics, Hazara University Mansehra, Pakistan

2. Department of Botany, Hazara University Mansehra, Pakistan

3. Center of Plant Biodiversity, University of Swat, Pakistan

drhahmad@gmail.com

Iron Weed (*Vernonia anthelmintica*) has immense genetic potential for cultivation as a commercial crop on marginal lands, particularly in the subtropical and cool temperate agroclimatic conditions of Pakistan. This article communicates the results of Vernonia germplasm evaluated for seed yield in the Mansehra District. Performance of the germplasm was evaluated through the application of different sowing methods, seed rates, herbicide application and plant density. The parameters evaluated were plant height, number of leaves per plant, number of branches per plant, leaf area, number of capitula per plant and seed yield per hectare. Analysis of variance showed highly significant difference for yield component traits. The correlation coefficient indicated that seed yield had highly significant and positive correlation with number of capitula per plant and number of branches per plant, significant and positive correlation with plant height and non-significant positive correlation with leaf size and number of leaves per plant. Similarly seed yield had very strong, highly significant and positive regression with 7.867 and 5.602 regression coefficients for number of capitulum and number of branches, respectively. Weak, positive and significant regression with 5.221 regression coefficient for plant height and weak, positive but non-significant regression with 3.858 and 5.602 regression coefficient for leaf area and number of leaves, respectively. It is concluded that both the planting method and herbicide application has evident effect on seed yield in Iron Weed. Our results revealed that in the rain fed conditions, the broadcast method, with herbicide spray before sowing provides maximum yield.

Keywords: Vernonia anthelmintica, Production Technology, Seed yield, Pakistan

# FARMER-SCIENTIST INTERFACE FOR DEVELOPMENT OF VARIETIES AND THEIR PROTECTION

Munish Nagpal

Sub Divisional Officer (Civil) and Sub Divisional Magistrate Ratia, Dist. Fatehabad, Haryana, Govt. of Haryana

munishnagpal1@gmail.com

Survey of literature reveals that Farmers world over have been able to develop through selection and even hybridization improved local strains and varieties of various crop commodities. Farmers' right is a concept to help support grass root innovators to develop/identify plant materials with their own intellectual propriety. This concept has been developed and adopted in FAO by all member countries, India being one of the first countries in the world to have passed legislation granting Farmers' Rights in the form of the Protection of Plant Varieties and Farmers' Rights Act, 2001. India is a gene rich country with vast traditional knowledge. Farmers' Rights are important as India is a center of biodiversity and farmers have evolved large number of local strains which serve as reservoir of genes against abiotic and biotic stresses and po- tential bio resources to mitigate effects of Climate change. Since Farmers and scien- tists can develop improved varieties through participatory plant breeding activities, it is important to have Plant Variety Protection Rights for both farmers as well as Plant Breeders. As per Seed Bill passed by Government of India, both Farmers and Breeders rights are protected. The Breeder is rewarded for his innovation by having control of the commercial market place but without being able to threaten the farmers' ability to independently engage in his livelihood, and supporting the livelihood of other farmers. Participatory plant breeding is an effective pathway to develop strains of crop varieties adapted to local conditions and to maintain genetic diversity among the varieties cultivated. The term, participatory plant breeding refers to a set of breeding methods, characterized by many different potential forms of interaction between farmers and breeders. The plant breeders and farmers worked together to produce improved varieties of maize for the low-resource farmers of the Panchmahals district of Gujarat, India. Initially, farmers developed and released GM-6 for cultivation in hill areas of Gujarat and Toria varieties in Haryana, Bikaneri Narma in Rajasthan etc. states of India.

Keywords: Farmer's variety, Seed Bill, Participatory plant breeding,
Plantvariety protection, farmers-scientists interface

# ANALYSIS OF THE RELATION BETWEEN THE PLOIDY LEVELS OF *HYPERICUM PERFORATUM* L. AND THE AMOUNT OF HYPERICIN PRODUCED

Gülsemin SAVAŞ TUNA[1], Gözde DUYU[1], Kardelen UZUN[1], Gülru YÜCEL[2], Ahsen YILMAZ[3], Metin TUNA[4]

1. Ebru Nayim Science High School, Tekirdağ, Turkey
2. Namık Kemal University, Faculty of Science and Letters, Department of Biology, Tekirdağ, Turkey
3. Namık Kemal University, Faculty of Medical, Department of Biochemistry, Tekirdağ, Turkey
4. Namık Kemal University, Faculty of Agriculture, Department of Field Crops, Tekirdağ, Turkey

glsvs@yahoo.com

*Hypericum perforatum* L., commonly known as St. John's Wort, produces hypericine, which is used in the treatment of many diseases. The amount of hypericin produced varies according to the ploidy level of the plant. In this study a comparison is made between the ploidy levels of H. perforatum L. populations present in the natural flora of Turkey and the amounts of hypericin produced by plants that were collected from the same geographical area but had different ploidy levels.

Seeds from 39 Hypericum perforatum L. populations collected from 23 different geographical areas of Turkey were planted in multipods and seedlings were obtained. In the flow cytometry analyses it was found that the nuclear DNA contents of the populations varied between 0.8 and 2.38 pg2C-1 and the populations had three different ploidy levels. One of the populations was diploid (0.76–0.84 pg2C-1), 38 of the populations were tetraploid (1.36–1.73 pg2C-1) and 5 of the populations were hexaploid (2.15–2.56 pg2C-1). Three plants from each of the İzm1a (diploid), İzm2 (tetraploid) and İzm1b (hexaploid) populations that were collected from the same geographical area were chosen and hypericin analysis was carried out according to a DAC 86 (DAC 1986) codex. In the analyses, it was found that the mean hypericin amount in diploid plants was 2.49%, while it was 1.27% in tetraploids and 1.43% in hexaploids.

As a result of the study, it was found that diploid plants produced more hypericin compared to tetraploid and hexaploid plants. It is recommended that the ploidy levels should be primarily determined in the studies on increasing the amount of hypericin, comparing the amounts of hypericin produced by plants from different areas or cultivation.

Keywords: *Hypericum perforatum*, ploidy level, hypericin produced

# SYRINGA BREEDING IN NIKITSKY BOTANICAL GARDENS

Yuriy Plugatar, Zinaida Klimenko, Vera Zykova

Nikita Botanical Gardens – National Scientific Center, Yalta, 298648,
Russian Federation

zykova_vera@mail.ua

Syringa collection of Nikitsky Botanical Gardens (NBG) has been forming since 1813. 18 Syringa species and about 100 cultivars were successfully introduced. The most perspective cultivars were chosen for landscaping of the Crimea and future breeding work. Syringa breeding was initiated in 1941 by Nikolay Kostetsky and continued by Klymenko Vera, Klymenko Zinaida, Alexandr Grigoryev, who bred cultivars adapted to the Crimean soil and climatic conditions and characterized by highly ornamental properties. Nowadays scientific objective of Syringa breeding in the Crimea is to obtain new cultivars with the following characteristics: high level of drought-resistance; early periods of flowering; pure and bright color capable not to fade; large sized simple or double flowers and inflorescences. Method of combined breeding was in use. NBG selectionists bred about 30 cultivars and formed hybrid fund including 100 hybrid seedlings as a result of 12 crossing combinations. After long-term test there were 10 new perspective forms more, marked out in this hybrid fund. Cultivars “Sevastopol waltz “ and “Eltigen” were included into assortment of federal project “Victory Syringa” in 2014 Analyzing inheritance of morphologic characteristics of flowers and inflorescences in conducted crossings it was found out that maternal parent form has prevailed effect on flower form and doubling while paternal parent form – on flower and inflorescence size.

The study was funded by research grant (№ 14-50-00079) of the Russian Scientific Foundation.

Keywords: Syringa, cultivar, breeding, Crimea

# GENOFOND FOUNDATION OF GARDEN ROSE DOMESTIC CULTIVARS IN NIKITSKY BOTANICAL GARDENS

Yuriy Plugatar, Zinaida Klimenko, Vera Zykova

298648, Urban Vil. Nikita 15,5, Yalta, The Republic Of Crimea, Russian Federation

klimentina55@mail.ru

Foundation of garden rose genofond collection in Nikitsjy Botanical Gardens (NBG) was initiated in 1812. It included rose cultivars and species from various regions of the world. In 1824 they were basis for breeding investigations which were grounded at the same time with plant introduction. The study objective was to breed abundant and multi flowering cultivar, resistant to fungal diseases under conditions of South Russia. Out of the total studied cultivars, species and forms (more than 6 thousand), it was marked out 100 of the most valuable cultivars-donors with important economically biological characteristics, 43 tolerant cultivars and 16 of the most mutable cultivars, which were used in breeding investigations. Different hybridization methods (intervarietal, closely related, remote), sampling of seedlings out of freely pollinated seeds within collection plantations, clonal selection and experimental mutagenesis (radiation and chemical) were applied in terms of breeding. A new system of garden rose complex breeding that combines different methods of hybridization and experimental mutagenesis was developed and tested. It made possible to extend spectrum of form-building processes for rose culture, shorten breeding terms of highly ornamental cultivars. Conducted researches resulted in formation of genofond including 300 domestic cultivars, hybrid and mutagenic forms, that belong to 9 garden rose groups (Grandiflora, Groundcover, Floribunda, Hybrid Tea, Miniature, Polyantha, Rambler, Rosa Kordesii, Shrub), for cultivation on south of Russia, where 14 of them were zoned.

The study was funded by research grant (№ 14-50-00079) of Russian Scientific Foundation.

Keywords: Introduction, genofond, garden roses, cultivar, breeding, mutagenesis

# PHENOLIC COMPOUNDS IN THE INFLORESCENCES OF LAVANDIN (LAVANDULA X INTERMEDIA EMERIC EX LOISEL)

Paliy Anfisa, Rabotyagov Valeriy

Nikita Botanical Gardens – National Scientific Center, Yalta, 298648,
Russian Federation

onlabor@yandex.ru

Lavandin (Lavandula x intermedia Emeric ex Loisel) is a promising aromatic crop with high yield and content of essential oil. Furthermore, Lavandin produces phenolic compounds able to scavenge radicals. In Nikita Botanical Gardens are maintained long-term work on the introduction and selection of Lavandin, as a result of which a number of commercially valuable cultivars and forms have been obtained. Phenolic compounds content and their component composition were investigated in the inflorescences` extracts for 2 cultivars and 6 varietal forms of Lavandin. Eleven phenolic compounds were identified by liquid chromatography method, including hydroxycinnamic acids, flavones glycosides and flavanone. Maximum concentrations were found for p-coumaric acid and apigenin glycoside. It has been demonstrated that tested cultivars and varietal forms of Lavandin are promising sources of flavonoids and hydroxycinnamic acids.

This study was funded by a research grant No 14-50-00079 of the Russian Science Foundation.

Keywords: Lavandin; cultivars; varietal forms; phenolics; hydroxycinnamic acids; Flavonoids

# PLANT GENETIC RESOURCES, CRYOPRESERVATION, PLANT BIOTECHNOLOGY

Dzhunusova M.[1], Morgounov A.[2], Botalinov R.[3], Jumakadyrova N.[4]

1. Kyrgyz-Turkish Manas University
2. CIMMYT
3. Agriculture Co-operative
4. Kyrgyz State Center for Variety Testing 56, Avenue Mira, Bishkek, Kyrgyzstan

mdzhunusova@gmail.com

Evaluation productivity and biology special of donors to resistance yellow rust of bread wheat in Chui regions in conditions of Kyrgyzstan. The crosses were performed between resistant and susceptible Kyrgyz varieties with resistance germplaSm from CIMMYT, ICARDA and introduction varieties from Central Asia. Conducted a one-two backcrosses. As standards, the yield was taken Kyrgyz varieties Tilek and Intensivnaya. We are used as a control universal international susceptible standard - Morocco. Methods of research: Hybrid analysis, breeding, field and laboratory researches. We are selected from hybrids F2-4. (hybrid and transgressive segregation). According to the study of genetics and breeding obtained germplasm to resistance to yellow rust and higher productivity. In the basic hybrid analysis, selected of 9 donors to resistance yellow rust with connection high productivity. In studying the breeding value of selected lines we carried out genetic differentiation on the basis TKW based on the degree of destruction yellow rust. resources, Now creation new perspective varieties bread wheat to resistance biotic and abiotic factors as Janym, Ajar, Manas.

Keywords: Bread wheat, resistance, yellow rust, quality, breeding, seed production.

# WILD TETRAPLOID OAT SPECIES: A NEW CHALLENGE TO IMPROVE OAT CULTIVATION IN MOROCCO

Nezha Saidi[1], Chaouki Al Faiz[2], Naima Shaimi[1], Mohamed Bouksaim[3],
Gideon Ladizinsky[4]

1. INRA, RU Plantbreeding, ConservationandValorisation of Plant Genetic Resources, RCAR-Rabat, P.O.Box 6570, Rabat Institutes, 10101, Rabat, Morocco
2. INRA-Rabat, Dpt. of Plant Genetic Resources, Avenue de la Victoire, B.P. 415, Rabat, Morocco
3. INRA, RCAR-Rabat, Foodprocessing laboratory, Mohamed Belarbi Alaoui Street, P.O.Box: 6356, Rabat Instituts, Morocco.

4. PrincipalInvestigator, USAID, Project No. TAMOU 97-053, Washington, DC 20523, U.S.A

Morocco is the centre of diversity for genus Avena, counting the existence of 29 spe- cies among the 30 taxa which belong to this genus. Two tetraploidoat species A. magna- Murph and Terrell., endemic of Morocco, and A. murphyi Ladiz. endemic of Southern- Spain, found to be of great nutritive value since their groat protein content exceeds that of the common oats by 30 to 40%. Due to their economic value, the National Institute for Ag-riculturalResearch (INRA) Morocco boosted a research programme aiming the improve-ment of the Moroccan hexaploid cultivars by transferring to the mthetetraploid high groat protein content in order to improve their groat nutritive value; through hybridisation- work. Groat technological analysis of the derivative lines revealed that the groat protein content of the developed hexaploid lines was improved by 4 to 56 % and 1 to 18 % by A. magna and A. murphyi respectively. Derived lines have also shown a good grain beta-glucan content ranging from 1,37 % to 6,05 %. Grainyield of the lines derived-from the cross involving A. murphyi was improved by 7 to 22 Qx/ha, compared to th- at of their hexaploid parents Amlal (37 Qx/ha) and Zahri (22 Qx/ha) respectively. As for resistance to diseases, the developed lines have shown a good resistance to crown rust, powdery mildew and barley yellow dwarf virus. Two developed lines issued from the cross- with A. murphyi are recently suggested forregistration at the national catalogue to be con-ceived for human consumption.

Keywords: Oats, hexaploid oat (2n=6x=42), tetraploid oat (2n=4x=28),
interspecific crosses, groat nutritive value, disease resistance,
variety registration

# EUCARPIA
# MEETING ROOM

# POTENTIAL LINE DEVELOPMENT WITH HIGH SEED YIELD, OIL YIELD AND OLEIC ACID BY HYBRIDIZATION BREEDING IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

Sabri Erbaş, Hasan Baydar

Süleyman Demirel Üniversitesi Ziraat Fakültesi Tarla Bitkileri Bölümü,
32260, Isparta, Turkey

sabrierbas@sdu.edu.tr

The study was carried out to determine agronomic (flowering time, maturing time, plant height, branches number per plant, head number per plant, head diameter, seed number per head, harvest index, 1000 seed weight and seed yield) and quality (oil content, husk ratio, oil yield and fatty acid composition) characters of F5 and F6 generations derived from a cross between Dinçer 5-118 (spineless-red flower) x Montola 2000 (spiny-yellow flower) in 2018 and the research was carried out in 2014. 12 lines of F5 generations, 5 lines of F6 generations and 6 cultivars (Dinçer 5-118, Montola 2000, Remzibey-05, Balci, Linas and Olas) were used as plant material. The lowest seed yield was found in Montola 2000 (80.3 kg/da) cultivar. The highest seed yield was observed in F5-82 (308.1 kg/da), followed by F5-31 (286.0 kg/da), F5-88 (265.3 kg/da), F6-37 (258.6 kg/da) and F6-189 (250.0 kg/da). The oil content of cultivars and lines ranged between 28.5-36.0% and highest oil content was determined at F6-98 line. Linoleic acid content of Dinçer 5-118 was 79.11%, oleic acid content for Montola 2000 was 76.90%. Seven lines contained high oleic acid (66.81-82.94%), Seven lines contained mid-oleic acid (36.19-57.11%), and three lines contained low oleic acid (16.34- 17.01%). As a result, 10 lines were selected based on seed and oil yield, oil content and oleic/linoleik acid when compared with parents and other cultivars. These lines will be used for adaptation and stability trials at five locations (Isparta, Eskişehir, Konya, Edirne and Şanlıurfa).

Keywords: Safflower, Carthamus tinctorius, line development, yield, oil content, oleic acid

# VALIDATION OF FIELD RESISTANCE TO LATE LEAF SPOT BY USING A MOLECULAR MARKER IN GROUNDNUT

Engin YOL[1], Hari D. UPADHYAYA[2], Bülent UZUN[1]

1. Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya, Turkey
2. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

enginyol@akdeniz.edu.tr

Groundnut or peanut (*Arachis hypogaea* L.) is an important oilseed crop which is valued as a rich source of high quality edible oil, protein, minerals and vitamins. It offers nutritional and economic benefits to the consumers and farmers, respectively. However there are many biotic and abiotic constraints to groundnut production in various eco-agricultural systems. The late leaf spot (LLS) is one of the most widespread and damaging foliar diseases of groundnut and it can reduce pod and fodder yields to an extent of over 50%, also affects adversely quality of seeds. Much of the global groundnut breeding efforts therefore have been directed to develop cultivars with high yields and also incorporating genes conferring resistance or tolerance to LLS disease. Integration of molecular marker aided selection with field based breeding is important to enhance the precision and speed of developing peanut cultivars with LLS resistance. In this perspective, many LLS resistance-related molecular markers have been developed to aid in the selection processes. The SSR marker, PM 384, is one of these markers and showed significant association with LLS resistance (Shoba et al. 2012, Euphytica, 188:265-272). The groundnut collection including 39 genotypes was employed for validating LLS resistance-linked marker (PM 384) and identifying resistant individuals. These genotypes were evaluated in the field with nine point disease scale to screen the genotypes for sources of resistance to LLS. Plants with a disease score of 1-3 and 6-9 were designated as being resistant and susceptible, respectively. After field evaluation, field scored genotypes were validated by LLS resistance using the linked marker, PM 384.

Acknowledgments: This study was supported by the Ministry of Science, Industry and Technology of Turkey and the Scientific Research Projects Coordination Unit of Akdeniz University (grants SANTEZ-01527-STZ-2012-2 and FDK-2014-140, respectively).

Keywords: Marker-assisted selection, selection, peanut, molecular markers, foliar disease

# EVALUATION OF GRAIN YIELD AND QUALITY CHARACTERISTICS OF SOME SAFFLOWER (*CARTHAMUS TINCTORIUS* L.) GENOTYPES WITH BIPLOT ANALYSES

Hasan Keyvanoğlu[1], İsmail Demir[2], Yusuf Arslan[3], İlhan Subasi[1]

1. Central Research Institute of Field Crops, Ankara, Turkey
2. Ahi Evran University, Agriculture - Faculty Department of Field Crops, Kırşehir, Turkey
3. Abant Izzet Baysal University - Faculty of Agriculture and Natural Sciences, Department of Field Crops, Bolu, Turkey

hasankeyvanoglutarm@gmail.com

In this research, yield components and quality traits of some safflower genotypes selected among preliminary yield trials in Ankara ecological conditions in the cropping season of 2014. The field experiment was conducted according Augmented design with 30 introduction material from 3 domestic safflower varieties (Remzibey, Dinçer, Balcı) obtained from Eskişehir Transitional Zone Agricultural Research İnstitute. According to the results of this study, there was high variation among accessions seed yield (78.4-343.1 kg/da), crude oil ratio (19-38%), Linoleic fatty acid composition (11.1-80.52%) and crude protein ratio (11.3-18.5%). Biplot analysis was used to investigate the relationships between grain yield and quality traits. In the evaluation using the Biplot graph, oleic acid and crude oil ratio were involved in the group I while crude protein ratio, stearic acid and palmitic acid were involved in the group II. On the other linoleic acid were involved in the group III. According to the results of research, genotypes showing high performance in terms of examined traits were selected for plant breading research.

Keywords: Biplot analyses, safflower, quality traits, grain yield, fatty acid composition

# THE COMPARISON OF SESAME (*SESAMUM INDICUM* L.) POPULATIONS SUPPLIED FROM DIFFERENT REGIONS OF TURKEY BASED ON QUALITATIVE AND QUANTITATIVE TRAITS

Aynur Bilmez Özçınar[1], Tahsin Söğüt[2]

1. Siirt Üniversitesi, Turkey
2. Dicle Üniversitesi, Turkey

a.bilmez_21@hotmail.com

This study carried out in the experimental area of Dicle University Faculty of Agriculture, Department of Field Crops in 2014 growing season. A total of 110 diverse sesame accessions (107 local and 3 cultivars as check) collected from Mediterranean, Aegean and Southeastern Anatolia Region of Turkey were sown on 3 May 2014.The experiment laided out in an augmented experimental design with eleven replications. Each plot has a size of 1.4 x 5 m2 with two rows (with a row to row spacing of 70 cm and plant to plant spacing of 10 cm).A total of 24 morphological and agronomical characters of 110 sesame material were evaluated following to IPGRI (International Plant Genetic Resources Institute) descriptors of sesame, and the obtained data was evaluated according to their qualitative and quantitative. The analysis of variance of the data was done and grouped according to the method of multiple comparisons (JMP Statistical Package Program).Correlation coefficients were determined by calculating the relationships between the traits.As a result of this study, it was determined sesame materials which have high yield and agro-morphological performance to provide an infrastructure for use in breeding programs.

Keywords: Sesame, Population, Qualitative Characteristics, Quantitative Characteristics

# GENETIC VARIATION IN CARBON ISOTOPE DISCRIMINATION AND ESTIMATED-WATER USE EFFICIENCY IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

Afifuddin Latif Adiredjo[1], Philippe Grieu[2]

1. Brawijaya University, Faculty of Agriculture, Department of Agronomy, Plant Breeding Laboratory, Malang 65145, Indonesia

2. Université de Toulouse, INP - ENSAT, UMR 1248 AGIR (INPT-INRA), Castanet-Tolosan 31326, France

al.adiredjo@gmail.com

Leaf carbon isotope discrimination (CID) has been proposed as an indirect tool for selection of water use efficiency (WUE) in several C3 plants. However, it is rarely used in sunflower. To evaluate the genetic variation of CID and the genetic correlation between CID and estimated-WUE, CID was measured in a population of recombinant inbred lines (RILs) of sunflower (Helianthus annuus L.). Estimated-WUE, called “potential” WUE (WUEp), was calculated as the ratio of assimilation potential (Ap) to transpiration per day at flowering (Ef). The CID was significantly varied among RILs and there was significant negative genetic correlation between CID and WUEp. Wide genetic variability for CID is reflected by its high heritability, where the heritability of the CID was higher rather than the WUEp. CID can be used as an indicator to determine WUE and appears to be a valuable trait in breeding to improve WUE for the sustainability of sunflower crops and industries.

Keywords: Sunflower - genetic variation - CID - WUE

# EFFECTS OF DROUGHT ON MORPHOLOGICAL TRAITS OF SOME SUNFLOWER LINES

Veli PEKCAN[1], Goksel EVCI[1], M. Ibrahim YILMAZ[1], Suna BALKAN NALCAIYI[2], Şeküre ÇULHA ERDAL[2], Nuran CICEK[2], Yasemin EKMEKCI[2], Yalcin KAYA[3*]

1. Trakya Agricultural Research Institute, PO Box: 16, 22100 Edirne, Turkey
2. Hacettepe University Science Faculty, Biology Dept, 06100 Ankara, Turkey
3. Trakya University Engineering Faculty, Genetic and Bioengineering Dept, 22100 Edirne, Turkey

yalcinkaya22@gmail.com

As a summer crop, sunflower is influenced a lot from environmental conditions so sunflower yield changes frequently year by year. On the other hand, in the recent years temperatures increased daily or periodically due to global warming. Therefore, new breeding studies should focus mostly to develop sunflower hybrids having highly drought tolerance. Based on these priorities, the study was conducted to evaluate the effects of drought stress on plant height, head diameter, flowering and physiological maturity period of some male inbred lines developed previously by Trakya Agriculture Research Institute (TARI). In this study, there were big changes among male lines on tolerance levels of yield traits against controlled conditions to drought. The significant effect of drought stress was determined on head diameter among examined yield traits. However, plant height affected less from drought stress. While head diameter of plants reduced up to 50%, drought stress conditions decreased the days of flowering up to 20% (about one week) of flowering time and about 15% (about 11-12 days) of physiological maturity period. Sunflower lines were screened for improved drought tolerance based on drought factor index (DFI) calculated head diameter values.

Key words: Drought tolerance, Inbred lines, Sunflower, Yield traits.

# SUNFLOWER BREEDING

Maria Pacureanu-Joita

National Agricultural Research and Development Institute Fundulea, Romania

mariapacureanu2@yahoo.com

Sunflower served as a decorative plant, long time after its arrival in Europe (in the 16th century). Large - scale use of sunflower as an oil seed crop started in Russia in the 1830s. Sunflower selection begun simultaneously with its expansion as an oil crop. Around the end of the 19th century, farmer's selection was practiced and it was aimed at improving the available sunflower populations. The beginning of scientifically grounded sunflower breeding date to 1912, when a program of varietal development was established. First methods applied in sunflower breeding were mass and individual selection for specific characteristics. Under the leadership of V.S. Pustovoit, a method was developed for obtaining high-yielding varietal populations based on individual selection and seed reserve that is used through the selection cycle. Using this method, the oil content in seed was increased from 35% to 53%. The resistance to the parasite Orobanche cumana and some diseases was incorporated into sunflower varieties. Another step in sunflower breeding was made by G. Pustovoit when it was introduced interspecific hybridization (crossing H. tuberosus with cultivated sunflower). Extensive genetic studies on sunflower inbreeding and heterosis were conducted in the second half of the 20th century by a large number of researchers. Practical utilization of heterosis in sunflower begun with the discovery of a stable source of cytoplasmic male sterility, discovered by Leclerq in 1969, in the wild sunflower H. petiolaris. After the discovery of the first cms and first restorer gene (by Kinman, 1970), a large number of breeding centers for developing sunflower hybrids were established. The first objectives in sunflower breeding programs place emphasis on high seed yield and high oil content. The selection must be targeted on genotypes with high oil content in kernels to obtain a high oil yield per unit. For a successful realization of high yields it is necessary to improve a range of properties and characteristics, such harvest index, resistance to biotic and abiotic stresses, earliness, adaptability. In recent period, introgression of genes for herbicides resistance (imidazolinone and sulfonylurea) from wild Helianthus species has become a topical breeding objective for both oil and confectionery sunflower. Detection of genes for modified oil quality of sunflower and their introduction into productive genotypes are important objectives. The new mutant have a high oleic acid content or palmitic or stearic acid. Developing hybrids with modified tocopherols (alpha, beta, gamma and delta) is an important breeding objective because this feature may increase storage life of oil. Defining an ideal plant type, for specific agroecological conditions is also important in sunflower breeding.

Keywords: Sunflower, breeding, seed yield, oil quality, resistance to herbicides.

# THE EFFECTS OF IRRIGATION, NITROGEN LEVELS AND PLANT POPULATION ON YIELD AND QUALITY CHARACTERISTICS IN CONFECTIONARY SUNFLOWER (*HELIANTHUS ANNUUS* L.)

Veli Pekcan[1], Enver Esendal[2]

1. Trakya Tarımsal Araştırma Enstitüsü, Edirne
2. Namık Kemal Üniversitesi Tekirdağ Ziraat Fakültesi Tarla Bitkileri Bölümü, Tekirdağ

velipekcan@hotmail.com

Confectionary sunflower in Turkey is cultivated widely in Eastern and Central Anatolia and in recent years, a significant increase is observed in the production area. This study was conducted during 2010 and 2011 in Edirne to investigate the effects of irrigation (S0: no water, S1: irrigation at the start of flowering, S2: irrigation at the start and complation of flowering), nitrogen (N) dosages (0, 50, 100, 150, 200 kg/ha) and plant populations (47620, 35710, 28570 ve 23810 plants/ha) on confectionary sunflower's yield, aspects of yield and quality characteristics. The study was set up in a Randomized Complete Block Design in split-split plots with 4 reps. According to the results of the study, as irrigation number increases, duration of physiological maturity, plant height, head diameter, thousand kernel weight (TKW), seed yield, grain width and length increase, but oil content decreases. N application of 150 kg/ha N gave the highest TKW, grain width and length, while 100 kg per hectare N application gave the highest shell ratio. Plant height, head diameter and grain yield varied with 100 kg and 150 kg per hectare nitrogen application for two years. As nitrogen dosage increas- es, oil content decreases and the highest oil content was obtained with no nitrogen application. As the plant population per hectare decreases, duration of flowering and physiological maturity, head diameter, TKW and shell ratio increase, but plant height, grain yield and oil content decrease. The highest effect in the study was obtained with irrigation applications. A 25.2% increase in grain yield in 2010 and 42.9 % in 2011; a 12.7 % increase in grain width in 2010 and 23.7 % in 2011; a 5.8 % increase in grain length in 2010 and 12.6 % in 2011, respectively were received in S2 application. As a result, when we consider the demands of producers, snack companies and consumers in confectionary sunflower cultivation, confectionary sunflower should be planted as 35710 plants/ha in density, irrigation should be done twice during flowering and 120-140 kg nitrogen per hectare should be applied

Keywords: Confectionary Sunflower, Irrigation, Nitrogen, Plant Populations

# CONFECTIONERY SUNFLOWER UNDER CONVENTIONAL AND ORGANIC PRODUCTION SYSTEMS

Nada Hladni, Siniša Jocić, Vladimir Miklič, Dragana Miladinović, Zvonimir Sakač

Institute of Field and Vegetable Crops, Novi Sad, Serbia

nada.hladni@ifvcns.ns.ac.rs

The main aim of confectionery sunflower breeding is increase in yield, content and quality of protein, decrease in seed oil content and improvement of seed oil quality, with reduction in hull content. In recent past, there has been a steady increase in global demand for organic foods because of health risks posed by the conventional method of production. IFVCNS has accepted the challenge of organic production in research and commercial activities, due to the increased demand for organic products in Serbia. The aim of this research is to examine the effect of both organic and conventional production systems on the seed protein content, seed oil content, 1000 seed weight, total number of seeds per head and fatty acids content of confectionery sunflower. Trials were set up including 22 confectionery NS hybrids, created and produced in the breeding program of IFVCNS, in the period of two years under conventional and organic growing systems, as a randomized block design with three replications. Mean values of 1000 seed weight (114.9g; 100.9g) and total number of seed (908;802) were higher in the conventional than in the organic production system. Mean value of seed protein content under the conditions of the conventional production system was lower than under the conditions of organic production (16.4%; 18.0%), while the type of production had no effect on mean oil content (35.6;35.9%). Palmitic, stearic and linoleic acid content exhibited higher mean values under the organic production system, while oleic acid content was higher in the conventional production. Testing under different agricultural production systems can be useful in identifying sunflower hybrids with broad adaptability.

Keywords: Confectionery sunflower, hybrids, organic and conventional production

# GENOME-WIDE SNP DISCOVERY AND IDENTIFICATION OF QTL FOR AGRONOMIC TRAITS IN SUNFLOWER (*HELIANTHUS ANNUUS* L.) USING A GENOTYPING BY SEQUENCING (GBS) APPROACH

Ibrahim Celik[1], Duran Zararsiz[2], Anne Frary[3], Sami Doganlar[3]

1. Department of Molecular Biology and Genetics, Izmir Institute of Technology, Urla, Izmir, Turkey
2. Agromar, Karacabey, Bursa, Turkey
3. Department of Molecular Biology and Genetics, Izmir Institute of Technology, Urla, Izmir, Turkey

icelik@iyte.edu.tr

Recently developed plant genomics approaches (LD mapping and genome-wide selection) require many molecular markers distributed throughout the plant genome. As a result, the availability of an increasing number of markers is essential for maintaining highly efficient and accurate plant breeding programs. In this study we identified SNP loci in sunflower using a genotyping by sequencing (GBS) approach in an intraspecific F2 mapping population. A total of 271,445,770 reads were generated by the Genome Analyzer II next-generation sequencing platform and 29.2% of the reads were aligned to unique locations in the reference genome. A total of 46,278 SNP loci were identified. This study increased the number of sunflower specific SNP markers by 71.4%. In addition, a SNP-based linkage map was constructed for QTL identification for yield related traits (plant height, head diameter and seed setting at head center). This is the first report of discovery of sunflower-specific SNPs by the GBS approach and QTL mapping using a high density SNP-based linkage map. The SNP markers and QTL identified in this work will be valuable molecular genetics tools for sunflower breeding.

Keywords: Genetic linkage map, Illumina Genome Analyzer II platform,
plant height, head diameter, seed setting at head center

# CHARACTERIZATION OF MICRNAS HAVING ROLE IN OLIVE OIL BIOSYNTHESIS MECHANISM

Hüseyin Tombuloglu, Guzin Tombuloglu, Mehtap Aydin

Fatih University, Department of Biology, 34500, Buyukcekmece-Istanbul, Turkey

htombuloglu@fatih.edu.tr

Olive tree (*Olea europaea*) is one of the main cultural, characteristic and economically important plants which are broadly planting especially in the Mediterranean region. The olive oil yield of the olive trees is changing between the cultivars. In this study, we investigated the olive oil production responsible microRNAs (miRNAs) between efficient cultivar (Ayvalik) and inefficient wild type cultivar (Delice) of olive trees. After the construction of non-coding small RNA libraries, miRNAs were analyzed by using next generation sequencing method and their functions were predicted by using some comparative bioinformatics tools. At the end of the study, 350 and 341 miRNAs were found in Delice and Ayvalık cultivars, respectively. Secondary structures of some miRNA were represented to exhibit characteristics of plant-specific miRNAs. Expression level of each miRNA was analyzed. It was found that the expressions of 59 miRNAs were significantly changed in Delice cultivar between mature and immature olive fruit. This number was detected as 34 in Ayvalik cultivar. In addition, expression profile of some selected miRNAs was verified by using RT-qPCR analysis. miRNA target genes were detected by using bioinformatic tools. As a result, it was shown that most of the miRNAs target the transcription factors. Among those, five different miRNA target gene was selected and their expressions was tested with RT-qPCR. In conclusion, it is argued that differentially expressed miRNAs may have role in the olive oil biosynthesis.

Keywords: Olive, oil production, microRNAs, Ayvalik, Delice, next generation sequencing, RT-qPCR

# GENETIC VARIATION OF OLEIC ACID CONTENT IN IOPRI'S OIL PALM BREEDING POPULATIONS

Edy Suprianto, Heri Adriwan Sirega, Hernawan Yuli Rahmadi, Nanang Supena,
Abdul Razak Purba

Indonesian Oil Palm Research Institute (IOPRI) Jl. Brigjen Katamso No. 51
Medan 20158

edygrey@gmail.com

The breeding objectives of oil palm (*Elaeis guineensis Jacq.*) have been focused on the increasing of oil yield as well as the improvement of oil quality. Palm mesocarp oil, known as crude palm oil (CPO), typically contains about 35%-40% oleic acid, 40-50% palmitic acid and about 10% linoleic acid. A palm oil with a higher proportion of oleic acid is preferred and it could mean new market opportunities for edible palm oil. Study of genetic variation of oleic acid content has been carried out in Indonesian Oil Palm Research Institute (IOPRI) to identify genetic materials having high oleic acid contents among breeding populations. Research has been conducted on 323 dura x pisifera/tenera crosses from second cycle of reciprocal recurrent selection (RRS) scheme tested on four locations in North Sumatra and Riau, Indonesia. Identification of oleic acid content has also been conducted on existing varieties as well as oil palm germplasm collections including E. oleifera derived materials. Relatively large variation on oleic acid content have been found among the tested crosses, with the ranged between 20 % to 57.84%. Oil palm varieties derived from La Mé and SP 540 materials showed high oleic acid content with average 44.3% and 42.3%, respectively. Oil with high oleic acid content has been identified on wild E. oleifera accessions from Suriname, about 64-67% of oleic acids. With relatively large genetic variation, it may be possible to create medium-high (55%-65%) oleic acid oil palm cultivars with conventional methods. Some QTL linked to oleic acid content found in other study may help to accelerate IOPRI's breeding program for development of high oleic acid oil palm cultivars.

Keywords: Oil palm, germplasm, oleic acid, breeding, recurrent selection

# HIGH YIELDING AND DROUGHT TOLERANT GENOTYPES DEVELOPED THROUGH MARKER-ASSISTED BACK CROSSING (MABC) IN CHICKPEA

Srinivasan Samineni[1], Rajeev K Varshney[1], Sobhan Sajja[1], Mahendar Thudi[1], Veera Jayalakshmi[2], A Vijayakumar[3], D M Mannur[4]

1. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Telangana, India
2. Regional Agricultural Research Station, Nandyal 518 502, Andhra Pradesh, India
3. University of Agricultural Sciences, Dharwad 580 005, Karnataka, India
4. Agricultural Research Station of UAS-Raichur, Gulbarga 585 101, Karnataka, India

s.srinivasan@cgiar.org

Chickpea (*Cicer arietinum* L.) is the second largest grown food legume crop in the world after common bean. This crop is largely grown under rainfed conditions in Asia and sub-Saharan Africa where terminal drought is the major production constraint. Generation of large scale genomic resources in chickpea during the recent years has made it possible to improve the complex traits like drought tolerance. A "QTL-hot-spot" harbouring QTLs for several root and drought tolerance traits was transferred from the drought tolerant line ICC 4958 to a leading chickpea cultivar JG 11 (ICCV 93954), and a widely adapted cultivar Bharati (ICCV 10) in India. A set of 20 BC3F4/BC3F5 introgression lines (ILs) of JG 11 and 22 of Bharati were evaluated at three to four locations (Patancheru, Nandyal, Gulbarga and Dharwad) in Southern India over two years during 2011-12 to 2014-15. Many lines giving at least 10% higher yield than the recurrent parents JG 11 and Bharati were identified at each location and in each growing condition (rainfed/irrigated). As the introgressed genomic region also influences seed size, most ILs had bigger seed than the recurrent parents. These results are very encouraging and demonstrate the effectiveness of marker-assisted breeding in improving terminal drought stress tolerance in chickpea.

Keywords: Chickpea, drought tolerance, MABC

# EFFECT OF POST-EMERGENCE HERBICIDE IMAZETHAPYR ON PHENOLOGICAL AND AGRONOMIC TRAITS IN CHICKPEA BREEDING LINES

Sobhan Sajja[1], Srinivasan Samineni[1], Mayur Gadekar[1], Veera Jayalakshmi[2],
A Vijay- akumar[3], Mohammad Yasin[4], Rajeev K Varshney[1]

1. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Telangana, India
2. Regional Agricultural Research Station, Nandyal 518 502, Andhra Pradesh, India
3. University of Agricultural Sciences, Dharwad 580 005, Karnataka, India
4. RAK College of Agriculture, Sehore 466 001, Madhya Pradesh, India

s.sobhan@cgiar.org

Chickpea is sensitive to herbicides and manual weeding is currently the only option for weed control in many developing countries in arid and semi-arid regions of the world. The farmers in these countries need herbicide-tolerant varieties to use post-emergence herbicides to control weeds. In this direction, a study was conducted with 21 breeding lines at four locations in India (Patancheru, Bijapur, Nandyal and Sehore) during post-rainy season of 2014-15. The trial was conducted under field conditions in RBD with four replications in both control (hand weeding) and sprayed (herbicide: Imazethapyr @ 750 ml/ha) treatments. The herbicide was sprayed 30 days after sowing. Herbicide effect was studied on phenological (days to flowering and maturity) and agronomic (number of primary and secondary branches, plant height, seed yield, 100-seed weight and harvest index) traits. The results indicated that time to flowering and maturity was delayed up to 16.5 and 18.5 days, respectively. Herbicide had no effect on primary branches, while the number of secondary branches was increased up to 12. Plant height was severely reduced by 18cm. The reduction in seed yield was observed up to 49%, whereas 100-seed weight was increased across locations. Location-specific superior lines (Nandyal: ICCIL 04016, ICCIL 04004, ICCV 10114; Patancheru: ICCIL 04007; Bijapur: ICCV 04516, ICCV 10, ICCV 97105, ICCIL 01026, ICCV 09106; Sehore: ICCV 08102) were identified. These lines can be used as potential sources for developing herbicide tolerant varieties in chickpea. Weed management through herbicides is economical and facilitates minimum tillage methods, which help preserve topsoil.

Keywords: Chickpea, herbicide tolerance, Imazethapyr, phenology, agronomical traits

# DETERMINATION OF EFFECT OF CHEMICAL MUTAGEN EMS ON MORPHOLOGICAL CHARACTERISTICS OF TAEK A-3 AND TAEK C-10 MUTANT SOYBEAN VARIETIES IN M1 GENERATION

Zafer SAĞEL, M. İhsan TUTLUER, Hayrettin PEŞKİRCİOĞLU,
Yaprak KANTOĞLU, Burak KUNTER

Sarayköy Nuclear Research and Training Center, Sarayköy, Ankara, Turkey

Today beside ionizing radiation, chemical mutagens are also using in crop improvment and Ethylmethanesulphonate (EMS) is on of the most widely used chemical mutagens in the field of plant breeding.

This research work was carried out to determine the effect of chemical mutagen (EMS) on seedling height TAEK A-3 and TAEK C-10 soybean varieties were used as the test plants and effect of presogking time determined.

In greenhouse and field experiments five different EMS dose (0 (Control), 0,025, 0,050, 0,075 ve 1,0 M) and in greenhouse 3 different presoaking time (0, 6 and 18 hours), in the field 2 different presoaking time (0 and 6hours) were applied.

After chemical mutagen application in the green house germination percentage and seedling height base EMS dose and presoaking time effect had been determined. Different effects of EMS on M1 germination of soybean of different characterics (no. of plants, plant height, no of pods and seedyield) were determined after field condination. As a result it can be said tht in both soybean varieties, seedling height was reduced as the EMS concentration was increased. But there was no distinct influence of presoaking time on the seedling height in both soybean varieties. Both soybean varieties the average percentage of germination increased with increasing pre-soaking time.

In field experiment It was concluded that by 6 hours presoaking the harmful physiolojical effect of EMS could be decreased.

Keywords: Soybean, Induced mutation, mutation breeding, chemical mutagen, EMS

# COMPARATIVE ANALYSIS OF SEED STORAGE PROTEIN PROFILES AND AGRONOMIC TRAITS TO EVALUATE GENETIC DIVERSITY AMONG THE SOYBEAN [*GLYCINE MAX* (L.) MERR.] GENOTYPES

Ömer Dursun, Emine Arslan, İrfan Özer

The Graduate School of Natural and Applied Science of Selcuk University 42050, Konya, Turkey

earslan@selcuk.edu.tr

This research aimed to investigate the genetic diversity among 12 soybeans (*Glycine max*) genotypes (A3935-NE3399-Defience-Arısoy-Atakişi-Ataem7-Nova-Bds07-Bds11-Bds21-Bds25-BDS27) using seed storage proteins and agronomic traits. Mature seeds of 12 Glycine max genotypes were collected. Total protein was isolated from seeds collected for each genotypes. Sodium Dodecyl Sulphate-Polyacrylamide Gel Electrophoresis was perfomed by a standard method on a vertical slab gel. Genetic similarity among genotypes was estimated basing on Nei's homology. Seventy one polypeptide bands in range of 9.159 kDa to 148.904 kDa were recorded. Cluster analysis was performed using UPGMA in Bio1D++ computer program. Similarity coefficients of 12 genotypes belonging to Glycine max ranged 75-98% with low diversity of genetic variation in protein profiles avarage Euclidian distance used for agronomic data ranged from 11.42 to 60.93. Those results showed that some genotypes were revealed in same groups in dendograms obtained according to both protein profiles and agronomic traits.

Keywords: Soybean, Glycine max, genotypes identification, seeds storage proteins, agronomic traits.

# IS AUSTRALIAN FABA BEAN INDUSTRY VULNERABLE TO RUST (*UROMYCES VICIAE-FABAE*)

Richard Trethowan[1,2], Sami Hoxha[1], Abdus Sadeque[2], Peng Zhang[1],
Kedar N. Adhikari[2]

1. The University of Sydney, Plant Breeding Institute, Cobbitty, NSW 2570, Australia

2. The University of Sydney, IA Watson Grains Research Centre, Narrabri,
NSW 2390, Australia

kedar.adhikari@sydney.edu.au

Faba bean (*Vicia faba* L.) is one of the oldest grain legumes grown in many countries. Faba bean rust, caused by Uromyces viciae-fabae, is a serious disease of faba beans in most faba bean growing areas in the world. Experiments were conducted to assess the genetic variation for rust resistance in Australian faba bean germplasm and to determine the genetic basis of rust resistance in the selected germplasm. Resistant lines were identified, subsequently crossed to agronomically suitable parents and the ensuing progeny were evaluated for resistance. Many derived lines showed a higher level of resistance than the current cultivars. Genetic studies from the seedling test of F2 and F3 progenies derived from two different sources of resistance showed three distinct responses, highly resistant, moderately resistant and susceptible. However, no homozygous families with an intermediate response were found in the F3 progeny test, hence, this infection type could not be attributed to independent gene(s). The F2 and F3 segregation ratio from both crosses indicated a single dominant gene was responsible for conferring resistance in each resistant parent. The resistant parent in one cross was a selection from the commercial cultivar Doza and in another it was Ac1655. Doza has been used widely in the breeding program as a source of resistance. Genetic uniformity in the germplasm due to this single source of resistance can exert pressure for pathogen mutation making faba bean vulnerable to rust. Therefore, identification and utilization of different sources of resistance is suggested in the breeding program.

Keywords: Faba bean rust, genetic analysis, grain legumes, resistance breeding, rust resistance

# ON FARM CONSERVATION OF A LENTIL LANDRACES IN MOROCCO WITH AN AD-VALUE ON ADAPTABILITY AND QUALITY

M. Taghouti[1], F. Gaboun[2], Nadia Benbrahim[1]

1. Plant Breeding, Conservation And Enhancement Of Phyto-genetic Resources Research Unit, National Instituteof Agricultural Research, Rabat, Morocco
2. Biotechnology Research Unit, National Institute of Agricultural Research, Rabat, Morocco

nadiabenbrahim@gmail.com

Lentil (*Lens culinaris Medik.*) is produced in Morocco by farmers using mainly landraces. However, they are threatened by both improved varieties and climate change. ZPop1 is a Zaer landraces which is appreciated by farmers for its specific adaptation and its high quality. In order to strengthen its on farm conservation throughout its marketing under a distinctive sign of origin and quality (GI), this study undertake (1) to analyze agricultural practices and seed management, (2) to assess genetic diversity using agro-morphological and biochemical traits (SDS-PAGE) and (3) to improve ZPop1 by selecting performed lines within participatory approach. In this context, this study is based on a survey from 41 lentil farmers and collected lines from both farmer's fields and experimental trials. The results showed (i) that Zpop1 had been on farm conserved thanks to its adaptability and the seed exchange network; (ii) a high genetic diversity according to heterozygosis rate (He = 0.338), allele frequency (Na = 1.938) and Shannon index (SWI = 0.499), (iii) the average of Zpop1 polymorphism (58.7%) is ranged between 21.7% to 91.3%, and a lack of genetic diversity in Aghbal accession according to Shannon index (SWI = 0.124), heterozygosis level (He = 0,085) and frequency allele (Na = 1,043). The selection was emphasis on earlier and productive lines which are produced by green seed coat and medium size. A Sustainable program of Zpop1 in situ conservation is needed to both ensure poor farmer food security and integrate lentil national breeding program as genetic pool of biotic and abiotic tolerance.

Keywords: Lentil, landraces, genetic diversity, on farm conservation, agro-morphology, SDS-Poly-Acrylamide Gel Electrophoresis

# EVALUATION OF PEA (*PISUM SATIVUM* L.) GERMPLASM FOR WINTERHARDINESS IN CENTRAL ANATOLIA, TURKEY

Azize Homer[1], Mevlüt Şahin[1], Ümran Küçüközdemir[2]

1. Central Research Institute for Field Crops, Ankara, Turkey
2. Eastern Anatolian Agricultural Research Institute, Erzurum, Turkey

ademirbas@hotmail.com

Winter pea can be grown in rotation with cereal crops in Central Anatolia, Turkey. However, winterkill can occur during severe winters. The objective of this study was to screen pea accessions for winter survival and identify genotypes with differential winterhardiness for future crop development. Twenty-five accessions originating from five countries were evaluated under field and laboratory conditions. Field trials were planted on two dates in Haymana, Ankara, and a single date in Ulaş, Sivas, Turkey during the fall of 2014. Winterhardiness was evaluated as the percentage of surviving plants. Differential survival of genotypes was observed at both locations. On average, winterkill was greater in Ulaş than in Haymana, and survival rate ranged between 12 to 100 percent. Turkish accessions, TR 79404 and TR 80194 had survival percentages comparable with the three winterhardy controls (Turkish cultivars "Taşkent" and "Özkaynak", U.S. cultivar "Melrose"). The European and U.S. accessions, included in the trials for their previously reported winterhardiness, showed high levels of winterhardiness, and could be used in breeding programs. In the laboratory, no plants survived at -12 and -16 °C. Screening at -8 °C generated differential survival among winterhardy controls and European accessions. Significant positive correlations ($r = 0.63 - 0.85$, $P < 0.0001$), between the test environments for the percent survival were found. Furthermore, in separate field trials at the same two locations, 17 Turkish, four UK, four Bulgarian, one French, and three US accessions, plus five controls were screened; and 14 of these, including Turkish accession TR 79407, had high survival rates.

Keywords: Pea, winterhardiness, germplasm, screening

# RELIABLE HOUSEKEEPING GENES FOR QRT-PCR OF PEA GENOTYPES GROWN UNDER DIFFERENT BORON TREATMENTS

Ahmet Tamkoç[1], HASAN CAN[2], Nimet Can[2], Mehmet Hamurcu[2],
Erdogan Esref Hakki[2]

1. Selcuk University, Faculty of Agriculture, Field Crop Department
2. Selcuk University, Faculty of Agriculture, Department of Soil Science and Plant Nutrition

hasancan194@yahoo.com.tr

The amount of protein contained makes legumes a very improtant nutrient source not only for the human dietary program, but also that of the animal feeding. Pea is one of the most preferred fodder in the cultivation of farm animals. Central Anatolia in Turkey, which is an important large agricultural area in terms of animal-husbandry, as the major plant growth and production limiting factors has semi-drought climatic conditions with a considerable amount of boron stressed soil sutructure. Boron deficiency as well as boron toxicity problems leading to inefficient plant metabolic activities as well as damages on the plant tissues are common in this region thus negatively influencing plant growth, development and also yield. The aim of this study was to acquire extensive knowledge on the expression profiles of selected widely used housekeeping genes. Pea genotypes were grown under boron-deficient and boron-toxic conditions in comparison with control plants with regular amounts of boron in the growth media. Ten differents genes (EF-I-Beta, EF-I-alfa, PP-II-A, Alfa-tubulin, Beta-tubulin, GAPDH, TF-II-A, Histone 3, Helicase and S18) were utilized in the screening study. In the growht media 0, 2, 20 and 200 ppm boron dossages were applied and plants were harvested on day 7 after treatments where the visual responses against boron were observed. qRT-PCR results were evaluated using the alternative softwares NormFinder, geNorm and BestKeeper. The most appropriate reference genes for pea genotypes grown under B stress conditions were determined as PP-II-A, tub, Helicase and S18, in sequence.

Keywords: Boron, House Keeping Gene, Reference gene, Pea, qRT-PCR

# ASSESSMENT OF SUMMER DROUGHT TOLERANCE IN 154 HALF-SIB FAMILIES OF AFALFA (*MEDICAGO SATIVA* L.) UNDER MOROCCAN FIELD CONDITIONS.

Paolo ANNICCHIARICO[1], Imane THAMI ALAMI[2], Yahya LAHRIZI[3], Abdelaziz BOUIZGAREN[2]

1. Consiglio per la Ricerca e la sperimentazione in Agricoltura (CRA), Centro di Ricerca per le Produzioni Foraggere e Lattiero-Casearie, ITALY
2. National Institute of Agronomical Research (INRA) Rabat Morocco
3. Faculty of Science and Technics Fès Morocco

bouizgaren_abdelaziz@yahoo.fr

The drought summer tolerance of 154 half-sib (HS) families of alfalfa *(Medicago sativa* L.) was evaluated under field conditions in semi-arid area of Morocco. The HS families were obtained by crossing three alfalfa cultivars (Mumuntanas, ABT10 and Erfoud) originated from three contrasting environments. The trial was installed in December 2013 according to alpha lattice designs with 5 replications. Each replication contains 14 incomplete randomized blocks. Each block contains 11 plots corresponding to a HS family represented by 42 plants. A moderate water deficit was applied during April and May, followed by a severe water stress without irrigation applied from June to the end of august. We assessed some agro-physiological and biochemical parameters related to water stress tolerance during May. The results showed a high variation in dry matter yield (DMY) among the HS families which varied from 6 to 18 T/ha. 10% of HS families had a good persistence to summer stress (less than 2.4% of plant mortality). These two parameters were negatively correlated. Significant variations were noted among HS families for majority of physiological and biochemical parameters evaluated. We noted that DMY was positively correlated with stomatal conductance, chlorophyll fluorescence, leaf chlorophyll content, leaf soluble sugar content and leaf proline content. These parameters provide the main indicators to assess the selection of HS families to summer drought tolerance. The selected HS families will be used to create a synthetic variety with a large adaptation to arid and semi-arid regions suffering from water scarcity in summer.

Keywords: Alfalfa (Medicago sativa L.), summer drought, persistence,
agro-physiological and biochemical parameters.

# IMPROVEMENT OF NEW SAINFOIN (*ONOBRYCHIS VICIIFOLIA SCOP.*) LINES VIA IN VITRO MUTAGENESIS TECHNIQUE

Ramazan Beyaz[1], Cengiz Sancak[2], Mustafa Yıldız[2]

1. Ahi Evran University, Faculty of Agriculture, Department of Soil Science and Plant Nutrition, Asık Pasa Campus, 40100, Kırşehir, Turkey
2. Ankara University, Faculty of Agriculture, Deparment of Field Crops, Dıskapı, 06110 Ankara, Turkey

ramazanbeyaz@gmail.com

Approximately 20% farmland are affected by salt and about 4 million acres of farmland are lost due to salinization every year in the world. To utulize from these farmland and to continue sustainable agriculture, need to improve new tolerant varieties againts adverse environmental conditions. Therefore, many of studies, which have been done by plant breeders, have been focus on this issues. The purpose of this study was to improve new tolerant sainfoin lines againts salt stress. For this purpose, the seeds of sainfoin were irridiated by source of cobalt-60 at 0 (as a control), 400, 500 and 600 Gy dose levels of gamma rays. Irradiated seeds were sown into the magenta caps containing MS-basal medium with 150 mM NaCl to select tolerant ones during germination (as an important phase to show their capacity of tolerance) under in vitro conditations. After that, these planlets were transferred to greenhouse and again applied 150 mM NaCl stress for 14 days to select tolerant ones during plant seedling phase under in vitro conditations. Then, survived plantlets were transferred to field. As a result of this study, 49 number of putative mutant planlets were selected both in vivo and in vitro conditions among nearly 6000 seedlings.

Keywords: Sainfoin, Salt Tolerance, *In vitro* mutagenesis

# GENOME SIZE AND CHROMOSOMAL DIVERSITY IN THE GRASS *GENUS DACTYLIS* L.

Metin Tuna[1*], Hüseyin Keles[1], Gülsemin Savaş Tuna[3], İlker Nizam[1],
Eyüp Erdem Teykin[2] ,

1. Namik Kemal University, Faculty of Agriculture, Department of Field Crops, Tekirdağ, Turkey
2. Namik Kemal University, Faculty of Agriculture, Department of Agricultural Biotechnology, Tekirdağ, Turkey
3. Ebru Nayim Science High School, Tekirdağ, Turkey

mtuna@nku.edu.tr

The genus Dactylis consists of only one species with approximatelly 20 subspecies. The basic chromosome number in the genus is X = 7. Ploidy varies from diploid to hexaploid within the genus while commonly used forage form known as Dactylis glomerata L. is tetraploid. Morphology of the Dactylis chromosomes varies from metacentric to sub-metacentric while they are similar to each other. Previous cytogenetic studies of the genus Dactylis L. were limited to chromosome counts and construction of karyotypes on the basis of Feulgen staining. Morphological similarity of Dactylis chromosomes makes it difficult to identify them by classical methods and pair with their homologs. Therefore, these karyotypes are of limited use for genome analysis. New molecular cytogenetic methods were not used in Dactylis prior to this study. The objective of this study was to characterize Dactylis genomes by using new molecular cytogenetic methods. Flow cytometry was used to determine genome size of the taxons as the distribution of highly repetitive DNA sequences (45S and 5S rDNA) on chromosomes were studied by in situ hybridization analysis. Based on the results of the study, there was a considerable level of genom size variation within and between Dactylis taxons due to probably incomplete crossing brarriers between populations regardless ploidy levels. The 5S rDNA sites were highly conserved, while 45S rDNA sites had wide variability. Simultaneous fluorescence in situ hybridization with 5S and 45S rDNA probes were useful for chromosome identification and pairing homologous. The results of this study add new informations on genome structure of genus Dactylis

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Keywords: Cytogenetics, Dactylis, FISH, genome size, flow cytometer

# THE VARIATION OF CRUDE PROTEIN AND TOTAL FAT OF THE MAIN GRASSLAND PLANTS, IN VARIOUS STAGES OF GROWTH, IN "KOSTILATA" SUBALPINE GRASSLAND IN THEODORIANA, ARTA, GREECE

Ch. Koutsoukis[1,2], K. Akrida-Demertzi[2], P. G. Dermetzis[2], Ch. Roukos[1],
Ch. Voidarou1 and S. Kandrelis[1*]

1. Technological Educational Institute of Epirus, Department of Agricultural Technologists, Faculty of Agricultural Technology Food Technology and Nutrition, Kostakioi - Arta, GR 47100 Arta, Greece
2. University of Ioannina, Department of Chemistry, Section of Industrial and Food Chemistry, Food Chemistry Lab.,GR 45110 Ioannina, P.O.Box 1186, Greece

sotkan@teiep.gr

The chemical composition of different plant parts varies, both within the plant itself, as well as among different plants, which is due to their structure, stage of growth and phenological characteristics. In this study, the results of a research conducted in 2013, in a subalpine ecosystem in Epirus (Greece) are presented. The objectives of this research were the determination of crude protein and total fat (ether extract) of the ecosystem's main grassland plants, per group (grasses, legumes, other forbs), at different stages of growth. These plant species were: a) grasses (*Alopecurus gerardii Vill, Stipa pennata* L., *Phleum alpinum* L.), b) legumes (*Trifolium repens* L, *Lathyrus aphaca* L, *Lotus corniculatus* L.) and c) other forbs (*Ranunculus repens* L., *Achillea millefolium* L. and *Geranium lucidum* L.). The results showed that: a) the largest amount in crude protein was found in Trifolium repens L. with a percentage of 17.05%, with a statistically significant difference only with grasses, b) in all plant species, the largest amounts of crude protein and total fat was observed during the initial stage of plant growth, showing a gradual decrease until the final stage of growth, c) statistically significant differences appeared in the amount of crude protein and total fat, between the same plant species, at different sampling dates, and between different plant species in the same sampling dates and d) the amount of total fat in all plant species was on average 3%.

Keywords: Subalpinegrassland, crude protein, total fat.

# HYBRID PIGEONPEA: RESEARCH TO REALITY

Sameer Kumar C V, Vijay Kumar R, Hingane A, Saxena R

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru 502 324, Telangana, India

c.sameerkumar@cgiar.org

Cytoplasmic and genetic male sterility based hybrids in field crops led to tremendous increase in productivity by exploiting the genetic principles of heterosis. Pigeonpea is an often-cross pollinated important grain legume in rainfed cropping systems, globally cultivated in 5 million hectares. The productivity in the crop is hovering around 800 kg/ha for the past 6 decades which is unacceptably low. The phenomenon of hybrid vigor was successfully exploited in the crop by identifying sources of male sterility from the wild relatives. It took three decades of research efforts to develop stable maintainers, complete restorers and heterotic hybrid combinations. The hybrids ICPH 2671, ICPH 2740 and ICPH 3762 were released for general cultivation by the farmers in different agroecoregions of India and a number of other hybrids are in the pipeline. Yield advantage of 30 to 40% (rainfed) and 50 to 60% (irrigated) was realized in farmers' fields over the local varieties. Seed production technology was standardized by exploiting male sterility and entomophily thereby appreciable amounts of hybrid seeds were harvested from the seed parent. Conventional and genomic approaches are underway to identify candidate genes responsible for fertility restoration, elite parents with resistance to fusarium wilt and sterility mosaic disease and heterotic gene pools to breed adaptive hybrids for different niches across the globe.

Keywords: Pigeonpea, hybrids, cytoplasmic male sterility

# INHERITANCE AND STABILITY OF SOME AGRONOMIC TRAITS OF AFRICAN YAM BEAN (*SPHENOSTYLIS STENOCARPA* (HOCHST EX. A. RICH) HARMS)

Kehinde, O.B[1], Adewale, B. D.[2]

1. Plant Breeding and Seed Technology, Federal University of Agriculture, PMB 2240, Abeokuta, Nigeria
2. Department of Biological Sciences, Ondo State University of Science and Technology, PMB 353, Okitipupa, Nigeria

d.adewale@gmail.com

African yam bean (AYB), Sphenostylis stenocarpa, an indigenous African pulse has immense nutritional significance. The understanding of inheritance pattern and stability status of agronomic trait is primary to their genetic improvement. Thirty AYB genotypes were evaluated for 100 seed weight (100SW), seed weight per pod (SWP), days to 50% flowering (D50F) and days to seedling emergence (DSE) in a randomized complete block design of three replications. The study was conducted at Ibadan, Ikenne, Mokwa and Ubiaja in Nigeria. Genotypic variation was significant ($p \leq 0.05$) for all characters except DSE. Location and Genotype x Location interaction was significant ($p \leq 0.05$) for the four characters. D50F had the least genotypic and phenotypic coefficient of variation (GCV and PCV) of 10.26% and 11.05% respectively. The highest GCV, PCV and genetic advance occurred in SWP at 34.55%, 37.88% and 64.94% respectively. Broad sense heritability ranged between 77.61% (DSE) to 89.07% (100SW). Repeatability was highest (13.83%) in 100SW. The performance of TSs87, TSs91 and TSs125 was highly significant for DSE and 100SW. The joint regression analysis identified TSs24 and TSs82 as the most stable genotypes for DSE and SWP with regression coefficient (bi) of 0.94 and 0.97 and deviation from linearity (Sdi2) of 0.028 and -0.028 respectively. The most stable genotypes for D50F and 100SW were TSs61 and TSs84 with b = 1.015 and 1.017 respectively. The study revealed potential breeding values of four agronomic traits in AYB.

Keywords: African yam bean, accessions, underutilized species, agronomic traits, joint regression analysis

# RESISTANCE TO STRESS AND CALCIUM BINDING PROTEIN TYPE IN PLANTS

Saadia Karbou[1,2,3*], Yasmina El Bahloul[1], Brahim Benaji[2], Mohammed Bouksaim[3], Majda Taoudi Benchekroun[2]

1. UR Amélioration des Plantes Conservation et Valorisation des Ressources Phytogénétiques -Centre Régional de la Recherche Agronomique de Rabat
2. Université. Hassan II - Casablanca. FSAC, Laboratoire Microbiologie, Pharmacologie, Biotechnologie et Environnement.
3. Laboratoire Eco valorisation, Centre Régional de la Recherche Agronomique de Rabat

skarbou@gmail.com

In the fear of global warming, accompanying to the rapid growth of the world population, it is essential to find new sources of increasing nutritional vegetable rates and to provide solutions for food security in these conditions.

New resources biotechnology research can be exploited for fighting against stress due to global warming for plants.

Calcium binding protein plays an essential role in the homeostasis of the intracellular calcium balance. In our current study, we believe that this protein molecule also plays an important role in addition to resistance to drought, and a direct role (more or less direct) to the quality and quantity of oil products by plants from arid and Saharan climate, such as argan tree in Morocco.

This molecule may be used as an essential biomarker for resistance to drought and increased crop yields of oily plants.

Keywords: Homologous function, Protein calcium-binding, drought,
biotechnology, oily plants

# USING THE NEW INTRODUCED SPECIES - SAFFLOWER IN THE CONDITIONS THE CENTRAL REGION OF THE RUSSIAN FEDERATION

S.K. Temirbekova, Yu.V. Afanaseva

Federal State Scientific Institution "All-Russia Selection-Technological Institute of Horticulture and Nursery", Russia, Moskow

sul20@yandex.ru

As a result at the Center of the gene pool and bioresources of plants of Institute was created cultivar of safflower tinctorius named "Krasa Stupinskaya". Vegetation period from germination to maturity in the years with different meteorological conditions is 105-130 days. Duration of flowering is about a month. Stem is erect, branching, naked, height is about 83-90 cm. Leaves are sessile, lanceolate, elliptic, with small spines. Inflorescence - a basket with a diameter near 1.5-3.5 cm. One plant can from 5-7 to 20-50 and more baskets. Seed's coat is hard, it is difficult to crack, reach 40-50 % from the mass of seeds. The seeds do not fall off after their maturation. The weight of 1000 seeds - 48-51 g. Productivety in our zone is 0.8-1.0 t/ha. Safflower seeds contain 32-38 % of fat, the yield of oil - 240 liters kg/ha. Absolute fat content in the treated seeds reaches more than 60 %, and it is fit for food. This cultivar does not affected by pests and diseases, except for enzyme-mycotic exhaustion of seeds (EMES). In wet years EMES causes seed's mass destruction by such diseases as Alternaria, Fusarium and others and as a result is a poor quality of seeds.

Keywords: Safflower, oil, new variety, diseases

# POSTER PRESENTATIONS PAPER LIST

# EVALUATION OF DIFFERENT GENOTYPES OF GROUNDNUT FOR RESISTANCE TO FOLIAR DISEASE IN NORTH EASTERN REGION OF SOUTH AFRICA

Maureen N Tshikunde, John B.O Ogola, Edna C Kunjeku

Department of Plant Production, University of Venda, Private Bag X5050,
Thohoyandou 0950, South Africa

ochandaogola@yahoo.com

Foliar diseases such as early leaf spot caused by Cercospora arachidicola, late leaf spot caused by Phaeiosariopsis personata and leaf rust caused by Puccinia arachidis are some of the most important factors constraining groundnut production. Therefore the development and use of resistant genotypes is important in ensuring high and sustainable production of groundnuts especially amongst smallholder farmers. This study assessed 16 genotypes of groundnuts for resistance to early leaf spot (ELS), late leaf spot (LLS) and groundnut leaf rust at a representative site of NE South Africa in the 2012/2013 cropping season. Fifteen of the genotypes (ICGV 06138, ICGV 06139, ICGV 06142, ICGV 06143, ICGV 06144, ICGV 06145, ICGV 06146, ICGV 06149, ICGV 06150, ICGV 06151, ICGV 07106, ICGV 07120, ICGV 06175, ICGV 06176, ICGV 06183) were from the Thirteenth International Foliar Disease Resistant Groundnut Varietal Trial Nursery and the sixteenth was a local commercial cultivar, Inkanyezi, that was used as a standard check. The disease incidence and severity were assessed on a weekly basis from 5 weeks after emergence until physiological maturity, using a 9 point ordinal scale together with a diagrammatic scale developed by ICRISAT for late leaf spot and rust screening. All 15 improved cultivars showed reasonable tolerance to foliar leaf spots when compared to the local check, Inkanyezi, which exhibited higher susceptibility to early leaf spot, late leaf spot and rust up to 12 weeks post-emergence. Clearly the fifteen improved genotypes may offer smallholder farmers greater option in managing foliar diseases.

Keywords: Groundnuts, early leaf spot, late leaf spot, groundnut leaf rust, disease assessment, disease incidence, disease severity

# GENOTYPIC VARIATION IN PHYSIOLOGICAL TRAITS, GROWTH AND YIELD OF 16 MEDIUM MATURITY GROUNDNUT (*ARACHIS HYPOGEAE* L.) LINES UNDER RAINFED CONDITIONS

Mokgaetji D Maja[1], John B.O Ogola[1], Cherian Mathews[2]

1. Department of Plant Production, University of Venda, Private Bag X5050, Thohoyandou 0950, South Africa
2. DARDLA, P/Bag X11318, Nelspruit-1240, South Africa

ochandaogola@yahoo.com

The north Eastern South Africa is characterized by low and poor distribution of rainfall that often lead to drought, especially terminal drought. Groundnut genotypes that mature within the rainy season but not too early to result in low yield may be beneficial in this region. This study aimed at assessing genotypic variations in agronomic performance and selected physiological traits of 16 groundnut genotypes at Thohoyandou, NE South Africa in the 2013/2014 cropping season. Fifteen of the genotypes were from the Thirteenth International Medium duration Groundnut Varietal Trial Nursery and the sixteenth was a local commercial cultivar, Inkanyezi that was used as a standard check. The experiment was laid in a randomized complete block with three replications. Chlorophyll content, stomatal conductance and intercepted radiation (IR) were measured at 71, 90 and 106 DAE using chlorophyll meter, leaf porometer and ceptometer, respectively. Crop biomass and grain yield were determined at harvest maturity. There was no variation in chlorophyll content, crop biomass and grain yield amongst the genotypes. The effect of genotype on stomatal conductance and IR was significant and the medium maturity genotypes recorded greater stomatal conductance and IR compared with the local check INKANYEZI. The lack of variation in crop biomass and grain yield amongst the genotypes was likely due to the excessively high amounts of rainfall received during the cropping season which was 146% greater than the long term average for the site

Keywords: Groundnuts, chlorophyll content, crop biomass, grain yield, intercepted radiation, stomatal conductance

# ROLE OF SUPEROXIDE DISMUTASES IN SUNFLOWER DEFENSE RESPONSE TO DOWNY MILDEW

Tatiana Sestacova, Angela Port, Maria Duca

Center of Molecular Biology, University of the Academy of Sciences of Moldova 3/2,
Academiei str., MD-2028, Chisinau, Republic of Moldova

tatiana.shestacova@gmail.com

Reactive oxygen species (ROS) elicit the defense of plant and are the first line of defense against pathogenic attack, while being characterized by both cytotoxicity to phytopathogen and host cells. Plants have a wide network of pathways for ROS production and scavenging, essential for maintance of ROS level within cell and signaling. The purpose of this study was determination of role of different SODs (MnSOD II, MnSOD I, CuZnSOD II and CuZnSOD I) in leaves of five sunflower genotypes (Drofa Rf, Drofa CMS, Drofa F1 hybrid and two isogenic lines 393A / 393B) in normal and infected with Plasmopara halstedii plants grown in field. Study of gene expression for four superoxide dismutases revealed that for all investigated genotypes highest expression level was for chloroplastic CuZnSOD I, but the lowest values of expression were characteristic for mitochondrial MnSOD I. Mn-SOD genes studied under natural infection in the field showed increased expression in case of weakly infected plants. The most significant intensification of the transcriptional activity was observed in Drofa Rf genotype, which also was characterized by the presence of the Pl6 resistance gene and showed no signs of systemic or medium infection in the field. It was observed reprogramming of synthesis in direction of chloroplast SOD accumulation, which can be explained by the fact that at later stages of infection occurs the phenomenon of chlorosis caused by the destruction of chloroplasts, thereby, the synthesis of CuZnSOD I is a mechanism of chloroplast protection against oxidative stress.

Keywords: Sunflower, downy mildew, superoxide dismutases, defense response, resistance, gene expression

# DEFENCE-RELATED GENES IN ADVANCED STAGES OF SUNFLOWER-BROOMRAPE INTERACTION

Tatiana Sestacova[1], Ion Gisca[2], Aliona Cucereavii[2], Angela Port3, Maria Duca[3]

1. Center of Molecular Biology, University of the Academy of Sciences of
   Moldova, 3/2, Academiei str., MD-2028, Chisinau, Republic of Moldova

2. AMG-Agroselect Comert Company, Republic of Moldova

3. Center of Molecular Biology, University of the Academy of Sciences of
   Moldova, 3/2, Academiei str., MD-2028, Chisinau, Republic of Moldova

tatiana.shestacova@gmail.com

Plants have developed during evolution a large set of defense mechanisms to pathogens. At the molecular level one of the most important resistance mechanism is synthesis of defense-related proteins, such as PR-proteins (Pathogenesis-Related) and plant defensins, which are considered as markers for SA-dependent and JA-dependent SAR respectively. Thus, the aim of this study was to establish implication of PR5 and defensin genes in sunflower resistance to broomrape in advanced stages of infection. Seven sunflower lines (resistant MS-2161A, tolerant MS-2039A and susceptible MS-2098A, MS-2091A, MS-2077A, MS-2067A and MS-1589A) grown in normal and infected with three broomrape populations (Tulcea, Romania; Soroca and Anenii Noi, Republic of Moldova) soil were used in this study. In conducted research RT-qPCR was used for determination of transcriptional activity of studied genes. Defensin and PR5 genes significantly changed their expression in better part of studied cases (e.g., PR5 was up-regulated up to 235-fold in non-symptomatic plants of MS-2039A infected with broomrape from Soroca). It has to be mentioned, that in common the highest values of transcript accumulations in responses to pathogen were detected for PR5 gene (3-235 fold), marker of Systemic Acquired Resistance (SAR). According to the results obtained in this study, it was clearly showed implication in defensive response of PR5 and defensin genes in advanced stages of broomrape infection in sunflower.

Keywords: Sunflower, broomrape, defence-related genes, resistance, gene expression

# NUTRITIVE VALUES OF SOYBEAN UNDER ARID ENVIRONMENT

Salem Alghamdi

King Saud University

salem@ksu.edu.sa

Soybean (*Glycine max* (L.) Merr.) is considered one of the main legume crops worldwide. The crop is grown on a large scale in the world as a rich source of vegetable protein and oil for human food. It is also used widely for the manufacturing concentrates for feeding livestock, particularly poultry production. Soybean seeds are used in Asia and other parts of the world to prepare a variety of industrial products and foods, fermented and dried, including soy milk, soy sauce, meat substitutes and other industrial products. Preliminarily estimation of proximate composition for each genotype is recorded. The crude protein composition genotypes varied widely and ranged between 35.63 to 43.13 %, with a mean value of 39.02 %. Moisture content ranged from 3.08 % to 5.88% while ash content in soybean genotypes ranged from 4.55% and 6.88 %with average of 5.44%. Total fat varied from 16.92 to 23.61 with a mean value of 23.61. Phytochemicals and antioxidants activities from twenty four genotypes of Soybean were determined. Differences were observed in total phenolics and flavonoid components. GC MS analysis showed total 90 phytochemical, of which the major components identified by gas chromatograph are predominantly composed of phenoliccopounds. Phenol, 2,6-dimethoxy-, 2-Methoxy-4-vinylphenol, 3,5-Dimethoxyacetophenone, 1,2-cyclopentanedione and Hexadecanoic acid, methyl ester were detected in most of the genotypes except few. These phytochemicals are responsible for various pharmacological actions like antimicrobial and antioxidants activities.

Keywords: Soybean, Nutritive values, Arid Environments

# VARIATION OF SOLUBLE CARBOHYDRATES IN SOYBEAN VARIETIS

Snezana Mladenovic Drinic, Aleksandra Sudaric, Vesna Peric, Mirjana Srebric, Dragan Kovacevic

Maize research institute Zemun Polje, Belgrade, Serbia

msnezana@mrizp.rs

Soybean, one of the major food and feed sources, contains about 40% protein, 20% oil, 35% carbohydrates and 5% minerals. Approximately half of carbohydrates are low molecular weight sugars, oligosaccharides, and small amounts of starch, while the other half are structural polysaccharides. Sucrose, stachiose and raffinose make up the majority of the water soluble carbohydrates in soybean seed. The objective of this research was to determine the variation in carbohydrate profile for seven soybean genotypes with HPLC method. Genotype differences were detected for all the soluble carbohydrates among the analyzed soybean genotypes. Olligosaccharids range from 4.34% in Lana to 5.03% in Selena. Sucrose was the predominant olligosaccharids accounting for an average of 46% of the total water soluble carbohydrates. Sucrose makes up 42.1%-48.49%, stachyose 29.10%-34.94% and raffinose 8.48%-13.38% of the total soluble carbohydrates in soybean seed. Small amounts of monosaccharides glucose, galactose and fructose (<1%) has been found. Raffinose and stachyose was positively correlated and each was negatively correlated with sucrose. Correlation between total water soluble carbohydrates and proteins was significant negatively (-0.45) as well as correlation between protein and oil (-0,64), but correlation between sugars and oil was positive (0,11). The soyfood market prefer soybean with high sucrose, low raffinose and stachyose content. The high sucrose variety Laura contains low stachyose and raffinose may be valuable for future genetic studies and soyfood industry.

Keywords: Soybean, carbonhydrates, oligosaccharids, HPLC

# GENETIC DIVERSITY AND CULTIVAR IDENTIFICATION OF DATE PALM (*PHOENIX DACTYLIFERA* L.) USING INTER-PRIMER BINDING SITE (IPBS) MARKERS

Ahmed Al-najm, Shuming Luo, Nabil Ahmad, Richard Trethowan

The University of Sydney, Plant Breeding Institute, Cobbitty, Australia

aaln4661@sydney.edu.au

Date palm (*Phoenix dactylifera* L.) is a monocotyledonous and dioecious perennial species, and it is one of the world's oldest cultivated fruit crop in many arid areas. Understanding the genetic relatedness among genotypes is important for effective date palm improvement. Five inter-primer binding site (iPBS) markers were used to survey genetic diversity and determine varietal differences among 54 and 12 date palm (Phoenix dactylifera L.) genotypes from Australia and Iraq, respectively. The PCR of these five iPBS primers (dominant markers) produced a total of 111 bands (100% polymorphic) ranging from 180 to 3500 bp. The PIC value for these five primers ranged from 0.2135 to 0.3289 with a mean value 0.2816. The mean expected heterozygosity (0.218), mean unbiased expected heterozygosity (0.229) and Shannon's information index (0.33) indicated a high level of inbreeding among the accessions tested. The resulted dendrogram from ordination and cluster analysis showed that the genetic relationships among all accessions could be separated into geographic origin; specifically Iraqi female cultivars, Australian female cultivars, Australian male accessions and related species, with a few exceptions. Date palm accessions cultivated in Australia and Iraq are highly divergent and the abundant genetic diversity observed provides a solid basis for date palm improvement in Australia. The iPBS PCR-based genome fingerprinting technology used in this study is low-cost and effectively differentiated accessions of date palm and their related species.

Keywords: Genetic diversity, Germplasm, Plant breeding

# FEATURES OF SOME CULTIVARS OF ESSENTIAL OIL ROSE *IN VITRO* MICROPROPAGATION

Natalya A. Yegorova[1], Irina V. Mitrofanova[1], Irina V. Stavtzeva[2]

1. Nikita Botanical Gardens – National Scientific Centre, Yalta, 298648, Russian Federation
2. Research Institute of Agriculture of the Crimea, Kievskaya str. 150, Simferopol, 295493, Russian Federation

yegorova.na@mail.ru

To increase the efficiency of breeding and seed growing of essential oil rose, one of the important essential oil plants cultivated at South of Russia, it is necessary to use biotechnological methods for accelerated multiplication of valuable genotypes, obtaining healthy planting material and further creation in vitro collections. The aim of this work was investigation the development of meristems of 5 essential oil rose cultivars at the first stages of in vitro micropropagation. The investigated plant materials were essential oil cultivars ‘Lany’, “Raduga”, “Lada”, “Michurinka”, “Festivalnaya” (Rosa spp.). As initial explants the meristems with leaf primordia from lateral buds of field-growing plants were used. The peculiarities of meristem morphogenesis and influence of some factors on this process at the first and second stages of micropropagation were revealed. It is shown that at the meristem introducing in vitro stage the multiple microshoots formation was obtained with a frequency rate up to 92%. Maximum capacity to form adventitious shoots was characterized cultivar “Raduga”, and the minimum – “Festivalnaya”. The increasing of rose micropropagation efficiency at the second stage by multiplication of shoots and shoot microcuttings was shown. Selection the culture medium (MS with BAP, gibberellic acid, IAA, glucose), which provides multiplication rate up to 4.6-15.7 per cycle, was depended on genotype and multiplication cycle. The multiplication rate at 3-4 cycles was increased, reaching maximum for cultivar “Raduga”(15.7) and “Michurinka” (13.2) and then at 5-7 cycles it was decreased.

This study was funded by a research grant No 14-50-00079 of the Russian Science Foundation.

Keywords: Essential oil rose, meristem, micropropagation, multiplication rate

# THE EFFECTS OF DIFFERENT DOSES OF GAMMA RAYS ON IN VITRO ADVENTITIOUS SHOOT REGENERATION IN SAFFLOWER

Hümeyra Yaman[1], Nilgün Bayraktar[2], Banu Efeoğlu[1]

1. Republic of Turkey Ministry of Food, Agriculture and Livestock, General Directorate of Agricultural Research and Policy. Central Research Institute for Field Crops, Biotechnology Research Center, Yenimahalle- Ankara/ TURKEY.
2. Ankara University Faculty of Agriculture. Field Crops Department, Dıskapı-Ankara/TURKEY

humeyrayaman@hotmail.com

The purpose of this study was to determine the effects of different doses of gamma rays in vitro adventitious shoot regeneration in safflower Dincer variety. In order to determine the best regeneration medium, different combinations of cytokinine and auxin types (TDZ (1-4 mg / L) X NAA (0-4 mg/L), BAP (1-4 mg/L) X NAA (0-4 mg / L)) were tested. It was observed that the most suitable of medium containing 1 mg/L TDZ. Regenerated shoots were rooted on MS medium supplemented with 0,5 mg/L NAA. Then, seeds of safflower containing 10-11% moisture were treated with 200, 300, 400, 500, 600 Gy doses of gamma rays using Co60 source. Callus ratio, ratio of explants forming shoot, number of shoots per explant, rooting ratio, root number per shoot, mean root length and survival ratio were determined in all dose applications. It was observed that when the doses were increased almost all parameters were markedly increased up to 400 Gy dose applications.

Keywords: Safflower, adventitious shoot regeneration, tissue culture, gamma ray

# ANALYSIS OF PROTEIN POLYMORPHISM IN DIFFERENT SUNFLOWER GENOTYPES

Duca Maria, Port Angela, Rotaru Tudor, Capatina Ana

Center of Molecular Biology, University of the Academy of Sciences of Moldova, 3/2, Academiei str., MD-2028, Chisinau, Republic of Moldova

portang@yahoo.com

One of the main goals of the sunflower improvement programs remain to be obtaining of new hybrids with advanced characters more pronounced at the qualitative level. It is considered that heterosis increases plant and organ size as well as plant productivity. In this context, the qualitative and quantitative analyses of seed proteins in 4 sunflower hybrids and their parental forms have been performed. Protein concentration was determined colorimetrically according to Bradford (1976); denatured proteins were separated by SDS PAGE electrophoresys according to Laemmli U.K. (1970). It was established that the concentration of total soluble proteins from the fat-free flour at investigated forms varies between 20-54%. In majority of investigated cases the direct proportional dependence between protein content in dry mass at parental forms and their hybrids was established. The electrophoretic analysis of total proteins demonstrates that the polypeptides spectrum is similar in all analysed genotypes, although some differences have been evidenced. Thus, 30 polypeptide bands with the relative molecular mass between 15 122 kDa were revealed in seeds of investigated forms. It was established that inheritance of polypeptide bands from the paternal line by hybrid offspring happened in 7 cases, from the maternal form by hybrid in 2 cases, and in 12 cases has been revealed the appearance of a new polypeptide at hybrid, which are most likely under the control of different allele genes.

Keywords: Sunflower, hybrids, proteins, polymorphism

# IMPROMENT OF EDIBLE OIL QUALITY IN KALE (*BRASSICA OLERACEA VAR. ACEPHALA*)

Fatih Seyis, Emine Aydın, Muhammet İkbal Çatal

Faculty of Agriculture and Natural Sciences, Recep Tayyip Erdogan University

fatih.seyis@erdogan.edu.tr

Kale (*Brassica oleracea var. acephala*) is vegetable plant at the Eastern Black Sea Region with high traditional value. Mainly the leaves of this plant are used to prepare traditional meal. On the other hand, we know that cabbage (*B. oleracea* L.) is one of the diploid parents of rapeseed (*B. napus* L.). The traditional oil quality of rapeseed have been changed using the low erucic acid mutants found in the gene pool of rapeseed (*B. napus* L.) and with time the 00-qualiy forms were developed in rapeseed (*B. napus* L.). İn B. oleracea low erucic acid mutants were detected in the 1990's and these cabbage genotypes were used to develop interspecific hybrids with low erucic acid content. These three cabbage genotypes, namely Kashirka, Ladozhskaya and Eisenkopf will now be used to transfer the edible oil quality into kale (*B. oleracea var. acephala*) using classical and biotechnological methods within the frame of a new staring project with the aim to develop a kale plant (*B. oleracea var. acephala*) with double use for the Eastern Black Sea Region. The breeding work will be discussed in detail.

Keywords: Kale, breeding, quality, B. oleracea

# BROOMRAPE (*OROBANCHE CUMANA WALLR.*) CONTROL BY BREEDING IN SUNFLOWER

Maria Joita Pacureanu, Luxita Risnoveanu, Anton Florin Gabriel

National Agricultural Research and Development Institute Fundulea, Romania

mariapacureanu2@yahoo.com

Broomrape (*Orobanche cumana Wallr.* has a long history of parasitism on sunflower, starting with Russia and followed by countries in Europe and Asia. There has been a constant tug-of-war between sunflower breeders and Orobanche cumana, with frequent changes in which side has the upper hand. Almost as soon as the breeders find a source of resistance to the latest race of the parasite, broomrape responds by evolving another virulent race. Sunflower selection for broomrape resistance makes use of different methods for testing breeding materials (in the field, greenhouse or at the molecular level), looks for resistance sources in certain wild species of genus Helianthus and has so far produced significant results. Dominant genes for resistance to races A,B,C,D,E and F have been found and incorporated into cultivated sunflow- er genotypes. In the last years, new broomrape populations have been discovered in several countries (Turkey, Spain, Romania, Russia, Ukraine, Bulgaria). None of the existing commercial hybrids resistant to the race F have proven resistant to these new populations of the parasite. Greenhouse work conducted at Fundulea institute in 2013 - 2015 period has managed to obtain two sunflower lines that are resistant to all the new populations of the parasite. The rapid changes in broomrape race composition have forced sunflower breeders and geneticists to not only search for genes for resistance to new races of the parasite, but, to also look for alternative solutions to the problem of broomrape control. Wild Helianthus annuus L. resistant to imidazolinones was first identified in Kansas, USA, in 1996 year. The use of imidazolinone resistance in sunflower breeding through the introduction of IMI-resistance into cultivated sunflower provides a broad spectrum of weed control and is specially effective in controlling Orobanche in sunflower. In the breeding program at Fundulea institute we are developing now the new sunflower lines, having genes for resistance to the new races of broomrape parasite as well as genes for resistance to IMI herbicides.

Keywords: Broomrape, sunflower, new races, genetic resistance, herbicide control

# EFFECTS OF 24-EPIBRASSINOLIDE ON LIPID PEROXIDATION AND ANTIOXIDATIVE ENZYMES ACTIVITIES IN BRASSICA JUNCEA L. UNDER LEAD STRESS

Eda Dalyan[1], Elif Yüzbaşıoğlu[1], Ilgın Akpınar[2], Esra Gülmez[2]

1. Division of Botany, Department of Biology, Faculty of Science,
Istanbul University, Süleymaniye, Istanbul

2. Institutes of Sciences, Istanbul University, Vezneciler, Istanbul

akpinarilgin@gmail.com

The effects of 24-epibrassinolide (24-EBL) on lipid peroxidation and antioxidative enzyme activities were studied in the roots of B. juncea L. (var. P71) seedlings exposed to lead (Pb) stress. The surface sterilized seeds were given treatments of different concentrations of EBL (10-12, 10-10, 10-8 and 10-6 M) and Pb (2 mM) in combination for 7 days in the Petri plates. After 7 days, root length were determined and, malondialdehyde (MDA) and total protein content, and the activities of antioxidative enzymes (guaiacol peroxidase (POD), catalase (CAT), and superoxide dismutase (SOD)) were analyzed in the roots of seedlings. While Pb stress caused to decrease in root length and protein content, it increased MDA content and the activities of antioxidant enzymes except for SOD. It was observed that the length of root decreased also when subjected to Pb stress in combination with 24-EBL. MDA content diminished significantly in all EBL concentrations compared to Pb. The amount of total protein also increased with decreasing EBL concentration. Furthermore, the activities of all antioxidative enzymes shown increase depending on EBL concentration compared to control. While CAT activity decreased in all EBL concentrations by comparison to Pb, the activity of POD diminished in only 10-12 and 10-8 M EBL applications. Also, it was not found significant difference between control and Pb application in the activity of SOD. However, it was observed increased SOD activity in roots treated with 10-6 M EBL. Conclusively, purpose of the present study was to contribute to a better understanding of the protective role of 24-EBL on regulation of antioxidant enzymes and its possible link in amelioration of Pb stress in plants.

Keywords: Epibrassinolide, lead stress, lipid peroxidation, peroxidase, catalase, superoxide dismutase.

# GENOTYPING SOYBEAN WITH SSR MARKERS ASSOCIATED WITH FLOWERING TIME AND SEED MATURATION

Saule Abugalieva, Shynar Anuarbek, Lyubov Volkova, Yerlan Turuspekov

Institute of Plant Biology and Biotechnology, 45 Timiryazev street, 050040 Almaty, Kazakhstan

absaule@yahoo.com

Soybean is one of the major legume crops in the World and Kazakhstan. In this study we genotyped a collection of 120 cultivars and perspective lines of soybean (*Glycine max* (L.) Merrill. The genotypes originated from different world regions belonged to maturity groups between 000 and I. Genetic diversity of this collection studied using 23 microsatellite markers, which according to published reports were associated to plant adaptation. In total 86 alleles were detected at all 23 SSR loci. The number of alleles per locus ranged from 2 to 7 with an average of 3.7. The maximum of seven alleles were observed at the loci of Satt063 on chromosome Gm14 and Satt458 on chromosome Gm17, respectively. The number of effective alleles ranged from 1.04 to 5.7 with an average 2.8. Genetic diversity according to Shannon (0.097-1.841; mean 1.005) and Nei (0.039-0.825; mean 0.540) indices were determined. Polymorphic index content (PIC) was also calculated which ranged from 0.038 to 0.802 with average of 0.491. A genetic distance matrix and a UPGMA cluster analysis were conducted based on the microsatellite markers data. Obtained genotypic results, phenological and phenotypic data of the collection grown in three regions of Kazakhstan will be used in association analysis for high adaptability and productivity in three regions of Kazakhstan.

Keywords: Soybean, genotyping, microsatellite markers, flowering time, seed maturation

# THE DETERMINATION OF CONSUMER PREFERENCES RELATED TO EXTERNAL QUALITY FEATURES IN TURKEY

Fatma Pınar Öztürk, Gökhan Öztürk, Emel Kaçal, Dilek Karamürsel,
Alamettin Bayav, Meltem Ali Emre

Fruit Research Institute Eğirdir, Isparta, Turkey

pinar1010@yahoo.com

To be aware that quality is the most important criterion of consumer acceptance has been required to take into account “the quality desired by the consumers” at breeding programs especially in the last 30 years. Therefore firstly the consumer acceptance criteria must be defined for target market. In the study was aimed to determine the acceptance degree of domestic consumers with regard to external quality features of pear fruit in Turkey. Primary data of study were obtained from questionnaires prepared by the visual sensory analysis method. Questionnaires were made with 91 panelists held Growtech fair in Antalya in 2014. Panelists gave scores between 1 and 10 for each color and shape options. ANOVA and basic statistics were utilized in the evaluation of data. Consumer preferences at domestic market related to external quality features in Turkey have been yellow-green, bright yellow and light green, pyriform-shaped and medium-sized pear.

Keywords: Fruit quality, Consumer preferences, fruit peel colour, shape

# NDVI CHARACTERISTICS, PRODUCTIVITY AND DROUGHT TOLERANCE OF PRECOCIOUS SOMACLONAL SOYBEAN LINES IN CONTRASTING AREAS OF KAZAKHSTAN

Didorenko S.V., Abugaliyeva A.I., Rozhanskaya O.A., Spryagaylova Y.N.,
Erzhebaeva R.,

Kazakh research Institute of agriculture and Plant growing, Almalybak v., Kazakhstan

svetl_did@mail.ru

The culture of somatic cells is a new source of plant diversity. Using somaclonal variation in the selection, can create new forms, which will serve as donors of economically valuable traits. The 15 soybean lines somaclonal varieties SibNIIK 315 and Dean were studis in 2014 -2015gg. on the field of the Kazakh research Institute of agriculture and Plant growing (KazRIAPG), Almaty (740 meters above sea level, 43 ° 15 'with. sh., 76 ° 54'. d.) and East Kazakhstan Agricultural Research Institute (EKARI), Ust -Kamenogorsk (49 ° 57 'with. sh., 82 ° 37'. d.). The growing season in terms of Almaty region ranged from 81-88 days, and in the conditions of the East Kazakhstan 82-103 days. Most late-ripening varieties somaclones SibNIIK 315 - R 207-10, R184-4 and Dyna's - R155-2 grade in eastern Kazakhstan conditions ripened for 103 days. The most productive line with a mass of seeds per plant 13,1-14,7g. - R176-5, R 165-11, R 198-12, R162-17, R155-2. To reveal drought-resistant forms of somaclonal lines were grown under conditions of drought provoked by the greenhouse complex KazRIAPG. The most productive patterns R-177-5, R-165-11, R-186-8, R-170-1 characterized as increased seed weight per plant, and increased the number of stomata in the flowering stage (12,8-17,6sht / field) and the number of hairs (20,0-24,5 pieces / box). Measurement of standardized difference vegetation index (NDVI), showed the highest rate in the phase of loading beans from somaclonal lines R -177-5, R-186-8, R-165-11 and R-290-11 (0,79 - 0, 81), while the standard variety SibNIIK 315 he was at the same stage of development 0,74- 0,75. NDVI measurements confirm the results of the accumulation of biomass more intensive development of somaclonal lines compared with the standard.

Keywords: Soybean, somaclones, yield, maturity, drought resistance

# ACHIEVEMENTS IN OIL CROPS BREEDING IN SERBIA

Sinica Jocic, Sandra Cvejic, Ana Marjanovic-jeromela, Nada Hladni, Dragana Miladinovic

Institute of Field and Vegetable Crops, Maksima Gorkog 30., 21000 Novi Sad, Serbia

nada.hladni@ifvcns.ns.ac.rs

Breeding oil crops in Serbia has numerous achievements contributing to both local and European research and production. It is also faced with many challenges, common to the other breeding programs in Europe and worldwide. The Institute of Field and Vegetable Crops (IFVCNS), from Novi Sad, Serbia has long tradition in breeding and production of major oil crops, such as sunflower and rapeseed. Sunflower breeding program started fifty years ago, focused on different open-pollinated varieties development. After discovery of cytoplasmatic male sterility (CMS) and restorer (Rf) sources the breeding work was primarily aimed to hybrid research and development. Sunflower breeders have created methods, defined main directions for breeding and build up models of ideal hybrids for the different agro-ecological conditions. A rich collection of genetically divergent material has been developed: over 7000 inbred lines, collection of 500 accessions of annual and perennial wild species from genus Helianthus and their interspecies hybrids. The final results of intensive breeding programme are over 500 released hybrids in Serbia and other countries. Well-developed cooperative programs with over 30 institutes and companies enabled the exchange of genetic material resulting over 150 joint hybrids. Rapeseed (*Brassica napus* L.) has been receiving an increased attention in Serbia during past few decades, due to the production of bio-diesel, where rapeseed is considered the most quality crop for this purpose. Today, the IFVCNS remains the only institution in Serbia dealing with rapeseed breeding, biotechnology, agronomy, seed production and other forms of research. Breeding strategies at IFVCNS related to rapeseed are based upon the basic research of seed yield components and seed yield and quality, with emphasis on oil and protein composition. So far, at IFVCNS there have been developed eleven autumn-sown rapeseed cultivars, two spring-sown rapeseed cultivars and one hybrid registered in Serbia and other countries. Beside sunflower and rapeseed numerous other plant species are also regarded as a possible oil source of various quality parameters. Collection of IFVCNS minor oil crops included research on castor oil plant, flax, sesame, safflower, mustard, false flax, caper spurge, mary thistle, chufa sedge, coriander, dill, okra and lens.

Keywords: Oil crops, sunflower, rapeseed, minor oil crops, breeding

# MOLECULAR AND MORPHOLOGICAL CHARACTERIZATION OF TURKISH OPIUM POPPY (*PAPAVER SOMNIFERUM*) GERMPLASM FOR BREEDING AND CONSERVATION

Ibrahim Celik[1], Huseyin Camci[2], Arzu Kose[2], Ferda Celikoglu Kosar[2],
Sami Doganlar[1], Anne Frary[1]

1. Department of Molecular Biology and Genetics, Izmir Institute of Technology, Urla, Izmir 35430, Turkey
2. Anatolia Agricultural Research Institute (AARI), Eskisehir, Turkey

icelik@iyte.edu.tr

Opium poppy (*Papaver somniferum* L.) is an important medicinal crop which is the only source of many alkaloids. Despite the importance of this crop, few studies have characterized opium poppy germplasm with crop-specific molecular markers. Turkey is a diversity center for opium poppy, therefore, molecular and morphological characterization of Turkish opium poppy germplasm is essential for both conservation and efficient breeding. In this study, morphological and molecular diversity of 103 Turkish opium poppy landraces and 15 cultivars were analyzed. Potentially useful morphological variation was observed for morphine content, plant height, and capsule index. However, the landraces exhibited limited breeding potential for stigma number, seed and straw yield. As expected, the accessions had low molecular genetic diversity (average 0.11). Both morphological and molecular analyses showed distinct clustering of cultivars and landraces. The present study also indicated that morphological data was less efficient than molecular data for core set selection in Turkish opium poppy.

Keywords: Core set, microsatellites, morphine content, Papaver somniferum, SSR

# EXOGENOUS ASCORBIC ACID INCREASES RESISTANCE TO SALT OF CARTHAMUS TINCTORIUS

Banu Aytül Ekmekçi

Anadolu University, Science Faculty, Biology Depertmant

hilooglumuhip@gmail.com

Salinity stress has negative effects on agricultural yield throughout the world, affecting production whether it is for subsistence or economic gain. This study investigates the inductive role of vitamin C and its application mode in mitigating the detrimental effects of irrigation with diluted (10, 20 and 30 %) NaCl + water on Carthamus tinctorius plants. The results show that 10% of salt water exhibited insignificant changes, while the higher levels impaired growth by reducing seed germination, dry weights of shoot and root, water status and chlorophyll contents. However, irrigation with salt water enhanced carotenoids and antioxidant enzyme activities. The detrimental effects of salt water were ameliorated by application of 100 ppm ascorbic acid (vitamin C). The inductive role of vitamin was associated with the improvement of seed germination, growth, plant water status, carotenoids, endogenous ascorbic acid and antioxidant enzyme activities. Moreover, vitamin C alone or in combination with 30% NaCl water increased the intensity of protein bands as well as synthesized additional new proteins with molecular weights of 205, 87, 84, 65 and 45 kDa. This could increase tolerance mechanisms of treated plants towards water salinity.

Keywords: Salinity, stress, vitamin C, antioxidant, NaCl, enzyme.

# DIFFERENTIAL GENE EXPRESSION IN SOYBEAN GENOTYPES UNDER DROUGHT STRESS

Evanthia Champla[1], Ourania I Pavli[2]

1. Laboratory of Plant Breeding and Biometry, Department of Crop Science, Agricultural University of Athens, Iera Odos 75, 11855 Athens, Greece
2. Laboratory of Genetics and Plant Breeding, Department of Agriculture, Crop Pro duction and Rural Environment, University of Thessaly, Fytokoy Str, 38446 N. Ionia, Volos, Greece

gskaracis@aua.gr

In response to drought, plants induce a series of developmental, morphological and molecular adaptations, aiming at safeguarding all necessary activities. In this study, we determined the expression of genes related to drought tolerance in soybean plants subjected to limited water availability. The deduced transcript levels were comparatively analyzed with non-stressed soybean plants. Drought stress experiments were carried out using a known resistant and a susceptible to drought variety. The genotypes under study were subjected to drought stress a) in vitro, using solidified MS medium, with decreased osmotic potential by adding polyethylene glycol (PEG) 6000 (PEG 0%, 2,5%, 5%), for 12 days and b) in field conditions using two different irrigation regimes: full (80% FWC) and insufficient(40% FWC). Response to drought was assessed on plants that were subjected to stress for a period of 4 and 6 days. All analyses were performed on 4 independent biological repeats per treatment. For transcriptomics, an in silico survey allowed for the selection of genes whose expression is related to soybean's response to drought. Following total RNA isolation, RNA samples were treated with DNase. First-strand cDNA was reverse transcribed and target cDNAs were used as template in quantitative real-time PCR reactions (qRT-PCR), using gene specific primers. Differences of cDNA template amounts were normalized using the expression level of the ubiquitin gene. Primers were designed using Primer Express. Deduced data are discussed and suggested as candidate functional markers to be employed for the purposes of screening and identifying drought tolerant genetic material in soybean.

Keywords: Soybean, drought tolerance, gene expression, qRT-PCR,
functional marker

# EMBRYO RESCUE STUDIES IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

Hümeyra Yaman[1], Cuma Karaoğlu[1], Hasan Keyvanoğlu[2], İlhan subaşi[2], Yusuf Arslan[3]

1. Biotechnology Research Center, Central Research Institute for Field Crops, 06220 Yenimahalle/Ankara/Turkey.
2. Department of Oil Crops, Central Research Institute for Field Crops, 06220 Yenimahalle/Ankara/Turkey.
3. Department of Field Crops, Faculty of Agriculture and Natural Sciences, Abant Izzet Baysal University 14280 Abant/Bolu/ Turkey

humeyrayaman@hotmail.com

Genetic exchange of gene characters is possible with hybridization between closely related plant species. However, development of embryos is in possible due to the differences between parental genomes in some cases. Survival rate of F1 plants is low when the chromosome numbers of hybrid plants are different. Classical breeding programs are being carried out for Safflower which is an important oil plant in our country to expand the genetic base and to get efficient lines of it. Also we carry out tissue culture studies. After hybridization of different species or genus of plants, haploid plants can be obtained by the isolation of immature embryos and culturing them in vitro on basal medium. Thus, embryo rescue operations were studied on safflower. We studied optimization stage of the embryo how many days later must be taken after hybridization, the sterilization method and nutrient media used during regeneration stage. Different hormone concentrations containing 3 basal media and 6 genotypes were used in the study. We also recorded extracted number of embryos, the number of shoots turned from embryos, the number of plants regenerated and the regeneration rate values. The regeneration rate was varied between 0-100%. The best values were attained with R9 regeneration medium used in the wheat embryo rescue study. The highest rates of regeneration are attained from the genotype 114/3 and 122/2 respectively. Plantlets were rooted in medium containing 0.5 mg/L NAA. Then, 2 weeks later they were transferred into the pots in greenhouse conditions.

Keywords: Safflower, tissue culture, embryo rescue, regeneration rate.

# INVESTIGATION OF THE EFFECT OF EMS (*Ethyl Methanesulfonate*) TREATMENT OF FATTY ACID RATIO IN SAFFLOWER (*Carthamus tinctorius*)

İlhan Subaşı[1], Dilek Başalma[2], Yusuf Arslan[3], Hasan Keyvanoğlu[1]

1. Field Crops Central Research Institute-Şehit Cem Ersever Cad.
   No: 9-11 Yenimahalle ANKARA
2. Ankara University, Agricultural Faculty, Ankara-Turkey
3. Abant Izzet Baysal University, Faculty of Agriculture , Golkoy

ilhansubasi@gmail.com

Safflower is an important oil plant with 13-46% oil in its seeds. Safflower has quality oil in terms of fatty acids. This oil is consists of unsaturated fatty acids at the ratio of 90%. Safflower oil is linoleic acid-rich. In recent years especially safflower varieties with high oleic acid have been breeded because of suitability for frying and having high storage stability. Mutagen treatments are commonly used method for modification of fatty acid composition. The aim of this study is to examine the effect of EMS (Ethyl Methane Sulfonate) which is in alkalizing agent group as a chemical mutagen, to fatty acid composition of safflower oil. In our research with using 20 seeds of Linas cultivar 7 different EMS doses (control, 0,24%, 0,4%, 0,64%, 0,8%, 1,6%, 2,4 %) and 5 different times (control, 2h, 3h, 4h, 5h) were treated. After the treatments seeds were sowed on 27.04.2015 and harvested in August. The main fatty acids of control safflower oil is determined as 73% linoleic acid, 12% oleic acid, 5,8% palmitic acid and 2,2% stearic acid. Compared to the control the highest decrease among the fatty acids was determined in oleic acid as 8,39% (32,78% decrease) for treat of 2 hour and 0,64% EMS (2h-0,64). It is followed by linoleic acid 61,1% (17,05% decrease) 3h-0,24; palmitic acid 4,94% (15,77% decrease) 3h-0,24 and stearic acid 1,94% (13,78% decrease) 4h-1,6 respectively. On the other hand in some treatments there were increases in oleic acid, stearic acid and linoleic acid content. As the increasing values oleic acid was 14,77% (18,27% increase; 4h-0,24 treatment), stearic acid was 2,51% (11,76% increase; 3h-0,64 treatment) and linoleic acid was 76,77% (4,21% increase; 3h-0,64 treatment). Also it was determined that lauric acid which was not seen in the control was increased in some treatments and reached to 14,94% with 2h-0,64 treatment.

Keywords: Safflower, Carthamus tinctorius L., Mutation, Modification, Fatty acids

# IDENTIFICATION OF CHLOROPHYLL CONTENT IN SOYBEAN (*GLYCINE MAX* (L.) MERRILL) BY USING SOIL PLANT ANALYTICAL DEVELOPMENT (SPAD)-502 METER

Mustafa Polat, Rüstem Üstün, Birgül Güden, Engin Yol, Bülent Uzun

Department of Field Crops, Faculty of Agriculture, Akdeniz University,
Antalya, Turkey

birgulguden@akdeniz.edu.tr

Soybean, (*Glycine max* (L.) Merrill), is one of the most significant legume crop known as a source of oil and protein in the world. At the same time, provide vegetable protein for people on diets and feed supply for animals. Chlorophyll content that give information about productivity and physiology of plant is an important trait and a valuable tool for determination drought tolerance in plants. Traditionally, measurement of chlorophyll contents required leaf extraction with organic solvents and spectrophotometric determination in solution is required for pigment analysis with wet chemical methods and this implication is time-consuming and requiring intensive hand-labor. Non-destructive methods have been developed for measurement of chlorophyll content such as Soil Plant Analytical Development (SPAD)-502 meter which is rapid, inexpensive, portable and suitable for field use. In the present investigation, measurement of chlorophyll contents was performed for each genotypes in a soybean collection consisting of 124 genotypes with using SPAD-502 meter. The SPAD readings for each accession were replicated 3 times at different dates. The results represented that the highest and the lowest chlorophyll contents in the soybean collection were determined by 40.53 µmol/m2 and 19.01 µmol/m2, respectively. The acquiring SPAD data in the soybean collection would be highly useful for selecting accessions suitable for second crop farming in southern Turkey as it is providing some indication about water-use-efficiency and drought tolerance of the materials.

Keywords: Chlorophyll, Soybean, SPAD.

# MAPPING OF QUANTITATIVE TRAIT LOCI ASSOCIATED WITH BLUSH SKIN IN EUROPEAN PEAR *PYRUS COMMUNIS* L.

Solomon Ntladi, Kenneth R Tobutt, Rouvay Roodt-Wilding, Jan P Human

ARC Infruitec Nietvoorbij, Private Bag X5026, Stellenbosch 7599, South Africa

ntladim@arc.agric.za

The European pear breeding programme at ARC Infruitec-Nietvoorbij in South Africa is known for breeding cultivars with blush skin using traditional breeding methods. The blush skin trait is of considerable economic value. However, to date, genetic control of blush skin in European pear is not well understood. In the study, an F1 progeny derived from a cross between “Flamingo” (blush skin) x “Abate Fetel” (light blush, mostly russeted) was used to construct a framework map of microsatellite markers previously mapped in pear and apple, and to locate QTLs associated with blush skin. Fruit skin colour was scored visually over three seasons in 121 seedlings and 137 microsatellites corresponding to 187 loci were analysed. Map construction with JOINMAP4.0 and preliminary QTL analysis using MapQTL6.0 revealed two putative QTLs on LG 5 and LG 9 explaining 18.9% and 12.4% of the variance, respectively. These results provide better understanding of genetic control for blush in pear. A Pc-MYB10 gene involved in anthocyanin development in fruit skin that was previously mapped to LG9 by another group is a candidate gene for one of the QTLs. Markers linked to these QTLs would be useful for marker-assisted selection in the pear breeding programme for blush skin.

Keywords: Microsatellites, QTL, marker assisted selection

# BIOTECHNOLOGICAL APPROACHES OF PERSIMMON EXPLANTS INTRODUCTION *TO IN VITRO* CULTURE

Irina V. Mitrofanova, Natalya N. Ivanova

Nikita Botanical Gardens National Scientific Center, Yalta, 298648,
Russian Federation

irimitrofanova@yandex.ru

Persimmon belongs to the family Ebenaceae Gurke, genus Diospyros L. Persimmon fruit are rich in vitamins and polyphenolic substances, carotenoids, leucoanthocyans, organic compounds, potassium, calcium, iron, iodine and contains 13 organic acids, carotene, colorants and tannins. The collection of Nikita Botanical Gardens includes 82 cultivars and 3 species of persimmon. The aim of the study was investigation of features of in vitro introduction process for some valuable persimmon cultivars for their cleaning up and micropropagation. As initial explants meristems and vegetative buds from 6 cultivars in February-September were collected. Aseptic persimmon culture (80%) was obtained by consequentially immersing of explants in 70% C2H5OH, 1% Thimerosal and 0.08% AgNO3. For in vitro chemotherapy into the medium ribavirin (1-30 mg l-1) was added. Explants development was induced on MS medium supplemented with BAP, zeatin and IBA. Microshoots regeneration was obtained on MS medium with 0.4-0.8 mg l-1 zeatin. Number of microshoots formation was depended on the mother plant. At the earlier stages of the culture 2-3 microshoots per explant in cv. “Nikitskaya Bordovaya”, 1-2 – in cvs. “Zvezdochka”, “Zolotistaya” and “Mechta” were obtained. Under each new subculture number of regenerated microshoots increased and in the 3rd one it was 3-6 microshoots per explant. Thus, in our research we have determined the type of initial explant, optimal time of explants introduction, sterilization conditions, types of the culture medium and growth regulators for induction of persimmon explants development.

This study was funded by a research grant No 14-50-00079 of the Russian Science Foundation.

Keywords: Persimmon, cultivar, explant introduction, microshoot,
regeneration in vitro

# SELECTION OF PRUNUS CERASIFERA PLUM SPECIES IN ISPARTA, KUTAHYA CITIES AND EVALUATION OF ROOTSTOCK CHARACTERISTICS

İbrahim Gür, Hakkı Koçal, Mehmet Aksu, Ömer Faruk Karamürsel,
Hasan Cumhur Sarısu, İsmail Demirtaş

Fruit Research Institute, 32500 Eğirdir, Isparta, TURKEY

igur03@hotmail.com

Plums are fruit groups that have lots of varieties with high diversity and adaptation capability in Asia, Europe and North America. Plum’s origin is East Asia, Middle Asia and Caucasia including P. cerasifera Ehrh. species and it has also a great variety diversity. P. cerasifera Ehrh. is the most commonly species for using seedling rootstock for plums. The seedling rootstocks of plums which are including Prunus cerasifera Ehrh. species in Turkey are used as rootstock for European Plums Japanese Plums and cherry plums. The species are not only used as rootstocks for different plums genus but also are used for peach, apricot, almond and cherry species. In this study, 50 Prunus cerasifera Ehrh. plum types were selected from Isparta and Kütahya cities with high diversity in 2012 year. Selected plum types were planted in Eğirdir Fruit Research Institute. Stem diameter, canopy width, canopy height and thorn density of plants were evaluated in 2015 year. It was determined Sph 5, Gdz 5, and Gdz 1 types have weak development capacity; Gdz 6, Kpl 14 and Kpl 15 types have strong development capacity. In the next phase of the study, the types selected will be propagated by vegetative method and graft compatibility of selected rootstock types will be determined with some peach, plum and apricot varieties.

Keywords: Clone, P. cerasifera, selection, rootstock breeding

# SHOOT PROPOGATION STUDIES ON SELECTED WILD SOUR CHEERY TYPES IN VITRO CONDITIONS

Şafak Sekmen, Hasan Cumhur Sarısu, Zehra Babalık, İbrahim Gür, Melih Aydınlı
Eğirdir Fruit Research Institute 32500 Eğirdir/Isparta, Turkey

safaksekmen@gmail.com

*Prunus avium* L. and *Prunus mahaleb* L. rootstock are generally used in sweet cheery and sour cherry production in Turkey. These rootstocks have some negative effects for soil and ecology conditions for that reason adaptable seed and clone rootstocks should be used for his aim, 38 different wild sour cheery types were collected from 2002 and were planted and stored in Eğirdir Fruit Research Institute farmland. In this study Y8, S2, S12, KS6, D4 and D1-1 types were selected from 38 type and propagation studies were done with these types. Study was conducted in Eğirdir Fruit Research Institute in 2015. Apical and lateral shoot peaks were used as explant in the propagation and different hormones and concentrations were used. Effects of the 6 different combinations for shoot development ratio, shoot propagation, shoot number and shoot length were evaluated. Highest success in shoot propagation was determined from 1.0 mg/I BAP, 1.5 mg/I GA3 and 0.1 mg/I NAA with MS nutrient combination, some types will be studied with other studies to get the best propagation combination in the next stages.

Keywords: Rootstock, in vitro propagation, sour cheery

# BREEDING OF EARLY RIPENING SWEET CHERRY CULTIVARS

İsmail Demirtaş, Mehmet Aksu, Hasan Cumhur Sarısu, Ömer Faruk Karamürsel, İbrahim Gür, Hakkı Koçal, Yılmaz Sesli, Fatma Pınar Öztürk, Zehra Babalık, Melih Aydınlı

Fruit Research Institute, 32500 Eğirdir, Isparta, Turkey

idemirtas66@hotmail.com

Turkey holds the first place in the world cherry production with about 400.000 tones, however it can only export %10-15 of this production. “0900 Ziraat” cultivar constitutes almost all of this cherry export by itself. This high quality cultivar is known as “Turkish cherry” in the word. Depending on only one cultivar causes gaps in the export, thus leading to profit loses for cherry growers and exporters. Growers wish to produce cherries outside the peak production periods to take advantage of higher market prices. This has been a high priority for many breeding programs and a wider maturity range has supported increased planting of cherries. “Breeding of new sweet cherry varieties” named project was started at Fruit Research Institute in 2007. In this study as method was followed classical crossing breeding method. E. Burlat, E. Rivers, P. Bernard and 0900 Ziraat cultivars were used as parents. The goal of project is to develop new high quality and early ripening sweet cherry cultivars with high consumer preference. So far, 2000 genotypes from different crosses were obtained. Traits of pregenies are being evaluated.

Keywords: Breeding, Prunus avium L., Early ripening, Quality

# DETERMINATION OF THE REFERENCE GENES SUITABLE FOR GENE EXPRESSION STUDIES IN RESPONSE TO DROUGHT STRESS IN PEACH

Mehmet Aksu[1], Mehtap Şahin Çevik[2*]

1. Ministry of Food Agriculture and Livestock, Fruit Research Institute, Eğirdir, Isparta, Turkey
2. Süleyman Demirel University, Faculty of Agriculture, Department of Agricultural Biotechnology, Isparta, Turkey

msahincevik@yahoo.com

Drought causes considerable yield losses in agricultural production and limits the lands used for agriculture. Plants have developed certain adaptation mechanisms to survive under drought stress. In recent years, studies have been conducted to reveal the mechanisms of drought adaptation and tolerance in plants. These studies showed that expression of the many genes changed in significantly under abiotic stresses in plants. Gene expression studies have been carried out among stress responsive genes to determine individual genes and level of changes in the expression of these genes during stress treatments in plants. In gene expression studies, determining gene expression levels correctly requires the use of reference genes which show no changes in their expression, need to be identified for each plant type and each stress condition. In this study, genes showing no changes in their expression levels in response to drought stress in peach were determined. For this purpose, drought stress was applied to peach plants for 30 days and leaf samples were collected from these plants prior to stress treatment and on the 7, 9, 11, 15, 20, 27 and 30 days of drought stress treatment. Total RNA was isolated from these leaves using CTAB+LiCl method. Expression levels of actin (ACT), translation elongation factor 2 (TEF 2), RNA polymerase subunit (RP II), and ubiquitin 10 (UBQ 10) genes were determined from total RNA using real time RT-PCR. The results showed while TEF 2, RP II and UBQ 10 reference genes showed significant changes in their expression, no significant changes in the expression of actin gene was observed in peach under drought stress. Therefore, as a result of this study, use of actin as a reference gene in gene expression studies in peach under drought stress is recommended.

Keywords: Abiotic stress, drought, Prunus persica, reference gene, real-time PCR

# DETERMINATION OF EXPRESSION LEVELS OF SOME WRKY GENES DURING DROUGHT STRESS IN PEACH

Mehmet Aksu[1], Mehtap Şahin Çevik[2*]

1. Ministry of Food Agriculture and Livestock, Fruit Research Institute, Eğirdir, Isparta, Turkey
2. Süleyman Demirel University, Faculty of Agriculture, Department of Agricultural Biotechnology, Isparta, Turkey

msahincevik@yahoo.com

In recent years, studies conducted in different plants showed that WRKY transcription factors (TF) play a role in resistance to abiotic and biotic stresses. Peach (*Prunus persica* L.) is an important fruit species among stone fruits. As in other fruit species, drought cause reduction in production areas and yield losses in peach. In this study, the expression level of some WRKY TF during drought stress in peach was determined. For this purpose, peach plants were treated with drought stress for 30 days and leaf samples were collected from these plants before the stress treatment and on the 7, 9, 11, 15, 20, 27 and 30 days of drought stress treatment. Total RNA was isolated from these leaves using CTAB+LiCl method. The expression of five different WRKY genes in response to drought stress was determined by real time PCR method using total RNA. The results showed expression pattern of WRKY genes were different and significant differences were observed in expression levels of these WRKY genes during drought stress in peach. As a result of this study, it is thought that some of the WRKY TFs analyzed in this study may have a role in the drought stress adaptation and tolerance in peach.

Keywords: Abiotic stress, drought, gene expression, transcription factors, Prunus persica, real-time PCR

# DETERMINATION OF SUSCEPTIBILITY OF SOME APRICOT CULTIVARS TO THE SHOT-HOLE (*STIGMINA CARPOPHILA*) DISEASE UNDER NATURAL INOCULUM CONDITIONS

Yusuf Öztürk, Hakkı Koçal, Şeyma Reyhan Erdoğan, Hamza Şenyurt, Mesut İşci
Fruit Research Institute, Eğirdir, Turkey

yosuf_ozturk@hotmail.com

This study was conducted in Eğirdir Fruit Research Institute for two years for the purpose of determining the susceptibility of some apricot cultivars to the shot-hole disease, which is one of the most important fungal diseases affecting stone fruit trees and especially apricot caused by the fungus Stigmina carpophila. In the study, reactions of 9 domestic and 10 foreign (in total 19) apricot cultivars to the disease under natural inoculum were analyzed. Disease evaluations were made on fruits and leaves separately. As a result of leaf evaluations, the highest disease severities were determined to be on cultivars Çağataybey (32.30%), Sakıt-7 (26.30%) and şekerpare (25.03%), respectively, and the lowest on cultivars Wilson Delicious (11.41%), Ivonne Liverani (12.54%) and Borsi Rozsa (14.35%). In fruit evaluations, however, the highest disease severities were found to be on cultivars şekerpare (50.87%), Sakıt-7 (50.15%) and Sakıt-2 (49.85%), and the lowest on cultivars Aprikoz (17.45%), Zard (17.69%) and Hasanbey (21.28%). A moderate positive correlation was observed between leaf and fruit disease severities. No statistical difference was detected between leaf and fruit disease severities by ripening periods. Disease severity was found to be higher on fruits than leaves and on domestic cultivars. Determination of disease resistances of domestic-foreign apricot cultivars with high fruit quality is thought to provide great advantage in selecting the parents to be used as a source of resistance in breeding studies.

Keywords: Apricot, shot-hole disease, Stigmina carpophila, cultivar reactions

## AN OVERVIEW ON FRUIT BREEDING IN TURKEY

Emel KAÇAL[1], Fatma AKINCI YILDIRIM[2], Gökhan ÖZTÜRK[1], Melih AYDINLI[1]

1. Fruit Research Institute, 32500 Eğirdir, Isparta, Turkey
2. Suleyman Demirel University, Faculty of Agriculture,
   Department of Horticulture, Isparta, Turkey

emel.vural@gmail.com

Turkey has a rich biodiversity and it is home to many ancient civilizations. Breeding and culture of fruit species in Turkey is based on many years. According to archaeological excavations, an advance fruit culture has been made in Anatolia 4-5 thousand years ago. Central Asian Turks who has a deep rooted fruit growing traditions, also made a significant contribution to this culture. In scientific terms, fruit breeding studies began after the establishment of the republic and gained momentum over time. Generally these studies have been carried out identification of genetic resource and selection of superior fruit types into the biodiversity. In this context, studies have been made in many species including walnut. New breeding programs have been established in different objectives and used advanced techniques (tissue culture and molecular methods) in breeding methods the last 15-20 years. Although the primary objective of breeding programs to develop new varieties, in recent years, rootstock breeding programs also began to gain speed such as apple, plum and sour cherry fruit. Breeding studies in Turkey carried out by mainly universities and research institutes. From the 2000s to today, it is possible see to develop variety and rootstock studies by private sector. Thus, it is foreseen to increase of medium and long term breeding programs.

Keywords: Turkey, fruit, variety, hybridization, selection

# DEVELOPMENT OF EMBRYO SAC AND POLLEN TUBE GROWTH IN PEAR CROSSES

Gökhan Öztürk[1], M. Atilla Aşkın[2], Recep Ali Emre[1], Emel Kaçal[1],
Hasan Cumhur Sarısu[1]

1. Meyvecilik Araştırma Enstitüsü Eğirdir/Isparta
2. Süleyman Demirel Üniversitesi, Ziraat Fakültesi, Bahçe Bitkileri Bölümü

irem_gokhan@hotmail.com

In this study, Williams, Deveci and Ankara cultivars were crossed as controlled with Santa Maria, Mustafabey, Coscia, Dr Jules Guyot, Beurre Hardy and Beurre Precoce Morettini cultivars. Whether there is a incompatibility state between main and pollinator cultivars, seed number obtained from crossing, embryo sac formation in mother parents and pollen tubes growth according to pollinator varieties have been examined. It was not observed any incompatibility state between main and pollinator cultivars. The average number of seeds per fruit chanced according to years and pollinator varieties. At examination of embryo sac growth was determined that embryo sacs were ready of for fertilization after 7 days from anthesis. Pollen tube growth in controlled pollination applications was one or two days earlier from free pollination and determined in 3-4 days.

Keywords: Pyrus communis, embryo sac growth, pollen tube growth

# THE NEW TABLE GRAPE CANDIDATES IN TEKİRDAG VITICULTURAL RESEARCH INSTITUTE

Onur Ergönül, Cengiz Özer, Mehmet Sağlam

Tekirdag Viticulture Research Institute, Turkey

onur.ergonul@gthb.gov.tr

Turkey is among the leading grape growers countries and ranks fifth (462.295 ha) and sixth (4.234.305 ton) in terms of vineyard area and grape production, respectively. Grape production is characterized with Sultanina growing especially in Aegean region. The share of grapes in total fresh fruit is 21-23 percent (Söylemezoğlu et al, 2015). Many regional grape varieties being inadequate to export are still continuing economic importance in local markets. However, curiosity and demand to new grapecultivars of grape growers and consumers have increased. Different ecologies at grape growing regions provide marketing the grapes in wide time range. In Turkey, in spite of being important gene source of grape and one of the biggest grape producers, number and quantity of favorite table grape cultivars are insufficient at the market. Early or late maturing attractive crossbred- new table grape cultivars will be good alternative for table grape growing regions. Breeding programs to develop new grape cultivars have been initiated at state research institutions. Seedless and seeded F1 populations were formed with different crosses at the Tekirdağ Viticultural Research Institute and Yalova Atatürk Horticultural Central Research Institute. Seedlessness has been inherited to the progenies from stenospermic grap egenotypes like Sultanina. In these grapes, seeds abort soon after fertilization, so that consumers do not sense the rudimenter seeds. Table grape market needs to extra properties like big size, attractive color, early or late maturing addition to seedlessness. The project studies had been initiated to release new table grape cultivars having these features in Tekirdağ Viticultural Research Institute and ten table grape cultivar were registered while eight genotypes are in registration process (Özer et al. 2012). This article will focus on the quality characteristics of eight table grape candidates developed by crossbreeding studies.

Keywords: Table, grape, cultivars, new

# FROST DAMAGE IN APPLE AND IMPORTENCE OF BREEDING LATE BLOOMING APPLE VARIETIES

Turgay Seymen, Şerif Özongun, Figen Akyüz, A. Nilgün Atay, Emel Kaçal

Fruit Research Institute, Eğirdir/Isparta, Turkey

turgayseymen@mynet.com

80.8 million apple was produced in the World according to 2013 year data and Turkey is in the 3rd rank with 3.128.450 tones. Apple has been cultivated in 81 cities of Turkey. When produced apple varieties have been evaluated %43.3 were Red Delicious group varieties, %26.4 were Golden Delicious group varieties, %7.9 were Amasya varieties, %3.9 were Granny Smith varieties and others had ratio of %18.5.

Apple gets less damage from spring frosts than fruit species. All precautions were done for frost damage (wind machines, irrigation etc.) in big apple orchards in March 2014 and April 2015 but frost damage had been occurred in Konya, Karaman cities and same valleys. In 2014 Turkey's apple production decreased from 3.1 million tones to 2.5 million tones because of frost damage. Some production decrease is expected in 2015 year. Standard apple varieties used in Isparta generally blooms in the 4th week April. But local apple varieties Demir and (Type 31 and Type 4) apple types blooms in the first week of May in Isparta ecological conditions. Breeding late blooming varieties will be useful for the prevention of frost damage and to get new high quality apple varieties. Breeding late blooming apple varieties will be good for regions with extreme weather conditions. For this reason late time blooming local apple varieties and standard late time blooming apple variety studies are very important.

In our study it was aimed to determine local/foreing apple varieties blooming time and pomological characterizes for future breeding studies.

Keywords: Apple, breeding, frost damage, bloomig of late

# DEVELOPMENT OF DWARF AND SEMI-DWARF RESISTANCE APPLE ROOTSTOCK AGAINST ERWINIA AMYLOVORA, A CAUSAL AGENT OF FIRE BLIGHT DISEASE

Şerif Özongun[1], Hüseyin Basım[2], Turgay Seymen[1], Esin Basım[2], Figen Eraslan[1], Derya Baki[2]

1. Eğirdir Fruit Research Institute, Turkey

2. Akdeniz University, Faculty of Agriculture, Turkey

serifozongun@yahoo.com

This work has been done in 2014 and 2015. The aim of work is to develop resistant apple rootstocks against Erwinia amylovora, a causal agent of Fire Blight disase. A hundred nineteen wild apple rootstocks grown from their seeds obtained from Samsun, Artvin, Bayburt, Gümüşhane, Tokat ve Amasya province in the Black Sea region of Turkey and 330 other genetic apple rootstocks were used as rootstock materials of this work. Different domestic and foreign strains of Erwinia amylovora were adjusted into 1x108 cfu/ml and inoculated by spraying onto fresh leaflets of apple rootstocks in 80-85% relative humidity and isolated growth conditions. Tests were done as 5 replicates for each apple rootstock and the each rootstock were tested against Erwinia amylovora twice in different time. The results of sensitivity of the rootstocks were evaluated by measuring Fire Blight symptoms progressed from tip of the shoots to bottom during 2-weeks time period. In this work, the results including sensitivities of the apple rootstocks against Erwinia amylovora, a causal agent of Fire Blight Disease, as a part of "the resistant apple rootstock breeding project" will be presented.

Keywords: Apple, Rootstock, Breeding, Fire Blight

# SOME POMOLOGICAL AND MORPHOLOGICAL CHARACTERISTICS OF APPLE VARIETIES/TYPES WHICH HAVE RESISTANCE GENES FOR APPLE SCAB

Figen Akyüz, Turgay Seymen, Şerif Özongun

Fruit Research Institute, Eğirdir/ISPARTA, Türkiye

fgnersln@hotmail.com

Apple scab, caused by the fungus Venturia inaequalis, is a major fungal disease for apples, it causes much economic loses in our country. In a research which was conducted in 2012, 96 apple varieties/types had been evaluated for apple scab resistance and resultant 8 native varieties/types was determined that have 3 or more resistance genes. In this study was conducted on these 8 varieties/types (Kalkandelen, Malus spp (Gemlik-2 çöğür anacı), Coll-22, 15, 25, 60, 72 ve 473E) in 2012-2013 years. 8 varieties/types was defined pheneological characteristics (time of beginning of the flowering and harvest time), pomological characteristics (fruit weight, fruit width, fruit height, fruit firmness and malic acid), morphological characteristics (tree vigor, type of bearing) and was observed sensory analysis (fruit taste, juiciness).

Keywords: Apple, Venturia inaequalis, resistance

# COMPARISON THE ESSENTIALS OILS OF LAURUS NOBILIS OF THREE MONTHS (APRIL, MAY AND JUNE)

OULD YEROU Karima[1*], Meddah B[1], Tir touil A[1,2]

1. Laboratory of Bioconversion; Microbiological engineering and safety,

2. Laboratory Research on Biological Systems and Geomatics (LRSBG)

1. 2. Faculty of Science; Biology Department; University of Mascara -Algeria

mhanine11@yahoo.fr

Laurus nobilis is an aromatic plant, widespread in Algeria and widely used by local people as a source of spice and for its medicinal properties. The essential oil of this plant is the subject in this work a comparative study of this dune extraction HE three months: April, May and essential oil June.L'extraction was performed by steam distillation and performance the highest (1.5%) was determined in the month of May, in this month, the laurel plant was fully flowered in favorable soil and climate conditions for biosynthesis of the essential oils that makes the yield increases considerably.

Keywords: Laurus nobilis, Algeria, essential oil, steam distillation, yield.

# A GENERAL REVIEW OF THE BIOTECHNOLOGY ON RHODODENDRON IN TURKEY

Sevil Saglam, Bahadır Altun, Tuğba Yücel Yazıcı, Ozlem Uner, Zekeriya Doğan

Ahi Evran University, Faculty of Agriculture, Department of Agricultural
Biotech- nology, 40100, Kirsehir, Turkey

saglamsevil@gmail.com

Rhododendrons (*Rhododendron* spp.) are one of the most important flower crops in the world and have an economic value in ornamental, medicinal and landscaping trade. However, these plants have not been recognized by Turkey. Biotechnology is any technological application that uses biological systems, living organisms or derivatives thereof, to make or modify products or processes for specific use. It has provided an abundance of their trade and production Micropropagation, cell culture and molecular characterisation as well as gene technology are being highlighted. Plant biotechnology have enormous potential to improve the efficiency and precision of conventional plant breeding via biotechnological tools on Rhododendrons. In this review, we present an overview of the advantages of plant biotechnology tools and its applications in plant breeding from Rhododendron species in Turkey. We also consider reasons why biotechnology has had only a small impact on Rhododendron's plant breeding so far and suggest ways in which the potential of biotechnology can be realized. Finally, we discuss reasons why the greater adoption of biotechnology in the future is inevitable, the extent of its use will depend on available resources, especially for Rhodedendron luteum Sweet. and Rhododendron ponticum L. in Turkey. Achieving a substantial impact on Rhododendron improvement by biotechnology tools represents the great challenge for agricultural and forest scientists in the next years. We are also to strengthen the resource investigation of species and habitats for Rhododendron and studies on their biotechnology; to make sure the priorities of species and habitats for conservation and also to establish information database.

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Keywords: Rhododendron tissue culture genetic transformation, molecular characterization, biotechnology, plant breeding, Turkey ornemental plants

# THE POSSIBILITY OF USING PHENOLIC COMPOUNDS IN BREEDING TO FIRE BLIGHT RESISTANCE

Melih Aydınlı, Gökhan Öztürk, Emel Kaçal

Fruit Research Institute, 32500, Eğirdir, Isparta, Turkey

maydinli@gthb.gov.tr

Fire blight (*Erwinia amylovora* Burr.) is a bacterial disease causes serious economical yield loses on pome fruits such as pear, apple and quince belong to Rosaceae family. Resistance level varies to cultivars in apple and pear. Phenolic compounds produced as secondary metabolites have been known that serve as defensive element, provides resistance against disease depending on the amount in plant and play an important role in plant genetic resistance. The studies conducted so far has been determined that cultivars have more phenolic compounds have been more resistance to fire blight. However, the specific amount of some phenolic substances is more important on resistance than the total amount of phenolic substances in plant. At the studies made pear and apple has been determined that more effective different phenolic compounds with regard to fire blight resistance. Pear cultivars in resistance to fire blight have higher arbutin content. It has been determined that epicatechin concentration in pear leaves and chlorogenic acid concentration in apple leaves increased after artificial fire blight inoculation. As a result of, some special biochemical compounds found in plants have been involved in resistance mechanisms against to fire blight disease. On the resistance breeding studies using as biochemical markers of these compounds could be a parameter for distinguishing resistant and susceptible plants, and it can be considered as early selection criteria.

Keywords: Fire Blight, Resistance Breeding, Phenolic Compounds

# IMPACT OF DROUGHT STRESS ON PHYSIOLOGICAL TRAITS, YIELD AND YIELD COMPONENTS OF FIELD GROWN DURUM WHEAT (*TRITICUM DURUM* DESF.) AND BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

Allahverdiyev T.I.

Plant Physiology and Biotechnology Department, Research Institute of Crop
Husbandry Ministry of Agriculture, Baku AZ1098, Pirshagi Sovkhoz-2,
Azerbaijan

tofig_1968@mail.ru

Drought is a serious problem for wheat production worldwide including in Azerbaijan. We studied some morphophysiological traits of wheat genotypes grown under irrigated and rain-fed conditions, their yield and yield components. Water shortage led to decrease of stomatal conductance (gs), photosynthesis rate (Pn), transpiration rate (E), mesophyll conductance (gm), increase of intercellular CO2 concentration (Ci). The changes of gs more affected on E than Pn. Drought caused reduction of relative water content (RWC), Chl(a+b) and Car(x+c) contents. The Chl(a+b)/Car(x+c) ratio was decreased under water stress. The RWC of studied durum and bread wheat genotypes less affected by water stress than gas exchange parameters and pigments content. Proline content was increased under rain-fed condition. Area (LA) and dry mass of leaves per stem, leaf area index (LAI) of genotypes significantly reduced from pre heading to grain formation. Drought led reduction of plant height and peduncle length of wheat genotypes. Water stress resulted in a decrease of yield components (spike mass, spike length and width, number of spikelet, number and mass of grain per spike, thousand kernels mass) and yield of durum and bread wheat genotypes. The Chl(a+b) content, Pn and yield of bread wheat genotypes were relatively higher than durum wheat ones. Physiological traits may be reliable for selection of drought resistant wheat genotypes.

Keywords: Gas exchange parameters, chlorophyll a,b, leaf area, relative water content, yield

# IS GENETIC EROSION REAL THREAT FOR LOCAL TAJIK WHEAT MATERIALS

Bahromiddin Husenov, Munira Otambekova, Alexey Morgounov

Tajik Agrarian University, 146, Rudaki Ave., 734003, Dushanbe, Tajikistan

bahromiddin@gmail.com

Tajikistan is blessed with wide genetic diversity of crop species, especially cereals. Academician Nikolay Vavilov visited Tajikistan three times (in 1916, 1919 and 1929) and indicated that it is the country of the must visit for botanists and plant breeders. Following Vavilov a number of expeditions were carried out to investigate the diversity of small grain cereals, especially wheat and rye. Wheat landraces still significantly contribute to food security in remote rural areas. They are valuable locally adapted genetic material, which can be used for improving modern wheat varieties. However, nowadays genetic erosion seems to be real threat for local wheat material in Tajikistan. The outcomes of wheat landraces inventory conducted with the technical support of FAO-SEC and CIMMYT-Turkey revealed that landraces are grown in limited areas, by small farms and mainly in the mountainous regions. The number of farmers growing landraces is decreasing every year. In addition the risk of loss of genetic diversity with the change in farmers from one generation to the next is high. Though, majority of wheat diversity collected and stored in the National and International Genebanks, higher priority needs to be given to in-situ or on-farm conservation. For beneficial usage of landraces, wheat breeders and organizations dealing with ex-situ conservation have to have close collaboration with identified farmers, who still maintain crop diversity.

Keywords: Wheat landraces, plant breeding, conservation, genetic erosion.

# DETERMINATION OF GENETIC DIVERSITY ON SOME *TRITICUM MONOCCOCUM* L. GENOTYPES WITH SSR MARKERS

Ayşe Yıldız[1], Kürşad Özbek[1], Fatma Ruveyda Alkan[1], İsa Özkan[2]

1. The Central Research Institute for Field Crops, Şehit Cem Ersever Street
   No. 9-11, Yenimahalle /Ankara, Turkey
2. General Directorate of Agricultural Research and Policies,
   Yenimahalle /Ankara, Turkey

varolyildiz@hotmail.com

In this study, 24 T. monoccocum, from different locations, were used from Turkish Seed Gene Bank (TSGB) collections. To obtaine DNA, firstly single seed grain was rented with homogenizer (RoscheMagnaLyser), afterwards according to Biotecon-Foodproof DNA Isolation Kit Protocol, DNA isolation were carried out. Quantity and quality of DNA were performed using Nanodrop Spektrofotometer. The average DNA amount and quality were determined respectively; 714 ng/µl and 1.8 (260/280 OD). Eight SSR markers; selected from microsattelits and showing high polymorphism in wheat (Xgwm 666, Xgwm 136, Xgwm 312, Xgwm 205, Xgwm 617, Xgwm 427, Xgwm 570 and Xgwm 635 ), were used for determining genetic differences among 24 T. monoccocum genotypes as described Röder et al., 1998. Agarose gel electrophoresis (1,3 %) was performed for observation of bands which occur at the end of the SSR-PCR experiment. Samples were run at 150 volts for about 1.5 hours. Afterwards, the DNA bands were displayed with Kodac Gel Logic 200 visualization system. Results show that the highest polymorphism were determined in Xgwm 136, Xgwm 666 and Xgwm 570 primers respectively, the lowest polymorphism were determined Xgwm 617, Xgwm 205 and Xgwm 427 primers respectively.

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Keywords: T. monoccocum, Genetic diversity, SSR.

# SELECTION OF NEW WHEAT VARIETIES TOWARDS RESISTANCE TO MAJOR RUSTS IN TAJIKISTAN

Bahriddin Soliev, Munira Otambekova, Hafiz Muminjanov, Zebuniso Eshonova
Production Cooperative Named After L. Murodov, Hisor Rayon, Tajikistan

munira.otambekova@gmail.com

Wheat production is affected by series of biotic stresses in Tajikistan, where yellow rust and leaf rust present higher threat. During last ten years there were five epidemics of the yellow rust in Hisor valley of Tajikistan. In parallel to the public a private wheat breeding program initiated by Production Cooperative named after Latif Murodov with active involvement of farmers in screening of advance lines, selection of superior varieties, maintenance breeding, variety demonstration and seed multiplication. A smooth-running wheat breeding program has now been established. Selected advanced lines from the international nurseries go to the observation nursery for further testing and seed multiplication. Lines selected from the observation nursery are moved through a sequence of preliminary yield trials (PYT), yield trials (YT), and multilocation yield trials (MYT) before the best lines are submitted as cultivars for official testing and release. With the support of IWWIP program in Turkey we screened 38 wheat varieties currently grown in Tajikistan and 19 advanced breeding lines from our breeding program towards yellow rust and leaf rust. Results showed that advanced lines relatively were less affected by both yellow rust and leaf rust in comparison to varieties in artificial tests.

Keywords: Wheat breeding, diseases resistance, yellow rust, leaf rust, private breeding

# CHANGES IN THE ELECTROPHORETIC ANALYSIS OF SOLUBLE LEAF PROTEINS OF TWO WHEAT CULTIVARS IN RESPONSE TO HEAT STRESS

Banu Efeoğlu[1], Serpil Terzioğlu[2]

1. Ministry of Food, Agriculture and Livestock, Biotechnology Research Center, Yenimahalle, Ankara, Turkey
2. Hacettepe University, Faculty of Science, Department of Biology Ankara, Turkey

befeoglu@hotmail.com

The effects of heat stress at 37°C and 45°C for 8 h on the seedlings of bread wheat (*Triticum aestivum* L.) cv. Karacadağ and durum wheat (*Triticum turgidum* L.) cv. Fırat cultivars differing in sensitivity was investigated by means of 2-D SDS polyacrylamide gel electrophoresis. The analysis of protein patterns of leaves showed that while 37 proteins at 37°C, 8h and 53 proteins at 45°C, 8h were newly synthesized in Karacadağ cultivar; 5 proteins were repressed and 16 proteins were newly synthesized at 37°C, 8h and 35 proteins were repressed and 1 protein was newly synthesized at 45°C, 8h in Fırat cultivar compared to their controls. Since Karacadağ was determined as heat tolerant and Fırat as heat sensitive cultivars in the previous screening of two cultivars, the proteins newly synthesized under heat stress conditions may be associated with the heat resistance capacity of such genotypes.

Keywords: Wheat cultivars, heat shock proteins, heat stress, two dimensional electrophoretic analysis.

# FREE PROLINE IN THE REACTION OF WHEAT TO HEAVY METALS

Tazhibayeva T.L.[1*], Abugalieva A.I.[2], Massimgaziyeva A.S.[2]

1. Al-Farabi Kazakh National University, 71 Al-Farabi avenue, Almaty, 050040, Kazakhstan
2. Kazakh Scientific Research Institute Agriculture and Plant Growing, Almalybak, Almaty Region, Kazakhstan Tamara.

tazhibayeva@kaznu.kz

Heavy metals (HM) are considered as one of the abiotic stressful factors of environment caused irrational activity of human-being. We earlier showed increase of free proline level for sprouts of wheat cultivars in the response of HM (2010 - 2014). It is interesting to compare the obtained data with an experiments of free proline content in the 25 wild wheat, introgression forms, received with the wild genes and faculty wheat having a metal stress. So that, genotypes with higher resistance to abiotic stresses are involved in research a priori. Level of a metal stress in plants was controlled on biometric indicators of growth 7 – day seedlings and roots. We tested HM ($Zn2 +$, $Cu2 +$, $Cd2 +$) in concentration of 20 mg/l in the nutritious solution.

It is established that HM cause increase of free proline level in all genotypes of wheat, and wild and faculty forms are characterized by higher of proline content even in control. Specificity in reaction of introgression forms on effect of various metals is found, the content of proline raised in 2 and more times, and growth indicators decreased, especially under the influence of Cu2+, for example at (Bezostaya 1 x Ae.triaristata) x Komsomolskaya. Zn2+ for several introgression forms caused stimulation of growth processes that was connected with the increasing of proline level. Under the influence of Cd2+ there was a considerable accumulation of free proline in faculty varieties Intensive and Memory 47 in winter option. Wheat cultivars are more susceptible to the impact of HM, than wild and introgression forms that is interfaced to growth of intracellular concentration of proline. It is shown that free proline should be used for differentiation of the studied wheat on effect of heavy metals.

Keywords: Free proline, heavy metals, wild and cultivars of wheat, introgression and faculty forms, growing of roots and seedlings

# CHARACTERISTICS OF THE SYNTHETIC WHEAT ROOT SYSTEM DUE TO THE DROUGHT RESISTANCE

Aigul Abugaliyeva[1], Alexey Morgounov[2]

1. Laboratory Head, Kazakh Research Institute of Agriculture and Plant Growing, Yerlepessov street, 1, 040909, Almalybak, Kazakhstan
2. Head, International Winter Wheat Improvement Program, CIMMYT, P.K. 39 Emek, 06511, Ankara,Turkey

kiz_abugalieva@mail.ru

Great importance given to the root system in increasing the wheat yield especially in regions with insufficient moisture. Characteristics of the root system with WinRHIZO using implemented: a) 8 -10 day seedlings; b) cut the aboveground part after three weeks; c) the aboveground part not cut. The most powerful root system with a maximum degree on 7 from 10 characteristics was allocated the genotype 231- (Bezostaya 1 x Ae.triaristata) x Karligash; on 4 from 10 characteristics was allocated a hybrid combinations: 1674 - Zhetysu x Tr.timopheevi (length, area, PA and roots volume). On 3 from 10 characteristics - 1671 - Zhetysu x Tr.militinae (roots mass, fresh leaves, branching). On development of the root system at later stages allocated genotypes 231 (Bezostaya 1 x Ae.triaristata) x Karligash on 9 from 12 characteristics, in step of 8-10 day seedlings and genotype 1721-9 (Bezostaya 1 x Tr.militinae) x Tr.militinae (10 from 12 characteristics) and 3 from 12 characteristic the genotype 1712 (Erythrospermum 350 x Tr.militinum). Cutting of overground part considered as a stress, which induces the development of the root system, which connected with drought resistance. Genotypes 1727 (Erythrospermum 350 x Tr.kihara) and 1671 (Zhetysu x Tr.militinae) after cutting characterized the maximum sign value, exceeding maximum values for genotypes that have formed its root system without cutting overground part, that is, by inducing the secondary root system formation. These samples marked by drought resistance in 2014-2015 harvest, with a high NDVI and proline content in leaves.

Keywords: Root system, wheat, wild relatives, drought resistance

# INVESTIGATION OF SUBUNITS OF HIGH MOLECULAR WEIGHT GLUTEIN IN SOME PURE LINES IN WHEAT BREEDING PROGRAMMES

Ayşe Yıldız[1], Ayten Salantur[1], Mehmet Doğan[2], Stuart Lucas[3]

1. The Central Research Institute for Field Crops, Sehit Cem Ersever St.,
No 9-11 Yenimahalle, Ankara, Turkey
2. Ankara University, Faculty of Sciences Department of Biology Tandogan,
Ankara, Turkey
3. Sabanci University, Nanotechnology Research and Application Centre Tuzla,
Istanbul

varolyildiz@hotmail.com

It is possible to evaluate the potential of being quality bread of wheat by using HMWG subunits. In this study, 91 Red Bread Preliminary Yield Trial (RPYT) materials developed as a result of wheat breeding programmes of Central Research Institute for Field Crops have been used as material. Extraction of proteins of High Molecular Weight Glutein (HMWG) and Sodium Dodecyl Sulfate - Polyacrylamide Gel Electrophoresis (SDS-PAGE) analysis have been carried out with the modified application according to method (UPOV, 1994) stated in bread wheat kind property document of 'International New Plant Variation Protection Union' (UPOV). Extraction of glutein proteins has been done by using one single seed from one spike for each genotype. As standard genotype to determine HMWG, Pavon, Opata, Gabo, Orca, Kadett Clement, Chinese Spring have been used.

HMWG subunits of obtained proteins have been determined by using SDS-PAGE method (UPOV, 1994). Electrophoresis process has been carried out with at 45mA and 20oC 16 hours- application by using 10 µl glutein protein with 3% loding gel and 14% separation gel. Obtained gel compositions after electrophoresis process have been done by photographed after staining with Coomassie Brillant Blue- G250.

"2*, 7+8 and 2+12" combination has been determined in 18 pure lines and has been the most common (19.8%) observed combination in this study of which 13 different HMWG subunits combinations have been determined. Other common combinations are "2*, 7+8 and 2+12" combination in 15 lines (16.5%) and "1, 17+18 and 5+10" combination in 13 lines (14.3%). Quality score value 9-10 shows high quality, 8 shows promising, value 5 and under shows low quality. While 48 pure lines (52.8%) have been evaluated with 10 quality score, only quality score value of 5 pure lines (5.5%) has been determined changing between 4 and 5. These scores has an important place in quality breeding. It is very important in the aspect of allowing removal of low quality genotypes in early periods in breeding programmes especially requiring more workforce and time.

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Keywords: High Molecular Weight Glutein (HMWG), breeding, SDS-PAGE, quality.

# NDVI CHARACTERIZATION OF SYNTHETIC AND WILD WHEAT RELATIVES, WHEAT DOUBLE HAPLOIDS, OF NAKED BARLEY AND OATS, SORGHUM, SOYBEAN AND WINTER RAPE

Aigul Abugaliyeva[1], Alexey Morgounov[2], Aigerim Massimgaziyeva[3],
Kenebay Kozhakhmetov[3], Vladimir Chudinov[4], Rauan Zhapayev[5]

1. Laboratory Head, Kazakh Research Institute of Agriculture and Plant Growing, Yerlepessov street, 1, 040909, ALmalybak, Kazakhstan
2. Head, International Winter Wheat Improvement Program, CIMMYT, P.K. 39 Emek, 06511, Ankara, Turkey
3. Kazakh Research Institute of Agriculture and Plant Growing, Yerlepessov street, 1, 040909, ALmalybak, Kazakhstan
4. Karabalyk Agricultural Research Station, Kostanay, Kazakhstan
5. Kazakh Research Institute of Agriculture and Plant Growing, ALmalybak, Kazakhstan and CIMMYT, Kazakhstan

kiz_abugalieva@mail.ru

The standardized index of plant cover difference (NDVI) researched cultural, synthetic forms of wheat and wild relatives, double haploids wheat (winter and spring forms) naked/membranous barley and oats, early maturing sorghum varieties, soybeans and winter forms of rape in Kazakh Research Institute of Agriculture and Plant Growing (2013-2015) on collection, breeding and agronomic experiments. The observations made in the south and the north of Kazakhstan. The maximum NDVI value indicates a phase of booting as in winter and spring in molds. For synthetic wheat forms the NDVI index varied (starting from the tillering phase to milk ripeness) from 0.24 to 0.82, for wild relatives 0,32-0,80; for varieties 0,18-0,81, double haploids 0.49 -0.80, naked oats 0,23-0,78, barley 0,41-0,79, rape 0.25-0.75 and soya 0,18-0,81. We compare the dynamics of biomass accumulation for the wild and cultural forms and their hybrids. Genotypes ranked according to the degree of reaction to stressful conditions. Allocated among the wild relatives - Tr.kiharae, synthetic Zhetysu x Tr.timopheevi, Erithrospermum 350 x Tr.kiharae, Bezostaya 1 x Ae.cylindrica. The work executed within the framework of the program O 0722 the Ministry of Agriculture.

Keywords: NDVI, wheat, synthetics, double haploid, naked oats, barley, soybeans, sorghum

# RESISTANCE OF SOME INTERNATIONAL FACULTATIVE WINTER WHEAT MATERIALS TO RUST IN 2014

Kadir Akan[1], Zafer Mert[1], Fatih Özdemir[2], Alexey Morgounov[3], Mesut Keser[4]

1.The Central Research Institute for Field Crops, Sehit Cem Ersever Cd.
No. 9-11, Yenimahalle, Ankara, Turkey;

2. Bahri Dağdaş International Agricultural Research Institute, Ereğli Yolu Üzeri
2. Km. P.K. 125, 42020 Konya

3. CIMMYT, Turkey Office, P.K. 39, 06511 Emek, Ankara, Turkey

4. ICARDA, Ankara, Turkey

kadir_akan@hotmail.com

Bread wheat is one of the most important cereal crops in Turkey. The purpose of this study was to assess seedling and adult plant stripe/leaf/stem rust reaction at the Central Research Institute for Field Crops in 2014.

We tested 100 genotypes from the Facultative Winter Wheat Observation Nursery. These materials were developed by the International Winter Wheat Improved Project (IWWIP). For seedling plant reactions were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. Seedling reactions were recorded 14 days post inoculation on either 0-4 (LR and SR) or 0-9 scales (YR). For adult plant reactions; each genotype was sown by hand in a 1 m row in October 2013. Susceptible cultivars Morocco, Little Club, Michigan Amber and Seri 82 were sown around the experimental field and Little Club was also used as the susceptible control in every 10th row. For stripe rust spore suspensions in mineral oil were inoculated to plants at two different times. Materials were also evaluated under natural epidemic condition at Seydiler/Kastamonu in 2014. Stripe and stem rust development on each entry was scored on the modified Cobb scale when the susceptible check Little Club reached 80-100S disease severity in June 2014. Coefficients of infection below 20 were considered to be resistant.

Forty six (46%), 15 (15%) and 33 (33%) genotypes were resistant to YR, LR and SR at the seedling stage respectively. Fifty nine (59%) and 9 (9%) genotypes were resistant to YR and SR at the adult stage respectively. These resistant lines were determined for breeding program.

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Keywords: Rusts (Puccinia spp), genetic resistance, reaction test

# SPRING WHEAT STEM RUST RESISTANCE NURSERY REACTIONS TO STRIPE, LEAF AND STEM RUSTS

Zafer Mert, Kadir Akan

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

kadir_akan@hotmail.com

Rust diseases (*Puccinia* spp.) are the most important biotic stresses in Turkey. On the other hand rust diseases limit wheat yield and quality in Turkey. The aim of the Central Research Institute for Field Crops's spring wheat stem rust resistance nursery (SWSRRN) germplasm development program is to identify genotypes resistance to the rust diseases. In this study, 55 genotypes from the SWSRRN materials were used. For this purpose, seedling test were conducted for yellow leaf and stem rust. Evaluations were carried out at the research facilities of CRIFC at İkizce and Yenimahalle in Ankara and Kastamonu (stem rust) in the 2014 season.

For adult plant reactions; the genotypes were inoculated with local Pst populations (virulent on Yr2, 6, 7, 8, 9, 25, 27, Sd, Su, Avs) and ; the genotypes were observed with local Pgt populations (avirulent on Sr24, Sr26, Sr27, and Sr31). Stripe and stem rusts development on each entry were scored using the modified Cobb scale when the susceptible check cv. Little Club had reached 80S infection severity in June and August 2014. Coefficients of infections were calculated and values below 20 were considered to be resistant. For seedling test; the seedling was inoculated with local Pgt, Pst and Pt (avirulent on Lr9, Lr19, Lr24, and Lr28) populations. Stripe, leaf and stem rust development on each entry were scored after 14 days with 0-4 and 0-9 scale for leaf-stem rust and yellow rust, respectively.

Twenty six (47%) (seedling) genotypes and 30 (55%) (adult stage) genotypes were resistant to local Pgt, 18 (33%) (seedling) were resistant to the local Pt, and 9 (16%) (seedling) genotypes and 22 (40%) (adult stage) genotypes were resistant to local Pst, The resistance sources to stem, leaf, and stripe rust were determined in this research.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/14/A12/P01/002)

Keywords: Rusts (Puccinia spp), genetic resistance, reaction test

# LEVERAGING GERMPLASM POOL FOR NEW VARIETY: HIGH PROTEIN KERNEL OIL PALM

Mohd Din Amiruddin, Noh Ahmad, Rajanaidu Nookiah, Ahmad Kushairi Din and Wan Nooraida Wan Mohamed

Advanced Biotechnology & Breeding Centre, Malaysian Palm Oil Board, 6 Persiaran Institusi, Bandar Baru Bangi, 43000 Kajang, Selangor, Malaysia

mohddin@mpob.gov.my

Oil palm, Elaeis guineensis germplasm collections from Angola, Cameroon, Gambia, Ghana, Guinea, Madagascar, Nigeria, Senegal, Sierra Leone, Tanzania, Congo and Elaeis oleifera germplasm collections from Brazil, Colombia, Costa Rica, Honduras, Panama, Suriname, Peru and Ecuador, including a commercial DxP control were screened by the Malaysian Palm Oil Board (MPOB) for protein kernel content. Random samples from the germplasm were analysed using the Kjedahl method. Analysis of variance (ANOVA) showed highly significant differences among the eleven countries for Elaeis guineensis and among the eight countries for Elaeis oleifera. However, the coefficient of variation (CV) varies among the countries from 8.60% to 21.86% for E. guineensis and from 4.51% to 9.92% for E. oleifera. At the family level, ANOVA also showed highly significant differences, indicating high genetic variability for the trait among the families for both species. For E. guineensis, ANOVA showed no significant differences between the dura and tenera fruit forms. Coupled with the high heritability estimates (h2B 100%), the development and improvement of the trait can be expedited. Highest protein kernel content for E.guineensis was found in Madagascar germplasm with mean of 26.23% and ranged from 20.74 % to 29.44% whereas for E. oleifera, highest protein kernel content was found in Surinam germplasm with mean of 19.62% and ranged from 16.29% to 22.97%. Families with high protein kernel content and additional samples from the E. guineensis and E. oleifera germplasm collection need to be screened further in breeding and improvement programmes before the trait can be commercially exploited.

Keywords: Screening, high protein kernel content, oil palm germplasm,
Elaeis guineensis, E. oleifera, breeding, crop improvement

# GENETIC DIVERSITY OF SOME MOROCCAN LENTIL GENOTYPES AND THEIR INTERACTION WITH DIFFERENT ENVIRONMENTS

J. Mbasani Mansi, N. Benbrahim, F. Gaboun, Z. A. Triqui and R. Mentag

Faculty of Sciences, Mohammed V University, Avenue Ibn-Batouta, Po Box 1014, 1000 Rabat, Morocco

mansimbas@gmail.com

Lentil (*Lens culinaris Medik.*) is produced for its seeds that are rich in proteins and minerals. It is commonly used in rotation with cereal crops because of its potential to improve the fertility of soils. In Morocco, this legume is commonly produced by farmers using both varieties and landraces. However, no information is available on the adaptation potential of genotypes to different agro-ecological environments. In this context, trials were conducted on three different bioclimatic environments (Atlantic bour intermediate, semi-arid and mountain) with 15 genotypes (10 landraces, and 5 varieties). Furthermore, genetic diversity of these genotypes was assessed using agro-morphological and molecular markers. Combined analysis of variance across three environments indicated a highly significant effect of both Environment and GxE interaction. Within the three environments, yield average was higher for varieties than for landraces. However, two landraces (NBr and MBS) and one variety (Zaa) showed a stability yielding in all tested environments. For phenotypic variability, results of field performance showed a high level between genotypes for most of agro-morphological traits. Thus, genotypes were clustered in six genotypic groups. RAPD analysis showed different clustering patterns with high polymorphism information content (PIC = 0.88). Finally, Moroccan landraces showed a good adaptation potential to different environments. Sustainable program of genetic resources conservation is needed. Also, these landraces are promising candidate for initiating a breeding program for yield improvement. Further research should be carried out in order to screen those accessions for tolerance to abiotic and biotic stresses.

Keywords: Agro-morphology, genetic diversity, genotype-environment interaction, landraces, lentil, PIC, RAPD, varieties

# GENE ACTION AND COMBINING ABILITY ESTIMATES USING CYTOPLASMIC-GENIC MALE STERILE LINES TO DEVELOP PIGEONPEA HYBRIDS FOR RAINFED CONDITION

K.B.Saxena[1], Sameer Kumar[2], R. Vijaya Kumar[2], A.N. Tikle[3]

1. International Crops Research Institute for the Semi-Arid Tropics
2. International Crops Research Institute for the Semi-Arid Tropics, Patancheru
3. RAK College of Agriculture, Sehore, India 466 001

antiklepb@gmail.com

Pigeonpea is the major source of vegetable protein in Indian diet. Pigeonpea is the only food legume where cytoplasmic-genetic male sterility is being exploited for commercial use of making hybrids. The discovery of stable CMS system and breeding of commercial hybrids has become a landmark in increasing the productivity of this crop. Keeping in view the combining ability estimates were worked out through Line x Tester analysis of 10 hybrids developed by crossing five CMS lines with two male testers to know the genetic architecture of yield attributes- Days to maturity, branches/plant, pods/plant, seed yield, wilt resistance and pollen fertility. Analysis of variance revealed significant differences among genotypes, crosses, lines, testers and line x tester interactions for most of the traits. Preponderance of non-additive gene action was realized by higher values of specific combining ability compared to general combining ability. The average degree of dominance were more than unity (>1) and predictability ratio was less tha unity (<1) for all the traits, signifying non-additive gene action resulted from dominance, over dominance, epistasis and various other interactions. Hence, heterosis breeding is effective for increasing yield potential of hybrids in pigeonpea.The estimates of GCA effects indicated male parent ICPL 87119 as good general combiner for days to maturity and pollen fertility while ICP 2043 is good general combiner as female parent. Cross combinations ICP 2043 x ICP 87119 and ICP 2078 x ICP 87119, ICP 2048 x ICP 20108 , ICP 2092 x ICP 20108 were desirable combinations for yield and other traits.

Keywords: Cytoplasmic-genic male sterility (CMS); General combining ability (GCA); Specific combining ability (SCA); heterosis, epistasis

# THE EFFECT OF SOWING DATES ON PHENOLOGY OF FABA BEAN (*VICIA FABA* L.)

Najeeb Alharbi, Kedar Adhikari, Helen Bramley

Plant Breeding Institute, The University Of Sydney, 107 Cobbitty Road, Cobbitty,
Nsw 2570, Australia

najeeb.alharbi@sydney.edu.au

Faba bean (*Vicia faba* L.) is an important cool-season grain legume because of the high nutritional value in their seeds. Matching phenology of a crop to the environment is an important key to improving adaptation and increasing yields. Therefore, a field experiment was conducted at Narrabri in New South Wales, Australia. Ninety-six diverse faba bean genotypes were evaluated under three sowing dates (16 April, 7 May and 26 May 2014) in two replications for the effect of sowing dates on phenological and physiological traits. The results revealed that sowing dates, genotype and their interactions significantly affected the thermal time (°C-d) and days to 50% anthesis and maturity, and seed filling duration. A variation found among the genotypes in vernalisation requirements. Ac0805#4912 took 1365.9 °C-d in the first sowing and shorter in the other sowings (1143.5 and 1012.9 °C-d), indicating that it required vernalisation to flower. In contrast, 11NF008b-8 took 787.9, 851.3 and 886 °C-d in the three sowings, indicating it had no effect of vernalisation. Thermal time to 50% anthesis and maturity, days to maturity and seed filling duration decreased with delayed planting, while days to 50% anthesis increased. Seed filling duration strongly negatively associated with days to 50% anthesis (r= -0.8), while strongly positively correlated to maturity (r= 0.9). These results suggest that, sowing time highly influenced the phenological and physiological traits, which reflected on the final yield production. Further evaluation of phenological and physiological parameters in faba bean genotypes under field conditions is highly recommended.

Keywords: Phenology, sowing dates, environment.

# GENETIC VARIABILITY IN ROOT AND SHOOT TRAITS IN A CHICKPEA RECOMBINANT INBREED LINE POPULATION UNDER TWO WATER REGIMES

Imtiaz Muhammad[1], Houaslı Chafıka[2], El Bouhmadi Keltoum[3]

1. International Center for Agricultural Research in the Dry Areas (ICARDA),
2. Institut National de la Recherche Agronomique du Maroc, Centre Régional de Settat, Settat 26000, Maroc.
3. Laboratoire d'Ecologie et d'Environnement, Faculté des Sciences Ben M'Sik, Casa, Maroc

houaslichafika@gmail.com

Nearly 90% of the world's chickpea (*Cicer arietinum* L.) crop is grown under rainfed conditions where terminal drought stress affects the reproductive phase and results in important yield losses. Studies in various crops have shown the importance of a deep root system for extracting moisture under terminal drought stress. The objective of this study was to evaluate the genetic variability in root and shoot characters among 94 recombinant inbred lines subjected to two water regimes (control and stress) and to study some of the phenotypic correlations that could help improve drought tolerance in chickpea. The drought tolerant line 'ILC3182' and the drought susceptible line 'ILC3279' as well as the progeny of their cross consisting of 94 F6 recombinant inbred lines were subjected to dry and normal water regimes in the greenhouse. The experiment was laid out as a completely randomized factorial experiment with two replicates. Root and shoot traits were evaluated and compared. The data showed statistically significant effect of water regime, genotype and of the interaction of the two. Several statistically significant correlations between all traits were observed in both water regimes indicating their potential utility in selecting for drought tolerance. Drought tolerance indices were well associated with all other measured traits. This population is a potential candidate for molecular studies dealing with genetics of shoots and root traits linked to drought tolerance.

Keywords: Chickpea, Drought, tolerance, genetic improvement.

# EFFECTS OF BENEFICIAL MICROORGANISMS ON PLANT DEVELOPMENT THROUGH BIOTECHNOLOGICAL PROCESSES

Arzu ÜNAL, Banu EFEOĞLU

Ministry of Food, Agriculture and Livestock Biotechnology Research Center
Yeni- mahalle-Ankara / TURKEY

There are many studies about sustainability of metabolic processes and their mechanism of action through microbial activity and continuous exchange of material in literature (Kacar, 1984). Studies reveal that microorganisms, which have potential of being a biological fertilizer and a biological control agent for plant production, can be used against stresses created by abiotics/biotics factors in different ecosystems and guide future studies about subject (Imriz et al., 2014). Beneficial soil microrganisms function in areas such soil quality, crop production, and plant health. These studies were focused on detoxification of heavy metals (Wani et al. 2010; Ma et al. 2011), degradation of toxicants including pesticides (Ahemad and Khan and 2012), salt tolerance (Mayak 2004), biological warfare of plant pathogenes (Hynes et al. 2008; Tozlu, et al. 2012), recycling and increased availability of plant nutrients (Çakmakcı 2009), supporting plant development by producing phytohormones and enzymes (Dejordjevic et al. 1987; Ferreira et al. 1987).

Intensive agriculture entails the use of excessive fertilization. High- input farming practices achieving high yields have created environmental problems and degradation in natural resources. A biotechnological goal is to use different strains of selected rhizosphere microorganisms to minimize synthetic fertilizer application and to maximize plant growth and nutrition. Plant Growth Promoting Rhizobacteria (PGPR) are able to exert a beneficial effect upon plant growth. Therefore, they are used as biofertilizers in agriculture. Bio-fertilizers (BG) are of great importance in sustainable agriculture. The wide genetic variation within microbial species explains the high potential of the microorganisms to adapt to different environments. Therefore, there is a need to develop specific selected strains with higher effectiveness under a wide range of experimental conditions (Çakmakçı, 2005).

Crop growth and development are closely related to the nature of the soil microflora, especially those in close proximity to plant roots, i.e., the rhizosphere. Thus, it will be difficult to overcome the limitations of conventional agricultural technologies without controlling soil microorganisms. This subject takes place in research subjects in Ministry of Agriculture and Livestock-Biotechnology Research Center. Storage and assay of enzyme activity in Aspergillus and Rhizobium species isolated from local sources are performed in Microbial Biotechnology Laboratory in this center.

Keywords: Biotechnology, sustainable agriculture, beneficial microorganism, plant growth.

# A SEARCH FOR CANDIDATE GENE FOR COWPEA POWDERY MILDEW RESISTANCE IN THE SOUTHERN GUINEA ECOLOGY OF NIGERIA

Amazue, U. Esther[1], Adewale, B. Daniel[2]

1. Department of Crop Science, University of Nigeria, Nsukka, Nigeria
2. Department of Biological Sciences, Ondo State University of Science and Technology, Okitipupa, Nigeria

ugamazue@yahoo.ca

The need to identify candidate gene for resistance to powdery mildew (PM), a major fungal foliar disease of cowpea in Southern guinea savannah of Nigeria has necessitated this research. An experiment involving 13 cowpea genotypes was laid out in a randomized complete block design (RCBD) of two replications at the Botanical Garden, University of Nigeria, Nsukka, Nigeria. Each genotype was scored for susceptibility to the disease. Four parents were afterward selected for progeny generation through a 2 x 2 factorial mating design. The F1 hybrids were evaluated in RCBD of two replications on the field for powdery mildew resistance. The scored data was transformed by arc sine method before subjection to analysis in SAS (version, 9.3). Analysis of variance (ANOVA) revealed significant ($P<0.01$) differences among the 13 genotypes in their susceptibility to PM. The male, female and the interaction of both significantly ($P<0.001$) differed. Additive genetic variance (510.07) was higher than the dominance genetic variance (387.67). Additive gene action was prominent in this study. The broad and narrow sense heritability estimates were: 99.9% and 56.8% respectively. The average degree of dominance was 1.23 and the genetic advance was 62.09. Heterosis which signifies resistance to PM was observed in the crosses between Nsukka-BA x IT89KD-374-57, IT90K-59 x IT89KD-374-57 and IT90K-59x Nsukka-1B. The identified resistant genotypes (IT90K-59, Nsukka-BA and IT- 89KD-374-57) would be resources for further breeding programme. Powdery mildew cowpea resistant cultivar development could be achieved through hybridization programme since the major contribution to the inheritance of the trait is additive.

Keywords: Powdery mildew, inheritance, genetic advance, gene action, F1 hybrids, heterosis

# ASSESSING AN OPTIMAL LOW INTER-PLANT DISTANCE TO APPROACH NIL-COMPETITION AND SCREEN INDIVIDUAL PLANTS FOR TOLERANCE TO VIRUSES IN LENTIL

Dimitrios Vlachostergios[1], Chrisanthi Foti[1], Ioannis Mylonas[1],
Evaggelia Sinapi- dou[2], Alexios Polidoras[3], Epameinondas Paplomatas[4],
Elissavet Chatzivassiliou[4], Ioannis Tokatlidis[2]

1. Fodder Crops and Pastures Institute 413 35 Larissa, Greece
2. Dep. of Agricultural Development, Democritus Un. of Thrace,
   68200 Orestiada, Greece
3. School of Agriculture, Aristotle Univ. of Thessaloniki, Thessaloniki, 54124, Greece
4. Dep. of Crop Science, Agricultural University of Athens, 11855, Greece

itokatl@agro.duth.gr

Disease-induced spatial heterogeneity might be desirable in lentil breeding to recognize the susceptible genotypes and select the potentially tolerant ones. At very low densities an increased disease incidence has been recorded while the discrimination between infected and healthy plants was easier. However, low densities expand the experimental area inducing extra spatial heterogeneity. Since spatial heterogeneity can have serious effects on the precision of field experimentation in plant breeding, an optimal inter-plant distance was investigated so as to compromise absence of competition and lower spatial heterogeneity. A number of 1000 individual plants of the landrace "Lefkada" were screened at two adjacent trials, positioned according the zig-zag configuration of the honeycomb model. The inter-plant distance was 50 and 80 cm, corresponding to total trial surface of 220 and 576 m2, respectively. Severe virus and vascular infections were recorded in both trials resulting in 50% (50 cm) and 56% (80 cm) of the plants to die or to fail to produce any seed, and leading to huge spatial heterogeneity. Nevertheless, higher mean yield per plant by 30% and lower CV by 14% at the inter-plant distance of 50 cm (4.71 g and 140%) compared to 80 cm (3.61 g and 162%) evidenced that undesirable spatial heterogeneity was greater at 80 cm. Although results might be data specific and further research is imperative, the conclusion was that the inter-plant distance of 50 cm is more appropriate than that of 80 cm for lentil honeycomb breeding. This research has been co?financed by the European Union (European Social Fund - ESF) and Greek national funds through the Operational Program "Education and Lifelong Learning" of the National Strategic Reference Framework (NSRF) - Research Funding Program: THALES. Investing in knowledge society through the European Social Fund.

Keywords: Breeding, disease, inter-plant distance, spatial heterogeneity

# EARLY SELECTION OF COFFEE PLANTS (COFFEA CANEPHORA) WITH DESIRABLE CUP QUALITY TRAITS BY USING HERITABLE METABOLIC MARKERS

Roberto Gamboa Becerra[1], Óscar González Ríos[2],
María Cecilia Hernández Hernán- dez[2], Robert Winkler[1]

1. Department of Biotechnology and Biochemistry, CINVESTAV Irapuato, Guanajuato, Mexico
2. Instituto Tecnológico de Veracruz, Veracruz México

rgamboa@ira.cinvestav.mx

Coffee is the second most valuable traded commodity around the world. Mexico is one of the main exporters and the globally leading producer of organic coffee, with Coffea arabica and C. canephora as the two main cultivated species. *Currently*, there is a need for new strategies for the genetic improvement of coffee plants, conventional breeding takes too long time for responding timely to market demands, climatic variations and new biological threads such as the fungus Hemileia vasta- trix. Selection assisted by genetic markers is limited, since the correlation with the plant phenotype and final product quality is usually poor. Thus, we developed an un-targeted metabolomic approach to identify highly heritable metabolites inked to coffee cup quality in early development stages of C. canephora plants. We employed a maternal half sibs approach to estimate the metabolites heritability. Leaves at early plant development stage and fruits were collected. Roasted coffee samples were subjected to sensorial evaluation by a trained board. Sample extracts were analyzed by Ultra performance Liquid Chromatography (UPLC) coupled to an ion trap mass spectrometry analyzer (MSn). Data were processed with MZmine, metabolites were identified by MSn spectra with the MassBank server (http://www.massbank.jp/ BatchSearch.html) and a custom SpiderMass database. Metabolites heritability was calculated by linear regression progeny-progenitor. We allow new insights about heritability of metabolites in C. canephora and identification of cup quality-related markers. Our novel metabolite markers-assisted strategy drastically accelerates the selection of C. canephora plants and suggests a new approach for accelerated and more focused breeding for other crops.

Keywords: Early selection, Coffea canephora, highly heritable metabolites,
cup quality metabolite markers

# AGRO-MORPHOLOGICAL CHARACTERIZATION OF CHICKPEA GENOTYPES USING MULTIVARIATE ANALYSIS TECHNIQUES

Muhammad Afzal, Salem S Alghamdi, Hussein H Migdadi, Megahed H Ammar

Legume Research Unit, Molecular Biology Lab, Department of Plant Production, College of Food and Agriculture, King Saud University, Riyadh, Saudi Arabia.

afzal_uaf@hotmail.com

Chickpea is a cool season legume crop, inexpensive source of protein and energy. Genetically diverse lines were used to determine the diversity among cultivars, provide better opportunity to find the gene combinations from genotypes differed from parents. The experiment was conducted to determine the genetic diversity of 52 chickpea accessions from ICARADA and international using randomized complete block design (RCBD) with three replications at King Saud University, Riyadh, Saudi Arabia during 2014. The genetic variation was determine by 13 different agronomical superior traits. Analysis of variance results showed highly significant difference with all agronomic traits. The high variance values were observed for plant height (cm), days to 50 % flowering, days to maturity, number of pods/plant, 100 seed weight (g) and biological yield. Hundred seeds weight strongly positively correlated with number of seeds/pod and number of pods/plant. Seed yield/plant (g) reveled strong positive correlation with plant height (cm), number of primary branches, number of secondary branches, number of pods/plant, 100 seeds weight, biological yield, harvest index, while strong negatively correlate with days to 50 % flowering and days to maturity. PCA showed 83.27 % genetic diversity for first five PCs. First components analysis (PC1) showed 39.06 % while PC2 20.99 % of the total respectively. Plant height, number of primary branches, 100 seeds weight (g), number of pods/plant, number of seeds/pod, leaf area, biological yield, harvest index and seeds yield/plant (g) showed positive relation for genetic diversity in PC1 while days to 50 % flowering, days to maturity, number of seeds/pod, biological yield and seed yield/plant (g) has positive contribution in second component (PC2). The chickpea genotypes were divided into four main clusters. Cluster II, Cluster III and Cluster IV showed variance 52.55, 48.39 and 41.43 % respectively.

Keywords: Chickpea, PCA, Cluster Analysis, Genetic Diversity

# USE OF DIFFERENT MOLECULAR MARKERS FOR RESISTANCE TO ASCOCHYTA BLIGHT IN CHICKPEA

Duygu Sarı, Cengiz Toker

Department of Field Crops, Faculty of Agriculture, Akdeniz University,
Antalya, Turkey

duygusari@akdeniz.edu.tr

Chickpea (*Cicer arietinum* L.) is a self-pollinated important food legume, highly valued as a good source of protein (%20-%23). It is grown in an area of 13.5 million hectares with total production of about 13.1 million tonnes in the world. It is divided into two groups as kabuli and desi on the basis of plant characteristics. Desi types are smaller and darker in colour, while Kabuli types are larger and rounder, and they are usually beige or cream in colour. Both chickpea types are susceptible to Ascochyta blight caused by Ascochyta rabiei (Pass.) Labr. This is the most damaging disease of chickpea causing yield losses of up to 100% and having a global distribution. Sources of resistance to ascochyta blight have been identified and resistance breeding has become an important objective of chickpea improvement programmes. The usage of genetic markers associated with resistance genes facilitates the selection of cultivars through marker-assisted selection (MAS) programs. The DNA-based markers, such as RAPD, ISSR, DAF, SSR, SCAR, RGA, AFLP were used to identify QTLs related to blight disease. Veryfing these markers and mapping of their locations is the preliminary point for developing of blight resistant varieties. Also, these markers can assist in MAS for resistance breeding.

Keywords: Ascochyta blight genetic, markers-assisted selection, mapping

# EVALUATION OF VARIATION IN NEBYAN BEAN (*PHASEOLUS VULGARIS*) POPULATIONS COLLECTED FROM SAMSUN, TURKEY

Sağlam, F[1], Balkaya, A[2], Kandemir, D[3]

1. Samsun Directorate of Provincial Food Agriculture and Livestock, Samsun, Turkey
2. University of Ondokuz Mayıs, Faculty of Agriculture, Horticulture Department, Samsun, Turkey
3. University of Ondokuz Mayıs, Samsun Vocational School, Samsun, Turkey

abalkaya@omu.edu.tr

Nebyan beans are very important genetic resources and farmers grow local varieties that they select and maintain for a long time in Nebyan region, Samsun. This region is located within the boundaries of Cerekli, Fındıklı, Kösedik, Aydınpınar, Ormancık, Ku°kayası, Düzköy and Çiftlik villages in Ondokuz Mayıs district, Samsun. In this study, nineteen populations of Nebyan bean were collected from different eco geographical areas of Nebyan region in 2011 year. Each genotype were analyzed for 27 traits. Nebyan bean populations characterized according to their morphological, earliness, and yield traits. Principal Component Analysis (PCA) as a result of examination in connection with identifying traits 27 units independently axis 8 principal components, are obtained. These axes, which represents 88.49% of the total variation was found. Principal Component axis; pitch, the first harvest time, leaf color, average seed weight, pod thickness, total pod weight / plant, seed width, pod width, pod tip length, pod color, post-harvest period, pod curvature, plant height, 100 seed weight , cross-sectional shape, bract leaf length, leaf length and leaf width was determined that features stand out. In addition, cluster analysis was applied to the data and determined that populations are clustered in three groups. A dendrogram to evaluate the similarity between populations are regulated. It revealed high variation. Investigation on the plant characteristics, variability of the evaluation will be conducted in the future to vegetable breeders in breeding populations of green beans belonging to the desirable properties may be helpful in determining. The obtained results will use to apply for trademark and geographical indication report on behalf of namely Nebyan beans for Ondokuz Mayıs district by the Turkish Patent Institute.

Keywords: Snap bean, genetic resource, Nebyan, characterization, variation, breeding

# DIVERSITY AMONG CROATIAN COMMON BEAN (*PHASEOLUS VULGARIS* L.) LANDRACES

Klaudija Carovic-Stanko[1], Mirjana Herak Custic[2], Martina Grdisa[1], Boris Lazarevic[2], Monika Vidak[1]

1. University of Zagreb, Faculty of Agriculture, Department of Seed Science and Technology, Svetosimunska 25, HR-10000 Zagreb, Croatia
2. University of Zagreb, Faculty of Agriculture, Department of Plant Nutrition, Svetosimunska 25, HR-10000 Zagreb, Croatia

mvidak@agr.hr

Common bean (*Phaseolus vulgaris* L.), once known as the poor's man meat, has re- cently gained attention as functional food being a valuable source of high-quality protein. In Croatia common bean is traditional, but unfortunately, neglected crop. It is cultivated in low input production systems. The landraces are adapted to local environments and growing conditions, showing a great variability in morphological and agronomic traits. In order to assess morphological diversity and protein content we analysed 300 Croatian common bean landraces. The accessions grouped into seven clearly defined clusters representing distinct morphotypes commonly known by their traditional names: tresnjevac, zelencec, biser, dan noc, puter, tetovac and kukuruzar. The protein content in raw seeds ranged from 16.69 to 27.88%. The results will allow the identification of most promising landraces to be used for breeding purposes.

Keywords: Common bean, landrace, protein content, morphological diversity

# FUNGAL DISEASES OF PROTEIN CROPS IN AEGEAN REGION

Tijen Taşkın

Gençlik cad. No:6 Bornova-İzmir

tijen.taskin@gthb.gov.tr

Protein crops such as bean, faba peas, lupins, alfalfa and clover have a huge potential for farmers, feed industry, food industry and breeding industry. Leaves and stems of protein crops are high in protein and serve as an excellent and nutritious food for humans and feed for many domesticated animals. One of the major threats to the protein-rich leguminous crops is yield and quality loss due to diseases. Like most crops, legumes is attacked by many disease- causing organisms. Fungal diseases cause significant damage on protein crop fields in Aegean region. In this study, it is intented to determine the fungal diseases which cause losses in protein crop production. Fungal pathogens will be detected in the samples brought to laboratory from different provinces (Balıkesir, Denizli, İzmir and Uşak) during 2013-2015. Anthracnose (Ascochyta rabiei), wilting (Fusarium oxysporum), rust (Uromyces ciceris-arietini) in chickpea, Fusarium wilt (Fusarium oxysporum) in bean and root rot (Rhizoctonia solani and Fusarium spp.) in cowpea were detected. Management practices aimed at reducing loss from fungal disease, are based on factors, selection of an appropriate multiple disease-resistant variety, and use of other disease management practices including environment modification, crop rotation, irrigation, and fungicides. Detection and identification of disease problems are essential for managing the impact of diseases on protein crops production.

Keywords: Fungal diseases, protein crops, Aegian region

# THE EVALUATION OF PLANT DIVERSITY (GENETIC RESOURCE) STUDIES IN PLANT BREEDING

Banu Kadıoğlu, Sibel Kadıoğlu

East Anatolian Agricultural Research Institute (DATAE)
25090-Aziziye/ Erzurum, Turkey

sibel.kadioglu@hotmail.com.tr

Plant breeding is as ancient as human history. Them mankind that had to eat, had fed on plants that they gathered, saved the big and sturdy seeds of the plants they liked for next year and cultivated them. This can be considered as mankind taking wild species in culture (utilizing genetic variation) and plant breeding (gross selection). Culture plants are being developed by using natural variation from different genetic sources and by classic breeding methods. One of the most important and the basic aims of plant breeding is to sustain genetic variation in plant level and to obtain new plants with wanted inherited features by using variations in genetic structures and natural propagation of the plants. Breeder tries to develop new methods as well as using the classic ones and tries to find the ways to use and evaluate variation of the plantation in the geography he recites.

Turkey, where main genome and variation centers are located, is placed in three phytogeography regions. There are 12 thousand species and subspecies. Four thousand of these are endemic species. In order to protect this prosperity and provide sustainability it is required to collect and protect the local species that are main material of the plant breeding, the village populations, the primitive relatives of the culture types, the transition species, the breed species, the breeding lines and the imported materials.

Plant genetic sources are used in global studies on plant growth in a way to disseminate around the world with its one or two important features and continuity. In this context, the seed gene banks subsidiary to ministry of food, agriculture and livestock, breeding studies carried out by the investigation institutes and researches of the genetic resources providing gene flow are evaluated, the current situation of genetic resources and breeding researches are presented.

Keywords: Plant breeding, plant diversity, genetic resource, seed gen bank,
TAGEM projects

# SEED GENE BANKS INFORMATION SYSTEM

Bengü KOYUNCU, Canan YAĞCI TÜZÜN, Kürşad ÖZBEK

Central Research Institute for Field Crops, Turkish Seed Gene Bank, Şehit Cem
Ersever Street, No: 9-11 Yenimahalle/Ankara

esmer.benguu@gmail.com

Conservation of national plant diversity especially genetic resources of some cultivated plant species are extremely important for sustainable plant production. There are two seed gene bank in our country within Ministry of Food Agriculture and Livestock with the aim of collection, documantation, conservation and molecular-morphological characterization of plant genetic resources. It is needed the existence of a suitable, reliable and sustainable national database in order to minimaze the wasted time/labor in field studies and damage to nature. Researchers especially breeders can reach the material which has higher viability rate, qualified and characterized with this database. Passport (plant name, altitude, coordinates, habitat informations etc.) and storage information of 45.789 (as of August 2015) materials which were collected and conserved in Turkish Seed Gene Bank from 1988 to present-day were arranged for suitable formation to prepare the Seed Gene Banks Information System (SGBIS) with pre-studies.

Designed software system was developed with Microsoft C # Asp.Net 4.0 as an object oriented programming language to perform faster, safer and flexible searching and real-time recording of material. Software was designed with ER model and SQL R2 program was selected as database. Passport, storing, characterization, evaluation, socio-economical and eco-geographical data of materials were placed in database columns to access more detailed information. A star network topology was used in local area network to protect against cyber attacks. Researchers especially breeders will access information of plant genetic resources in seed gene banks before started their studies with this software.

Keywords: Plant conservation, plant genetic resources, seed gene bank,
plant diversity, database for conservation, software for seed gene bank

# ASSESSMENT OF GENETIC DIVERSITY IN RYE COLLECTION WITH ISSR MARKERS

Natiga Nabiyeva

AZ1106, Azadlig Ave155, Baku, Azerbaijan

gen_eht@yahoo.com

The genetic diversity of 83 samples of cultivated and wild rye (*S. cereale* L., *S. segetale* L., *S. sylvestre* H.) accessions, conserved in the National Genebank of Azerbaijan has been assessed. The research was carried out by polymerase chain reaction using 6 ISSR-primers (ISSR2, ISSR6, ISSR7, UBC808, UBC811, UBC827). Electrophoresis of the synthesized amplicons revealed only 49 bands, 47 of which were polymorphic. The greatest number of bands (11 bands) was registered upon reaction with ISSR2. The average level of genetic polymorphism designed for all primers was 95.2%. The DNA amplification with 4 (ISSR2, ISSR6, UBC808, UBC827) primers revealed a 100% level of polymorphism, indicating the feasibility of their application to the study of the genetic diversity of rye. The dendrogram based on the cluster analysis has identified 11 distinct groups of samples of plants. The largest group divided into 2 subgroups brings together 68 samples, allowing to consider them as the similar genotypes. Two groups include 3 rye samples, and one group - 2 rye samples. 7 samples from the studied collection are separated into separate groups according to the analysis data, indicating the isolated structure of the genome of these plants, distinguished from all other genotypes.

Keywords: Rye, genetic diversity, ISSR markers, polymorphism

# INTRASPECIFIC DIVERSITY ESTIMATION IN SOME SPECIES OF MEDICINAL PLANTS

Ana Mutu, Oleg Budeanu, Steliana Clapco, Rodica Martea

Center of Molecular Biology, University of the Academy of Sciences of Moldova,
3/2, Academiei str., MD-2028, Chisinau, Republic of Moldova

anisoara.mutu@gmail.com

Intraspecific diversity is a key element in the evolution of organisms. Aromatic and medicinal plants present a rich and available sources of bioactive compounds with lower polyvalent side effects than those produced by chemical synthesis. A relatively inexpensive technique, which ensures simple and rapid identification of genomic polymorphism, is RAPD-PCR. The aim of conducted research was to estimate genetic diversity of medicinal plants with economic importance in Republic of Moldova O. vulgare and *H. officinalis* L. (family Lamiaceae), which is characterized by a high content of essential oils with varied composition and multiple curative properties, applying RAPD-PCR technique. Efficiency of RAPD primers for intra- and inter-population polymorphism assessment in different genotypes of H. officinalis and O. vulgare, collected from experimental fields and spontaneous flora, was demonstrated. Analysis of electrophoretic profiles obtained after amplification with arbitrary primers for O. vulgare genotypes collected from different populations revealed higher level of polymorphism (45.0 %) of spontaneous forms comparatively with the experimental culture (36.4 %). The highest molecular polymorphism for O. vulgare ssp. was revealed by RAPD-PCR analysis with primers OPB10, OPG10 and UBC215. In the case of H. officinalis L. the maximum number of polymorphic bands (12 fragments) was generated by primer OPJ01, followed by OPA9 and OPB03 (8 fragments). The most primers showed a high degree of molecular polymorphism depending on tested primers and particularities of studied species.

Keywords: Polymorphism, medicinal plants, RAPD-PCR

# STUDY OF GENETIC DIVERSITY OF MOROCCAN GRAIN SORGHUM (*SORGHUM BICOLOR* L. MOENCH) VARIETIES BASED ON MORPHOLOGICAL AND MOLECULAR MARKERS

Rajae Alloudane[1], Nourdin El Mourabit[2], Said Barrijal[1*]

1. Department of Biology, Faculty of Sciences and Technics of Tangier,
University of Abdelmalek Essaadi, Morocco

2. National Institute of Agronomy research, Tangier, Morocco

barrijal@yahoo.fr

The study of the genetic diversity of Moroccan grain sorghum (*Sorghum bicolor* L. Moench) varieties constitutes a necessary step that can be exploited in the programs of improvement and valorization of this marginalized cereal. A total of 16 accessions collected from northwest area of Morocco were analyzed using fourteen morpholigical traits (grainyield,biomassyield,graincolor, inflorescence length) and four nuclear microsatellites markers (ISSRs) to determine the genetic relationships among landraces .cluster analysis based on morphological traits revealed three major distinct groups with one landrace forming independent cluster. Based on molecular markers, seven clusters were observed

The four ISSR markers used reveal a relatively important genetic variability. With a polymorphism rate of 98 ,99 %, an average number of allel 2,7 per locus .Molecular markers clearly separated landrraces within and between groups than morphological markers.

Keywords: Sorghum bicolor L. Moench; morphological markers, ISSR Markers; Genetic Variability

# SOME FRUIT CHARACTERISTICS OF GENOTYPE OF MELON (*CUCUMIS MELO*) WITH THE ORIGIN OF LAKES REGION (GOLLER BOLGESI) IN TURKEY

Fatih Erdoğan[1], Mustafa Paksoy[2], Önder Türkmen[2]

1. Fruit Research Institute, 32500 Egirdir, Isparta/Turkey
2. Selçuk University, Agriculture Faculty, Department of Horticulture, 42031 Konya/Turkey

ferdoganx@hotmail.com

97 pieces of local melon (*Cucumis melo*) genotype collected in 6 cities in Lakes Region (Göller Bölgesi) in Turkey forms the material of this study. In order to conduct morphological characterization and inbreeding activities, the genotypes were unrepeated planted in Eğirdir (Horticultural Research Institute of Eğirdir) district of Isparta on June 12, 2013 so that each genotype is consisted of 20 seedbeds. In this study; fruit shape, fruit weight, fruit length, the diameter of the fruit, diameter of pistil scar, the flesh thickness, the skin thickness, fruit shape of apex, and aroma presence measurements and observations were made.

Keywords: Melon, Cucumis melo, fruit characteristics, Lakes Region

# VARIABILITY OF MORPHOLOGICAL TRAITS OF TWO FIBRE FLAX POPULATIONS

Sylwia Lewandowska[1], Jan Szopa-Skórkowski[1], Andrzej Kotecki[2], Henryk Bujak[2]

1. Wroclaw University of Environmental and Life Sciences, Department of Genetics, Plant Breeding and Seed Production, Poland, 50-363 Wroclaw, Plac Grunwaldzki 24 A
2. Wroclaw University of Environmental and Life Sciences Department of Crop Production Poland, 50-363 Wroclaw, Plac Grunwaldzki 24 A

henryk.bujak@up.wroc.pl

Biologically active flax fibers can be used to produce fabrics dressing supporting the treatment of difficult healing wounds. The subject of research were two genetically modified populations of type M and B in which fiber an increased synthesis of antioxidants was found. The first form was a type M of flax, which has genetically modified cells containing a three-gene construct containing cDNA encoding the enzymes of the polyhydroxybutyrate synthesis. In contrast, the second type B has genetically modified cells containing monogenic construct encoding βglucanase enzyme. Flax fibers obtained from type M producing polyhydroxybutyrate and B plants producing polyamines can be used to produce a fabric forming a basis of a new dressing supporting the period of difficult wound healing process.

The research material was line B14 derived from population of type B and line M50 derived from population of type M. The populations were reproducing in separate Ohio self-pollinated plant breeding method. 50 plants, characterized by a good height and a good technology stalk length, were selected from every individual plot. Directly after harvesting 8 morphological traits were analyzed. Student's t-test showed a significant difference between the tested lines for stalk thickness, number of branches on the stalk, capsule and seed number and seed mass per plant. In terms of plant height, technology stalk length, number of branches per panicle the populations did not differ from each other. Line M50 stands out favorably than line B14 in terms of majority morphological tested traits.

Keywords: Agronomic traits, antioxidants, fiber flax, variability

# EVALUATION OF SOME WILD RELATIVES, HYBRIDS AND CULTIVATED POTATOES USING CT AND MTDNA MARKERS

Mousa Torabi Giglou*, Panahandeh Jaber, Seyed Abolghasem Mohammadi, Fariborz Zaree Nahandi, Alireza Motallebi Azar, Jadwiga Sliwka

Moghan College of Agriculture and Natural Resources, University of Mohaghegh Ardabili, Parsabad Moghan, Ardabil Province, Iran

m.torabigiglou@gmail.com

Potato has a large number of wild relative species, and most of all wild species of potatoes are in the same gene pool, so there are many ways, to cross cultivated potatoes with them and exploitation of the useful properties, but there are some barriers like cytoplasmic sterilities, characterized by different chloroplast and mitochondrial DNA type, that are important for designing efficient breeding programs and mating combinations as well as nuclear chromosomal DNA that contribute to some special characteristics like various types of male sterility. Cytoplasmic DNA diversity and relationships of 45 potato genotypes of three ploidy and EBN levels, belonging to 16 species (wild relatives, selected hybrids and cultivated potatoes), was assessed via mitochondrial and chloroplast markers. DNA was extracted from … by the CTAB method (Doyle and Doyle 1987) and adjusted to a concentration of 25 ng/l. We used 5 chloroplast DNA (ctDNA) marker primers (T, S, D, SAC and A) to find different ctDNA types and 1 mitochondrial DNA (mtDNA) marker (ALM_4 / ALM_5 marker) to recognize mtDNA types α, β and γ. These primers were used alone or in multiplex reactions. PCR products of A, T, SAC markers and multiplex reactions were digested with BamHI enzyme for 3 hours at 37˚C. After finding chloroplast and mitochondrial DNA types, cytoplasmic types of genotypes were assigned according to Hosaka and Sanetomo (2012). The cytoplasmic genome of the common potato is characterized by the presence of T-type chloroplast DNA (ctDNA). Wide cytoplasmic diversity was observed in studied potato germplasm. According to markers banding pattern types, results showed 10 cytoplasm types. The most prevalent type in 2EBN genotypes was D/α and all promising hybrids, as well as tested cultivars showed T/β type. Mexican diploids with B genome and S. commersonii accessions with A genome came together in W/γ type. Among Mexican potatoes, 7 diploid genotypes possessed W-type cyto- plasm characterized by α, γ and σ-types of mtDNA. All of allopolyploid 2EBN 4x genotypes including S. papita, S. hjertingii, S. polytrichon and S. stoloniferum acces- sions had D/α type cytoplasm and only two accessions plt/62 and fen/37 had D/γ type. Out of the hybrids, St1.K and A.K possessed T/β type, SB.K showed W/α, and two promising hybrids; stbr-p and stbr-w were qualified as D/α, whereas S. andigena and commercial cultivars Agria and Satina possessed T/β type. Studied S. acaule accessions showed different cytoplasm types. Genotypes acl/67, acl/76, and acl/49 showed W/β, D/β, M/α and P/β cytoplasm types respectively. The only P/β cytoplasm was observed in phu/op genotype whereas other studied S. phureja genotype had D/α type.

Keywords: Cytoplasm type, chloroplast DNA, cultivated potatoes, diversity, hybrids, mitochondrial DNA, multiplex PCR, Solanum, wild relatives.

# BREEDING SYSTEM OF SOME IRANIAN POPULATIONS OF *LEONURUS CARDIACA* L. (LAMIACEAE)

Fatemeh Borna[1,2*], Nabil. M. Ahmad[1], Shuming Luo[1], Richard Trethowan[1]

1. Plant Breeding Institute, Faculty of Agriculture and Environment, University of Sydney, Cobbitty, NSW 2570, Australia
2. Department of Horticulture, Faculty of Agriculture, the University of Tehran, Iran

fatemehborna@gmail.com

Motherwort (*Leonurus cardiaca* L., family Lamiaceae) is the only species of the genus Leonurus found in Iran, and has many uses in folk medicine. The objective of this research was to assess the floral structure, phenology and sexuality (including pollen and stigma biology) of three Iranian populations (Sarab, Dargaz and Khansar). Exploring these characteristics can identify the breeding system in L. cardiaca and provide a basis for the genetic improvement of secondary metabolites that may have human health benefits. The results showed that the perfect (bisexual) flowers are protandrous as the stigma becomes receptive between two to three days post-anthesis and anther dehiscence. However, the timing of anthesis of flowers within each inflorescence and flowers of different inflorescences on each plant may be synchronous leading to the possibility of geitonogamous pollination. The studied populations varied in flowering time by up to 20 days. The earliest flowering population was Khansar and the latest was Dargaz. Controlled pollination tests indicated a high percentage of self-pollination (>87%) in all three populations because each inflorescence was crowded with flowers at different developmental stages. On the other hand, controlled cross pollination produced high fruit setting. The cross between Sarab and Dargaz produced more than 95% fruit set, while the cross between Dargaz and Khansar produced only 50%. This is a clear indication of the differences in compatibility between these populations.

Keywords: Floral biology; Motherwort; crosspollination; Pollen viability; Stigma receptivity

# GENOFOND OF HYBRID TEA ROSES IN NIKITSKY BOTANICAL GARDENS

Yuri Plugatar, Zinaida Klimenko, Svetlana Plugatar

Yalta, the Republic of Crimea, Russia

gardenroses@mail.ru

The first cultivars of hybrid tea roses were taken to Nikitsky Botanical Gardens (NBG) in 1950s. They were intensively started to introduce and breed in 1955. Nowadays NBG genofond of hybrid tea roses includes 144 cultivars, where 50 cultivars belong to domestic breeding as a result of different hybridization methods and experimental mutagenesis. Under conditions of South Coast of the Crimea (SCC) hybrid tea roses cultivated in open ground, are enough frost-resistant and don`t need cover for wintering. Some of them present prolonged remontant blooming up to 150-180 days. Though some cultivars are damaged by fungal diseases of foliage, shoots and buds during summer-autumn period. After many years of introduction study it was determined that hybrid tea roses are of high adaptability, perspective for cultivation under SCC conditions and usage in breeding and landscaping. 17 early-blooming cultivars were found out and assortment of 33 cultivars of domestic and foreign hybrid tea breeding was developed and recommended for cultivation on South of Russia.

This study was funded by a research grant No 14-50-00079 of the Russian Science Foundation.

Keywords: Breeding, introduction, genofond, hybrid tea roses, mutagenesis, hybridization.

# OPTIMIZATION OF DNA ISOLATION METHOD FOR DETERMINATION OF GENETIC VARIATION WITH ISSR-PCR METHOD IN SAINFOIN (*ONOBRYCHIS SP.* L.)

Ayşe Yıldız[1], Burcu Pulluk Uğur[2], Sümer Aras[2], Erol Karakurt[1]

1. The Central Research Institute for Field Crops, Şehit Cem Ersever Cd.,
   No 9-11, Yenimahalle, Ankara, Turkey
2. Ankara University, Faculty of Sciences Department of Biology
   Tandogan, Ankara, Turkey

varolyildiz@hotmail.com

Besides being an important species of forage production sainfoin (*Onobrychis sativa* Lam.), having quality and high food yield, is a legume plant which is useful for improving soil fertilisation and features and preventing erosion. Cultivated under dry conditions, production of grass by using poor and barren soil increase the sainfoin value. In the world almost 160 sainfoin species are known. Turkey is one of important developing centre for this species and it is known that there are 52 sainfoin species (60 taxon).

Sainfoin has very rich genetic variation in terms to resistance to dryness, salinity, diseases and pests. Determination of resistant varieties against the biotic and abiotic stress conditions and identification of these in term of genetics are quite important for protection of gene sources and developing new varieties in sainfoin breeding programmes. Therefore, besides morphological identifications molecular identifications will provide an effective use of genetic variations in breeding programmes. For this purpose DNA marker systems having high polymorphsim rate and not affected by environmental conditions as ISSR, SSR and AFLP are the most used methods for identification of genetic variation.

The purpose of this study is to carry out ISSR studies in one plant and populations of some sainfoin varieties collected from Central Anatolia Region, in order to determine the outstanding genotypes at molecular level. For this reason 3 different nucleic acid isolation methods have been used for obtaining DNA with appropriate quality and quantity. These techniques include two different CTAB and one commercial kit methods. In the first method of CTAB average concentration 224 ng/µl and standard deviation 101,42 ng/µl, in the second method of CTAB average concentration 553,6 ng/µl and standard deviation 553,12 ng/µl and in commercial kit method average concentration 35,8 ng/µl and standard deviation 18,32 ng/µl have been found.

Acknowledgement: This study was financed and supported by General Directorate of Agriculture Research and Policy, Republic of Turkey Ministry of Food, Agriculture and Livestock

Keywords: DNA isolation, Sainfoin, ISSR, Genetic variation, Optimization

# GENETIC RESOURCES AND PROGRESS IN POTATO AND VEGETABLE BREEDING IN KAZAKHSTAN

Temirzhan E. Aitbayev, Bakhytbek M. Amirov

Nauryz st., Stlm. Kainar, Karasai District, Almaty Region, 040917, Kazakhstan

bamirov@rambler.ru

In Kazakhstan production of potato, vegetables and melons are an important sector of agriculture to provide a year-round supply of complete and balanced food. According to statistics in 2014 in the Republic the area of potato totaled 184,8 thousand ha, gross yield - 3,344 million tons. Vegetables were cultivated on an area of 137,7 hectares, from which were collected 3,241 million tons. Under the melons and watermelons were allocated 82,3 ha with the gross yield of 1,713 million tons. In spite of the significant production of potato and vegetables in the country yet there is an acute shortage of them in the off-season, when the prices of many vegetables soar, and the assortment of domestic vegetables remains very poor. Therefore breeding and releasing of new varieties with the best economic-valuable traits are of high importance. Before 1991 breeding research at the Kazakh Research Institute of Potato and Vegetable Growing had covered only seven crops - potato, onion, tomato, cucumber, pumpkin, watermelon and melon, and The Soviet Union's Register of selection achievements had included 12 varieties of potato and vegetables of Kazakhstan breeding program. In Kazakhstan in recent years has been rapidly evolving and expanding breeding research. Today the breeding research has been expanded to 25 kinds of vegetables and the gene pool of Kazakhstan amounts 12000 accessions of vegetables from 97 countries and 2000 accessions of potato from 40 countries of the world. As of 2015 the State Register of breeding achievements includes over 130 local varieties of potato and vegetables.

Keywords: Potato, vegetables, gene pool, breeding, production

# MORPHOLOGICAL CHARACTERIZATION OF VETCHES IN THE SEMI-ARID REGION OF SETIF USING FUZZY LOGIC INFERENCE SYSTEM

K. Abed-Cheniti[1], S. Bouharati[2]

1. Department of Agronomy, Faculty of Nature and Life, Setif 1 University,
2. Laboratory of Intelligent Systems, Faculty of Technology,
   Setif 1 University, Algeria

khalissacheniti@gmail.com

In agriculture, preventing the performance of a plot is paramount. In this study, we tried to predict the performance of the species or varieties of leguminous in a semi-arid region. Several variables are taken into account such as the numbers of leaves, flowers, stem height ... etc. Knowing that these variables are characterized by uncertainty and vagueness, we proposed a data analysis tool based on artificial intelligence techniques, including the principles of fuzzy logic. The result was very satisfactory. Program established to predict the performance of a land just from imprecise input variables of the system. Thus in this context, the main objective of this work is to characterize morphologically certain species of vetch in the semi-arid region of Setif in Algeria, to determine the most discriminating variables and find the most relevant and most effective varieties meeting the food needs of our breeding both quantitatively and qualitatively. As the data characterizing these parameters are distinguished by their vagueness and uncertainty, we found it useful to apply the principles of artificial intelligence (fuzzy inference) that are perfectly suited to these data.

Keywords: Leguminous, Vetches, morphological characteristics, semi-arid region, fuzzy logic system.

# ACHIEVING LONG TYPE PEPPER POPULATION RESISTANT TO TOMATO SPOTTED WILT VIRUS (TSWV)

İbrahim ÇELİK*, Ramazan ÖZALP, Nejla ÇELİK, İlknur POLAT, Görkem SÜLÜ
Batı Akdeniz Tarımsal Araştırma Enstitüsü
celik_ibrahim@yahoo.com

Pepper is widely grown vegetable crops after the tomato and watermelon in the world. One of the most important disease effects on pepper production is wilt caused by Tomato Spotted Wilt Virus (TSWV). The best way for the control of this disease is use resistant varieties. In this study, improving TSWV resistant populations to use on long type variety breeding studies was aimed. Three resistant cultivar as resistant crossed with susceptible Serademre 8. F1 plants raised from these crosses were tested against TSWV. The resistance tests were performed both mechanical inoculation and molecular methods. Virulent strain isolated from infected pepper plant was used disease material in the mechanical inoculations. TSWV linked CAPS marker (SCAC 568) was used in the molecular test method for verification classical test method. Developed three population generated from crossed three resistant genitors with susceptible plants were self-pollinated five generations. Resistance test performed in each generation and resistant plants were choosing for self-pollination to achieve next generation. Totally, 399 plants from population one, 520 plants from population two and 98 plants from population three were developed as homozygote resistance in five generation. These populations seem to be contains good characters for using in TSWV resistant long type pepper breeding studies varieties.

Keywords: Pepper, TSWV, Molecular Markers

# EVALUATION OF NEW MELON VARIETIES IN ECOLOGICAL CONDITIONS OF SOUTHERN KAZAKHSTAN

I. I. Umbetaev[1], S.P. Makhmajanov[1], B.M. Amirov[2]

1. Laboratory st., v. Atakent, Makhtaaral district, South Kazakhstan region, 160525, Kazakhstan;
2. Nauryz st., Stlm. Kainar, Karasai District, Almaty Region, 040917, Kazakhstan

bamirov@rambler.ru

In Kazakhstan melon is the leading vegetable crop with planting area accounting for over 46 thousand ha of them around 40 thousand ha is concentrated in Southern Kazakhstan. In recent years, demand for Kazakh melons grows in Russia and Europe. For conveyor delivery of melon products to the market for producers advisable to have different varieties of melons with varied ripening which would possess along with good taste a high shelf life quality and transportability. During 2012-2014, at the Kazakh Research Institute of Cotton Growing were carried out environmental testing of 8 mid-early maturing and 12 mid maturing melon varieties from domestic and foreign breeding program. As the results have shown, all the varieties of melon were well adapted to the average soil salinity and groundwater table at a level of 1,5-2,0m. Among the mid-early maturing melons the most high-yielding varieties were cv “Muza”, cv “Shugyla” and cv “Mayskaya”, ensuring, respectively, 8,4; 8,5 and 10,6% of additional yield to the yield of test cv “Chempionka” (32,4 t/ha). Of the tested 12 mid maturing melon varieties by high yields were distinguished cv “Zhuldyz”, cv “Karakai”, cv “Zhienshar”, cv “Torpedo” (Djian) and cv “Yuzhanka 12” shown, respectively, 22,6; 32,8; 35,5; 42,8 and 59,3% increase to the yield of test cv “Gulabi Oranjevaya (36,0 t/ha).

Keywords: Melon, trial, variety, yield

# SOME PHLOEM MIRNAS ARE INDUCED BY CADMIUM STRESS TO COMMUNICATE OVER LONG DISTANT PLANT ORGANS

Huseyin Tombuloglu[1], Guzin Tombuloglu[1], Mehtap Aydin[1], Abdugaffor Ablazov[1], Serdal Sakcali[2]

1. Fatih University, Department of Biology, 34500, Buyukcekmece-Istanbul, Turkey

2. Suleyman Demirel University, Department of Biology, Isparta, Turkey

htombuloglu@fatih.edu.tr

Cell to cell and/or organ to organ communication is essential for plant development and growth. In this process, some biomolecules (RNAs and proteins) can move from one cell to another by using specific symplastic network connected via plasmodesmata. Meanwile, distance cells and organs can communicate via plant vascular bundle. microRNAs (miRNA) are the potential signal molecules which are directed to move over long distances. In this study, it is addressed to find phloem mobile microRNAs that are induced upon Cadmium (Cd) stress. Pumpkin (Cucurbita maxima) phloem exudates were collected from 21-day old seedlings which were exposed to toxic level of Cd. Control (no treatment), 24h and 48h samples were processed for miRNA analysis. In total, expression of 14 miRNAs were analyzed from each sample. Among them, miR159, miR160, miR162 and miR167 were found to be overexpressed in phloem exudates. It is implied that those miRNAs can be important for long distance signal transduction mechanism under Cd stress conditions. The results can contribute to understand organ to organ communication of plants under Cd stress. Also, the results shed light on miRNA-mediated signal transduction and organ-to-organ communication strategy of plants.

Keywords: Mobile miRNA, Phloem, long distance communication, Cadmium.

# DEVELOPING OF HYBRID PEPPER (*C. ANNUUM* L.) VARIETIES FOR PROTECTION CULTIVATION

Ramazan Özalp, İbrahim Çelik

Batı Akdeniz Agricultural Research Institute, Antalya, Turkey

ramazanozalp@yahoo.com

Pepper (*Capsicum annuum* L.), is one of the most important vegetable species produced in both open fields and protected cultivation in Turkey. It has a big market value due to various fruit types. There is a need for developing new varieties because of the changing market demands. Long, charliston, capia and bell fruit types of pepper were studied in this breeding programme with three stages. Firstly, inbred lines were crossed with two tester lines to determine combining ability and heterotic pattern. Secondly, specific combination hybrids were made by considering heterotic groups and promising hybrids were determined. Thirdly, yield performances of promising hybrids were tested with control commercial varieties. Yield trials and morphological characterizations of hybrids were done in randomized complete block design (RCBD) in the single crop-growing seasons in unheated glasshouses of Batı Akdeniz Agricultural Research Institute (BATEM) and the hybrids were also demonstrated to private sector during the growing term. As a result, two of long pepper, three of charliston pep- per, three of capia pepper and two of bell pepper candidate hybrids were determined. A total of 10 candidate pepper hybrid varieties and 20 inbred lines were introduced to the private and public sector in "Products Catalog". Some ınbred lines were sold to private sector for their breeding studies. And two pepper hybrid varieties were regis- tered as "Özge" (sweet long pepper) and "Özalp" (charliston pepper) in May, 2015. The rights of seed production and sale of "Özalp" variety were transferred to private seed company for 5 years.

*This study is a part of "Improvement of F1 Hybrid Vegetable Varieties and Qualified Lines in Turkey" project (KAMAG-109G029) that is supported by Scientific and Technological Research Council of Turkey (TUBITAK).

Keywords: Pepper (*Capsicum annuum* L.), pepper breeding, combining ability, heterotic pattern, morphological characterization, hybrid variety

# THE NEW TABLE GRAPE CANDIDATES IN TEKIRDAĞ VITICULTURAL RESEARCH INTITUTE

Onur Ergönül, Cengiz Özer, Zeliha Orhan Özalp, Mehmet Sağlam

Viticultural Research Institute, Breeding and Genetic Department, 59100 Tekirdağ, Turkey

onur.ergonul@gthb.gov.tr

Turkey, in spite of being important gene source of grape and one of the biggest table grape producers, the number and quality of qualified table grapes are insufficient. The main variety is Sultanina for both domestic and foreign markets. High quality, early or late maturing, attractive hybrid table grape cultivars will be good alternative for table grape growing regions and improve dynamism of the sector. For this purpose, conventional breeding studies with the priority of seedlessness have been carried out Tekirdağ Viticulture Research Station (TVRS) since 1974. Parents were seeded genotypes as female progenitor while seedless genotypes as pollinator. The four new table grape cultivars were released in 2011 and registration procedure was started in 2012 for eight candidates. New grape candidates were selected from cross combinations of Italia x Reçel Üzümü, Çınarlı Karası x Tekirdağ Çekirdeksizi, Ribol x Güz Üzümü, Amasya Beyazı x (16xA-101). The five of Candidate cultivars are seedless while others are seeded. The data related with quality, yield, growth and ripening time of eight table grape candidates are presented in this study.

Keywords: Breeding, table grape, seedlessness.

# IMPROVEMENT OF QUALIFIED LINES UNDER CHILLING STRESS IN CUCUMBER (*CUCUMIS SATIVUS* L.)

Volkan Gözen, Akın Tepe, Filiz Öktüren Asri, E. Işıl Demirtaş, Levent Keskin

Department of Vegetables and Ornamental Plants, Bati Akdeniz Agricultural
Reseach Institute, Antalya, TURKEY

vgozen@hotmail.com

Cold temperature damage is a common problem for early-planted cucumber in Turkey. Chilling temperatures (-120C) can cause significant damage to cucumber plants. This study was conducted as a sub-project of “Improvement of F1 Hybrid Vegetable Varieties and Qualified Lines in Turkey” supported by TÜBİTAK 109G029 at the Vegetable and Ornamental Plant Department of Batı Akdeniz Agricultural Research Institute (BATEM) between 2010 and 2014. The objective of the present study was to improve chilling tolerant lines from cucumber gene pool. To determine the performance chilling stress of genotypes, experiments were carried out in both growth chamber and greenhouse during the winter and early spring. The approach was based on chlorophyll contents (Chl), the electrolytic relative leakage rate and chilling injury index in cucumber seedlings at the first true-leaf stage in a growth chamber (RH = 60%) with a photoperiod of 12 h light (250 µmol m-2s-1)/12 h darkness, and seedling were exposed at 5 °C for 8 hours. Chilling tolerance genotypes were selected and inbred. Inbred lines were obtained with six times inbreeding by using single seed descent metod. Generative period tests were performed for yield an yield component under growing greenhouse conditions during winter and early spring season. As a result of this study, 7 qualified lines were improved at the end of the project. Furthermore, these pure lines have been sold to four domestic seed companies by BATEM, in order to be utilized in their breeding programmes for improving a new F1 hybrid varieties

Keywords: Cucumber, chilling stress, breeding, pure-line selection, yield and yield components

# SCREENING COMMERCIAL TOMATO CULTIVARS FOR TOMATO SPOTTED WILT VIRUS RESISTANCE USING A SW-5 LOCUS SPECIFIC MARKER

Gülderen Koca, Bayram Çevik

Süleyman Demirel University, Faculty of Agriculture, Department of Plant Protection. Isparta, Turkey

bayramcevik@sdu.edu.tr

Tomato spotted wilt virus (TSWV) is one of the major disease problem in the tomato growing regions of Turkey andthe world. Sw-5 gene from wild tomato species Solanum peruvianum confers resistance to TSWV. Although the resistance was incorporated into commercial tomato cultivars through classical breeding, many cultivars commonly grown cultivars are still susceptible. In this study, the presence of Sw-5 TSWV resistance gene in different tomato cultivars from different seed companies operating in Turkey was determined. Seeds of 71 different tomato cultivars were germinated and the genomic DNA was isolated from seedlings, the presence of the Sw-5 gene conferring resistance to TSWV was determined Sw-5-2 locus specificmarkers by PCR method. The results showed that while 53 of 71 cultivars contained the Sw-5 locus, 18 cultivars did not have the Sw-5 locus. Among the 53 cultivars, 15 of them were resistant to TSWV, but 39 of them were susceptible. 14 of the resistant cultivars were determined to be heterozygote for sw-5 gene and only one was considered to be homozygous. Testing with Sw-5-2 locus specific markers showed that the presence of the Sw-5 resistance gene can effectively be identified in tomato. The results of this study also showed that most of the tomato cultivars commonly grown in Turkey contained Sw-5 locus conferring resistance to TSWV, but only one third of these cultivars actually had the resistant genotype and possibly resistant to TSWV.

Keywords: TSWV, tomato, MAS, molecular markers, disease resistance

# THE HYPOCOTYLS MORPHOLOGY OF PROMISING SALT TOLERANT WINTER SQUASH AND PUMPKIN ROOTSTOCK LINES AND GRAFTING COMPATIBILITY, SURVIVAL RATES WITH GRAFTED WATERMELON

Balkaya, A[1], Yıldız, S[2], Kandemir, D[3]

1. University of Ondokuz Mayıs, Faculty of Agriculture, Horticulture Department, Samsun, Turkey
2. University of Abant İzzet Baysal, Bolu Vocational School, Bolu, Turkey
3. University of Ondokuz Mayıs, Samsun Vocational School, Samsun, Turkey

mdilek@omu.edu.tr

Salinity is one of the major environmental factors that cause reduction in plant growth, development and productivity worldwide. The selected salt tolerant, three pumpkin lines and three interspecific hybrids of C. maxima x C. moschata were used in this study. Emergence rate, hypocotyls morphology, survival were determined. Grafting success of rootstocks differed between 46.0-100.0 %. It was determined that the grafting success of G29 (100 %) and G31 (85 %) pumpkin genotypes, G40 (87 %) interspecific genotypes with Crimson tide F1 watermelon cultivar is the highest. The grafted watermelon genotypes gave the highest vegetative growth compared to ungrafted control seedlings. The results showed that G29, G40 and G31 rootstock candidates have powerful rootstock potential for watermelon and it is a good resource for rootstock breeding programs.

Keywords: Winter squash, pumpkin, rootstock, resistance, watermelon, grafting, salt

# PROSPECTS OF KAZAKHSTAN IN ONION BREEDING

Bakhytbek M. Amirov, Vera O. Alpysbaeva, Zhuldyz-Saule S. Amirova

Nauryz st., Stlm. Kainar, Karasai District, Almaty Region, 040917, Kazakhstan

bamirov@rambler.ru

In 2014 among the vegetable crops in Kazakhstan, onion (*Allium cepa* L.) ranked second after tomato - its area was 22,9 thousand ha, with a production volume 608400 tons. More than 90% of its production area is concentrated in the southern and south-eastern regions of the country. As of 2015 in the State Register of breeding achievements included 32 varieties and F1 hybrids of onion, including 11 varieties of the Kazakh Research Institute of Potato and Vegetable Growing (KRIPVG).

Onion breeding research in Kazakhstan has been conducted since late 1940s. Over the years of studies hundreds of onion accessions of different geographic origin with a varied genetic diversity have been collected, more than 5,000 breeding material has been evaluated and studied.

Since the mid-1990s, into the country began to rapidly import foreign hybrid seeds of vegetable crops, including onions. Therefore, since 2007 in order to substitute them by domestic hybrids breeding gene pool has been refilled with new sterile forms of onion, introduced from the University of Wisconsin, USA, which made it possible to create a real original breeding base for the development of local inbred lines for further onion heterosis breeding in Kazakhstan.

Given the onion production area in Kazakhstan is mainly sown by foreign hybrid seeds, in recent years at KRIPVG a high priority has been given to the development of highly productive and disease-resistant varieties, and already there have been achieved some promising outcomes in breeding of onion sterile inbred lines.

Keywords: Onion breeding, productivity, diseases resistance, storability

# SSR (SIMPLE SEQUENCE REPEAT)-BASED ASSESSMENT OF GENETIC CHARACTERIZATION IN GENETIC RESOURCES OF VINEYARD IN SANLIURFA AND ADIYAMAN PROVINCES

Kürşat Alp Aslan[1], Nergiz Çoban[1], Selçuk Özcan[1], Hakan Usanmaz[1], Ebru Sakar[2]

1. Antepfıstığı Araştırma İstasyonu Müdürlüğü, Gaziantep, Türkiye

2. Harran Üniversitesi, Ziraat Fakültesi, Bahçe Bitkileri Bölümü, Şanlıurfa, Türkiye

kursatalp0272@msn.com

Southeastern Anatolia Region has a rich genetic diversity of grapes along with the area and production potential. Confusion of variety is observed result from different naming and variation of inter varieties in this region. Some of the oldest grape varieties which aren't used in cultivation seems to be increasingly faced with the risk of loss. It is aimed reduction of adverse conditions and selecting superior genotypes with this selection study. A total of 26 genotypes obtained result of selection. Ten SSR markers (VVMD27, VVMD28, ZAG83, VVMD5, VVMD7, VVMD24, VVMD31, VMC2h4, VVS2, VVMD5) were tested to using 28 genotypes including 26 local and 2 reference varieties to identify the genetic alleles profile. Genetic similarities between them was determined. Allele size, allele number, possibility of expected and observed heterozygosity and identification for each SSR locus was determined by fragment analysis system. The obtained results were evaluated in the dendrogram levels.

Keywords: Vineyard, selection, Sanlıurfa, Adıyaman, SSR

# THE POTENTIAL FOR ROOTSTOCK BREEDING OF SOME INBRED LINES AND LOCAL POPULATIONS IN EGGPLANT

H. F. Boyaci[1], A. Unlu[1], S. Kıran[2], E. Gumrukcu[1], S. Kusvuran[3], S. S. Ellialtioglu[4]

1. Bati Akdeniz Agricultural Research Institute, Antalya, Turkey
2. Soil Fertilizer and Water Resources Central Research Institute, Ankara, Turkey
3. Cankiri Karatekin University, Kizilirmak Vocational High School, Cankiri, Turkey
4. Ankara University, Faculty of Agriculture, Dept. of Horticulture, Ankara, Turkey

filiz_boyaci@yahoo.com

Eggplant is one of the important species from cultivated vegetables, having serious problem causing biotic and abiotic stress factors. To overcome these problems, use of grafting eggplant seems to be as an alternative solutions. A significant number of rootstock has been developed from wild relatives of eggplant for gathering multiple resistance genes in a plant. However, these rootstock have brought many problems such as incompatibility between the scion and stock, lack of seed germination ability, existing fruit quality etc. New Rootstock developed by using cultivar forms of eggplant may be revealed more successful results. Some of the attributes of inbred lines and local genotypes in eggplant that can contribute to rootstock breeding program is presented in this paper.

Keywords: Scion, biotic stress, abiotic stress, resistance, tolerance

# IDENTIFICATION OF COLD RESISTANCE OF LOCAL DIFFERENT GRAPE VARIETIES IN THE GAP REGION

Kürşat Alp Aslan[1], Nergiz Çoban[1], Selçuk Özcan[1], Hakan Usanmaz[1],
Serkan Kösetürkmen[1], M. İlhan Bekişli[2]

1. Pistachio Research Station, Gaziantep, Turkey
2. Harran University, Faculty of Agriculture, Department of Horticulture, Sanlıurfa, Turkey

kursatalp0272@msn.com

Turkey where it located in the most favorable climates for viticulture in the world has a rich farming potential with a very old and deep-rooted culture of viticulture. Our country is one of the gene centers of grapevines over the world and ecological conditions of our country is quite suitable. Viticulture is an important agricultural activity carried out in the Southeastern Anatolia Region since the very old years. Southeastern Anatolia Region provides 23% of the total grape production in our country. Production area is 129.624 hectares and the amount of production is 643.284 tons. Plant breeding is aimed that increases economic value of the plants which produced benefiting from genetic variations which occurred in several ways. Clone selection is used successfully in vegetative reproduction plants and especially in mixed populations. It is possible to encounter many different grape varieties and types in this region. It was stored 112 species and types of vineyard which has danger of extinction by this study. It were made phenological observations, determination of quality and yield properties. Our region occurred frost in 2014. It was not affected “Siyah Bandırma”, “Horoz Yüreği”and “Kızlar Tahtası”from local grape varieties by frost damage. The terms of yield and quality did not cause any loss due to frost.

Keywords: Vineyard, selection, GAP, frost, cold resistance

# RESISTANCE SCREENING OF ONION LAND RACES FROM TURKEY AGAINST STEM AND BULB NEMATODE (*DITYLENCHUS DIPSACI* (KUHN 1857) (*TYLENCHIDA: ANGUINIDAE*)

Elif Yavuzaslanoglu[1*], A. Ramazan Alan[2]

1. University of Karamanoglu Mehmetbey, Technical Sciences Vocational School, Department of Plant and Animal Production, Karaman, Turkey

2. University of Pamukkale, Faculty of Science and Literature, Department of Biology, Denizli, Turkey

eyavuzaslanoglu@kmu.edu.tr

Stem and Bulb Nematode (*Ditylenchus dipsaci* (Kühn 1857) (*Tylenchida: Anguinidae*) is one of the constraints of onion production in Turkey. It causes severe damage on onions and distributes in temperate climate conditions in the world. It is reported from Central Anatolian Plateau, Aegean, Trace and Black Sea Regions in Turkey. Due to the wide range of host spectrum and dormant stage in soil of the nematode, population control under field conditions is difficult. Use of resistant cultivars against stem and bulb nematode is one of the best control options. There is not any available source of onions resistant against D. dipsaci. Onion land races from Turkey provided by PAUBIYOM (Pamukkale University Plant Genetics and Agricultural Biotechnology Investigation and Application Centre) were screened against D. dipsaci under controlled conditions. Two out of thirty accessions were found promising with lower nematode multiplication. Accession 11 provided 0,7±0,4 (0-4,2) and 0,28±0,12 (0-1,2) fold multiplication and accession 26 provided 0,24±0,16 (0-1,8) and 0,01±0,01 (0-0,1) fold multiplication in two times repeated experiments. Suggestion of lower nematode multiplication rate onion materials in problematic areas is economically and environmentally one of the advantageous plant protection approaches.

Keywords: Resistance, nematode, onion, landrace, stem and bulb nematode, Ditylenchus dipsaci

# REGISTERED CUT FLOWER SPECIES BY MUTATION BREEDING IN THE WORLD

Özgül Karagüzel[1], Ayşe Serpil Kaya[1], Soner Kazaz[2], Uğur Kahraman[1], Selma Kösa[1]

1. Batı Akdeniz Agricultural Research Institute

2. Ankara University

tezkara@yahoo.com

Mutation techniques on ornamental plants have been used successfully for creating new superior varieties for many years in the world. Chrysanthemum, carnation, rose, gerbera, lilium, alstroemeria, statice, gladiolus, gentiana, latyrus, delphinium, cymbidium and tulip are used for creating new mutant varieties with mutation breeding on cut flowers, which have the highest commercial value among the ornamental plants. Most of the mutants were created by x or gamma ray. The most preferred quality criteria by the consumers are flower colour, flower shape, flower size, leaf characteristics (form, size and colour), early flowering and vase life (for cut flowers), and these quality criteria are considered on mutation breeding. All the records of certificated or commercial new plant species and varieties, which are created by mutation breeding in the world, are kept in FAO / IAEA database. In this article, the data about the number of created mutant, mutagens, doses, materials which were used and developed plant characteristic on cut flower species which are registered in this database, were compiled.

Keywords: Mutation, breeding, cut flowers, database

# THE RATE OF COLOUR DISTRIBUTION OF CREATED GENOTYPES ON STUDIES OF VARIETY DEVELOPMENT OF CARNATION

Ayşe Serpil Kaya[1], Özgül Karagüzel[1], Soner Kazaz[2], Uğur Kahraman[1]

1. Batı Akdeniz Agricultural Research Institute
2. Ankara University

ayserka07@hotmail.com

In the studies of the Variety Development of Carnation in Batı Akdeniz Agricultural Research Institute between 2012-2015, 45 spray and 5 standard genotypes which were created by clonal selection, were determined as superior. In this study, the rates of petal colours were observed as 19% red, 10% dark pink, 15%light pink, 5% white, 10% purple, %10 orange, 6% maroon, 7% yellow and 18% bicolour. CIELAB colour values, hue angels (h= arctan (b/a) and colour saturation values (C= (a2 +b2) 0.5) of genotypes were measured with Minolta CR 400. In this article, CIELAB colour values of genotypes with light pink colour flowers were mentioned.

Keywords: Carnation, clonal selection, hybridization, variety development, petal colour

# BIOTECHNOLOGY ASPECTS OF FRAGARIA X ANANASSA DUCHESNE CULTIVARS MICROPROPAGATION

Olga Mitrofanova, Nina Lesnikova-Sedoshenko, Raisa Babina, Irina Mitrofanova

Nikita Botanical Gardens-National Scientific Center, Yalta, 298648,
Russian Federation

irimitrofanova@yandex.ru

Strawberry is a famous and the most widely spread berry crop all over the world. It combines early fruit appearance with high and annual crop yield production. Strawberry fruits have high taste and dietary qualities and can be consumed fresh as well as in processed foods. Efficiency of strawberry culture is mostly set with the used cultivar. The other important problem for commercial culture is quality of planting material as even the best cultivar could disclose its fruiting possibilities only in the absence of harmful pests and diseases. Nowadays propagation of high quality planting material is impossible without using of modern biotechnology techniques. For 5 cultivars we developed some methods for micropropagation of plants through the meristem culture and direct shoot regeneration from leaf. All the mother plant material had been tested for absence of virus infections by ELISA-tests and then established to in vitro culture. Culture media were supplemented with ribavirin for suppression of residual virus infection in cultured explants. Murashige and Skooge medium have been modified and optimal concentrations for plant growth regulates (cytokinin and auxin) have been found out. Mean microshoots number at the stage of regeneration process induction was 9.5 ± 0.2 per explants for the cultivar "Honeoye" and 6.3 ± 0.1 – for the cultivar "Elsanta" and other cultivars. It was demonstrated that active microshoot regeneration starts after 1.5 - 2 months of explants in vitro culture. Optimal conditions for strawberry plantlets rooting in vitro and adaptation in vivo were determined.

Keywords: Strawberry, cultivar, explant, microshoot, regeneration and rooting in vitro

# ACHIEVEMENTS AND PROSPECTS OF KAZAKHSTAN IN ONION BREEDING

Bakhytbek M. Amirov*, Vera O. Alpysbaeva, Zhuldyz-Saule S. Amirova,
Gulnar M. Ibragimova

Kazakh Research Institute of Potato and Vegetable Growing, Nauryzst.,Stlm. Kainar,
KarasaiDistrict, AlmatyRegion, 040917, Kazakhstan

bamirov@rambler.ru

In 2014 among the vegetable crops in Kazakhstan, onion (*Allium cepa* L.) ranked second after tomato - its area was 22,9 thousand ha, with a production volume 608400 tons. More than 90% of its production area is concentrated in the southern and south-eastern regions of the country. As of 2015 in the State Register of breeding achievements included 32 varieties and F1 hybrids of onion, including 11 varieties of the Kazakh Research Institute of Potato and Vegetable Growing (KRIPVG). Onion breeding research in Kazakhstan has been conducted since late 1940s. Over the years of studies hundreds of onion accessions of different geographic origin with a varied genetic diversity have been collected, more than 5,000 breeding material has been evaluated and studied. Since the mid-1990s, into the country began to rapidly import foreign hybrid seeds of vegetable crops, including onions. Therefore, since 2007 in order to substitute them by domestic hybrids breeding gene pool has been refilled with new sterile forms of onion, introduced from the University of Wisconsin, USA, which made it possible to create a real original breeding base for the development of local inbred lines for further onion heterosis breeding in Kazakhstan. Given the onion production area in Kazakhstan is mainly sown by foreign hybrid seeds, in recent years at KRIPVG a high priority has been given to the development of highly productive and disease-resistant varieties, and already there have been achieved some promising outcomes in breeding of onion sterile inbred lines.

Keywords: Breeding, Onion, Productivity, Disease resistance, Storability

# USAGE OF MOLECULAR MARKERS FOR ESTIMATION OF THE GENETIC DISTANCE BETWEEN THE MAIZE INBRED LINES

Kamila Nowosad, Henryk Bujak

Wroclaw University of Environmental and Life Sciences Department of Genetics, Plant Breeding and Seed Production Poland, 50-363 Wroclaw, Plac Grunwaldzki 24 A

kamila.nowosad@up.wroc.pl

Correct division of derived inbred lines into heterogeneous groups enhances the growth in effectiveness of the maize hybrid breeding and lowers the costs of this process. For grouping of genotypes, analyses of genetic origin (lineages) and ones of genetic similarity, determined by the methods of molecular genetics, are applied. On the grounds of an analysis of similarity, inbred lines of the maize are assigned to five basic genetic pools, which guarantees that a high effect of heterosis will be acquired. Estimation of the genetic distance based on DNA polymorphism analysis represents a more objective method than analysis of the phenotypic diversity. Ones of the most use- ful for characterization of the maize inbred lines are SSR (Simple Sequence Repeat) markers. These markers enable to assess the diversification of lines as they display a high level of polymorphism, and are both species-specific and highly reproducible. The aim of the research was to define the genetic similarity between new inbred lines of the maize. The study material comprised 95 maize lines derived at Polish breeding companies. DNA, isolated from the maize seedlings, was used in molecular analyses with the employment of amplified microsatellite sequences, i.e. SSR markers. The revealed DNA polymorphism allowed to calculate the coefficients of genetic similarity between the studied maize lines, and subsequently to delineate a dendrogram illus- trating the genetic distance between them. The SSR starters applied enabled effective differentiation of the research material, and the results acquired indicate high diversi- fication of the maize lines under investigations. The fact that no distinction was drawn between the genotypes coming from Smolice and those from Kobierzyce testifies to a similar genetic background of the Polish breeding material. The dendrogram divided the studied genotypes into two main branches, one of which included two lines, and the other was further divided into three subgroups. The most abundant cluster was composed of 69 genotypes coming from Smolice and Kobierzyce. The performed analysis of principal components allowed to distinguish three groups with genotypes coming exclusively from one or the other breeding firm.

Keywords: Genetic distance, inbred lines, maize

# SELECTION ON EARLY FLOWERING STAGE OF LATE POPULATIONS OF CORN

Benko N.I.

AGROPLAZMA Ltd. 32, Akademika Lukyanenko st., Krasnodar, 350012,
Russian Federation

agroplasma@rambler.ru

Eight late populations of corn (FAO 600) were exposed to a recurrent selection on decrease of vegetation period. Every year 600 plants of each population were grown. Thirty plants with the earliest flowering periods were implicated for crossing (selection index - 5%). Pollen was used only from those plants, which had flowering silks. After the fifth cycle of selection, breeders have conducted a study on the effectiveness of selection and its influence on different traits. On the average, each cycle of selection in all populations has allowed to decrease the following periods: from germinating to flowering - 2,4 days; from flowering to ripening - 0,9 days; harvesting moisture level decreased up to 1.0%; number of leaves - 0.8 less. The given selection have caused to lower plant's height and height of cob's place; reduction of start of flowering stage between tassels and silks. Significant change in lodging resistance of plants was not observed.

In all experiments with different moisture level conditions, it was observed significant interaction between genotype x selection cycle.

Most populations, after their selection on early flowering, have increased their adaptation to conditions with lack of moisture.

Studying of different selection cycles in test-crosses, in regions with lack of moisture, has showed, that the selection has forwarded the increase of combining ability of populations for 'grain yield' trait.

The fifth cycle of selection, as for vegetation period, was close to hybrids with FAO 300.

Keywords: Corn populations, recurrent selection, early maturing.

# DYNAMICS OF LEAF TRANSPIRATION IN TWO CONTRASTING MAIZE (*ZEA MAYS* L.) HYBRIDS UNDER WATER STRESS AND BIOCHAR AMENDMENT

Leila Romdhane[1], Teofilo Vamerali[2], Marianna Bandiera[2] , Giuseppe Barion[2],
Giuliano Mosca[2], Leila Radhouane[1]

1. University of Carthage -Faculty of Sciences of Bizerte (7021 Jarzouna-Bizerte)
   Laboratory of Science and Agronomic Technical -National Institute of
   Agronomic Research of Tunisia, Street Hédi Karray- Ariana 2049
2. Department of Agronomy, Food, Natural Resources, Animals and the
   Environment, University of Padova, Viale dell'Università 16, 35020
   Legnaro, Padova, Italy

laila.romdhane1@gmail.com

A pot experiment was conducted at the experimental Farm of Legnaro (Padova, NE Italy) to study the dynamics of leaf transpiration in two maize (*Zea mays* L.) hybrids, i.e., one drought sensitive (S: P1921) and one drought tolerant (T: D24), under biochar addition in conditions of progressive limited water availability. The investigation compared two treatments: soil amendment with wood-derived biochar (1% w/w) vs. untreated controls, with five replicates.

The effects of water stress were evaluated by calculating the "linear plateau regression" obtained by relating daily relative transpiration (RT) over the fraction of transpirable soil water (FTSW).

Results showed that in both hybrid biochar was able to maintain a high rate of transpiration down to low FTSW values. The linear plateau regression model of un-amended D24 starts to decline earlier (82 % FTSW value) than in P1921(45% FTSW value), confirming the water-saving strategy of D24. Instead, soil amended with biochar allowed plants of both hybrids to transpire at their maximum down to lower FTSW, i.e., 45% and 22% in D24 and P1921, respectively.

It is concluded that biochar can delay the inhibition of transpiration in condition of limited water availability and it is most commonly observed the capacity of biochar to improve the water holding capacity, a fact that is attributed to the high surface area of biochar which helps it to increase water retention.

Keywords: Maize, drought tolerance, transpiration, water retention, biochar
amendment.

# EVALUATION OF SWEETCORN UNDER SWEETCORN- CHILLI PEPPER INTERCROPPING IN WEST JAVA, INDONESIA

Dedi Ruswandi, Jajang Supriatna, Meddy Rachmady, Neni Rostini

University Padjadjaran Bandung, Indonesia

dediruswandi2000@yahoo.com

Sweetcorn- chilli pepper intercropping is commonly applied to increase yield and profit by farmers in West Java, Indonesia. An experiment was set up in Kutamandiri-Sumedang, West Java from January up to April 2015 to select new sweetcorn hybrid and their parental lines for intercropping with chilli pepper. The evaluation of genetic materials was laid on a split plot design with two replications. The main plot consisted of four cropping system, whereas, the subplots were thirty eight sweet corn genotypes. The result showed that parental line of MSR 17.2.3 is the best combiner for plant heigh, while SR 17 is the best combiner for maturity and ear weight per plant. In addition the best combinations for high yield in both sole cropping and intercropping are MSR 12.6.7 x SR 4 and MSR 25.5.1 x SR 17. However, MSR 17.6.7 x SR 4 and MSR 17.6.7 x SR 17 were the best hybrid for intercropping based on land equivalent rasio, competitive ratio, and stress tolerance index analysis.

Keywords: Chilli pepper, GGE biplot, intercropping, Indonesia, sweetcorn, West Java

# RESPONSE OF DR UNPAD MAIZE HYBRID TO WATER USE AND FERTILIZER CONSUMPTION IN WEST JAVA, INDONESIA

Edy Suryadi, Nurpilihan Bafdal, Dedi Ruswandi

Fakultas Teknologi Industri Pertanian

dediruswandi3000@gmail.com

DR Unpad maize hybrid is developed to improve the maize production in West Java, Indonesia. The aims of this research was to select DR UNPAD maize hybrids that efficient in using water to dry condition but also respond to fertilization. The research was conducted from Mei to November 2009 in Cigadung, West Java, Indonesia. Four maize hybrids was planted and split plot design. The evaluation of maize hybrids was laid on a split plot design with two replications. The main plot consisted of four maize hybrids, namely; DR A, DR B, DR F, and Bisi 2. The subplots were having four combinations of fertilizer and water treatment. The biometric characters included plant height, numbers of leaf, yield per plot and weight of 100 seeds. The result showed that Organic Fertilizer can increase soil moisture, water availability and growth of maize. Thus, water Application 4 days with 50 % dosage of N P K fertilizer and 50 kg/ha Organic Fertilizer EMAS can increase the plant height of DR A maize hybrid. Maximum efficiency of irrigation was showed by water application for every 3 day with 100 % dosage of N P K fertilizer on BISI 2 hybrid and water application 3 days with 50 % dosage of N P K fertilizer and 50 kg/ha Organic fertilizer EMAS on DR F maize hybrid.

Keywords: Fertilizer, maize, water treatment, West Java

# THE INFLUENCE OF SOME PESTICIDES ON WHEAT AND CORN SEED GERMINATION

Port Angela, Ciobanu Lucia, Clapco Steliana, Savca Elena

Center of Molecular Biology, University of the Academy of Sciences of Moldova 3/2, Academiei str., MD-2028, Chisinau, Republic of Moldova

stela.clapco@gmail.com

The persistent organic pollutants are one of the most stringent environmental problems in the Republic of Moldova, due to the uncontrolled application of pesticides and lack of a proper management of dangerous waste. The negative effects provoked by pesticides appear on the different phenological stages of plant development depending on sensitivity and adaptive capacity of organism. In order to assess the impact of chemical pollution with pesticides Toxafen and Heptaclor on plants, germination and some morpho-physiological and biochemical parameters of wheat Auriu-273 and corn Moldovenesc-257, treated by pesticides in concentrations of 0,5-15%, have been studied. The germinative energy, water content, fresh and dry biomass, sprouts height, root system volume, total protein content and catalases activity, have been determined according to the standard methods. The germination test highlighted a more pronounced toxic action of pesticides during first 48 hours, demonstrating direct negative dose-effect correlation of the average intensity (r = -0,68) at corn and strong (r = -0,84) at wheat. Tested chemicals lead to the 2-6 smaller volume of root system and diminution by 11-64% of fresh and dry biomass content. Activity of catalases and the total protein content were 1,5 3,0 times higher in variants treated by Heptaclor. In those treated with Toxafen the enzyme activity increased only in roots with 18-54%, but the total protein content decreased on 48,1%. Investigated pesticides show the toxic action on germination, confirmed by the quantitative and qualitative variations of analyzed indices, the inhibitory effect being more pronounced in corn comparative to wheat.

Keywords: Pesticides, corn, wheat, germination.

# PHYSICOCHEMICAL ANALYSIS AND COLOR CHARACTERISTICS OF SUPERIOR OPEN-POLLINATED MAIZE LINES EVALUATED IN TWO CONTRASTING ENVIRONMENTS

Vasileios Greveniotis[1], Elisavet Bouloumpasi[2], Vasilia A. Fasoula[3],
Paraskevi Mitlianga[2]

1. Hellenic Republic Ministry of Reconstruction of production, Environment and Energy Rural Development , Hellenic Agricultural Organization “Demeter”, Industrial and Forage Crops Institute, National Center for Quality Control Classification & Standardizatio
2. Division of Agricultural Products Quality Control, Technological Educational Institution of Western Macedonia, Florina, Greece
3. Institute of Plant Breeding, Genetics & Genomics and Center for Applied Genetic Technologies, University of Georgia, 111 Riverbend Road, Athens, GA 30602, USA

vgreveni@mail.com

Prognostic breeding is an alternative crop improvement methodology that enables selection of plants for high crop yield potential by evaluating its two components, i.e., the plant yield potential and the stability of performance. Plant yield and stability are assessed concurrently in the absence of competition by utilizing two prognostic equations. Our selection strategy started in the F2 generation of the commercial maize hybrid Costanza and continued for 3 cycles. Superior plants and lines were selected on the basis of the two selection equations, the plant prognostic equation and the line prognostic equation, where x is the yield per plant, is the mean plant yield of the surrounding plants within the moving ring, is the overall mean plant yield of the trial, and s are the mean plant yield and standard deviation, respectively, of each line. A total of 15 high-yielding open-pollinated lines were developed and were extensively evaluated along with the F2 and Costanza, in randomized complete block experiments in two contrasting environments of Greece that differed greatly in altitude and soil chemical analysis. The objective of this study was to investigate the presence of variation for seed protein, seed oil, moisture, pH, ash contents and color characteristics (L, a, b parameters) among these superior selected lines. The statistical analysis revealed significant differences among these lines for all traits except oil content. Furthermore, our results revealed the presence of a strong genotype by environment interaction, suggesting that all the traits were affected significantly by the environment.

Keywords: Maize lines, prognostic equations, crop improvement, quality and color characteristics, genotype by environment interaction

# RUST REACTIONS OF LINES IN A WHEAT ADVANCE YIELD TRIAL NURSERY DEVELOPED BY THE MAIZE RESEARCH INSTITUTE IN 2014

Zafer Mert[1], Kadir Akan[1], Vesile Urin[2], Özge Helvacioğlu[2], Lütfü Demir[2], İzzet Özseven[2], Şinasi Orhan[2], Yavuz Ağı[2]

1. The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11, Yenimahalle, Ankara, Turkey
2. Maize Research Institute, Hanlı Köy Mahallesi Arifiye Cad. No:20 Arifiye/Sakarya, Turkey

kadir_akan@hotmail.com

Rusts (caused by *Puccinia spp.*) and flooding are the principal yield-limiting factors for wheat production in the Central Anatolian region and South Marmara Part of Turkey. The aim of the study was to determine resistance sources in an advance yield trial of flooding tolerant lines. Seedling tests involving all three rusts were carried out at Central Research Institute for Field Crops, Yenimahalle/Ankara, in 2014. For seedling plant reactions were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. Seedling reactions were recorded 14 days post inoculation on either 0-4 (LR and SR) or 0-9 scales (YR). For adult plant reactions, the test materials were inoculated with local Pst populations. Stripe rust development on each entry was scored on the modified Cobb scale when the susceptible check Little Club reached 80-100S disease severity in June 2014. Coefficients of infection below 20 were considered to be resistant. Twenty five (56%), 11 (24%) and 24 (53%) genotypes were resistant to YR, LR and SR respectively. Thirty (67%) genotypes were resistant to stripe rust at the adult stage.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/12/A12/P01/01-004)

Keywords: Rusts (*Puccinia spp*), genetic resistance, reaction test

# USE OF SSR MARKERS FOR DIVERSITY ASSESSMENT AND POTENTIAL HETEROTIC GROUPING AMONG MAIZE INBRED LINES

Ana Nikolic, Jelena Bogosavljevic, Dragana Ignjatovic-Micic, Zoran Camdzija, Milomir Filipovic, Snezana Mladenovic Drinic, Milan Stevanovi

Maize Research Institute Zemun Polje, Belgrade, Serbia

msnezana@mrizp.rs

Knowledge about genetic diversity enables successful development of maize inbred lines and determination of their heterotic grouping. It is well known that creation of high yielding maize hybrids directly depends on the genetic distance between parents. Simple sequence repeats (SSRs), one of the most robust marker class were used for assessment of genetic diversity and heterotic grouping of 27 maize inbred lines of Maize Research Institute "Zemun Polje" collection. A total of 195 alleles were amplified with 30 markers. Average number of alleles detected was 6.5. Polymorphic information content (PIC) values ranged from 0.29 to 0.85 with an average of 0.68. Genetic similarity detected was in a range from 0.46 to 0.93. The UPGMA clustering grouped inbreds into two clusters (except one line which was not grouped into any of the clusters, suggesting its loose relationship with the other inbreds) which were consistent with the pedigrees or known information about source materials. PCA showed moderate agreement with cluster analysis. Results of this analysis showed that SSR markers could be successfully used in breeding programs to help in selection of the most suitable parental lines for creating new improved maize hybrids.

Keywords: Maize, heterotic group, SSR markers

# DETERMINATION OF SOME QUALITY TRAITS AND RELATIONS AMONG FEATURES IN POPCORN INBRED LINES

Ahmet Öztürk[1], Şekip Erdal[1], Mehmet Pamukçu[1], H. Filiz Boyacı[1], Bayram Sade[2]

1. Batı Akdeniz Tarımsal Araştırma Enstitüsü Müdürlüğü / Antalya
2. Karatay Üniversitesi Rektörlüğü / Konya

aozturk20@gmail.com

Popcorn is different from other maize types with its popping ability. This study was carry out in Batı Akdeniz Agricultural Research Institute's (BATEM) Field Crops Department in 2014. Quality traits of thirty five popcorn in bred lines were examined. The experiment was conducted as a randomized complete design with three replications. In the research, kernel moisture value %15.6 (line 16) - %17.6 (line 1), popping volume 8.3 cm3/g (line 22) - 29.3 cm3/g (line 5), rate of unpopped kernels %1.8 (line 25) - %35.4 (line 35), kernel size 58.3 number/10g (line 12) - 102.3 number/10g (line 9), flavor test 2.7 (line 31) - 7.2 (line 22), softness in mouth 1.5 (line 10) - 4.0 (line 2) were changed respectively. As a result of the research 2, 5, 6, 7, 10, 13, 17, 24, 25 and 26 lines came into prominence from the point of quality. When the relationships between quality traits were investigated, significant and positive correlation at % 1 level was determined between softness in mouth and flavor traits. Also, significant and negative correlation at % 1 level was determined between rate of unpopped kernels and popping volume. On the other hand, % 5 significant and positive correlation was recorded in between popping volume and kernel size as well as flavor and grain moisture. Rate of unpopped kernels and kernel size correlated negatively at % 5 significant level. Similar results were determined between popping volume and flavor. According to the results promising lines in terms of quality traits selected and will be used in the future breeding studies.

Keywords: Popcorn, quality, popping volume, flavor, softness in mouth

# DEVELOPMENT OF WAXY (*ZEA MAYS CERATINA*) CORN HYBRIDS

Rahime Cengiz, Bülent Cengiz, Mesut Esmeray, M. Cavit Sezer, Niyazi Akarken, A.Eşref Özbey, Ahmet Duman

Mısır Araştırma Enstitüsü

rcengiz24@gmail.com

Waxy corn was found in China in 1908. Waxy corn starch has a different structure than normal maize. Normal maize includes 75% amylopectin and 25% amylose despite waxy maize includes 100% amylopectin. Amylopectin is a form of starch and consists of glucose subunits. The separation of amylose is composed of glucose molecules to subunits. Waxy characterized is controlled by a double recessive gene (wx). There is no waxy maize varieties have been registered in our country. Maize Research Insti- tute obtained waxy germplasm and hybrid varieties from abroad for starting breeding program of waxy corn in 2011. DH waxy lines were developed using DH (Doubled haploid) technique. In vivo techniques is used to obtain the maternal haploid maize lines focus in a short period of time. Starch analysis and iodine tests were made in obtained DH waxy maize lines. Five hybrid waxy varieties were developed as a result of crossbreeding between waxy maize lines. Waxy hybrid varieties has been experi- menting in 3 locations in 2015. Waxy hybrid varieties will be determined as results of yield trials and corn starch analysis, and will be registered.

Keywords: Waxy corn, breeding, starch, hybrid variety

# EFFECTS OF GRADUALLY RISING TEMPERATURE IN MAIZE (*ZEA MAYS* L.) SEEDLINGS: PHOTOSYNTHESIS CHARACTERISTICS AND PROTECTIVE MECHANISM

Elif Yüzbaşıoğlu[1], Eda Dalyan[1], Ilgın Akpınar[2]

1. Department of Botany, Faculty of Science, Istanbul University, Süleymaniye, Istanbul, Turkey
2. Institute of Sciences, Istanbul University, Istanbul, Turkey

akpinarilgin@gmail.com

The aim of this study was to understand the effect of varying degrees of temperature (30/25, 35/30, 40/35, 45/40 °C at 16/8 photoperiods) with controls growing at 25/20 °C in maize belong to C4 plant groups. Plants exposed to increasing temperatures for 5 days were subsequently exposed to heat stress and compared to plants experiencing heat stress for the first time (controls). Treatments at temperatures above 35 °C triggered to high temperature (HT) stress in maize seedlings. The stress injury measured as malondialdehyde (MDA), chlorophyll (a and b), carotenoid and anthocyanin content, maximum photosystem II efficiency (Fv/Fm) and leaf water status (RWC). MDA level was significantly increased at high temperature (35, 40, 45 °C). RWC was minumum level at 45 °C. Chlorophyll content was the highest at 35 °C and it was decreased at 40 and 45°C compared with 35 °C and also Fv/Fm was relatively affected to 40 and 45 °C. Non-enzymatic (carotenoids and anthocyanins) antioxidants were dramatically increased under high temperatures stress. There was significant increase in the activity of catalase (CAT), ascorbate peroxidase (APX), glutathione reductase (GR), however peroxidase (POX) and superoxide dismutase (SOD) activity did not changed under gradually rising temperature conditions. The result of this study temperature above 35 °C shown as stress effects on photosynthesis and lipid peroxidation and induced to enzymatic and non-enzymatic antioxidant activity in maize seedlings.

Keywords: Maize, high temperature stress, photosynthesis, antioxidant enzymes

# THE APPLICATION OF ISOELECTRIC FOCUSING (IEF) TO ESTABLISH SUCCESSFULNESS OF CONVERSION OF MAIZE INBRED LINES TO THE CMS TYPE (CYTOPLASMIC MALE STERILITY)

Milan STEVANOVIC, Jelena VANCETOVIC, Zoran CAMDZIJA, Jovan PAVLOV, Snezana MLADENOVIC-DRINIC, Grcic Nikola, Ksenija MARKOVIC

Maize Research Institute, Zemun Polje, Slobodana Bajia 1, 11185 Belgrade, Serbia

mstevanovic@mrizp.rs

The principal aim of this study was to determine genetic differences between original and inbreeding lines and their CMS and Rf variants by the use of isoelectric focusing (IEF). Seven maize inbred lines developed at the Maize Research Institute, Zemun Polje, were used in this study. Each of these seven (7) inbreds were investigated in five variants: with normal cytoplasm (N), with C type sterile cytoplasm (CMS-C), the fertile counterpart C (RfC), with S type sterile cytoplasm (CMS-S) and the fertile counterpart S (RfS). The biochemical characterisation of original and conversed maize inbreds was done by the application of the method of Ultra-thin Layer Isoeletric Focusing (UTLIEF) of storage proteins in maize seeds. It was established that protein profiles of CMS-Rf variants of inbreds 1, 3, 4, 6 and 7 were identical with original inbreds. By comparison of electrophoregrams of the original inbred 2 and its CMS-Rf variants it was established that the RfC variant differed in presence-absence of protein marker bands from both, the original inbred and remaining CMS-Rf variants of the given inbred. The analysis of protein profiles of the inbred ZPL5 showed that the RfC variant of this inbred line differed from remaining CMS and Rf variants. In future work, the application of protein markers may be a fast and simple method to establish whether the conversion of inbreds to CMS type is done well and entirely.

Keywords: Maize, cytoplasmic male sterility (CMS), inbred lines, isoelectric focusing (IEF)

# MITIGATION OF WATER STRESS EFFECT BY SELENIUM

Nesrine AISSA[1*], Mario MALAGOLI[2] , Michela SCHIAVON[2] and
Leila RADHOUANE[1]

1. University of Carthage –Faculty of Sciences of Bizerte (7021 Jarzouna-Bizerte) Laboratory of Science and Agronomic Technical -National Institute of Agronomic Research of Tunisia, Street Hédi Karray- Ariana 2049 (Tunisia)
2. DAFNAE, University of Padova, Agripolis 35020 Legnaro, Padova, Italy

nesrine.aissa@hotmail.fr

In the current context of climate change, abiotic stress remains a major constraint to the growth and productivity of crops.

Drought stress impact can be partly mitigated through genetic and physiological improvement for stress tolerance. The use of an effective ameliorant or a stress alleviant like selenium may offer a variety of potential solutions. This element has generated interest of many biologists due to its antioxidative properties.

Various morphological and physiological traits related to stress tolerance like plant growth; plant height, root-shoot ratio, relative water content and chlorophyll index were studied during three months on Sorghum (Sudan Grass III cultivar) in the Mediterranean regions.

A pot experiment was conducted at the experimental station (greenhouse) at Agripolis (Padova, Italy). Experimental design consists of six combinations of treatments: a control (100% ETM), two water regimes (70% and 35% ETM) with and without Selenium at low concentration (2%).

Results showed that Selenium may enhance the drought tolerance by improving leaf and stem growth and by decreasing root elongation. Selenium also had significantly increased the relative water content and chlorophyll index of treated plants.

These results suggested that selenium with others physiological and biochemical parameters have a major role in alleviating of drought stress.

Keywords: Sorghum, exogenous protectants, drought tolerance.

# IN VITRO ANDROGENESIS OF SYNTHETIC WHEAT IN ANTHER CULTURE

Erzhebaeva R., Abugaliyeva A., Kovalenko A.

Kazakh research institute of agriculture and Plant growing, Almalybak v.,
Kazakhstan

raushan_2008@mail.ru

Doubled haploid technologies have become key tools for plant breeding. Using these techniques, the speed and efficiency of plant improvement processes can be significantly enhanced. Anther culture-based technologies have the potential to regenerate large numbers of doubled haploid. The objects of the study were 20 genotypes of spring and winter synthetic wheat. Embryogenesis was induced in modified 3 mediums. Number embryo-like structures varied in different growth media and genotypes from 3 to 166 EC / 150 anthers of a petri dish. Selected 4 responsive genotypes: Kazakhstanskaya 10, 6625 x T.timopheevii-10, 6625 x T.timopheevii-13 (350 Erythrospermum kihara) x Erythrospermum 350-92. Embryogenesis induction was not observed in three genotypes. 8 samples showed low responsiveness to anther culture technology. They are formed as an average of from 0 to 8 embryo-like structures/ petri dish. The highest of microspore embryogenesis was obtained in AP medium for prescription ASPFG. In this medium it formed 200-300 embryo-like structures/ petri dish. Albino and green plantlets were regeneration from embryo-like structures. More than 50% of regenerants were albino. In total, 98 green plantlets were produced, transplanted and established in soil.

Keywords: Androgenesis, anther, microspore, growing medium, embryo-like
tructures, regenerated plants.

# RUST REACTIONS OF SOME TURKISH, BREAD WHEAT GENOTYPES IN WINTER ADVANCE YIELD TRIAL SET-2

Kadir Akan, Bayram Özdemir, Zafer Mert, Selami Yazar, Ayten Salantur,
Mehmet Emin Alyamaç, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

bozdemir40@yahoo.com

Rusts (caused by *Puccinia spp.*) diseases are one of the important diseases on cereal crops in Turkey and worldwide. Bread wheat (*Triticum aestivum*) is one of the important diseases on cereal crops in Central Anatolian Plateau. The purpose of the study was to determine the reactions of seedling and adult plant stage of some genotypes from rusts and bunt under artificial epidemic condition in Ankara location in 2013-2014 growing season.

We tested 24 genotypes from the some Turkish, bread wheat genotypes in winter advance yield trial-2 set. These genotypes were developed by The Central Research Institute for Field Crops (CRICF) Wheat Breeding Unit.

Seedling plants were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. For adult plant reactions; each genotype was sown by hand in a 1 m row in October 2013. Adult plants were inoculated with local Pst and with local Bt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7) population before planting.

Seedling reactions were recorded 0-4 (SR and LR) or 0-9 scales (YR). Adult plant reactions were scored on the modified Cobb scale when the susceptible check Little Club reached 80-100S disease severity in June 2014. Coefficients of infection below 20 were considered to be resistant. Bunt development on each entry was scored on the infected spike percent scale in August 2014. Of infection below 25% were considered to be resistant. Ten (42%), 8 (33%) and 11 (46%) genotypes were resistant to SR, LR and YR at the seedling stage respectively. Twelve (50%) and 13 (54%) genotypes were resistant to YR and BT at the adult stage respectively. The resistant lines will be useful to obtain resistant varieties.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/13/A12/P01/002)

Keywords: Rusts (*Puccinia spp*), genetic resistance, reaction test

# RUSTS AND BUNT RESPONSES OF SOME TURKISH, IRRIGATE WINTERBREAD WHEAT GENOTYPES IN YIELD TRIALS

Zafer Mert, Bayram Özdemir, Kadir Akan, Selami Yazar, Ayten Salantur,
Mehmet Emin Alyamaç, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

bozdemir40@yahoo.com

Rust (*Puccinia spp.*) diseases are very important that is one of the most significant biotic factors affecting wheat yield and quality in Central Anatolian Plateau. The purpose of this study was to identify the reactions of 72 Turkish, irrigate winter, bread wheat genotypes developed by the Central Research Institute for Field Crops (CRIFC) Wheat Breeding Unit and entered in yield trials.

Seedlings were inoculated with local Pst population (virulent on differentials carrying Yr2, Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), local Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pst population.  Reactions were scored for each entry at 14 days post-inoculation on standard 0-4 (LR and SR) or 0-9 (YR) scales. Adult plants were inoculated with local Pst population (virulent on differentials carrying Yr2, Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Bunt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7). Stripe rust development on each entry was scored using the modified Cobb scale. Coefficients of infection were calculated and values below 20 were considered to be resistant. Bunt was scored on the infected spike percent scale. Of the infections below 25% were considered to be resistant.

At the seedling stage, 13 (18%), 5 (7%) and 21 (29%) genotypes were resistant to SR, LR and YR, respectively. Forty six (64%) and 65 (90%) genotypes were resistant to YR and bunt at the adult stages, respectively. In conclusion, the utilization of these resistances is highly recommended in the breeding programmes.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/13/A12/P01/002)

Keywords: Rusts (*Puccinia spp*), genetic resistance, reaction test

# RUSTS RESPONSES OF SOME GENOTYPES OBTAINED FROM WILD EMMER X DURUM WHEAT CROSSES

Kadir Akan, Ayten Salantur, Zafer Mert, Selami Yazar, Bayram Özdemir,
Mehmet Emin Alyamaç, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

asalantur@mynet.com

Turkey is one of the important centers of certain plant genetic resources. Stripe/leaf/stem (*Puccinia spp.*) rust diseases are important fungal stress factors limiting yield and quality in Central Anatolia/Turkey growing areas. Two mega durum (T. durum Desf. ) cultivars (cv. Kızıltan-91 and cv. Çesit 1252) were crossed with pure wild type (T. araraticum (TUR 3379)) from single spike. These lines were developed by The Central Research Institute for Field Crops (CRICF) Wheat Breeding Unit. A total of 37 wheat genotypes from these crosses were tested to yellow, leaf and stem rusts.

Adult plant and seedling tests were conducted for yellow rust whereas only seedling tests were conducted for leaf rust and stem rust. Evaluations were carried out at CRIFC, İkizce, in the 2014 season. For adult plant stripe rust assessments, the materials were inoculated with a local Pst population (virulent on differentials carrying Yr2, Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA). Stripe rust development on each entry was scored using the modified Cobb scale. Coefficients of infection were calculated and values below 20 were considered to be resistant. Seedlings were inoculated with local Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pst population. Reactions were scored for each entry at 14 days post-inoculation on standard 0-4 (LR and SR) or 0-9 (YR) scales.

At the seedling stage, 35 (95%), 0 (0%) and 1 (5%) genotypes were resistant to SR, LR and YR, respectively. Only one (5%) genotype was resistant to YR at the adult stage.

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Keywords: T. *araraticum*, T. *durum Desf.*, Rusts (*Puccinia spp*), genetic resistance, reaction test

# RUSTS AND BUNT RESPONSES OF SOME TURKISH, IRRIGATE WINTERBREAD WHEAT GENOTYPES IN ADVANCE YIELD TRIALS

Zafer Mert, Selami Yazar, Kadir Akan, Ayten Salantur, Bayram Özdemir,
Mehmet Emin Alyamaç, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

yazarselami@yahoo.com.tr

Biotic and abiotic factors limit the effect on the potential of the Turkish wheat cultivars in Central Anatolian Plateau. Especially, the drought and some fungal diseases turn out to be the major reasons for the yield shortage and quality. The purpose of this study was to identify the reactions of 24 Turkish, irrigation winter wheat genotypes developed by the Central Research Institute for Field Crops (CRIFC) and entered in advance yield trials.

Adult plant and seedling tests were conducted for stripe rust whereas only seedling tests were conducted for leaf rust and stem rust and bunt. Evaluations were carried out at CRIFC, İkizce and Yenimahalle, in the 2014 season. For adult plant stripe rust assessments the materials were inoculated with a local Pst population (virulent on differentials carrying Yr2, Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA). Stripe rust development on each entry was scored using the modified Cobb scale. Coefficients of infection were calculated and values below 20 were considered to be resistant. Bunt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7) development on each entry was scored on the spike percent scale. Of the infections below 25% were considered to be resistant. Seedlings were inoculated with local Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pst population. Reactions were scored for each entry at 14 days post-inoculation on standard 0-4 (LR and SR) or 0-9 (YR) scales.

At the seedling stage, 3 (13%), 6 (25%) and 4 (17%) genotypes were resistant to YR, LR and SR, respectively. Twelve (50%) and 19 (79%) genotypes were resistant to YR and BT at the adult stage. According to this result, we can use Entry no1, 4, 12 genotypes for registration or resistance crossing programme for yellow rust and bunt in Central Anatolian Plateau.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/13/A12/P01/002)

Keywords: Rusts (Puccinia spp), genetic resistance, reaction test

# RUST RESPONSES OF SOME TURKISH, BREAD WHEAT GENOTYPES IN WINTER ADVANCE YIELD TRIAL SET-1

Kadir Akan, Selami Yazar*, Zafer Mert, Ayten Salantur, Bayram Özdemir,
Mehmet Emin Alyamaç, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

yazarselami@yahoo.com.tr

Bread wheat (*Triticum aestivum*) is the third largest cereal cultivated in the world and the second in terms of dietary intakes. However, yield and quality can be severely affected by the rusts and bunt diseases caused by the fungus Puccinia spp. and Tilletia spp. The purpose of this study was to assess seedling and adult plant rusts and bunt reaction test the Central Research Institute for Field Crops in 2014. We tested 24 genotypes from some Turkish, bread wheat genotypes in winter advance yield trial-1 nursery. These genotypes were developed by The Central Research Institute for Field Crops (CRICF) Wheat Breeding Unit.

Seedling plants were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. Seedling reactions were recorded 0-4 (LR and SR) or 0-9 scales (YR). For adult plant reactions; each genotype was sown by hand in a 1 m row in October 2013. Adult plant were inoculated with local Pst and with local Bt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7) population before planting. Yellow rust development on each entry was scored on the modified Cobb scale when the susceptible check Little Club reached 80-100S disease severity in June 2014. Coefficients of infection below 20 were considered to be resistant. Bunt development on each entry was scored on the spike percent scale when the susceptible check Yakar 99, 90-100% disease severity in August 2014. Of infection below 25% were considered to be resistant.

Seven (29%), 5 (21%) and 0 (0%) genotypes were resistant to YR, LR and SR at the seedling stage respectively. Fifteen (63%) and 18 (75%) genotypes were resistant to YR and BT at the adult stage, respectively. The resistant lines will be useful to obtain resistant varieties.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/13/A12/P01/002)

Keywords: Rusts (*Puccinia spp*), genetic resistance, reaction test

# REACTION OF WHITE GRAINED WINTER YIELD TRIAL BREAD WHEAT GENOTYPES MATERIAL TO RUST IN 2014

Kadir Akan, Mehmet Emin Alyamaç, Zafer Mert, Selami Yazar, Ayten Salantur, Bayram Özdemir, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11, Yenimahalle, Ankara, Turkey

eminalyamac@hotmail.com

Rusts (caused by Puccinia spp.) are the most destructive foliar disease of wheat in Central Anatolian Plateau/Turkey. The White Grained Winter Advance Yield Trial Bread Wheat nursery consisting of 72 winter bread wheat genotypes were tested for identification of resistance to prevailing seedling and adult plant for reaction tests to rusts and bunt diseases in 2014. These genotypes were developed by The Central Research Institute for Field Crops (CRICF) Wheat Breeding Unit.

Seedling plants were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. Seedling reactions were recorded 14 days post inoculation on either 0-4 (LR and SR) or 0-9 scales (YR). Adult plants were inoculated with local Pst and with local Bt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7) population before planting. Yellow rust development on each entry was scored on the modified Cobb scale. Coefficients of infection below 20 were considered to be resistant. Bunt development on each entry was scored on the spike percent scale when the susceptible check Yakar 99, 90-100% disease severity in August 2014. Of the infections below 25% were considered to be resistant.

Thirty five (49%), 13 (18%) and 8 (11%) genotypes were resistant to YR, LR and SR at the seedling stage respectively. Thirty eight (53%) and 57 (79%) genotypes were resistant to YR and BT at the adult stage respectively. The resistant lines will be useful to obtain resistant varieties.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/13/A12/P01/002)

Keywords: Rusts (Puccinia spp), genetic resistance, reaction test

# REACTIONS OF RED GRAINED WINTER YIELD TRIAL BREAD WHEAT GENOTYPES MATERIAL TO RUST IN 2014

Zafer Mert, Mehmet Emin Alyamaç, Kadir Akan, Selami Yazar, Ayten Salantur, Bayram Özdemir, Emin Dönmez

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

eminalyamac@hotmail.com

Bread wheat is important cereal crops in Turkey. Rusts (caused by Puccinia spp.) has been the most devastating disease of wheat production in Central Anatolian Plateau/Turkey. The purpose of this study was to assess seedling and adult plant yellow/leaf/stem rust reaction test in Central Research Institute for Field Crops in 2014. We tested 72 genotypes from the Red Winter Advance Yield Trial Bread Wheat Nursery. These genotypes were developed by The Central Research Institute for Field Crops (CRICF) Wheat Breeding Unit.

Seedling plants were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. Seedling reactions were recorded 14 days post inoculation on either 0-4 (LR and SR) or 0-9 scales (YR). For adult plant reactions; each genotype was sown by hand in a 1 m row in October 2013. Adult plants were inoculated with local Pst and with local Bt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7) population before planting. Yellow rust development on each entry was scored on the modified Cobb scale when the susceptible check Little Club reached 80-100S disease severity in June 2014. Coefficients of infection below 20 were considered to be resistant. Bunt development on each entry was scored on the infected spike percent scale when the susceptible check Yakar 99, 90-100% disease severity in August 2014. Of the infections below 25% were considered to be resistant.

Thirty two (46%), 8 (11%) and 18 (25%) genotypes were resistant to YR, LR and SR at the seedling stage respectively. Thirty five (49%) and 55 (76%) genotypes were resistant to YR and BT at the adult stage, respectively. The resistant lines will be useful to obtain resistant varieties.

This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/13/A12/P01/002)

Keywords: Rusts (Puccinia spp), genetic resistance, reaction test

# DROUGHT EFFECTS ON YIELD AND YIELD COMPONENTS IN DIFFER- ENT GROWING PERIODS OF THE SOME BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

İrfan Öztürk[1], Korkut K. Z[2]

1. Trakya Agricultural Research Institute, PO Box:16, Edirne, Turkey

2. Namık Kemal Uni. Fac. of Agr. Dep. of Field Crops. Tekirdağ, Turkey

irfanozturk62@hotmail.com

Drought stress is a severe abiotic stress and major constraint to wheat yield production. This research carried out in the experimental field of TARI during two years and 15 genotypes were planted as in completely randomized blocks design in split plot with tree replications. Kate A-1, Gelibolu, Pehlivan, Tekirdağ, Selimiye, Aldane, Bereket, Flamura-85 and Golia cultivars with some lines have been used. Drought treatments are placed on main parcel and genotypes on the sup-plot. Drought treatments were applied at several plant stages from stem elongation up to physiological maturating stage. In this research; grain yield, biological yield, harvest index, number of spike per square meter, spikelet number per spike, number of grain per spike and lengh of spike and pairwise comparison were investigated between these traits. Grain yield have been decreased in all cultivars on the drought condition. The highest grain yield with 658.3 kg/da was obtained from Bereket cultivar. As treatment the highest grain yield was determined with 763.8 kg/da on non-stress condition, Grain yield decreased in 40.1% in fully drought condition, 28.0% under stem elongation stage and 26.2% in grain filling period of drought. Drought stress more affected to grain yield at stem elongation stage according to grain filling period. From stem elongation stage to physiological maturating stage it was found positive and significant correlation between grain yield with biological yield, number of pike per square meter, number of grain per spike depending on drought stress increasing

Keywords: Drought, bread wheat, variety, yield, yield component

# RESISTANCE SCREENING OF WHEAT LAND RACES FROM IRAN AGAINST HETERODERA FILIPJEVI (MADZHIDOV, 1981) STELTER (TYLENCHIDA: HETERODERIDAE)

Elif Yavuzaslanoğlu[1*], I. Halil Elekçioğlu[2], M. Julie Nicol[3]

1. University of Karamanoglu Mehmetbey, Technical Sciences Vocational School, Department of Plant and Animal Production, Karaman, Turkey
2. Cukurova University, Faculty of Agriculture, Department of Plant Protection, Adana, Turkey
3. International Maize and Wheat Improvement Centre (CIMMYT), Ankara, Turkey

eyavuzaslanoglu@kmu.edu.tr

Cereal cyst nematode Heterodera filipjevi is widely distributed in wheat production areas in Central Anatolian Plateau and causes economical loss in high population levels under drought stress conditions. There are intensive studies on wheat breeding for quality characteristics, yield potential and resistance for pests, diseases and physiological disorders. Identification of resistance sources for different characteristics is the first step of breeding studies. Incorporation of nematode resistant wheat sources into breeding germplasm would increase wheat yield in nematode problematic areas. Therefore 31 wheat landrace accessions from Iran provided by CIMMIT (International Wheat and Maize Improvement Centre) were screened for resistance against Heterodera filipjvi Haymana, Ankara population under greenhouse conditions. Two resistant and two susceptible check varieties were included in the study. Wheat accessions were divided into 5 groups (resistant to highly susceptible) according to produced cyst numbers on plants.  CIMMYT named IWA 8604765 was most promising accession with mean 1,28±0,64 (0-5) cysts per plant. Two accessions were moderately resistant and 6 accessions were moderately susceptible.  Other accessions showed susceptible and highly susceptible reaction. Land races are very useful breeding sources, reduces the time and efforts for breeding studies.

Keywords: Resistance, nematode, wheat, landrace, cereal cyst nematode, Heterodera filipjevi

# EVALUATION OF SOME QUALITY PARAMETERS ON SOME LANDRACE DURUM WHEAT SAMPLES

Seda Külen, Turgay Şanal, Kürşat Özbek, Kazım Karaca

Tarla Bitkileri Merkez Araştırma Enstitüsü Şehit Cem ERSEVER Cad. No:9
Yenimahalle/ANKARA

tsanal@hotmail.com

Wheat and wheat based industry plays an important role in Turkish economy because of yield, consumption, export, and additivity to general economy. Our country is rich in landrace wheat populations. However, until recently these genetic resources are not used enough wheat breeding program in our country. Therefore, in order to be used effectively the national wheat gene sources, it is necessary to characterize their qual- ity characteristics. The objectives of this study were to determine some quality pa- rameters (SDS Sedimentation, protein (Dumas method), kernel hardness, gluto-graph, Ash content, yellowness (b*) (semolina colour) and thousand kernel weight) and to correlate every parameter with each other of the samples. The results were evaluat- ed as statistically significant. Based on the results a significant and positive correla- tion coefficient (-0.592**) was observed between ash content and protein. Wet gluten content showed positive significant correlations with protein (0.764**), ash content (0.405**), SDS Sedimentation (0.273**) and negative correlations with yellowness (-0.260*) and thousand kernel weight (-0.229*). Gluten index (%) showed positive significant correlation with SDS Sedimentation (0.677**).

Keywords: Landrace, durum wheat, SDS, yellowness, wet gluten, qluten Index, corelation

# EFFECT OF SPROUTING DAMAGE ON SOME QUALITY TRAITS OF BREAD WHEAT VARIETIES

Hasan Ay, Ahmet Akyol

Eastern Mediterranean Agricultural Research Institute, Adana, Turkey

hasanay2000@hotmail.com

This study was conducted during 2010-2011 growing sezons at ADANA. During the study 13 bread wheat varieties were used. The main objectives of the study are to determine pre-harvest sprouting damage on 1000 kernel and hectoliter weight at field conditions. Studies were conducted under field conditions. The test materials were tested in two topics. The first of them; each bread wheat variety artificially soaked with mini sprinkler system during 6 hours period of a day in a week at the harvesting time, than they have left for dried and harvested and non-irrigated wheat varieties and the second didn't irrigate and wheat varieties only harvest. Data of hectoliter and 1000 kernel weight of were used for determination of resistant varieties.

Results revealed that, with sprouting damage all bread wheat varieties had reduced 1000 kernel and hectoliter weights excep 1 variety with sprouting damage. All varieties susceptible to pro-harvesting germination spike. The conducted study suggested that generally harvesting time is rainy, earlier wheat varieties should be preferred so that varieties may escaped rainy season. Another suggestion, would prefer resistant wheat varieties.

Keywords: Pre-harvest sprouting damage, bread wheat, 1000 kernel and hectoliter weigh

# THE DETERMINATION OF MOLECULAR MARKERS OF RESISTANT GENES AGAINST NEW BROOMRAPE RACES IN SUNFLOWER

Yalcin Kaya[1], Necmi Beşer[1], Semra Hasançebi[1], Goksel Evci[2], Veli Pekcan[2], İbrahim M. Yilmaz[2], T. Hilal Ciftcigil[2]

1. Trakya University, Engineering Faculty, Genetic Engineering Department, Edirne, Turkey
2. Trakya Agricultural Research Institute, Edirne, Turkey

Turkish oil seed production is not enough for domestic consumption. This relevant gap is supplied by oil seed or crude oil imports with paying higher cost (3 billion $ at 2013). Therefore, the study on increasing of Turkish oil seed production and diminishing the current gap is vital in both strategical and economical aspects. Then ewraces of broomrape- which is one the most important factors reduced yield and quality in sunflower are observed in all of Trakya-Marmara region which has 70% of Turkish sunflower production and also in Çukurova and Black Sea Region as being increasing planted areas of sunflower recently in Turkey. Therefore, it is certainly necessary that new developing sunflowers are resistant to broomrape. The classical breeding research part of project were conducted in National Sunflower Hybrid Breeding Project having conducted by Trakya Agricultural Research Institute (TTAE) and broomrape resistance for MAS research was performed in Trakya University with collaborating university and public breeders. In the broomra- pe resistant in bredlines having higher seed and oil yield developed in TTAE, to determine effectively the homozygous plants using original markers for the segenes, two RAPD markers were discovered in the study. These marker fragments were sequenced and cloned and possible SCAR primers were designed. After obtaining of primers of these markers and then using of MAS effciciently in the National project, the project will gain the opportunity to be accelerated and efficient selection with using broomrape possible markers.

Keywords: Sunflower, broomrapeparasıte, molecularmarkers, rapd.

# BIOTECHNOLOGICAL IMPLICATIONS OF AN EXPERIMENTAL SYSTEM ALLOWING FOR GAMETE MANIPULATION IN WHEAT (*TRITICUM AESTIVUM* L.)

Zsolt Ponya, A. Anikó Dobosy

Kaposvár University, Hungary

ponyazs@yahoo.com

Although double fertilisation, a unique reproduction strategy characteristic of angiosperms, which involves two separate fusion events taking place deeply in maternal tissues and giving rise through extensive and well-concerted changes to the embryo and its nutritive tissue, the endosperm, was discovered well over a century ago (Nawaschin, 1898 and Guignard 1899), it is still an enigmatic process we know very little of. Thus, issues of overriding importance in developmental biology of angiosperms such as gamete recognition, egg cell maturation and activation by the sperm, molecular and cellular events leading to the asymmetrical cell cleavage of the angiosperm zygote and the control of the first steps of zygotic embryogenesis remain largely obscure.

Nevertheless, obtaining a profound insight into these mechanisms would provide not only information on these developmentally important processes, but would also facilitate the exploitation of the sexual route for gene delivery studies for plant breeding purposes.

In line with these considerations, an experimental system will be presented which involves in vitro gamete fusion of opposite sexes and microinjection of isolated egg cells elaborated for cereals hence allowing for addressing some of these issues as well as for gene/protein/fluorophore delivery into isolated female gametoplasts.

# DETERMINATION OF THE HIGH OLEIC TYPE SAFFLOWER LINES BY MOLECULAR MARKERS

Merve Güzel[1], Semra Hasançebi[2], Yalçın Kaya[2]

1. Trakya Agricultural Research Institute, PO Box: 16, 22100 Edirne, Turkey
2. Trakya University Engineering Faculty, Genetic and Bioengineering Dept, Edirne, Turkey

merveguzel@live.com

The safflower (*Carthamus tinctorius* L.) which belongs to Compositae family is an annual oil plant. The stems, leaves, flowers and seeds of the safflower have been used in different areas. Types of linoleic oils (Omega-6), such as cotton, sunflower, corn, peanut, soybean oil etc., are used in Turkey and around the world. This type of oils has low smoke point. The chemical structure of the oil produces carcinogenic compounds as a result of repeated frying operations. This is dangerous for human health. Because of this reason economic and healthy oil should be obtained. Types of oleic oils (Omega-9) have a higher smoke points than linoleic (Omega-6) ones. Oleic type oil is the best frying oils for that reason. High oleic safflower oil can be developed classical plant breeding studies, but this process involves a long period of time. Biotechnological methods especially marker assisted selection (MAS) could be used fast and efficiently in the development of new varieties. High oleic acid character is controlled recessive single gene (Ol) in safflower. Lower and higher oleic safflower lines were crossed in the study. DNA isolation was made from plant leaf tissues of F2 generation. Scanning was performed with marker assisted selection (MAS) after DNA isolation. SCAR markers IASCA 73, IASCA 74, IASCA 37 and IASCA 39 were used mapped in conjunction with a gene Ol. As a result; the determining of high oleic fatty acid content genes in cultivars was determined without generating plant seeds utilizing MAS in the study.

Keywords: Safflower, Marker assisted selection (MAS), High oleic acid, breeding

# MOLECULAR CHARACTERIZATION OF OAT LINES OBTAINED FROM DIFFERENT GENE BANKS USING SSR MARKERS

Ali Tekin, Erdem Aslan, Sevgi Herek, Tevrican Dokuyucu, Aydin Akkaya,
Hasan Gezginç, Yüksel Bölek, Halil Tekerek, Ziya Dumlupınar

Kahramanmaras Sutcu Imam University, Faculty of Agriculture, Department of Agricultural Biotechnology, Kahramanmaras, Turkey

ziyadumlupinar@yahoo.com

The molecular tools compared to wheat, maize and barley are less than oat however, in recent years a huge number of SSR and SNP markers were developed.

In this study, kinship of 384 Turkish origin oat genotypes obtained from different gene banks were investigated using SSR (simple sequence repeats) markers.

Three hundred and eighty four oat genotypes obtained from different gene banks were used as material. Oat genotypes were planted to the pots for DNA isolation from their leaves. After the PCR and electrophoresis the bands were scored and a dendogram was created.

Based on the molecular marker analysis, 384 oat genotypes genotyped by 40 SSR markers and those markers interrogated 130 loci. According to the dendogram generated by genotypic data, oat landraces showed a wide distribution and it is determined that oat landraces are basically 51% similar. Among the SSR markers used in the study, AB_AM_467, AB_AM_829 and AB_AM_874 were interrogated 5 loci thus, those markers were the most allelic ones. One of the most important results of the molecular analysis besides the kinship, the TL462 and TL464 were found identical as a result of 40 SSR markers with 130 loci.

In the research, the kinship of 384 Turkish origin oat lines was determined and crossing especially most diverse ones in the oat breeding programs might expand the genetic variations.

Keywords: Oat, Avena sativa, Avena byzantina, molecular characterization, SSR

# EVALUATION OF OAT LANDRACES OBTAINED FROM DIFFERENT GENE BANKS FOR AGRONOMIC TRAITS

Hasan Gezginç[1], Ali Tekin[2], Erdem Aslan[2], Abdulkadir Tanrıkulu[3], Sevtap Kartal[3], Tevrican Dokuyucu[3], Cengiz Yürürdurmaz[3], Aydın Akkaya[3], Ziya Dumlupınar[2], Sevgi Herek[3]

1. Doğu Akdeniz Geçit Kuşağı Tarımsal Araştırma Enstitüsü, Adana Yolu Üzeri 5. km Kahramanmaraş
2. Kahramanmaras Sutcu Imam University, Faculty of Agriculture, Department of Agricultural Biotechnology, Kahramanmaras, Turkey
3. Kahramanmaras Sutcu Imam University, Faculty of Agriculture, Department of Field Crops, Kahramanmaras, Turkey

ziyadumlupinar@yahoo.com

In this study 384 oat genotypes obtained from different gene banks, native to Turkey were investigated for agronomical traits with four commercial cultivars (Checota, Sebat, Faikbey and Seydisehir) for two years.

Oat landraces were evaluated for stem diameter (SD), plant height (PH), panicle length (PL), vegetative period (VP), grain filling period (GFP), days to maturity (DM), grain number per panicle (GNP), grain weight per panicle (GWP), thousand kernel weight (TKW) and single row yield (SRY) under Kahramanmaras conditions.

According to two years field trails, genotypes were found significant for SD, PH, PL, VP, DM, TKW and SRY while, years were found significant for SD, PL, VP, GFP, DM, GNP, GWP, TKW and SRY and year x genotype interactions were significant for PL, VP, DM, TKW and SRY.

The landraces performed better than the commercial ones for the most of the traits investigated. The SRW ranged between 4.65 g (TL444) to 202.1 g (TL614). And the genotypes with the higher SRY were TL708, TL714, TL734 and TL703 (167.85, 160.25, 153.90 and 149.7 g, respectively).

Keywords: Oat, Avena sativa, Avena byzantina, landraces, genetic resources

# YIELD AND STABILITY OF SOME MALTING BARLEY (*HORDEUM VULGARE* L.) GENOTYPES UNDER RAINFED CONDITIONS OF TURKISH HIGHLANDS

İsmail Sayım[1], Namuk Ergun[1], Sinan Aydogan[1], Taner Akar[2]

1. Central Research Institute for Field Crops, Ankara, TURKIYE
2. Akdeniz University, Faculty of Agriculture, Department of Field Crops, Antalya, TURKEY

ismail.sayim@gthb.gov.tr

In this research, grain yield of twenty advance malting barley lines were compared to two malting (Aydanhanım and Zeynelağa) and two feed (Tarm-92 and Larende) barley cultivars and also their response to adverse ecological conditions were investigated during 2013-2014 and 2014-2015 seasons trough five locations of Central Anatolia (İkizce, Altınova, Gözlü, Malya and Ulaş). Grand mean of the first year experiments over locations (İkizce, Gözlü, Malya and Ulaş) was 3261,0 kg/ha and advance line 10 with 3793,0 kg/ha grain yield outyielded all genotypes followed by advance line 17 with 3711,0 kg/ha and cv. Larende with 3707,0 kg/ha, respectively. In the second year of experiments over locations (İkizce, Altınova, Gözlü, Malya and Ulaş), grand mean was 4241,0 kg/ha and cv. Larende with 5448,0 kg/ha grain yield out-yielded all genotypes followed by advance line 10 with 5293,0 kg/ha by and advance line 8 with 4881.0 kg/ha and, respectively. Stability analysis showed that cvs. Aydanhanım and Tarm-92 and advance lines 1, 2 and 9 were the most stable genotypes. Additionally, advance lines 16, 11 and 17 were more stable especially for unfavourable conditions however, advance lines 10, 8, 7 and 3 together with cvs. Larende and Zeynelağa were in good adaptability to favourable conditions. As a result of this study, advance line 10 with two year high yielding performance were more promising genotype for moderate and high yielding environments.

Keywords: Malting barley lines, grain yield, environments, stability and adaptability

# YIELD AND STABILITY OF SOME BARLEY (*HORDEUM VULGARE* L.) GENOTYPES BASED ON DIFFERENT STABILITY PARAMETERS

İsmail Sayım[1], Namuk Ergun[1], Sinan Aydogan[1], Taner Akar[2]

1. Central Research Institute for Field Crops, Ankara, TURKIYE
2. Akdeniz University, Faculty of Agriculture, Department of Field Crops, Antalya, TURKEY

sinan.aydogan@gthb.gov.tr

In this research, response of grain yield of twenty advance feed barley lines four feed and malting (Tarm-92, Aydanhanım, Burakbey and Larende ) barley cultivars to diverse environments were compared by using parametric and non-parametric stability parameters during 2013-2014 and 2014-2015 seasons trough eighteen locations of Central Anatolia. There was a clear difference between stability parameters over two successive years and eighteen locations. Combination of grand mean and coefficient of variation (CV %) of the grain yield based on Eberhart and Russel parametric stability showed that cvs. Aydanhanım and Burakbey and Lines 3, 8, 10 and 15 were good yield performance and stable genotypes. Moreover, combination of another parametric stability parameters such as regression coefficient (bi) and variability (S2di) demonstrated that while cvs Aydanhanım and Tarm-92 and lines 6, 7, 8 and 21 were stable genotypes, cvs. Larende and Burakbey and Lines 2, 14 and 22 can be adaptable to high yielding environments. One of the another stability parameters, AMMI (Additive Main effects and Multiplicative Interaction) bi-plot graphs, showed that cv. Larende and lines 14 and 22 were unstable but they out-yielded the other genotypes during 2014-2015 season trough Malya, Altınova, and Ikizce locations. Additionally, cv. Burakbey and lines 2, 21 and 23 were also unstable but they out-yielded the other genotypes 2014-2015 season trough Gözlü and Konya locations. However, lines 13 and 15 were determined as stable ones based on AMMI bi-plot graphs. On the contrary to parametric stability parameters, cv. Larende and lines 11, 15 and 19 were stable ones based on non-parametric stability parameters such as Si(1) and Si(2). There was no any compromise between different stability parameters but cvs. Aydanhanım and Larende and Lines 3, 8, 10 and 15 were more stable ones based on different stability parameters in general.

Keywords: Barley, grain yield, AMMI bi-plot, parametric stability, non-parametric stability

# YIELD AND STABILITY OF SOME FEED BARLEY (*HORDEUMVULGARE* L.) GENOTYPES UNDER CENTRAL ANATOLIAN CONDITIONS

Namuk Ergun, İsmail Sayim, Sinan Aydogan, Taner Akar

Central Research Institute for Field Crops, Ankara, TURKEY

namuk.ergun@gthb.gov.tr

In this research, grain yield of twenty advance feed barley lines were compared to four feed and malting (Tarm-92, Aydanhanım, Çetin-2000 and Larende ) barley cultivars and also their response to adverse ecological conditions were investigated during 2014-2015 season trough five locations of Central Anatolia (İkizce, Altınova, Gözlü, Malya and Ulaş). Grand mean of the experiments over five locations (İkizce, Altınova, Gözlü, Malya and Ulaş) was 4338,0 kg/ha and advance line 103 with 5795,0 kg/ha grain yield outyielded all genotypes followed by cv. Larende with 5604,0 kg/ha and advance line 111 with 5222,0 kg/ha, respectively. The high yielding environment was İkizce location with 5229,0 kg/ha while Altınova location was the unfavourable condition with 3376,0 kg/ha. Stability analysis demonstrated that cv. Çetin-2000 and advance feed lines 103, 104 and 107 the most stable and high yielding genotypes. Additionally, advance feed lines 111, 117, 101 and 102 were more stable especially for unfavourable conditions however, advance feed lines 105 ve 109 were in good adaptability to favourable conditions. Tarm-92, the most commonly cultivated cultivar in Central Anatolia, was still the most stable genotype with close yield potential to grand mean. As a result of this study, advance line 103 with high and stable grain yield was the most promising genotype for Central Anatolia.

Keywords: Feed barley lines, grain yield, environments, stability and adaptability, Central Anatolia

# DETERMINATION OF QUALITY TRAITS OF SOME MALTING BARLEY VARIETIES AND LINES

Safure Güler, Dönüş Ermişer, Turgay Şanal, İsmail Sayım, Sinan Aydoğan, Namuk Ergün

Central Research Institute for Field Crops, Ankara, Turkey

safureguler@hotmail.com

This research was conducted to determine some quality traits of 4 malting barley varieties (Aydanhanım, Zeynelağa, Tarm-92, Larende) and 20 lines in 2013-2014 growing season in 4 locations (Ulaş, Malya, Gözlü, Altınova). In the study lines and varieties were evaluated in terms of physical characteristics, protein content and malting quality traits. According to results of study the lines 20, 21 and 2 had the highest malting quality values. The highest fine extract yield (78,6%) and friability value (62,4%) were determined with the line of 20. Although line 19 is coarse-grained, the lowest fine extract yield (73,5%) and friability value (26,7%) were determined. The highest fine extract yield was determined in Ulaş location. In this study, new malting barley genotypes were determined with advanced malt analysis. Thus, it will be possible to bring into use desired quality of malting barley genotypes that will meet the requests of malt and beer industry of Turkey and will be suitable for different ecological conditions of Middle Anatolia Region. Also, the most appropriate location for cultivation of malting barley was revealed.

Keywords: Barley Varieties, Malting Quality Traits, Fine Extract

# SOME IMPORTANT FOOD QUALITY CRITERIA OF HEXAPLOID OAT LINES OF A. SATIVA DEVELOPED IN MOROCCO

Rajae Manzali[1], Benchekroun, M[1], Douaik, A[2], Bouksaım, M[2], Saidi, N[2]

1. University Hassan 1st, Faculty of Sciences and Techniques, Department of Applied Biology and food processing, P.O. Box: 577, Settat, Morocco
2. INRA, RCAR-Rabat, P.O.Box 6570, Rabat Institutes, 10101, Rabat Morocco

raja.manz@live.fr

Epidemiological studies revealed that whole-grain intake can prevent against some diseases such as cancer, cardiovascular problems, diabetes and even obesity. Inter alia oat (*Avena sativa* L.) has long been recognized as a healthful and nutritious food, since it is a concentrated sources of dietary fiber, resistant starch oligosaccharides, and other nutrients and phytochemicals, especially antioxidants, including minerals and phenolic compounds, that have both dietary and therapeutic implications. In the present research, the used plant material was made of sixteen Moroccan hexaploid oat lines, issued from interspecific crosses using Moroccan hexaploid oat cultivars of A. sativa and two wild accessions of tetraploid oat species A. magna and A. murphyi, which were assessed for crude fiber content, β-glucan, proteins, fat, starch, minerals, total phenols and antioxidant compounds. Chemical analysis revealed high significant differences in content of proteins (9,67-17,44%), fat (3,06-10,96%) and crude fibre (9,15-23,99%). The highest β-glucan and protein contents mean value 6,05% and 17,29% respectively, were exceptionally noticed for some of the sixteen lines which could be conceived for human consumption. Moreover, the results have showed that all cultivars studied can be considered as a rich source of nutrients, polyphenols and antioxidants. As a consequence, according to the content and the quality of nutrients, the new developed oat lines could be in squad of the food products which can be included in diet formulation in Morocco.

Keywords: Oat, antioxidants, fiber, human consumption, health.

# EVALUATION OF SOME TECHNOLOGICAL QUALITY PARAMETERS OF ADVANCED BARLEY LINES AND CULTIVARS

Dönüş Ermişer, Safure Güler, Turgay Şanal, Sinan Aydoğan, Namuk Ergün,
İsmail Sayim

Tarla Bitkileri Merkez Araştırma Enstitüsü Ankara, Türkiye

safureguler@hotmail.com

This research was conducted to determine technological quality parameters of barley (*Hordein Vulgare*) varieties (Aydanhanım, Tarm-92, Çetin-2000, Larende) and 20 lines in regional yield trial supplied from 5 locations (Ulaş, Malya, Gözlü, Altınova and Haymana) on Field Crops Central Research Institute (FCCRI) in ecological conditions of 2013-14 year. In the study lines and varieties were evaluated in terms of physical characteristics, protein content and malting quality traits. According to results of study the lines 2, 14, 21, 5, 10 and 7 with Aydanhanım cultivar had high quality values. In Ulaş location have been determined highest malting (yield of extract fine and friability value) and physical quality parameters (large kernels (over 2.8+2.5 mm), thosand kernel weight and test weight). In this study, new malting barley genotips were determined with advanced malt analysis. According to GGE biplot analysis there were close relationship between malting quality parameters and protein content.

Keywords: Barley, ecologie, malt quality characteristic

# TO DETERMINE RESISTANT TO SPROUTING DAMAGE IN FIELD CONDITION AT SOME TRITICALE VARIETIES IN ÇUKUROVA REGION

Hasan Ay, Ahmet Akyol

Eastern Mediterranean Agricultural Research Institute, Adana, Turkey

hasanay2000@hotmail.com

This study was conducted during 2009-2010 growing sezons at ADANA. During the study 6 triticale varieties which were commonly produced in different geographic regions in Turkey. The main objectives of the study are to determine pre-harvest sprouting damage and resistance triticale varieties at field conditions. Studies were conducted under field conditions. The test materials were tested in two topics. The first of them; each triticale variety artificially soaked with mini sprinkler system during 6 hours period of a day in a week at the harvesting time, than they have left for dried and harvested and non-irrigated wheat varieties and the second didn't irrigate and wheat varieties only harvest. Data of hectoliter and 1000 kernel weight of were used for determination of resistant varieties.

Results revealed that, 6 triticale varieties had reduced 1000 kernel and hectoliter weights with sprouting damage. According to correlations, it was positive relationship with sprouting damage between 1000 kernel and hectoliter weight to control. It was also positive relationship between 1000 kernel weight and hectoliter weight to control. All triticales varieties susceptible to pro-harvesting germination spike. The conducted study suggested that generally harvesting time is rainy, earlier triticale varieties should be preferred so that varieties may escaped rainy season. Another suggestion, would prefer resistant varieties.

Keywords: Triticale, sprouting damage, resistatant, 1000 kernel, hectoliter weight

# GENETIC RELATIONSHIP BETWEEN PHYSIOLOGICAL PARAMETERS AND THE ROLE OF STABILITY FOR YIELD SUSTAINABILITY UNDER STRESS AND NON-STRESS REGIMES IN WHEAT

Saleem S[1,4*], M Kashif[1], M Hussain[3], A S Khan[1], M F Saleem[2], M Imtiaz[4] and M Y Ashraf[5]

1. Plant Breeding and Genetics Department, University of Agriculture Faisalabad, Pakistan
2. Agronomy Department, University of Agriculture Faisalabad, Pakistan
3. Wheat Research Institute Ayub Agriculture Research, Faisalabad, Pakistan
4. International Maize and Wheat Improvement Center (CIMMYT) Pakistan Office, CSI, Building, NARC, Park Road, Islamabad 44000, Pakistan
5. Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan

s.saleem@cgiar.org

Fifty wheat accessions were evaluated for stability against drought stress. All the studied parameters like chlorophyll a, chlorophyll b, turgor Potential and grain yield per plant decreased significantly under drought stress for all the fifty accessions except proline content which increased under drought stress. The accession 8126, O5BT014 and 9401 showed a stable performance under stress regime for chlorophyll a, b, turgor potential and ultimately produced better grain yield under stress regime. These accessions also showed high percentage increase for proline under drought stress. The presence of significant correlation of Chlorophyll a. b, proline content and turgor potential with grain yield at both genotypic and phenotypic level under drought stress also supported the above results. Hence, selection of those genotypes which give a stable performance under stress regimes can help to improve the overall grain production by compensating yield loss due to periodic drought spells and can also perform well under rainfed conditions.

Keywords: Breeding, Drought, Physiological Parameters, Yield.

# ADOPTION OF MODERN CULTIVARS AND HYBRIDS WIPED OUT THE TRADITIONAL VARIETIES: A CASE STUDY IN ZONE II AND ZONE III A OF BIHAR, INDIA

Chandan Roy, R. N. Sharma, S. C. Choudhury

Bihar Agricultural University, Sabour Bhagalpur, India

chandan.roy43@gmail.com

Aggressive introduction of modern cultivars, fragmented land holdings, changing land use pattern and climates and shift from subsistence agriculture to commercial agriculture increased rate of genetic erosion and loss of many traditional cultivars. Bihar state carriers rich biodiversity for rice and pulses crops. Zone II and Zone III A of Bihar covers 11.96% and 25.75% of the total geographic area of the state. To understand the change in the cropping system and their impact on agro-biodiversity of these zones the present study was carried out. A survey was conducted in February, 2014 in the selected districts of respective zones. Germpalsm collection and passport data documentation was recorded as per Moss and Guarino (1995). Geographic coordinates (latitude/lon- gitude) for each collection was recorded using GPS receiver. Subsequent regeneration and characterization of the germplasm is being undertaken by the concern breeders, so that details information will become available to the users. A drastic reduction of cereal germplasm observed in both the zones. Non-scented traditional rice varieties mostly wiped out due to availability of the modern cultivars. However, scented traditional rice cultivars are existing in pockets due to their local adaptation and suitability for milling than other improved scented cultivars. Decades before cultivation of boro rice in the zone II was prominent but with the introduction of winter maize hybrids reduced the boro rice cultivation. In the last decade, 12.35% area of rabi maize increased in the zone II. Maximum increase in area under maize was observed in the district Kishanganj (99.85%) followed by Madhepura (36.27%) and Katihar (22.48%). On the other hand, maximum area reduction of boro rice was observed in district Khagaria (20.63%) fol- lowed by Katihar (18.19%). The zone IIIA of Bihar is rich for traditional pulse culti- vars. In the last decade, drastic reduction of pulse crop area in Bihar as well as in zone IIIA was observed. Maximum reduction was found for Lathyrus (45.92%) followed by Chickpea (26.63%) in zone IIIA. Besides having good cocking quality, flavor and di- gestibility of the traditional cultivars, area and production of the pulse crop is reducing with the availability of wheat cultivars suitable for rainfed and limited irrigation condi- tions. Ex-situ conservation of local landraces of rice and pulse crops of Bihar is needed to shift into in-situ conservation process. Total of 18 cereals, 17 oilseed, 25 pulse crops, 17 vegetables and spices of traditionally grown cultivars were collected during the sur- vey and applied for farmer's variety registration under PPV&FRA, 2001. Most of the cereals and oilseed cultivars were collected from Zone II while most of the pulses were collected from Zone IIIA. Rice among the cereals, toria among the oilseeds and chick- pea among the pulses were dominating in number of cultivars in the collection.

Keywords: Traditional cultivars, Agrobiodiversity, PPVFRA2001

# SPRING- SOWN FIELD PRODUCTION IN KAZAKHSTAN: GIS-TECHNOLOGIES OF MAPPING

Abugalieva A.I.[1], Tazhibayeva T.L.[2], Salnikov V.G.[2], Assilbekova A.A.[2], Savin T.V.[1]

1. Kazakh Scientific Research Institute Agriculture and Plant Growing, Almalybak, Almaty region, Kazakhstan
2. Al-Farabi Kazakh National University, 71 Al-Farabi ave, Almaty, 050040, Kazakhstan

Tamara.Tazhibayeva@kaznu.kz

The spring-sown field is the main crop of grain production of Kazakhstan. For increase in export of grain at the world markets and ensuring domestic needs, it is necessary that the Kazakhstan grain was economic and ecologically safe. In this regard productivity, high quality, the balanced minerals, environmental resistance, in particular to a drought, are limiting for spring- sown field in our country and as well as other ones. We applied GIS-technology of mapping state test-sites for production of a spring-sown field located in various agro landscape zones of the republic. The software of ArcGIS 10 was for this purpose used. Saratovskaya 29 was the Grade standard. In - the first, we created the map - basis of agro landscapes with a geographical arrangement of 62 test-sites and kept in base of geodata. Secondly, analyzed a big information resource of data for the last more than 25 years on productivity and protein content, determined % of occurrence 1 + 2 classes of wheat by these indicators, and also, to an index of influence of the environment on quality of grain of a spring-sown field for each test-site. In – the third, collected and analyzed data on the content of zinc in grain of wheat which is grown up on these test-sites. In – the fourth, created a matrix on dryness indexes of various zones. In – the fifth, we created maps of geographical distribution of Kazakhstan zones on productivity, the maintenance of a protein, quality of grain, the content of zinc in grain and to dryness indexes. By drawing up the above maps the cartographical way of a qualitative background was used.

Mapping on the basis of GIS-technologies will allow to create system of timely forecasting of a crop and quality of grain, the accounting of regional specifics, including agro landscape, climatic, for formation of “exact” grain production.

Keywords: Spring-sown field, GIS-technology of mapping, ArcGIS 10,
agro landscape zones, test-sets, productivity, quality of grain,
a protein, the content of zinc in grain, a dryness index

# BREEDING OF CROPS WITH IMPROVED FUNCTIONALITIES

Güray Akdoğan

Department of Field Crops, Faculty of Agriculture, Ankara University
Dıskapi 06110 Ankara Turkey

gakdogan@agri.ankara.edu.tr

Functional characteristics of many traditional foods are being discovered and studied wisely to improve quality and quantity or gain new functions. Natural or processed foods contain increased/decreased amounts, modified, deleted or gained types of known biologically active compounds, which in defined healthy for human and animal dietary or industry. Starch is one of the most abundant storage products produced by plants and is widely used for human consumption, comprising 80% of the average daily caloric intake. It is also widely used in feed, fuel and industry. Various mutations in the genes involved in starch synthesis result in altered starch phenotypes which provide important information for understanding starch biosynthesis mechanisms and the function of isoforms. An increased understanding of the regulatory factors controlling storage starch biosynthesis will allow a more targeted approach to the alteration and manipulation of starch structures produced in crop plants. The major targets for the manipulation of starch structure in plants are the relative proportions of amylopectin and amylose and the chain length distribution of amylopectin. Several mutants have been obtained and described in various cereals and other species that contain starches composed of only amylopectin or that have a very high proportion of amylose. Nowadays, novel starches with improved functionalities (changes in gelatinization temperature, viscosity of cooked pastes and gels) have been produced in plants through the use of mutants and genetic modification. This report is prepared to present latest developments in crops with improved functionalities and, in particular, production of starch with improved functionalities.

Keywords: Altered starch phenotypes, amylose, amylopectin, waxy,
amylose extender, mutation

# RUSTS AND BUNT REACTIONS IN A BUNT RESISTANCE NURSERY IN 2014

Kadir Akan, Zafer Mert

The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11,
Yenimahalle, Ankara, Turkey

kadir_akan@hotmail.com

Rusts (caused by *Puccinia spp.*) and bunt (caused by *Tilletia spp.*) are the principal yield and quality-limiting factors for wheat production in the Central Anatolian region. The aim of the study was to improve resistance lines to rust and bunt. The aim of the Central Research Institute for Field Crops's Bunt Resistance Nursery (BRN) germplasm development program is to identify genotypes resistance to the rusts and bunt. In this study, 53 genotypes from the BRN materials were used.

FSeedling plants were inoculated with local Pst (virulent on differentials with Yr2 Yr6, Yr7, Yr8, Yr9, Yr25, Yr27, YrSd, YrSu, and YrA), Pt (avirulent on differentials with Lr9, Lr19, Lr24 and Lr28) and the Pgt (avirulent on differentials with Sr24, Sr26, Sr27 and Sr31) population. For adult plant yellow and bunt reactions; each genotype was sown by hand in a 1 m row in October 2013. Yellow rust development on each entry was scored on the modified Cobb scale when the susceptible check Little Club reached 80-100S disease severity in June 2014. Coefficients of infection below 20 were considered to be resistant. For bunt test; the experiment was conducted as the seeds of the total genotypes were inoculated artificially with local Bt (virulent on Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 and Bt-7) population before planting. Bunt development on each entry was scored on the infected spike percent scale when the susceptible check Yakar 99, 90-100% disease severity in August 2014. Below 25% were considered to be resistant.

Twenty (38%), 9 (17%) and 9 (17%) genotypes were resistant to YR, LR and SR at the seedling stage, respectively. Twenty six (49%) and 53 (100%) genotypes were resistant to YR and BT at the adult stage respectively. Potential resistant germplasm was determined.

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Keywords: Rusts (Puccinia spp), genetic resistance, reaction test

# IN VITRO TUBERIZATION FOR POTATO IMPROVEMENT AFTER GAMMA IRRADIATION

Souleymane Bado[1], Kaoutar El-Achouri[2], Said Zantar[2], Mouad Chentouf [2]

1. Plant Breeding and Genetics Laboratory (PBGL), Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, IAEA, P.O. Box 100, Wagramerstrasse 5, A-1400 Vienna, Austria
2. Institut National de Recherche Agronomique, Centre de Tanger, Tanger 90010, Morocco

elotmani.samira@gmail.com

Potato (*Solanum tuberosum* L.) is an important vegetable and staple food worldwide and ranks fourth after maize, rice and wheat. In Morocco, it is staple food for most of the population therefore the cultivation is extensively throughout the year. However the cultivated varieties have poor yield due to Potato virus Y and drought. In vitro culture of vegetatively propagated crops in combination with radiation induced mutation has proven to be a valuable method to broaden genetic variability. Mutation breeding aims to improve these traits in favoured the most cultivated variety “Kondor”.

Prior to mutation breeding, radio-sensitivity tests need to be performed to determine the optimal dose treatment for mutation induction. Since potato is a vegetatively propagated crop, and a tuber producer crop, the micro-tuberization strategies were adopted: 1) irradiation of in vitro cutting and immediate tuberization; and 2) tuberization of in vitro cuttings and irradiation of micro-tubers.

Radio-sensitivity tests showed varied responses in two treatments with respect to GR50 and LD50 (doses required for mutation induction). The micro-tubers were more resistant to gamma irradiation compared to the cutting tuberization. In addition the efficiency of the two strategies is being assessed on mutant population level in field conditions.

Keywords: Radio-sensitivity test, optimal dose, gamma irradiation, microtubers, mutation induction

# IMPROVEMENT OF POTATO VARIETIES WITH HIGHER IRON CONTENT AND YIELD BY MOLECULAR BREEDING

Ahmet Şahin, Emre Aksoy, Mehmet Emin Çalışkan

Nigde University, Faculty Of Agricultural Sciences And Technologies, Agricultural Genetic Engineering, 51240 Nigde

Potato is the fifth most produced crop in the world and accumulates high levels of carbohydrates, proteins, vitamins as well as iron in its stolons. Being one of the essential micronutrients, iron is found highly in nature although it cannot be absorbed readily by roots due to its low solubility in alkaline environments such as calcerous soils. Plants grown on such soils are often exposed to iron deficiency. Since majority of soil is calcerous in Turkey, unfortunately agriculturally important crops like potato are under constant iron deficiency, leading to lower potato yields. Iron deficiency in plants in turn affects the human health since the plants are the main iron source in human diet. Being the most important reason of anemia, iron deficiency continues to be a major public health problem both in Turkey and in the world. For this reason, the ultimate goal of this project is the development of potato varieties with higher yield and iron content. We first identified the homologs of Arabidopsis thaliana IRT1, IRT2 ve NAS4 in Solanum tuberosum with very high homology percentages (68%, 63% ve 60%, respectively) in pBLAST analyses and investigated the phylogenetic relationships of them. The expression levels of genes and proteins (IRTs and NAS) function if iron uptake and distribution in plants will be detected in 200 potato varieties under iron deficiency. Varieties showing the highest IRT and NAS levels will be determined. Then, the potato varieties with the highest iron content and yield will be determined among selected varieties.

Keywords: Bioinformatics, gene expression, iron deficiency, molecular breeding, potato, biofortification

# A MULTI-LOCATION EVALUATION OF COTTON FIBER TRAITS IN RELATION TO COTTON CULTIVARS.

Vasileios Greveniotis

Hellenic Republic Ministry of Reconstruction of production, Environment and Energy Rural Development, Hellenic Agricultural Organization “Demeter”, Industrial and Forage Crops Institute, National Center for Quality Control Classification & Standardizatio

vgreveni@mail.com

A multi-location evaluation of commercial cotton cultivars was conducted in Greece during 2014-2015. For this purpose four main cotton regions was selected: Thessaly, Sterea Ellada, Macedonia and Thrace. The five most cultivated commercial upland cotton (*Gossypium hirsutum* L.) cultivars were used for evaluation of their fiber traits fluctuations. 200 fields were recorded and four samples from each field were collected to analyze fiber traits. Genotypes x Environment interactions were computed in correlation to fiber trait fluctuations. Results suggest that there is a strong interaction between the five commercial cotton cultivars and the regions of cultivation for eight fiber traits. Two cotton cultivars were stable across environments in most of the fiber traits, but generally, each specific environment affected significantly fiber traits. This depicted the differences of genetic materials and the different breeding strategies of the breeding companies. Because of the presence of significant Genotype x Environment interactions, breeding of cotton must be based on a multi-location evaluation scheme that may result in more stable behavior of cotton cultivars across different environments. Acknowledgements: This research project is funded under the Action ‘Research & Technology Development Innovation projects (AgroETAK)’, MIS 453350, in the framework of the Operational Program ‘Human Resources Development’. It is co-funded by the European Social Fund and by National Resources through the National Strategic Reference Framework 2007-2013 (NSRF 2007-2013) coordinated by the Hellenic Agricultural Organisation “DEMETER” (Industrial and Forage Crops Institute - National Center for Quality Control Classification & Standardization / Scientific supervisors: Dr E. Maloupa- Dr. M. Darawsheh).

Keywords: Multi-location, interaction, fluctuations, cotton cultivars

# VALORIZATION OF OLIVE BY-PRODUCTS THROUGH VERMICOMPOSTING

Barhoum KHARBOUCH[1] Abdelhamid EL MOUSADIK[1], Sevastianos ROUSSOS[2], Nathalie DUPUY[3] , Hicham LAKHTAR[1], Sandrine AMAT[3]

1. Laboratoiry of Biotechnology and valorization of Natural Resource (LBVRN), Faculty of Sciences, University Ibn Zohr, Agadir, Morocco.
2. Team Ecotechnologies and Bioremediation, Avignon and Aix Marseille University; IMBE CNRS UMR-7263 / IRD-237, Box 421, Campus Etoile, Faculty St. Jerome, 13397 Marseille cedex 20, France.
3. Laboratory Instrumentation and Analytical Sciences (LISA), Aix-Marseille University Campus Sciences St Jerome, Marseille, France

kharbouch-barhoum@hotmail.fr

In Morocco, large quantities of olive by-products (olive mill wastes and pomace) are produced annually. These by-products create serious problems for the environment, particularly groundwater and surface. Although several biotechnological processes (composting, anaerobic digestion, evaporation…) have been proposed to dispose of or recover the waste, cost and technicality limited their application. This study aims to propose vermicomposting as a process adapted to the technical and economic requirements of the Souss region. This study aims vermicomposting mastery of several mixtures of olive waste in order to both enhance and improve the quality of fertilizing waste processing into vermicompost. Two mixtures M1 and M2 are prepared from the pomace, manure and sugar cane bagasse. The mixture M2 was soaked by the olive mill wastes diluted to ¼, the mixtures were inoculated earthworms of the species Eisenia foetida and Eisenia andrei. The results showed that the mixture M1 recorded biomass gain of 126 mg / worm against 12.5 mg / worm to the mixture M2. Similarly the reproduction rate of earthworms in the mixture M1 was 12.72 cocoon / week against a rate of 8.22 cocoons / worm for the M2 mixture. At the end of vermicomposting decreased C / N ratio was recorded for both mixtures (from 29 to 19.25 M1 and M2 from 38 to 27). This decrease demonstrates the stabilization and mineralization of organic matter in the vermicomposting process. The total phenols concentration contained in the mixture M2 is reduced by 76%. The phytotoxicity test of vermicompost obtained revealed no toxicity against the germination of tomato seeds (overall germination index >80%).

Keywords: Vermicomposting - Eisenia andrei – olive by-product -Bio-compost - Organic matter – phenols - phytotoxicity test.

# TEA (*CAMELLIA SINENSIS* (L.) O. KUNTZE) BREEDING ACTIVITIES IN TURKEY

Fatih Seyis, Keziban Yazıcı, Mustafa Akbulut

Faculty of Agriculture and Natural Sciences, Recep Tayyip Erdogan University

fatih.seyis@erdogan.edu.tr

Tea, *Camellia sinensis* (L.) O. Kuntze, is an drink and food material obtained after the processing of its fresh leaves with different methods, and is highestly consumed after water all over the world. Tea production on economic level are performed in about 30 countries inclusively these countries and Turkey. Turkey is on the 7. rank regarding the extent of tea plantation areas, on the 5. rank regarding dry tea production and on the 4. rank regarding annual individual consumption between tea growing countries. Tea, an conventional export product of our country, has an important place in the plant production of the Eastern Black Sea region and 203.000 farmers are labour with tea on 758.000 ha land. The Black Sea coastline contains at the meantime very important tea genetic resources. Currently, all tea plantations in Turkey are established by seedlings and show huge heterogeneity. Around, 1979's some selection studies were carried out on theses seedlings yo obtain promisin clones and some clones were created and released but not widely commercialized. The tea industry in Turkey solely consists of black tea production but more recently product diversification (gren tea, white tea etc.) has been initiated. Further, tea improvement activities concentrating on clonal selection to decrease seedling populations, collection, conservation, molecular and biochemical characterisation of tea genetic resources in the Black Sea region has also been initated.

Keywords: Tea breeding, Camellia sinensis, breeding activities

# HOW OLIVE VARIETIES AND SUBSTRATE CHARACTERISTICS CAN DETERMINE THE DIVERSITY OF PLANT-PARASITIC NEMATODE COMMUNITIES INFESTING OLIVE NURSERIES IN MOROCCO

T. Mateille[1], A. El Mousadik[2], H. Boubaker[2], S. Roussos[3], H. Lakhtar[2], H. Tazi[2], N. Ali[1], J. Tavoillot[1], Z. Ferji[4], A. Moukhli[5], M. Aït Hamza[2]

1. Institut de Recherche pour le Développement, Unité Mixte de Recherche Centre de Biologie pour la Gestion des Populations, Campus de Baillarguet, CS30016, 34988 Montferrier-sur-Lez Cedex, France
2. Université Ibn Zohr, Faculté des Sciences d'Agadir, Laboratoire Biotechnologie et Valorisation des Ressources Naturelles, BP 8106, 80000LBVRN, Agadir, Morocco
3. Institut de Recherche pour le Développement, Institut Méditerranéen de Biodiversité et d'Écologie marine et continentale Aix-Marseille Université ; Campus Sciences St Jérôme - Service 421 F-13397 Marseille cedex 20, - France
4. Institut Agronomique et Vétérinaire Hassan II, Campus d'Agadir, Département de Protection des Plantes, BP 18/S, 80000 Agadir, Morocco
5. Institut National de la Recherche Agronomique, Centre Régional de la Recherche Agronomique, BP513, Menara, Marrakech, Morocco

mohamed.aithamza@edu.uiz.ac.ma

Plant-parasitic nematodes (PPN) affect significantly the production of susceptible plants, including olive trees (*Olea europaea*), especially in the Mediterranean basin (Spain, Italy, Greece, Tunisia, and Morocco). Moreover, these parasites strongly affect young olive trees in nurseries and contribute to economic losses. PPN are everywhere detected in communities (i.e. species population mixtures). Knowing that plant pro- duction partly depends on parasite diversity, more information about PPN communi- ties and about interactions with their habitats is a prerequisite for the development of any control strategy. In this context, PPN communities were determined in 305 soil samples collected in 25 olive nurseries in Morocco (Souss, Haouz, Meknes-Tafilaate and Tanger-Titouane regions). The sampling was performed in spring 2013 and 2014. Morphobiometric observations revealed a significant diversity of PPN, belonging to 12 families and 22 genera. The most dominant PPN, which are known for their damages on Mediterranean olive, were Helicotylenchus spp. (86.5 %), Meloidogyne spp. (56.3%), Tylenchorhynchus spp. (50.4%), Trichotylenchus spp. (42.3%), and Rotylenchus spp. (37.2%). No disease symptoms were observed on roots. However, population levels of these nematodes were significant (up to 56,640 individuals /dm3 of fresh soil) in most of the olive nurseries. The contribution of physico-chemical characteristics of growing substrates (e.g. texture, pH and potassium content), and climate (maximum and min- imum average temperature) on the PPN diversity (abundance, richness, evenness and plant-parasitic index) and community patterns is discussed.

Keywords: Community; growing substrates; Morocco; nurseries; Olea europaea; Plant-parasitic nematodes; physico-chemical characteristics.

# SELECTION OF POTATO CLONES OBTAINED FROM HYBRID TRUE SEEDS

Rasool Asghari Zakaria[1], Leila Tarbali[1], Davood Hasanpanah[2], Omid Sofalian[1]

1. Department of Agronomy and plant breeding, Faculty of Agricultural Sciences, University of Mohaghegh Ardabili, Ardabil, Iran,
2. Agriculture Research Station of Ardabil, Ardabil, Iran

r-asghari@uma.ac.ir

In this research, the number of 80 potato clones at F2 generation obtained from hybrid true potato seeds of crossing among Lucca, Satina, Ceaser and Savalan cultivars were evaluated along with these control cultivars as an experiment based on augmented design with four replications. The traits of plant height, main stem diameter, number of main stems, tuber weight per plant, average tuber weight per plant, days to flowering, tuber yield and dry matter content were measured. Analysis of variance showed that there were significant differences among the control cultivars, between clones and control cultivars and among clones, for all traits. The best clones from viewpoint of tuber yield were the 35, 41 and 43 clones from the Luca X Caeser family. There was a significant positive correlation between tuber weight per plant with average tuber weight and the number of tubers per plant, and a significant negative correlation between tuber weight with days to flowering. In addition, the correlation between plant height and number of main stems and its diameter was significantly positive. Cluster analysis of the clones and control cultivars grouped them at six groups, which the clones from third and forth groups, in more traits such as tuber yield, tuber weight per plant, number of tubers per plant, plant height, number of main stems and stem diameter had a great values than overall average.

Keywords: Clone selection, True potato seed, yield

# EVALUATION OF 22 ALFALFA GENOTYPES FOR THEIR AGRONOMICAL CHARACTERISTICS AND THEIR YIELD POTENTIAL

Chrysanthi Pankou, Dimitrios Baxevanos

Institute of Industrial and Fodder Crops, Hellenic Agricultural Organization

cpankou@gmail.com

Alfalfa (*Medicago sativa* L.) is the most important forage crop grown worldwide because of its high nutritional quality for animal feed. The objective of this paper was the evaluation of 22 alfalfa genotypes for their yield potential and its components. The evaluated genotypes include eight greek varieties that are well adapted and widely cultivated in Greece (Cheronia, Florina, Ypati, Yliki, Pella, Lamia, Dolichi and Veria), thirteen foreign varieties known worldwide (Ultima, Talia, Prosementi, Padana, Maxima, Icon, Gea, Evergreen, Claudia, Blue ace, Almasa, 59N59 and 57Q53) and finally one ecotype (region of Serres, Greece). The experiment was conducted at the farm of the Institute of Industrial and Fodder Crops of Larissa in Greece and for the evaluation of the 22 genotypes a completely randomized design with three replications was applied. The performance of the 22 genotypes was assessed based on their yield in dry grass from the first three cuts of the current cultivation season and plant height before cuts. Eventually the evaluated varieties were classified and the specific data in combination with the performance of the varieties for the rest of the cultivation period will assist in the identification and isolation of the high yielding and best adapted varieties for cultivation in Greece. Research is part of the action “Research & Technology Development Innovation Projects - AgroETAK”, MIS 453350, in the framework of O.P. “Human Resources Development”, co-funded by ESF and National funds (NSRF 2007-2014), coordinated by the Hellenic Agricultural Organization “DEMETER”.

Keywords: *Medicago sativa*, dry grass yield, plant height, variety performance

# DETECTION OF NUCLEAR DNA CONTENT AND PLOIDY LEVELS OF *HYPERICUM PERFORATUM* L. POPULATIONS PRESENT IN THE NATURAL FLORA OF TURKEY USING FLOW CYTOMETRY

Gülsemin Savaş Tuna[1*], Gözde Duyu[1], Kardelen Uzun[1], Gülru Yücel[2], Metin TUNA[3]

1. Ebru Nayim Science High School, Tekirdağ, Turkey
2. Namık Kemal University, Faculty of Science and Letters, Department of Biology, 59030 Tekirdağ, Turkey
3. Namık Kemal University, Faculty of Agriculture, Department of Field Crops, Tekirdağ, Turkey

glsvs@yahoo.com

*Hypericum perforatum* L., also known as ″St John's Wort″ is a perennial, medicinal plant. The purpose of this study is to detect the ploidy levels of *H. perforatum* L. populations that are present in the natural flora of our country using the flow cytometry method for the first time.

The seeds of 39 *Hypericum perforatum* L. plants, which were collected from 23 different geographical regions of Turkey, were washed and dried and subsequently kept in 50 ppm GA and planted into multipods. The study was conducted under uncontrolled greenhouse conditions. During the flow cytometry analyses, it was found that the nuclear DNA content of the populations varied between 0.8 - 2.38 pg2C-1 and an intraspecific variation was seen. The populations consisted of three different ploidy levels and 2.4% of the analyzed samples were diploid, 86.3% were tetraploid, and 11.3% were hexaploid. During the analyses, it was also found that the variation within the intraspecific genome sizes was statistically significant; these differences were caused by the difference between the ploidy levels of the populations. The geographic areas from where the plants were collected did not have a statistically significant effect. A positive correlation was found between the height and nuclear DNA content during the study with tetraploids.

With this study, the ploidy levels of *H. perforatum* L. populations in Turkey were detected for the first time using the flow cytometry method. Furthermore, by collecting samples from different geographic areas, a small collection of genetic resources, which can be used for national and international scientific studies, was established.

Keywords: *Hypericum perforatum*, flow cytometry, nuclear DNA content,
ploidy level, genetic variation

# WINTER SURVIVAL OF COMMON VETCH (*VICIA SATIVA* L.) GERMPLASM IN CENTRAL ANATOLIA, TURKEY

Azize Homer[1], Mevlüt Şahin[1], Ümran Küçüközdemir[2]

1. Central Research Institute for Field Crops, Ankara, Turkey
2. Eastern Anatolia Agricultural Research Institute, Erzurum, Turkey

ademirbas@hotmail.com

Common vetch is an annual forage legume grown commonly as a spring crop in Central Anatolia, Turkey. Fall-sown vetch can yield more than the traditional spring sowing, using winterhardy cultivars. This study was conducted to determine if there is variability among germplasm for winterhardiness available from gene banks. Twenty-one Turkish and one Iranian accessions, plus three elite cultivars (two cold tolerant, one spring cultivar), were evaluated in two field trials in Haymana, Ankara, and one field trial in Ulaş, Sivas, Turkey during the 2014/15 season, and under controlled conditions. On average, higher level of winterkill occurred in Ulaş than in Haymana, and survival rate ranged between 13.7 to 91.9 percent. In Ulaş, the three highest surviving Turkish landraces TR 4474, TR 4492, and TR 15081, exhibited survival rates of 69.8, 56.1 and 54.5 %, respectively, compared to 82.1 and 91.9 % of cold tolerant controls. Under the controlled environment, only five accessions exhibited low level of survival at -8 oC and no plants survived at -12 and -16 oC. Correlation coefficients for the mean survival (%) of genotypes between test environments ranged from 0.37 to 0.83*** ($P < 0.001$). Moreover, in separate field trials at the same two locations, 24 Turkish accessions, one Bulgarian and one French accession together with four controls were screened, and six accessions TR 14790, TR 54404, TR 57557, PI 176795, PI 383799, and PI 542703 had survival rates comparable with the cold tolerant controls.

Keywords: Common vetch (*Vicia sativa* L.), winterhardiness, cold tolerance, germplasm, screening

# ESSENTIALS OILS OF LAURUS NOBILIS OF THREE MONTHS (APRIL, MAY AND JUNE) FROM ALGERIA

Ould Yerou Karima, Meddah B, Tir Touil A

Laboratoire of Bioconversion; Microbiological engineering and safety, Faculty of Science; Biology Department; University of Mascara - Algeria

mhanine11@yahoo.fr

Laurus nobilis is an aromatic plant, widespread in Algeria and widely used by local people as a source of spice and for its medicinal properties. The essential oil of this plant is the subject in this work a comparative study of this dune extraction HE three months: April, May and essential oil June.L'extraction was performed by steam distillation and performance the highest (1.5%) was determined in the month of May, in this month, the laurel plant was fully flowered in favorable soil and climate conditions for biosynthesis of the essential oils that makes the yield increases considerably.

Keywords: Laurus nobilis, Algeria, essential oil, steam distillation, yield.

# IDENTIFICATION OF NUCLEUS TYPES WITH THE SNPS IN ONION (*ALLIUM CEPA* L.) HYBRID BREEDING

Esra Cebeci, Fatih Hancı

Atatürk Central Horticultural Research Institute, Yalova, Turkey

esra.cebeci@gthb.gov.tr

Commercial onion (*Allium cepa* L.) production is based on open-pollinated and hybrid cultivars. The production of hybrid onion seed is economically feasible using systems of cytoplasmic-genic male sterility (CMS). Onion has biennial nature and shows strong self depression so molecular identification of cytoplasm and nucleus types might be helpful to development of sterile and maintainer lines. In many plants, single nucleotide polymorphism (SNP) markers are increasingly becoming the marker system of choice and the onion is one of them. In this study, researchers tried to evaluate cytoplasm and nucleus types of some onion accessions, collected from Turkey, using SNPs. Among accessions sterile and maintainer plants detected with molecular markers and some field works of the study still continues.

Keywords: Onion, molecular markers, CMS, SNPs, hybrid breeding

# MOLECULAR IDENTIFICATION OF CYTOPLASM TYPES OF TURKISH ONION (*ALLIUM CEPA* L.) GENOTYPES

Esra Cebeci[1], Hüseyin Padem[2]

1. Ataturk Central Horticultural Research Institute, 77102, Yalova, Turkey

2. Lumina, The University of Southeast Europe, 021187, Bucharest, Romania

esra.cebeci@gthb.gov.tr

Onion (*Allium cepa* L.) is grown worldwide for its fleshy bulbs which are used as food and medicinal purposes. It has biennial nature and strong self-depression, so breeding of inbred lines are taken a long period. The production of hybrid onion seed is economically feasible using the systems of cytoplasmic-genic male sterility (CMS). The identification of cytoplasm types with the molecular markers might be helpful to develop of sterile and maintainer lines. S-cytoplasm is the most common source of cytoplasmic-genic male sterility which is used to produce hybrid onion seed. Molecular characterization of N- and S-cytoplasm's and frequencies of nuclear non restoring allele allow onion breeders to determine the proportion of plants in open-pollinated populations that maintain CMS and can significantly reduce the investment required to identify individual sterile and maintainer plants. In our study, we applied the PCR-markers to identify the cytoplasm types of 113 Turkish onion genotypes. Among materials, it was found that, 22 of the genotypes possessed both S-and N-cytoplasm and 91 of the genotypes possessed only N-cytoplasm.

Keywords: Onion, Allium cepa, CMS, male sterility, cytoplasm types

# GENETIC SIMILARITY OF BROOMRAPE POPULATIONS FROM BALKAN REGION

Nataša Ćurčić[1], Igor Vukelić[1], Stevan Maširević[2], Dragan Škorić[3], Dejana Panković[1]

1. Faculty of Environmental Protection, Educons University, Vojvode Putnika 87, 21208 Sremska Kamenica, Serbia
2. Faculty of Agriculture, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia
3. Serbian Academy of Sciences and Arts, Belgrade Branch in Novi Sad, Nikole Pašića 6, 21000 Novi Sad

dejanapankovic@educons.edu.rs

Broomrape (*Orobanche cumana Wallr.*) can cause serious damages of sunflower yield in infested areas. The final goal of O. cumana genetic diversity studies is development of molecular tools for genetic identification. In this study seeds of twenty-four broomrape populations were collected in sunflower fields in Serbia, Romania and Bulgaria. Polymorphism of genomic DNA was examined with 18 RAPD primers, out of which five were highly polymorphic. Four to eight markers per primer were used for calculation of Jaccard coefficent of similarity (Jaccard index-JI) between broomrape populations. JI varied from 0.052 to 0.9, for highly disimilar and similar populations, respectively. Mean value of JI was 0.362. Cluster analysis (PAST v. 2.17c) revealed the separation of three populations sampled in location Krivaja in Serbia, from all other examined populations (bootstrap values ≥ 75). In addition high intrapopulational variability was observed for the sample from Bulgaria.

Acknowledgement: The research is co-financed by the Serbian Academy of Sciences and Arts (Project No.168).

Keywords: *Orobanche cumana Wallr.*, *Helianthus annuus* L., genetic diversity, molecular markers.

# INVESTIGATION OF PHYSIOLOGICAL PARAMETERS ON SOME DURUM WHEAT GENOTYPES

Kürşad Özbek*, Fatma Ruveyda Alkan, Nurgül Sarı, Rukiye Murat Duran,
Durmuş Deniz

Central Research Institute for Field Crops, Turkish Seed Gene Bank, Şehit Cem
Ersever Street, No: 9-11 Yenimahalle/Ankara

ozbekkursad@yahoo.com

This study was conducted in Central Research Institute for Field Crops, Yenimahalle locations, in dry conditions, 2014-15 vegetation season and the trial was conducted according to randomized complete block design with 3 replicates. In the study; 24 local durum wheat and 9 durum wheat varieties was used from Turkish Seed Gene Bank (TSGB) collections. Flag leaf chlorophyll content, flag leaf relative humidy content, flag leaf water retention index and canopy temperature parameters were investigated from durum wheat genotypes. At the end of the study; some important parameters was determined in terms of the statistical analyses. As a result of the physiological characterization we found that; maximum flag leaf chlorophyll content (SPAD) was 94.5 for 24. genotype and minimum 43,4 for 15. genotype, max flag leaf relative humidy content was 80 % for 25. genotype and minimum 40 % for 1. genotype, max flag leaf water retention index was 89,2 % for 10. genotype and minimum 60,5 % for 16. genotype, max canopy temperature was 34,1 °C for 2. genotype and minimum 19,5 °C for 33. genotype. Results of trials will be assessed as data on drought-resistant durum wheat varieties development in the Central Anatolian conditions.

Keywords: Landrace, durum wheat, drought.

# INVESTIGATION OF MORPHOLOGICAL PARAMETERS ON SOME DURUM WHEAT GENOTYPES

Kürşad Özbek*, Fatma Ruveyda Alkan, Nurgül Sarı, Rukiye Murat Duran,
Durmuş Deniz

Central Research Institute for Field Crops, Turkish Seed Gene Bank, Şehit Cem
Ersever Street, No: 9-11 Yenimahalle/Ankara

ozbekkursad@yahoo.com

Drought is one of the most important factor for limiting the yield of wheat. There is need for some morphological parameters of selection criteria on development of drought-resistant wheat varieties. This study was carry out in Central Research Institute for Field Crops, Yenimahalle locations, in dry conditions, 2014-15 vegetation season and the trial was conducted according to randomized complete block design with 3 replicates. In the study; 24 local wheat and 9 durum wheat varieties was used from Turkish Seed Gene Bank (TSGB) collections. Plant height, peduncle length, flag leaf area index, number of grains per spike, weight of grains per spike, awn length, awn dry weight and the 1000 seed weight parameters were investigated for durum wheat genotypes. At the end of the study; some important parameters was determined in terms of the statistical analyses. As a result of the morphological characterization we found that; maximum plant height was 144.7 cm for 20. genotype and minimum 66 cm for 11. genotype, max peduncle length was 55 cm for 20. genotype and minimum 19 cm for 12. genotype, max flag leaf area index was 61.08 cm2 for 24. genotype and minimum 10.30 cm2 for 15. genotype, max number of grains per spike was 63 for 33. genotype and minimum 22 for 15. genotype, maximum weight of grains per spike was 3.3 g for 16. genotype and minimum 0.7 g for 15. genotype, maximum awn length was 12.3 cm for 18. genotype and minimum 5.8 cm for 25. genotype, max awn dry weight was 0.4 g for 24. genotype and minimum 0.2 g for 15. genotype, max 1000 seed weight was 69.6 g for 20. genotype and min. 30,3 g for 17.genotype. The results are encouraging because of the high variation and valuable for durum wheat breeding programs in drought conditions in Central Anatolia.

Keywords: Landrace, plant height, number of grains per spike, awn length,
1000 seed weight.

# TAGEM DIGITAL HERBARIUM CATALOG

Kürşad Özbek*, Bengü Koyuncu, Şenay Boyraz Topaloğlu

Central Research Institute for Field Crops, Turkish Seed Gene Bank, Şehit Cem
Ersever Street, No: 9-11 Yenimahalle/Ankara

esmer.benguu@gmail.com

Turkey has a rich plant biodiversity and a high ratio of endemism due to its geographical and ecological conditions. Plant biodiversity in Turkey is also an important resource for plant breeding. But recording of biodiversity and opening the extensive database for researchers is of great importance. Herbarium specimens are useful for identification of plants and the determination of plant locations, abundance, habitat and flowering and fruiting periods. Having these information before the field studies is reduce the loss of important resources such as time, effort and cost. For this purpose, a Digital Herbarium Catalogue with open internet access has been created under the leadership of General Directorate of Agricultural Research and Policy / Turkey Seed Gene Bank. The number of samples available is reached to 2546 by transferring of some of herbarium specimens of Aegean Agricultural Research Institute/National Gene Bank and Nezahat Gokyigit Botanical Garden.

Designed database system was developed with Microsoft C # Asp.Net 4.0 as an object oriented programming language to perform faster, safer and flexible searching and real-time recording of material. Software was designed with ER model and Microsoft SQL Server 2008 R2 program was selected as database. Database of researchers in the design of recording column contains information that will support their work. TAGEM Digital Herbarium located in different institutions and organizations such as the National Botanic Garden of the catalog is planned in the near future be extended to cover herbarium collections. Thus, the flora of Turkey in international standards including the National Herbarium database will be created and thanks to this database researchers, who especially work in the field of biodiversity, will be able to access information accurate, easily and quickly.

Keywords: Plant conservation, plant genetic resources, seed gene bank,
plant diversity, digital herbarium

# INTERRELATIONSHIP BETWEEN 1000 SEED WEIGHT WITH OTHER QUANTITATIVE TRAITS IN CONFECTIONARY SUNFLOWER

Nada Hladni, Siniša Jocić, Vladimir Miklič, Dragana Miladinović, Miroslav Zorić

Institute of Field and Vegetable Crops, Novi Sad, Serbia

nada.hladni@ifvcns.ns.ac.rs

Breeding for increase of 1000 seed weight results in increased seed yield. Therefore it is considered an important criterion in the development of confectionary sunflower hybrids. In this paper, we studied mutual relationships between several quantitative traits on one side and 1000 seed weight on the other. Path coefficient analysis was used to separate direct and indirect effects of studied traits on 1000 seed weight, and to identify traits that could be used as selection criteria in sunflower breeding. The research was conducted during three vegetation seasons on 22 NS high-protein two-line confectionary sunflower hybrids, produced within the breeding program at IFVCNS. Strong and very strong correlations were found among the largest number of examined traits. With the analysis of simple correlation coefficients, very strong and strong positive correlation was determined between 1000 seed weight and length of seed (0.717**), seed hull ratio (0.609**), thickness of seed (0.549*). A strong negative interdependence was determined between 1000 seed weight and seed protein content (0.538*). Path coefficient analysis for 1000 seed weight at phenotypic level showed that the length of seed and thickness of seed had a very strong direct positive effect on 1000 seed weight (DE=0.849**; DE=0.748**). Width of seed had a strong negative direct effect on 1000 seed weight (DE=-387*). A weak direct negative effect of kernel protein content and seed hull ratio was established, whereas seed protein content had a weak direct positive effect on 1000 seed weight. This indicates that length and thickness of seed have high influence on 1000 seed weight.

Keywords: Confectionary sunflower, correlations, 1000 seed weight,
path coefficient analysis, quantitative traits,

# IMPLEMENTATION OF DROUGHT STRESS TO LOCAL DURUM WHEAT GENOTYPES FOR MICROARRAY STUDIES

Kürşad Özbek*, Rukiye Murat Duran, Ayşe Yıldız, Nurgül Sarı

Central Research Institute for Field Crops, Turkish Seed Gene Bank, Şehit Cem
Ersever St., No:9-11 Yenimahalle/Ankara

ozbekkursad@yahoo.com

We applied two different level of drought stress to 4 genotypes, which were selected from local durum wheat varieties, Çeşit 1252 and Triticum diccocoides L. as 3 biological and 2 technical repeat when grain filling process. After the anthesis, watering was performed in three different moisture contents in soils respectively, Control: (CTRL; SWC = %28), Medium level drought (MS; SWC=% 18) and Severe level drought (SS; SWC=%12,5). Genotypes which were subjected to the drought stress were planted in pots (16X16 cm) in to mixtures; soil, sand and peat (6: 3: 1) Genotypes were planted 5 plants per pot in temperature, humidity and photoperiodism controlled room. Then they were grown until they showing first 3 leaves in the light intensity of 500 m2s1, 10 C° temperatures and 60% relative humidity at day time, 7 C° temperatures and 60%relative humidity at night time in 12 h light 12 h dark conditions. After then samples were waited until harvested time in 22 C° temperature daytime, 18 C° temperature at night and 55% relative humidity for 16 hours light, 8 hours dark in 500 m2s1 light intensity. Relative humidity of all samples was adjusted to field capacity until the third day of anthesis. When the control plants were irrigated to the field capacity, water stress applied plants were waited to expected value of MS (18%) and SS (12.5%) relative humidity. Soil moisture content was calculated by weigh of pots 2 times a day. Weight of plants was taken into account when weigh of pots for watering. It took approximately 2-3 days for all genotypes in MS and SS humidity levels. Then irrigation was performed two times a day (early morning and late afternoon) to maintain the specified amount of moisture levels. The plants were harvested 9th day of stress application. Harvested plants were kept in -80C° for RNA isolation for use in microarray studies

Keywords: Wheat, Drought stress, Local variety, MicroArray

# NEW THREE SECONDARY GENES OF ZUCCHINI YELLOW MOSAIC VIRUS RESISTANCE

Abdulbasit Abbas AL JANABI, Sarab A. ALMUKHTAR*, Haider S. Keytan

Ministry of Science and Technology, Agriculture Research Office P.O. Box 765
Baghdad, Iraq

abd_lbasit@yahoo.com

Within a program of re-rooting of some vegetables including squash attention was get to the characteristics of resistance to viral diseases, including the Zucchini Yellow Mosaic Virus of squash, and the insect vectors of this virus. Coloration of leaf with white silver was one of these characters. Three shapes of white silvery color of leaf were differentiated. The first one is the full leaf silvery color: it includes the entire leaf upper surface that makes the leaf be seen not green and unattractive to viruliferous insects, it may appear early with the third leaf stage. The second shape is the netty white leaf: where all the vein of leaf colored whitely and the leaf appears like the spider net, and so it repellent the viruliferous insects. The third shape is the white spotted leaf: always appeared lately after the other shapes. It looks like florescence spots where they reflect the light in a way that repellent the insects like the bright reflective things do, and reduce the area of infection where it not happen in these spots. Studies of genetic behavior by hybridization with other race that haven't these characters and their separation in the second generation revealed that each shape of white or silver color controlled by one dominant gene of two alleles; and so they were simply inherited and transmitted to other races, but their appearance highly affected by genotype variation and environment factors.

Keywords: Vegetable breeding, virus resistance, cucurbits viruses, squash diseases, genetic resistance

# EFFECTIVE AGRONOMICAL AND MORPHO-PHYSIOLOGICAL TRAITS FOR SCREENING DROUGHT TOLERANT BREAD WHEAT GENOTYPES

Bennani, S[1*], Birouk A[2], Nsarellah, N[3], Tadesse, W[4]

1. National Institute of Agricultural Research, INRA Meknès, BP 578, Meknès, Morocco
2. Hassan II Agronomy and Veterinary Institute, Madinate Al Irfane, B.P. 6202. Rabat, Morocco
3. National Institute of Agricultural Research, INRA Settat, BP 589, Settat, Morocco
4. International Center for Agricultural Research in the Dry Areas, Biodiversity and Integrated Gene Management Program, B.P. 6299, Rabat, Morocco

sahar.bennani@gmail.com

Drought is one of the major abiotic stresses threatening bread wheat in Morocco. The breeding efforts are hampered by the lack of reliable selection criteria for this complex trait involving multitude of agro-morphological and physiological mechanisms. In order to investigate the best selection criteria to develop drought tolerant varieties, 40 bread wheat genotypes were evaluated under two locations representing the stressed and non-stressed environments, using randomized complete block design with three replications during 2014 cropping season. Several traits namely grain yield (GY), biomass (BY), number of plants (NP), spikes (NS), tillers per m² (NT), thousand grain weight (TGW), plant height (PH), plant vigor (PV), number of days to heading (NDH) and flowering (NDF), canopy temperature (CT), chlorophyll content (CC) and chlorophyll fluorescence (CF) were evaluated. The correlation analysis revealed significant positive association between GY, BY, TGW and NS in both conditions. In stressed environment, GY is also positively correlated with PV and PH and negatively correlated with CC and CT. Those results are in agreement with Principal Components (PC) Analysis which explained 52.8 % of total variation considering the first four PCs. The PC1 explained 21% of the total variation showing positive correlation with GY, TGW, NS, BY, PH, PV and negative correlation with CT, CC in stressed conditions. The positive correlation of BY, TGW and NS with GY confirmed that these characters are important for direct selection of high yielding and stable genotypes. Also, PV, CC and CT could be selected simultaneously as indirect selection criteria for drought tolerance.

Keywords: Bread wheat, drought tolerance, selection criteria, agronomic traits, morpho-physiological traits

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# PARTICIPANTS LIST

| Name | Surname | Country | Email |
|---|---|---|---|
| VIJAYAKUMAR | A. G | India | vijayuasd@gmail.com |
| MEHRAJ | ABBASOV | Azerbaijan | mehraj_genetic@yahoo.com |
| ABDALLA ELHASSAN YOUSIF | ABDALLA ELHASSAN YOUSIF | Sudan | abdomusa61@gmail.com |
| MOUKHLI | ABDELMAJID | Morocco | moukhli2000@yahoo.fr |
| ABUZAR | ABDULLAH | Pakistan | abuzar.abdullah@hotmail.com |
| ABDUGAFFAR | ABLAZOV | Turkey | ablazov3@gmail.com |
| SAULE | ABUGALIEVA | Kazakhstan | absaule@yahoo.com |
| AIGUL | ABUGALIYEVA | Kazakhstan | kiz_abugalieva@mail.ru |
| ADE AFRINA ARIFIN | ADE AFRINA ARIFIN | Indonesia | deyafrin@gmail.com |
| OLAWALE | ADENIJI | Nigeria | waleniji@gmail.com |
| DANIEL | ADEWALE | Nigeria | d.adewale@gmail.com |
| KEDAR | ADHIKARI | Australia | kedar.adhikari@sydney.edu.au |
| M. MUCHLISH | ADIE | Indonesia | mm_adie@yahoo.com |
| AFIFUDDIN LATIF | ADIREDJO | Indonesia | al.adiredjo@gmail.com |
| MUHAMMAD | AFZAL | Saudi Arabia | afzal_uaf@hotmail.com |
| MOSTAFA | AGHAEE-SARBARZEH | Iran | sarbarzeh@gmail.com |
| AGRIKCAP | AGRIKCAP | Japan | roysipinhou1972@yandex.ru |
| NANA | AGYEMAN BIRIKORANG | Ghana | nanakwesiagyeman@gmail.com |
| MUHAMMAD QADIR | AHMAD | Pakistan | mqadirahmad@gmail.com |
| RAMALA MASOOD | AHMAD | Pakistan | twin2001@yahoo.com |
| KHALIL | AHMAD | Pakistan | khalilpbguaf@gmail.com |
| ISRAR | AHMAD | Pakistan | iabotany32@gmail.com |
| HABIB | AHMAD | Pakistan | Drhahmad@gmail.com |
| HABIB | AHMAD | United Kingdom | drhahmad@gmail.com |
| ADNAN | AHMED | Bangladesh | greenuniversitydhaka@gmail.com |
| NESRINE | AISSA | Tunusia | nesrine.aissa@hotmail.fr |
| MOHAMED | AIT HAMZA | Morocco | mohamed.aithamza@edu.uiz.ac.ma |
| KADIR | AKAN | Turkey | kadir_akan@hotmail.com |
| GÜRAY | AKDOĞAN | Turkey | akdogangur@yahoo.com |
| GALIA | AKHMETOV | Kazakhstan | galiya87@hotmail.com |
| FATMA | AKIN | Turkey | akn.fatma+kongre@gmail.com |
| MUSTAFA | AKIN | Turkey | mustafaakin@bisab.org.tr |
| ILGIN | AKPINAR | Turkey | akpinarilgin@gmail.com |
| ZAHID | AKRAM | Pakistan | akramzahid@hotmail.com |
| MEHMET | AKSU | Turkey | mehmetaksu_43@hotmail.com |
| FIGEN | AKYÜZ | Turkey | fgn_ersln@hotmail.com |
| DR. MAHA ABD OUN HASAN | AL _ TAMEEMI | Iraq | dr_maha2008@yahoo.com |
| ADEL | AL SHIHI | Oman | 2000adel@live.com |
| MD ALAMGIR MIAH | ALAMGIR | Bangladesh | alamgir_magura@yahoo.com |
| ÖNDER | ALBAYRAK | Turkey | ondera@dicle.edu.tr |
| SALEM | ALGHAMDI | Saudi Arabia | salem@ksu.edu.sa |
| NAJEEB | ALHARBI | Saudi Arabia | najeeb.alharbi@sydney.edu.au |
| ASGHAR | ALI | Pakistan | asgharali_phb@hotmail.com |
| CUCEREAVII | ALIONA | Moldova | alionacucereavii@mail.ru |
| ALMIRA | ALIYA AZHAAR | Indonesia | almira710@gmail.com |
| JALAL | ALIYEV | Azerbaijan | aliyev-j@botany-az.org |
| ABDULBASIT | ALJANABI | Iraq | abd_lbasit@yahoo.com |
| NATIK | ALKUDSI | Iraq | natikalkudsi@yahoo.co.uk |
| NATIK | ALKUDSI | Iraq | sna_jj@yahoo.com |
| TOFIG | ALLAHVERDIYEV | Azerbaijan | tofig_1968@mail.ru |

| Name | Surname | Country | Email |
|---|---|---|---|
| AHMED | AL-NAJM | Australia | aaln4661@sydney.edu.au |
| RIYADH ABDULHASAN | ALSAEED | Iraq | riyadh_saeed@yahoo.com |
| NASSER | AL-SUHAIBANI | Saudi Arabia | mosalah@ksu.edu.sa |
| MOHAMMED | ALTAWEEL | Iraq | draltawel@yahoo.com |
| BAKTYBEKOV | ALYMKULOV | Kyrgyzstan | alymkulov.baktybek@mail.ru |
| ABDULRAZZAK A. JASIM ALZUBAIDI | ALZUBAIDI | Iraq | raz55iq@gmail.com |
| UGOCHI | AMAZUE | Nigeria | ugamazue@yahoo.ca |
| SHAKEEL | AMIR | Pakistan | dramirpbg@gmail.com |
| BAKHYTBEK | AMIROV | Kazakhstan | bamirov@rambler.ru |
| MOHD DIN | AMIRUDDIN | Malaysia | mohddin@mpob.gov.my |
| MEGAHED HELMI | AMMAR | Saudi Arabia | ammarrice@gmail.com |
| MOEZ | AMRI | Tunusia | amrmoez@gmail.com |
| ELIAS | ANASTASSOPOULOS | Greece | anastaso@teilar.gr |
| FATIMA | ANAYA | Morocco | anaya.fatima@gmail.com |
| PORT | ANGELA | Moldova | portang@yahoo.com |
| ALEXANDER EZEKIEL | ANGYU | Nigeria | alexangyu@gmail.com |
| SEMAI | ANNELA | Algeria | clostridium42@yahoo.fr |
| ASMAT | ARA | India | mirasmat35@gmail.com |
| MUHAMMAD AHMED | ARAIN | Pakistan | ahmedaraintj@gmail.com |
| ARIN | ARIANE CHAIRANI | Indonesia | arinchairani@gmail.com |
| ARJULA R REDDY | ARJULA | India | arjula.rama@gmail.com |
| MUHAMMAD ARSLAN AKHTAR | ARSLAN | Pakistan | arslanpbg@gmail.com |
| AHMAD | ARZANI | Iran | arzani@ucdavis.edu |
| HAMEED | ASAMADANY | Australia | halsamadani1979@hotmail.com |
| ABDYBEK | ASANALIEV | Kyrgyzstan | asanaly61@mail.ru |
| ZEMEDE ASFAW | ASFAW | Ethiopia | zasfaw49@yahoo.com |
| RASOOL | ASGHARI ZAKARIA | Iran | rrasghari@yahoo.com |
| ASIM ATA | ASIM ATA | Pakistan | asim.pbg@live.com |
| MUHAMMAD | ASLAM | Pakistan | aslampbg@gmail.com |
| KÜRŞAT ALP | ASLAN | Turkey | kursatalp0272@msn.com |
| AMRI | ASSIA | Algeria | amri.assia@yahoo.fr |
| ELIŞAN | ATAY | Turkey | ekarahan@dorukgroup.com.tr |
| RANA MUHAMMAD | ATIF | Pakistan | dratif@uaf.edu.pk |
| AUQUAARAQ | AUQUAARAQ | Gabon | rowlandsvtm@hotmail.com |
| FAISAL SAEED | AWAN | Pakistan | awanfaisal@yahoo.com |
| AWOL MOHAMMED | AWOL MOHAMMED | Ethiopia | mawol50@yahoo.com |
| HASAN | AY | Turkey | hasanay2000@hotmail.com |
| BAKHITBAY | AYBERGENOV | Uzbekistan | aybahit@rambler.ru |
| HANDAN | AYDIN | Turkey | handan.aydin@sesvanderhave.com |
| MEHTAP | AYDIN | Turkey | mehtapaydin23@gmail.com |
| MELIH | AYDINLI | Turkey | melihaydinli1985@gmail.com |
| SINAN | AYDOĞAN | Turkey | s_aydogan_@hotmail.com |
| MONININUOLA A. | AYO-VAUGHAN | Nigeria | folakevaughan@gmail.com |
| AYTEN | AYTEN DIZKIRICI TEKPINAR | Turkey | aytendizkirici@gmail.com |
| BARIŞ | AYYILDIZ | Turkey | ersel_tekin@hotmail.com |
| MOHAMMAD ABUL KALAM AZAD | AZAD | Bangladesh | akazad.hstu@gmail.com |
| MUHAMMAD TEHSEEN | AZHAR | Pakistan | tehseenazhar@gmail.com |
| IRUM | AZIZ | Australia | irum.aziz@sydney.edu.au |
| MOYASSAR | AZIZ | Iraq | moyassar_aziz@yahoo.com |
| SHIVA | AZIZINIA | Iran | sazizinia@ut.ac.ir |

| Name | Surname | Country | Email |
|---|---|---|---|
| SAIDMURAT | BABOEV | Uzbekistan | sai-baboev@yandex.ru |
| S. AHMET | BAĞCI | Turkey | bagcia@hotmail.com |
| MUHITTIN | BAĞCI | Turkey | muhittin.bagci@gthb.gov.tr |
| RAJAGOPAL | BALA | India | rajudevi@yahoo.com |
| AHMET | BALKAYA | Turkey | abalkaya@omu.edu.tr |
| SAIRA | BANO | Pakistan | sairakhan1441@gmail.com |
| SAID | BARRIJAL | Morocco | barrijal@yahoo.fr |
| SAID | BARRIJAL | Morocco | barrijal@yaoo.fr |
| BAHAR BANU | BATI | Turkey | bahar-banu@hotmail.com |
| HASAN | BAYDAR | Turkey | hasanbaydar@sdu.edu.tr |
| RISHI K. | BEHL | India | rkbehlprof@gmail.com |
| MARIA | BEIHAGHI | Iran | maria_beihaghi@yahoo.com |
| MERSHA TEZERA | BELAY | Ethiopia | mertez19@yahoo.com |
| BELIA | BELIA BERLIANI PUTRI | Indonesia | beliaberliani@gmail.com |
| NADIA | BENIBRAHIM | Morocco | nadiabenbrahim@gmail.com |
| BALDEEP SINGH | BENIWAL | India | baldeep.singh55@gmail.com |
| NIKOLAY | BENKO | Russia | agroplasma@rambler.ru |
| MALIKA | BENNACEUR | Algeria | bennaceurmalika@gmail.com |
| SAHAR | BENNANI | Morocco | sahar.bennani@gmail.com |
| LEILA | BENNANI | Tunusia | leilabennani83@gmail.com |
| MEHMET SINAN | BERKSAN | Turkey | msberksan@kar.com.tr |
| NECMI | BEŞER | Turkey | necmibeser@yahoo.com |
| RAMAZAN | BEYAZ | Turkey | ramazanbeyaz@gmail.com |
| NABIN | BHUSAL | India | nabin18_bhusal@yahoo.co.in |
| AYNUR | BILMEZ ÖZÇINAR | Turkey | a.bilmez_21@hotmail.com |
| OM PARKASH | BISHNOI | India | opbishnoi363@gmail.com |
| BAKHT MUHAMMAD | BM | Pakistan | sahara.malakand@gmail.com |
| FATEMEH | BORNA NASRABADI | Iran | fatemehborna@gmail.com |
| VIKTORIIA | BORYSOVA | Ukraine | v.borysova@maize.com.ua |
| ABDELAZIZ | BOUIZGAREN | Morocco | bouizgaren_abdelaziz@yahoo.fr |
| DRISS-ANOUAR | BOUTAZAMAT | Morocco | driss-anouar@hotmail.com |
| H. FILIZ | BOYACI | Turkey | filiz_boyaci@yahoo.com |
| ABOLFAZL | BOZORGMEHR | Iran | abolfazl_bozorgmehr@yahoo.com |
| AHMAD | BRAND | United Kingdom | ahmadbrand@yopmail.com |
| SUSAN K. | BROWN | United States | skb3@cornell.edu |
| UMAR | BUBA | Nigeria | umbfaruk2005@yahoo.com |
| TAMARA | BURAVTSEVA | Russia | t.buravtseva@vir.nw.ru |
| DANTER | CACHIQUE HUANSI | Peru | dcachique@gmail.com |
| ATABEY | CAHANGIROV | Azerbaijan | a.cahangir@hotmail.com |
| MEHTAP | CAKIROGLU | Turkey | mhtpckrgl@gmail.com |
| HASAN | CAN | Turkey | hasancan194@yahoo.com.tr |
| ESRA | CEBECI | Turkey | esra.cebeci@gthb.gov.tr |
| RAHIME | CENGIZ | Turkey | rcengiz24@gmail.com |
| LAROUK | CHAFIA | Algeria | laroukchafia@yahoo.fr |
| HOUASLI | CHAFIKA | Morocco | houaslichafika@gmail.com |
| EVANTHIA | CHAMPLA | Greece | evi_cha@windowslive.com |
| MIRIAM KARWITHA | CHARIMBU | Kenya | charimbu22y@yahoo.com |
| NOR MAYATI | CHE HUSIN | Malaysia | normayati@lgm.gov.my |
| HAFIZA MASOOMA NASEER | CHEEMA | Pakistan | masooma@uaf.edu.pk |
| MEJDA | CHERIF | Tunusia | cherif_majda@yahoo.fr |

| Name | Surname | Country | Email |
|---|---|---|---|
| RAVINDRA | CHIBBAR | Canada | ravi.chibbar@usask.ca |
| JIACHENG | CHUAN | China | chuanjiacheng@outlook.com |
| SERAP | COŞKUN | Turkey | serap.coskun@tarim.gov.tr |
| SAMEER KUMAR | CV | India | c.sameerkumar@cgiar.org |
| MEHMET | ÇAKMAK | Turkey | mehmet.cakmak@tarim.gov.tr |
| HASAN | ÇELEN | Turkey | hasan.celen@tarim.gov.tr |
| IBRAHIM | ÇELIK | Turkey | celik_ibrahim@yahoo.com |
| IBRAHIM | ÇELIK | Turkey | icelik@iyte.edu.tr |
| NURYA | ÇELİK | Turkey | tbb.5581@gmail.com |
| MEHMET | ÇETIN | Turkey | mehmet.cetin@antalyatarim.com.tr |
| SELÇUK | ÇETINKAYA | Turkey | selcukcetinkayaa@gmail.com |
| BAYRAM | ÇEVIK | Turkey | bayramcevik@sdu.edu.tr |
| ASLIHAN | ÇILINGIR | Turkey | aslihancilingir@hotmail.com |
| ÇAĞLAR | ÇOLAK | Turkey | caglar-colakfb@hotmail.com |
| GÜLBAHAR | ÇULHA | Turkey | glbhr.clh@gmail.com |
| ASHWIN | DAHAKE | India | ashwinbreedee18@gmail.com |
| ZEYNEL | DALKILIÇ | Turkey | zdalkilic@adu.edu.tr |
| DANIELKT | DANIELKT | United Kingdom | Danielkt@m4.blogrtui.ru |
| DAVAR MOLAZEM | DAVAR MOLAZEM | Iran | davarmolazem@gmail.com |
| MAHDI | DAVARI | Iran | mdavari@uma.ac.ir |
| CHUKWUNYERE SUNDAY | DAVID | Nigeria | worldmeteologicalorganization@gmail.com |
| ÖZLEM | DEĞER DEMIR | Turkey | ozlemdeger@ksu.edu.tr |
| ZIBANDEH | DEHGHANPOUR | Iran | zdehghanpour80@gmail.com |
| LUISA | DEL PIANO | Italy | luisa.delpiano@entecra.it |
| YUSUF | DEMIR | Turkey | ersel_tekin@hotmail.com |
| FATIH | DEMIREL | Turkey | speed-fd@hotmail.com |
| ISMAIL | DEMIRTAŞ | Turkey | idemirtas66@hotmail.com |
| ZÜBEYIR | DEVRAN | Turkey | zdevran@akdeniz.edu.tr |
| CHINYERE HANNAH | DICKSON | Nigeria | info@annpetersglobalconceptltd.com |
| ÇAĞIN DENIZ | DIKMEN | Turkey | cagindenizdikmen@gmail.com |
| YILDIZ | DILLI | Turkey | yildizd2008@gmail.com |
| ZORAN | DIMOV | Macedonia | dimov632002@yahoo.co.uk |
| MEHMET | DOĞAN | Turkey | mehmet_dogann@hotmail.com |
| AIBEK | DOLOTBAKOV | Kyrgyzstan | dolotbakov2012@mail.ru |
| DONALDJELA | DONALDJELA | Saint Kiss and Nevis | donaldkobikdf@outlook.com |
| PAMFIL | DORU | Romania | iro@usamvcluj.ro |
| MARIA | DUCA | Moldova | mduca2000@yahoo.com |
| ZIYA | DUMLUPINAR | Turkey | zdumlupinar@ksu.edu.tr |
| ÖMER | DURSUN | Turkey | genetikci4271@hotmail.com |
| MIRA | DZHUNUSOVA | Kyrgyzstan | mdzhunusova@gmail.com |
| EERBLEJULI | EERBLEJULI | Paraguay | lihakkrbrs@21cn.com |
| MEHMET | EFE | Turkey | mehmetefe@gmail.com |
| BANU | EFEOĞLU | Turkey | befeoglu@hotmail.com |
| EGORML | EGORML | Netherlands Antilles | egorm2002@outlook.com |
| BANU AYTÜL | EKMEKÇI | Turkey | baaslana@anadolu.edu.tr |
| KAOUTAR | EL ACHOURI | Morocco | al.kaoutar@gmail.com |
| YASMINA | EL BAHLOUL | Morocco | yasmina.elbahlou@onra.org.ma |
| SALAH | EL-HENDAWY | Saudi Arabia | shendawy@yahoo.com |
| KHALID | ELHINDI | Saudi Arabia | elhindikhalid2010@yahoo.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| M.SERCEN | ELIK | Turkey | m.sercen.elik@gmail.com |
| RECEP ALI | EMRE | Turkey | raemre@hotmail.com |
| DR. MÜFIT | ENGIZ | Turkey | mufitengiz@turkted.org.tr |
| ÜLKÜ | ER | Turkey | ulku_er@yahoo.com |
| SABRI | ERBAŞ | Turkey | sabrierbas@sdu.edu.tr |
| ŞEYMA REYHAN | ERDOĞAN | Turkey | seyma85tamer@hotmail.com |
| FATIH | ERDOĞAN | Turkey | ferdoganx@hotmail.com |
| ONUR | ERGÖNÜL | Turkey | onur.ergonul@gthb.gov.tr |
| NAMUK | ERGÜN | Turkey | namukergun@hotmail.com |
| DÖNÜŞ | ERMIŞER | Turkey | dermiser06@hotmail.com |
| RAUSHAN | ERZHEBAEVA | Kazakhstan | raushan_2008@mail.ru |
| VEHBI | ESER | Turkey | vehbieser@gmail.com |
| DR. GÖKSEL | EVCI | Turkey | gokselevci@hotmail.com |
| ASSAF | EYBISHTZ | Israel | assaf@tomatech.co.il |
| DEBBAH FADILA | FADILA | Algeria | fadila.pharma@gmail.com |
| ADNAN JABBAR | FAHAD | Iraq | adnan.jabbar45@yahoo.com |
| OUTTAR | FAHIMA | Algeria | outtar25@yahoo.fr |
| PROF. | FARHATULLAH | Pakistan | drfarhat@aup.edu.pk |
| BENSALAH | FARID | Algeria | bensalahfarid@yahoo.fr |
| AMJAD | FAROOQ | China | amjadfarooq81@hotmail.com |
| SHUKRI | FETAHU | Kosovo | shfetahu@hotmail.com |
| JéSSICA | FIGUEIREDO REZENDE | Brazil | jessica.rfigueiredo@gmail.com |
| NJOKA | FREDRICK | Kenya | njokafm@yahoo.co.uk |
| ABDELHAMID | GACEMI | Algeria | abdelhamid_gacemi@yahoo.fr |
| ROBERTO | GAMBOA BECERRA | Mexico | rgamboa@ira.cinvestav.mx |
| RASHMI | GAUR | India | rashmit129@gmail.com |
| HASAN | GEZGINÇ | Turkey | hasangezginc@hotmail.com |
| WALID GHIDAN | GHIDAN | Egypt | w_ghidan@hotmail.com |
| SAFFET | GIRAY | Turkey | saffetgiray@yahoo.com |
| VOLKAN | GÖZEN | Turkey | vgozen@hotmail.com |
| VASILEIOS | GREVENIOTIS | Greece | vgreveni@mail.com |
| ELENA | GULTYAEVA | Russia | gullena@rambler.ru |
| ELENA | GUMEROVA | Russia | gumeri@mail.ru |
| BIRGÜL | GÜDEN | Turkey | birgulguden@akdeniz.edu.tr |
| SAFURE | GÜLER | Turkey | safureguler@hotmail.com |
| IBRAHIM | GÜR | Turkey | igur03@hotmail.com |
| FATMAGÜL | GÜVEN | Turkey | fatmagulguven1988@hotmail.com |
| MERVE | GÜZEL | Turkey | merveguzel@live.com |
| SELDA | GÜZELKÜÇÜK | Turkey | selda.guzelkucuk@hmclause.com |
| OUABEL | HABIB | Algeria | ouabelhabib@hotmail.fr |
| HANINE | HAFIDA | Morocco | hanine1960@gmail.com |
| RIZKI | HAJAR | Morocco | rizki.hajar1@gmail.com |
| MEHMET | HAKAN | Turkey | mhmthkn84@mynet.com |
| MAHAMAT | HALIME | Chad | mahamathissenehalime@yahoo.fr |
| YOUNIS | HAMAD | Saudi Arabia | yhamad@ksu.edu.sa |
| BENYAHIA | HAMID | Morocco | hamidbenyahia2002@yahoo.fr |
| JAMIN PRIYOMINARJO | HARIYADI | Indonesia | hariyadiipb@rocketmail.com |
| HARTIZFER | HARTIZFER | Ireland | osbornesalterdc@yandex.com |
| ABDUL RAHIM | HARUN | Malaysia | rahim@nm.gov.my |
| THIKRA ABD OUN | HASAN | Iraq | thikra_appleid@yahoo.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| ALI | HASSAN | Egypt | profhass59@yahoo.com |
| MOHAMED YOUSIF | HASSAN ABASS | Sudan | mohamedarc114@yahoo.com |
| ZAHER | HAYAT | Morocco | hayatzaher@yahoo.fr |
| BUJAK | HENRYK | Poland | henryk.bujak@up.wroc.pl |
| SEVGI | HEREK | Turkey | sevgiherek@hotmail.com |
| NADA | HLADNI | Serbia | nada.hladni@ifvcns.ns.ac.rs |
| AZIZE | HOMER | Turkey | ademirbas@hotmail.com |
| KARIM | HOUMANAT | Morocco | karim_houmanat@yahoo.fr |
| NADIA | HOUMY | Morocco | houmy.nadia@gmail.com |
| ZETIAN | HUA | China | fanxiaoman819@163.com |
| BAHROMIDDIN | HUSENOV | Tajikistan | bahromiddin@gmail.com |
| IRADA | HUSEYNOVA | Azerbaijan | i_guseinova@mail.ru |
| NESRIN | HUSEYNZADE | Azerbaijan | h-nesli@mail.ru |
| IQBAL | HUSSAIN | United Kingdom | ihussains@yahoo.co.uk |
| MEHMET | HÜSEMOĞLU | Turkey | mehmet@smyrnatohumculuk.com.tr |
| USMAN | IJAZ | Australia | usman.ijaz@sydney.edu.au |
| HULYA | ILBI | Turkey | hulyailbi@gmail.com |
| GISCA | ION | Moldova | amurarescu@amg-holding.md |
| SHEIKH MUHAMMAD | IQBAL | Pakistan | iqbalsh65@hotmail.com |
| MUHAMMAD ZAFFAR | IQBAL | Pakistan | dr_zaffariqbal@hotmail.com |
| INNOCENT OSEMARE | ISEGHOHI | Nigeria | innocent.iseghohi@fuoye.edu.ng |
| ARIFUL | ISLAM | Bangladesh | aarif1982@outlook.com |
| ANZER | ISLAM | India | anzer.gene@gmail.com |
| AHMET | IŞIK | Turkey | aisik@trakyatarim.com |
| HÜSEYIN | İYİDOĞAN | Turkey | huseyin.iyidogan@tarim.gov.tr |
| ALI | IZANLOO | Iran | aizanir@gmail.com |
| VAHID | JAJARMI | Iran | vahid_jajarmii@yahoo.com |
| ABDULRAZZAK A. | JASIM ALZUBAIDI | Iraq | raz55iq@gmail |
| BETRAN | JAVIER | France | javier.betran@syngenta.com |
| SHUYE | JIANG | Singapore | shuye@tll.org.sg |
| VOLLMANN | JOHANN | Austria | johann.vollmann@boku.ac.at |
| TOROBEK | JOLDOSHEV | Kyrgyzstan | alatoopharm@mail.com |
| JOSEPHSER | JOSEPHSER | Tunusia | honey.triputen@mail.ru |
| HASAN | JOURANI | Iraq | hnjoor98@yahoo.com |
| MOHANRAJ | K | India | mohangene@yahoo.com |
| EMEL | KAÇAL | Turkey | emel.vural@gmail.com |
| EL HEIT | KADDOUR | Algeria | kaddy62003@yahoo.fr |
| JALIL JAWAD | KADHIM | Iraq | jalil.jawad63@yahoo.com |
| MADHUSUDAN | KADURAPPA | India | madhusudan_seeds@rediffmail.com |
| NANA ATAA | KAKRA IX | Ghana | gomoaojobitc@gmail.com |
| YASEMIN | KALAMAN | Turkey | yasemin.kalaman@tarim.gov.tr |
| JAVED | KAMAL | Pakistan | javed1743@yahoo.com |
| MOHAMMAD MOJTABA | KAMELMANESH | Turkey | kamelmanesh2000@yahoo.com |
| NOWOSAD | KAMILA | Poland | kamila.nowosad@up.wroc.pl |
| DİLEK | KANDEMİR | Turkey | mdilek@omu.edu.tr |
| SOTIRIOS | KANDRELIS | Greece | sotkan@teiep.gr |
| ONUR | KARAAĞAÇ | Turkey | onurkaraagac@hotmail.com |
| BURAK | KARACAÖREN | Turkey | burakkaracaoeren@yahoo.com |
| SEZGİN | KARADENIZ | Turkey | sezgin.karadeniz@tarim.gov.tr |
| ÖZGÜL | KARAGÜZEL | Turkey | tezkara@yahoo.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| EMRE | KARAHAN | Turkey | karahan_633@hotmail.com |
| CUMA | KARAOĞLU | Turkey | cumakaraoglu@hotmail.com |
| SAADIA | KARBOU | Morocco | skarbou@gmail.com |
| OULD YEROU | KARIMA | Algeria | mhanine11@yahoo.fr |
| MARJAN | KARRICA | Kosovo | arjani.d@gmail.com |
| DR. PARMEET | KAUR | India | waheguru.parmeet@gmail.com |
| CANAN | KAYA | Turkey | canan.kaya@gthb.gov.tr |
| YALÇIN | KAYA | Turkey | yalcinkaya22@gmail.com |
| AYŞE SERPIL | KAYA | Turkey | ayserka07@hotmail.com |
| YURY | KAZHURA | Belarus | kazhura@tut.by |
| KENNETHAHYNC | KENNETHAHYNC | Myanmar | mila.trunina.76@mail.ru |
| MESUT | KESER | Turkey | m.keser@cgiar.org |
| HARI | KESH | India | harikeshkaul@gmail.com |
| HASAN | KEYVANOĞLU | Turkey | hasankeyvanoglutarm@gmail.com |
| SHIVRAM | KHADKE | India | shivramkhadke@gmail.com |
| MARIA | KHALID | Pakistan | maria.khalid73@gmail.com |
| CHENITI | KHALISSA | Algeria | khalissacheniti@gmail.com |
| MUHAMMAD SARWAR | KHAN | Pakistan | sarwarkhan_40@hotmail.com |
| SAYYAR | KHAN | Pakistan | sayyarkhankazi@aup.edu.pk |
| M NASEEM ABBAS | KHAN | Pakistan | mnaseemabbas@yahoo.co.uk |
| MOHAMMAD | KHANJANI | Iran | mkhanjani@gmail.com |
| ANJU | KHARB | India | kharb.anju@gmail.com |
| BARHOUM | KHARBOUCH | Morocco | kharbouch-barhoum@hotmail.fr |
| WAHEEDULLAH | KHAWRIN | Afghanistan | waheedullah.official@gmail.com |
| ELENA | KHLESTKINA | Russia | khlest@bionet.nsc.ru |
| YASUKO | KIFUJI | Turkey | yasuko@uni.gen.tr |
| ALEKSANDR | KILCHEVSKY | Belarus | kilchev@presidium.bas-net.by |
| YÜCEL | KILIÇ | Turkey | yucel.kilic@limagrain.com |
| OSMAN | KILINÇ | Turkey | osman@bisab.org.tr |
| FERHAT | KIZILGEÇI | Turkey | ferhat_kizilgeci@hotmail.com |
| ZINAIDA | KLIMENKO | Russia | klimentina55@mail.ru |
| NINA | KONKOVA | Russia | ninakonkova.1@mail.ru |
| SUNEETHA | KOTA | India | ponnukota@gmail.com |
| TANMAY | KOTASTHANE | India | vilol.tanmay@gmail.com |
| DENIZ | KÖM | Turkey | denizkom@gmail.com |
| TEVFIK FIKRET | KÖSE | Turkey | tkose@dorukgroup.com.tr |
| MEHMET | KÖSE | Turkey | ersel_tekin@hotmail.com |
| LAMIN MOHAMMED | KPAKA | Nigeria | ngoacswi200@yahoo.com |
| AYDA | KRISNAWATI | Indonesia | my_ayda@yahoo.com |
| AYHAN | KULLEP | Turkey | ayhan.kullep@syngenta.com |
| ARUN | KUMAR | India | arun.bau4@yahoo.co.in |
| RAHUL | KUMAR | India | rahul.kumar1980@yahoo.co.in |
| KHABIBJON | KUSHIEV | Uzbekistan | kushiev@mail.ru |
| GALINA | KUZNETSOV | Russia | galva@ksc.krasn.ru |
| IBRAHIM | KÜÇÜK | Turkey | ibrahimkucuk@yahoo.com.tr |
| SEDA | KÜLEN | Turkey | sedakulen@gmail.com |
| BONA | LAJOS | Hungary | lajos.bona@gk-syeged.hu |
| SHOTA | LAMPARADZE | Georgia | mikats@mail.ru |
| KAKHA | LASHKHI | Georgia | b.erdemel@cgiar.org |
| NATASA | LJUBICIC | Serbia | ljubicic.natasa@gmail.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| DIANA YURIDIA | LÓPEZ LEY | Mexico | dyuridia@ira.cinvestav.mx |
| GUELORD | LUATI NDOMBASI | Zaire | guelordluatik@gmail.com |
| SHASHI | MADAN | India | svmadan12@gmail.com |
| HASSAN | MAHMOUDZADEH | Iran | mahmoudzadeh_h@yahoo.com |
| SUNDAY CLEMENT | MAKINDE | Nigeria | scmakinde@yahoo.com |
| MIKHAIL | MAKSIMENKO | Russia | mikhail.i.maksimenko@mail.ru |
| SUDHENDU | MANDAL | India | smandalbot@gmail.com |
| SONIA | MANSOURI | Tunusia | soniamansouri@yahoo.fr |
| RAJAE | MANZALI | Morocco | raja.manz@live.fr |
| GHEORGHE | MARIANA | Romania | mariana.gheorghe@limagrain.com |
| AIGERIM | MASSIMGAZIYEVA | Kazakhstan | miss.masimgazieva@mail.ru |
| GANOUDI | MATIKE | Morocco | ganoudi@gmail.com |
| CHIKELU | MBA | Italy | Chikelu.Mba@fao.org |
| JOSEPH | MBASANI MANSI | Morocco | mansimbas@gmail.com |
| ELTAIYB IBRAHIM HASSAN | MEDANI | Sudan | sulfab@yahoo.com |
| ABID | MEHMOOD | Pakistan | abidm9@gmail.com |
| RAVI | MEHNDIRATTA | India | dstiny896@gmail.com |
| GEETIKA | MEHTA | India | drgeetika1326@gmail.com |
| DIOUF | MEISSA | Senegal | dioufmeissa9@gmail.com |
| TECHALE BIHAN | MEKONNEN | Ethiopia | kanantnetsa@gmail.com |
| MUZAMIL HUSSAIN | MEMON | Pakistan | muzamilmemon37@gmail.com |
| TEMESGEN MATIWOS | MENAMO | Ethiopia | temesgen2008@hotmail.com |
| HARUN | MERAL | Turkey | harunmeral1299@gmail.com |
| GALIOLLA | MEYRMAN | Kazakhstan | sayshyer@mail.ru |
| MICHALVOM | MICHALVOM | Greenland | tina-sotskova@mail.ru |
| HUSSEIN | MIGDADI | Saudi Arabia | h.migdadi@gmail.com |
| RAIZ UL ROOF | MIR | India | imrouf2006@gmail.com |
| LIDIY | MIROSHNICHENKO | Russia | lidamir@mail.ru |
| IRINA | MITROFANOVA | Russia | irimitrofanova@yandex.ru |
| SNEZANA | MLADENOVIC DRINIC | Serbia | msnezana@mrizp.rs |
| HIVA | MOHAMADNEJHAD | Iran | hiwa.mohamadnejhad90@gmail.com |
| LAL AHAMED | MOHAMMAD | United Kingdom | lalahamed@gmail.com |
| SEYYED ABOLGHASEM | MOHAMMADI | Iran | mohammadi@tabrizu.ac.ir |
| CHERFAOUI | MOHAND SAID | Algeria | cherfa.ceres@yahoo.fr |
| MIGANAW MERAGIAW | MOLLAW | Ethiopia | misganme@gmail.com |
| OLGA | MOLODCHENKOVA | Ukraine | olgamolod@ukr.net |
| HASSAN | MONIRIFAR | Iran | monirifar@yahoo.com |
| ALEXEY | MORGUNOV | Turkey | a.morgounov@cgiar.org |
| BENHENNI | MOSBAH | Algeria | mosbahitgcbel@yahoo.fr |
| SEYED ABDOLLAH | MOUSAVI KOUPAR | Iran | abdy_mo@yahoo.com |
| BAKHT MUHAMMAD | MUHAMMAD | Pakistan | bm_undp@yahoo.com |
| MUJTABA | MUHAMMAD | Turkey | agriculturist2012@yahoo.com |
| MUHAMMAD SALEEM | MUHAMMAD SALEEM | Pakistan | aquras77@yahoo.com |
| ZHANNA | MUKHINA | Russia | agroplazma@gmail.com |
| HAFIZ | MUMINJANOV | Turkey | hafiz.muminjanov@fao.org |
| RENU | MUNJAL | India | munjalrenu66@gmail.com |
| MOHAMED SULIMAN | MUSTAFA | Sudan | bd1966mar8@gmail.com |
| ZEYNEP ÇISEM | MUTAFÇILAR | Turkey | cisemmutafzeynep@gmail.com |
| HÜSEYIN | MUTLU | Turkey | huseyin.mutlu@tarim.gov.tr |
| NATIGA | NABIYEVA | Azerbaijan | gen_eht@yahoo.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| ÇETIN | NACAR | Turkey | cetinnacar@gmail.com |
| MUHAMMAD | NAEEM ASLAM | Pakistan | naeembarki@gmail.com |
| MUNISH | NAGPAL | India | munishnagpal1@gmail.com |
| LAYACHI | NAIMA | Algeria | layachinaima@yahoo.fr |
| ANITA | NAMAYANDEH | United Kingdom | anitanamayandeh@yahoo.com |
| MOHAMMAD REZA | NAROUI RAD | Iran | narouirad@gmail.com |
| SENTHIL | NATESAN | India | senthil_natesan@tnau.ac.in |
| MUNIRA | NAVRUZBEKOVA | Tajikistan | munira_5@mail.ru |
| NAYUNDA SITORESTI | NAYUNDASITA | Indonesia | sitanayunda@gmail.com |
| FARHAD | NAZARIAN FIROUZABADI | Iran | nazarian.f@lu.ac.ir |
| SHAHID | NAZIR | Pakistan | shahidnazir82@gmail.com |
| MOUSSA | NDIAYE | Senegal | kndiaye77@yahoo.fr |
| NISA | NISA BUDI ARIFIANA | Indonesia | nisabudiarifiana@gmail.com |
| FULGENCE | NIYONGABO | Burundi | fulgeniyo@yahoo.com |
| ASO | NOBAKHT VAKILI | Iran | a.nobakhtvakili@gmail.com |
| ABID | NOORI | Afghanistan | abidnoori2030@yahoo.com |
| RAYMOND N. | NORMAN | Sierra Leone | slyacdo@gmail.com |
| YAHIA | NOURREDINE | Algeria | n_yahia@yahoo.fr |
| SOLOMON | NTLADI | South Africa | ntladim@arc.agric.za |
| RAFIQAH | NURAHMI | Indonesia | rafiqahnurrahmi@gmail.com |
| OCHANDA | OGOLA | South Africa | ochanda@univen.ac.za |
| ANKIT | OJHA | Nepal | kingofkings_ankit@yahoo.com |
| MURAT | OLGUN | Turkey | info@resa.gen.tr |
| MIKTAT | OLGUN | Turkey | info@olgunlar.com.tr |
| RASOUL | ONSINEJAD | Turkey | rasoul@troyatohum.com |
| ZELIHA | ORHAN ÖZALP | Turkey | zeliha.orhanozalp@gthb.gov.tr |
| MUNIRA | OTAMBEKOVA | Tajikistan | munira.otambekova@gmail.com |
| OTH MA | OTH MA | Morocco | othmane_malki@yahoo.com |
| ABLA RAKIA | OTHMANI SENDID | Algeria | othmaniabla@yahoo.fr |
| SIHAM | OUMOUSS | Morocco | siham.oumouss@gmail.com |
| CENGIZ | OZER | Turkey | ozercengiz@gthb.gov.tr |
| ÖZGE | ÖNDER | Turkey | ozgeonderr@hotmail.com |
| RAMAZAN | ÖZALP | Turkey | ramazanozalp@yahoo.com |
| ERKAN | ÖZATA | Turkey | erkan_ozata@yahoo.com |
| KÜRŞAD | ÖZBEK | Turkey | ozbekkursad@yahoo.com |
| BAYRAM | ÖZDEMIR | Turkey | bozdemir40@yahoo.com |
| ŞERIFE | ÖZER | Turkey | info@osm-agro.com |
| TOLGA | ÖZGEN | Turkey | tolga_amasya_05@hotmail.com |
| ERCAN | ÖZKAYNAK | Turkey | eozkaynak@yukseltohum.com |
| ŞERIF | ÖZONGUN | Turkey | serifozongun@yahoo.com |
| GÖKHAN | ÖZTÜRK | Turkey | irem_gokhan@hotmail.com |
| IRFAN | ÖZTÜRK | Turkey | irfanozturk62@hotmail.com |
| AHMET | ÖZTÜRK | Turkey | aozturk20@gmail.com |
| SÜLEYMAN CAN | ÖZTÜRK | Turkey | suleymanozturk@iyte.edu.tr |
| TUBA | ÖZYILMAZ | Turkey | tubaozyilmaz@windowslive.com |
| MARIA | PACUREANU JOITA | Romania | mariapacureanu2@yahoo.com |
| SURENDER | PAHUJA | India | pahujask66@gmail.com |
| MUSTAFA | PAKSOY | Kyrgyzstan | paksoy42@hotmail.com |
| ANFISA | PALIY | Russia | onlabor@yandex.ru |
| PROF. DR. IVAN | PANAYOTOV | Turkey | ivan_panayotov_wheat@yahoo.mail |

| Name | Surname | Country | Email |
|---|---|---|---|
| CHRYSANTHI | PANKOU | Greece | cpankou@gmail.com |
| GHULAM AHMAD PARRAY | PARRAY | India | parray_2005@rediffmail.com |
| MOACIR | PASQUAL | Brazil | mpasqual@dag.ufla.br |
| VELI | PEKCAN | Turkey | velipekcan@hotmail.com |
| ACHMAD YOZAR | PERKASA | Indonesia | achmadyozarp@yahoo.com |
| ILIEV | PETRU | Moldova | vierul_isphta@mail.ru |
| SURESHA P G | PG | India | surya.gpbr@gmail.com |
| MARIA | PINTEA | Moldova | mariapintea@yandex.ru |
| SVETLANA | PLUGATAR | Russia | gardenroses@mail.ru |
| YURI | PLUGATAR | Russia | plugatar@ukr.net |
| MUSTAFA | POLAT | Turkey | mustafapolat1003@gmail.com |
| ZSOLT | PÓNYA | Hungary | ponyazs@yahoo.com |
| LOLLIE AGUSTINA P. | PUTRI | Indonesia | lollie_agustina@yahoo.com |
| RENANE | RACHIDA | Algeria | rracha8@yahoo.fr |
| RAMIN | RAFEZI | Iran | raminrafezi@gmail.com |
| MD MOMINUR | RAHMAN | Bangladesh | mominagn@hstu.ac.bd |
| HIDAYAT | RAHMAN | Pakistan | rahman@yahoo.com |
| ILHAM | RAHMOUNI | Morocco | ilham.rahmouni@gmail.com |
| ALLOUDANE | RAJAE | Morocco | alloudan83@yahoo.fr |
| MOHAMMAD | RAMEZANI MALEKROUDI | Iran | ramgolband@yahoo.com |
| RAMLA MASOOD | RAMLA | Pakistan | ramlapbg@gmail.com |
| IQRAR AHMAD | RANA | Pakistan | iqrar_rana@uaf.edu.pk |
| BABITA | RANI | India | babitachahalkharb@gmail.com |
| RUMESH | RANJAN | India | rumeshranjan@yahoo.com |
| AWAIS | RASHEED | China | a.rasheed@cgiar.org |
| RENATOKR | RENATOKR | Martinique | helmutchol@4softsite.info |
| MARIANO | RESENDIZ | United States | mrese001@ucr.edu |
| LUXITA | RISNOVEANU | Romania | vasileelena303@yahoo.com |
| EUGENE | ROGOZHIN | United Kingdom | rea21@list.ru |
| LEILA | ROMDHANE | Tunusia | laila.romdhane1@gmail.com |
| DR NARAYAN ROY | ROY | Bangladesh | nroy_64@yahoo.com |
| CHANDAN | ROY | India | chandan.roy43@gmail.com |
| RSETHERTODEMA | RSETHERTODEMA | Laos | wengmei1001@tom.com |
| KHANBALA | RUSTAMOV | Azerbaijan | xanbala.rustamov@yandex.com |
| DEDI | RUSWANDI | Indonesia | dediruswandi2000@yahoo.com |
| RUTH O. ESCASINAS | RUTH | Philippines | ruthescasinas@gmail.com |
| AIMAN | RYSBEKOVA | Kazakhstan | aiman_rb@mail.ru |
| SEYED KAZEM | SABBAGH | Iran | sksabbagh@uoz.ac.ir |
| MUHAMMAD ABU BAKAR | SADDIQUE | Pakistan | abubakarpbg@yahoo.com |
| SHAHRIYAR | SADIGOV | Azerbaijan | shahriyar.sadikov@mail.ru |
| HOJJATOLLAH | SAEIDI | Iran | ho.saeidi@sci.ui.ac.ir |
| ZAFER | SAĞEL | Turkey | zafer.sagel@gmail.com |
| MEHMET | SAĞLAM | Turkey | saglams@mynet.com |
| SEVIL | SAĞLAM | Turkey | saglamsevil@gmail.com |
| FATIMA | SAHNOUNI | Algeria | sahnouni_fatima@yahoo.fr |
| NEZHA | SAIDI | Morocco | nezsaidi@yahoo.fr |
| SOBHAN | SAJJA | India | s.sobhan@cgiar.org |
| AHMED | SALAMH | Saudi Arabia | asalyest@gmail.com, |
| AYTEN | SALANTUR | Turkey | asalantur@mynet.com |
| SALMAN | SALEEM | United Kingdom | mrsalman146@gmail.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| REDA ABD ELMAKSOUD | SALLAM | Egypt | rida_rice@yahoo.com |
| GULMIRA | SAMENOVA | Turkey | gulmira.samenova@rofagroup.com |
| SRINIVASAN | SAMINENI | India | s.srinivasan@cgiar.org |
| MANOJ | SAPKOTA | Nepal | manoj34sapkota@gmail.com |
| NEBAHAT | SARI | Turkey | nesari@cu.edu.tr |
| DUYGU | SARI YOL | Turkey | duygusari@akdeniz.edu.tr |
| HASAN CUMHUR | SARISU | Turkey | hcumhurs@hotmail.com |
| GÜLSEMIN | SAVAŞ TUNA | Turkey | glsvs@yahoo.com |
| ISMAIL | SAYIM | Turkey | isayim2001@yahoo.com |
| HEINZ | SCHUTTE | Zaire | research@capstoneseeds.com |
| ŞAFAK | SEKMEN | Turkey | safaksekmen@gmail.com |
| YUSUF | SEN | Turkey | y.sen@enzazaden.com.tr |
| SEYED YAGHOB | SEYED MASOUMI | Iran | yamasoumi@yahoo.com |
| FATIH | SEYIS | Turkey | fatih.seyis@erdogan.edu.tr |
| TURGAY | SEYMEN | Turkey | turgayseymen@mynet.com |
| M. CAVIT | SEZER | Turkey | mehmetcavit.sezer@gthb.gov.tr |
| SYED AWAIS SAJID | SHAH | Pakistan | awaiskazmi44786@yahoo.com |
| MASOOD AHMAD | SHAKIR | Pakistan | masoodshakir7@gmail.com |
| KAIYRKUL | SHALPYKOV | Kyrgyzstan | alhor6464@mail.ru |
| MALIKA | SHAMEKOVA | Kazakhstan | shamekov@gmail.com |
| ELHAM | SHARIFZADEH | Iran | sharifzadeh.elham@yahoo.com |
| RAM | SHARMA | Uzbekistan | r.c.sharma@cgiar.org |
| GALIM | SHEGEBAEV | Kazakhstan | sakyshyer@mail.ru |
| ZAABOUBI | SIHAM | Algeria | zaaboubi.siham@yahoo.fr |
| OUROUADI | SIHAM | Morocco | siham.ourouadi@gmail.com |
| DIANE | SIMON ROZZETTO | Brazil | dsrozzetto@gmail.com |
| SATYAVIR | SINGH | India | dhandass@gmail.com |
| FRANSISCA MARIA KAK | SISCA | Indonesia | frsiscamkak@live.com |
| SUKHDEEP SINGH | SIVIA | India | sukhdeepsinghsivia@gmail.com |
| FOZIA KHAN | SIYAL | Pakistan | foziakhan2006@hotmail.com |
| QUAHIR | SOHAIL | Turkey | q.sohail@cgiar.org |
| BAHRIDIN | SOLIHOV | Tajikistan | yunuszod@yahoo.com |
| ILKNUR | SOLMAZ | Turkey | isolmaz@cu.edu.tr |
| AYED | SOUROUR | Tunusia | ayedsourour@yahoo.fr |
| HALE | SOYGAZI | Bahamas | hakki@bayindir.org |
| MARIA | STAMATOVA | Bulgaria | maredped@abv.bg |
| CLAPCO | STELIANA | Moldova | stela.clapco@gmail.com |
| MILAN | STEVANOVIC | Serbia | mstevanovic@mrizp.rs |
| VLAD | STOIAN | Romania | vlad.stoian@usamvcluj.ro |
| ILHAN | SUBAŞI | Turkey | ilhansubasi@gmail.com |
| RADIY | SULEIMENOV | Kazakhstan | rsuleimenov@mail.ru |
| NARGIZ | SULTANOVA | Azerbaijan | nargizsultanova@mail.ru |
| JUNIZA FIRDHA | SUPARNINGTYAS | Indonesia | junizafs.biokim47@gmail.com |
| EDY | SUPRIANTO | Indonesia | edygrey@gmail.com |
| EDY | SURYADI | Indonesia | dediruswandi3000@gmail.com |
| MUHAMMAD | SYAFII | United Kingdom | syafii_m@yahoo.com |
| AHMET | ŞAHIN | Turkey | ahmet.sahin@mail.nigde.edu.tr |
| MEVLÜT | ŞAHIN | Turkey | mevluts@yahoo.com |
| FATIH | ŞAHIN | Turkey | fathsahn00@gmail.com |
| TURGAY | ŞANAL | Turkey | tsanal@hotmail.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| HAMDI SEFA | ŞENOCAK | Turkey | sefa_senocak@hotmail.com |
| METE MURAT | ŞÖLEN | Turkey | bisab@bisab.org.tr |
| ENDER | TAMER | Turkey | endert@uni.gen.tr |
| TAMRAZ | TAMRAZOV | Azerbaijan | tamraz.tamrazov@mail.ru |
| ELENI | TANI | Greece | etani@aua.gr |
| ABDULKADIR | TANRIKULU | Turkey | atanrikulu@ksu.edu.tr |
| TIJEN | TAŞKIN | Turkey | tijen.taskin@gthb.gov.tr |
| TAMARA | TAZHIBAYEVA | Kazakhstan | tazhiba@list.ru |
| HAFSSA | TAZI | Morocco | hafssatazi@gmail.com |
| ERSEL | TEKIN | Turkey | ersel_tekin@hotmail.com |
| SULUHAN | TEMIRBEKOVA | Russia | sul20@yandex.ru |
| NACERA | TIGRINE | Algeria | tigkor12@yahoo.fr |
| ASHOK | TIKLE | India | antikle@yahoo.co.in |
| TAZHIHAN | TLEUBAEVA | Kazakhstan | life_0903@mail.ru |
| GHIZLANE | TOBI | Morocco | tobighizlane@gmail.com |
| IOANNIS | TOKATLIDIS | Greece | itokatl@agro.duth.gr |
| HÜSEYIN | TOMBULOGLU | Turkey | htombuloglu@fatih.edu.tr |
| TONTON | TONI MPEMBA | Zaire | tonimpembat@gmail.com |
| MOUSA | TORABI GIGLOU | Iran | m.torabigiglou@gmail.com |
| MIRANDA | TSERODZE | Georgia | miranda.tserodze@gmail.com |
| HISASHI | TSUJIMOTO | Japan | tsujimot@yokohama-cu.ac.jp |
| TUHARYKA | TUHARYKA | Greece | gruntkovskiyg@mail.ru |
| METIN | TUNA | Turkey | metintuna66@yahoo.com |
| YERLAN | TURUSPEKOV | Kazakhstan | yerlant@yahoo.com |
| AYTEN KÜBRA | TÜRKMEN | Turkey | aytenkubraturkmen@gmail.com |
| ÖNDER | TÜRKMEN | Turkey | turkmen@selcuk.edu.tr |
| UEAMAUBUCK | UEAMAUBUCK | Kenya | rock815571@tom.com |
| AHMET | UMAY | Turkey | ahmetumays@hotmail.com |
| TURGAY | UNVER | Turkey | turgayunver@gmail.com |
| SERGEI | USMANOV | Uzbekistan | S.tilibom2014@yandex.ru |
| BÜLENT | UZUN | Turkey | bulentuzun@akdeniz.edu.tr |
| ARZU | ÜNAL | Turkey | arzuunal@gmail.com |
| ANNISA IVANNA M | VANNA | Indonesia | anisvanna@gmail.com |
| ALKA | VASAN | India | alkavasan@yahoo.com |
| AKSHAY KUMAR | VATS | India | akshayvts@gmail.com |
| JOCHEM GEERT | VEGTER | Turkey | j.vegter@rijkzwaan.nl |
| PREETI | VERMA | India | preetiarskota2005@hotmail.com |
| MONIKA | VIDAK | Croatia | mvidak@agr.hr |
| NATALIA | VOLKOVA | Ukraine | natavolki@ukr.net |
| PANTEHA | VOSOUGH MOHEBBI | Iran | pantea.vm67@gmail.com |
| AGUNG | WAHYU SUSILO | Indonesia | soesiloiccri@yahoo.com |
| EBANGHA | WALTER OJONG | Cameroon | talk2walters@yahoo.com |
| LINHAI | WANG | China | linhai827@163.com |
| AIJAZ AHMAD | WANI | India | aijazbotku@gmail.com |
| HAMMA | WASSILA | Algeria | wassi_10@yahoo.fr |
| WILLIAMHAT | WILLIAMHAT | Chad | stanislavkulyd@mail.ru |
| KAMOLIDDIN | XUDARGANOV | Uzbekistan | sergeyusm@mail.ru |
| ASHA | YADAV | India | asha.agrarians@gmail.com |
| HARI SHANKAR | YADAVA | India | hsyadava.rvskvv@gmail.com |
| JAGDISH | YADAVENDRA | India | jpykmw99@gmail.com |

| Name | Surname | Country | Email |
|---|---|---|---|
| ŞADIYE | YAKTUBAY | Turkey | sadiyeyaktubay@yahoo.com |
| NASSER KOUADIO | YAO | Kenya | NYao@cgiar.org |
| BÜŞRA | YAPICI | Turkey | info@intpbc2015.org |
| MEHRDAD | YARNIA | Iran | m.yarnia@yahoo.com |
| TLILI-AIT-KAKI | YASMINA | Algeria | tliliyasmina@yahoo.fr |
| YAUDRYDARW | YAUDRYDARW | Marshall Islands | fanlongvpgfrj@21cn.com |
| CANER | YAVUZ | Turkey | caneryavuzmbg@gmail.com |
| ELIF | YAVUZASLANOĞLU | Turkey | elifs3@hotmail.com |
| SELAMI | YAZAR | Turkey | yazarselami@yahoo.com.tr |
| NATALIIA | YEHOROVA | Russia | yegorova.na@mail.ru |
| BAYAN | YESPEROVA | Kazakhstan | yesperova@gmail.com |
| GULCAN | YIKILMAZSOY | Turkey | gulcan.yikilmazsoy@gthb.gov.tr |
| MUSTAFA | YILDIRIM | Turkey | myildirimkm@gmail.com |
| AYŞE | YILDIZ | Turkey | varolyildiz@hotmail.com |
| FITNET | YILDIZ | Turkey | fitnetyildiz@gmail.com |
| KAMIL | YILMAZ | Turkey | kyilmaz60@hotmail.com |
| ENGIN | YOL | Turkey | enginyol@akdeniz.edu.tr |
| MOHD RAFII | YUSOP | Malaysia | mrafii@upm.edu.my |
| ALI | YÜKSEL | Turkey | ayuksel@yukseltohum.com |
| SERGEY | ZELENTSOV | Russia | vniimk-soy@yandex.ru |
| SINAN | ZENGIN | Turkey | sinzengin@gmail.com |
| NATALIA | ZHEMCHUZHINA | Russia | zhemch@mail.ru |
| LAIADI | ZIANE | Algeria | zlayadi@yahoo.fr |
| EVGENY | ZUEV | Russia | e.zuev@vir.nw.ru |
| VERA | ZYKOVA | Russia | zykova_vera@mail.ua |

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ABSTRACTS


Bu topraklarda
birlikte büyüyoruz
Çiftçimizin umutlarını ektiği her toprağı iyi tanıyor,
bu topraklardan dünyaya bereket saçıyoruz.
MAY
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Tohumda Kalite

## Karpuzunuzu kişiselleştirin!

Sandissima® kişisel kullanım ebatlarında, çizgili ve siyah çeşitleri ile bir karpuzdan çok daha fazlası.

Yükte hafif, lezzette ağır Sandissima® konsepti ile bir an önce tanışın!

## Türkiye'nin Yeni Kavun Markası!

Caribbean® turuncu meyve eti rengi, ekstra lezzeti ve uzun raf ömrü ile Türkiye'nin yeni kavun markası olmak için geliyor!

Suyunu hemen bırakmayan özelliği ve canlı turuncu rengi ile muhteşem meyve salataları da hazırlayabileceğiniz Caribbean® konseptini mutlaka deneyin!

## Ferahlatıcı, tatlı kavun!

mellissimo® mükemmel lezzeti ve tüketime hazır küçük ebatı ile yeni bir Piel de Sapo kavun konseptidir.

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Uzun İtalyan tipi biberlerden oluşan Palermo® konsepti, farklı renk seçenekleri ile de çok yakında sofralarınıza renk katmaya geliyor!

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Gençlik mh. 1330 sk. ● Güneş apt. No: 11/6 ● Antalya - Türkiye ● www.rijkzwaan.com.tr
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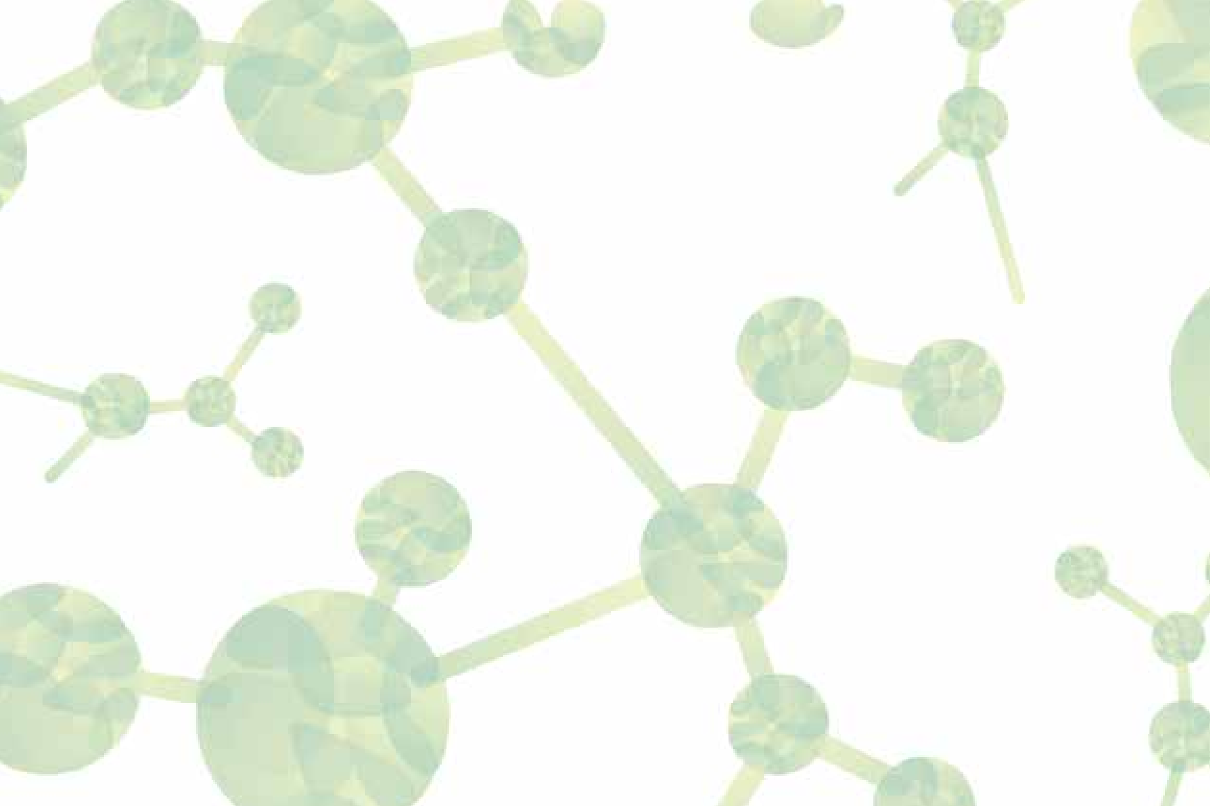

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