Plant Genetic Resources and their Exploitation in the Plant Breeding for Food and Agriculture

BOOK OF ABSTRACTS

18th EUCARPIA
Genetic
Resources
Section
Meeting
May 23-26, 2007
Piešťany
Slovak Republic

SLOVAK AGRICULTURAL RESEARCH CENTRE NITRA
RESEARCH INSTITUTE OF PLANT PRODUCTION PIEŠŤANY

EUCARPIA

European Association for Research on Plant Breeding
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Organizers:
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Piešťany, 2007

18th EUCARPIA GENETIC RESOURCES SECTION
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PLENARY LECTURES

PLANT GENETIC RESOURCES AS A BASE OF FOOD FOR DIVERSE AND HEALTHY DIETS

Peter Ruckenbauer[1], Heinrich Grausgruber[1], Wolfgang Palme[2] and Johann Vollmann[1]
[1]Department of Applied Plant Sciences and Plant Biotechnology, University of Natural Resources and Applied Life Sciences Vienna, Gregor-Mendel-Str. 33, 1180 Vienna, Austria; [2]HBLFA Schönbrunn, Grünbergstr. 24, 1130 Vienna, Austria; (email: peter.ruckenbauer@boku.ac.at)

At the World Food Summit in 1996, the global community agreed to the goal to halve the number of starving people by 2015. In regard to this ambitious goal crop diversity is essential to provide food security in the long term. The thousands of different crop varieties that have been developed over centuries by farmers and plant breeders, together with their wild relatives, carry the genes that will allow humanity to tailor its future plant food supply. The Food Pyramid shows that the groups of foods that should be consumed most to provide the body with protein, carbohydrates, vitamins and minerals are of plant origin, i.e. cereals and vegetables. However, apart from energy intake nutrition is taken on new meaning in the 21st century. Emphasis is now given on foods which can promote well-being and health, and help to reduce the risk of diseases. Several terms are used to describe these bioactive compounds and the foods that contain them, e.g. phytochemicals, nutraceuticals or functional foods. Therefore, the coming challenges comprise not only the supply of energy but also the intensified exploitation of nutritional and other added-values of food crops. In the following examples are given how plant diversity (can) contribute(s) to modern diets.

Cereal products should make-up a major part of the daily diet. A health benefit against heart disease and certain cancers is only provided if a significant part is consumed as whole grains and if the products are low in fat. Consumers, however, often dislike whole-grain products because of their strong flavour and uncommon colour and texture. Hard white wheat, until now only grown on a limited scale, combines good milling and baking characteristics and mild, sweet flavour due to lower amounts of polyphenols and tannins in the bran layers. Whole-grain bread made from white wheat looks and tastes more like the traditional white bread the majority of consumers prefer, but exploits the positive effects of dietary fibre. By contrast intensive pigmented grain types such as yellow, blue, brown-red, purple or black seeded forms of wheat, barley, rice or maize can be used for the production of specialty foods and beverages. In consequence of the antioxidative effects of pigments such as anthocyanins or carotenoids a potential health benefit can be expected from such food products as long as food processing does not destroy or alter the valuable phytochemicals. Beta-glucans, natural gum polysaccharides, are most abundantly in barley and oats. Since their cholesterol-lowering effect was approved functional foods based on barley or oats have gained significant momentum in recent years. Moreover, oats and barley products have the advantage that they can be labeled as GM-free compared to many sterol-containing products based on soybean, canola or maize. Consumers' growing interest in traditional foods that convey 'naturalness' has also stimulated cultivation of neglected and underutilized cereals such as hulled wheats or naked barley in the last decades.

Besides cereals the bulk of our diet should be made-up by vegetables. Consumption of vegetables is largely influenced by lifestyle, but also by trends in society and nutrition. The increasing market share of convenience products does not exclude vegetables. Pre-packed baby leaf salads enhance diversity by including crops as lollo rosso, radicchio, green cos, spinach, orach, swiss chard, mustard, mizuna, arugula or rocket, which on their own are consumed to a lesser extent. Besides the attractiveness such diversity it is healthy too. Leafy salad vegetables are important contributors of vitamins, minerals and phytochemicals with antioxidant activity. The growing interest in Asian kitchen put new vegetables to the perspective of European consumers. Edible soybean (edamame), chinese cabbage, pak choy, oriental celery, oriental cucumbers and gourds, bitter melon etc. are not entirely nameless anymore.

Vegetable oils are an important part of the diet and should preferred compared to animal fat. Edible oils are produced from oil fruits (olive, palm) or industrial crops (soybean, canola, sunflower, cotton etc.). The reservation of consumers against oilseed crops 'designed' by transgenic approaches can increment the interest in hitherto underutilized oilseeds. A promising low-input oilseed is false flax. Cold-pressed camelina oil is a good source of alpha-linolenic acid which an affect several cardiovascular risk factors. The cholesterol-lowering effect of camelina oil was demonstrated to be comparable to that of rapeseed and olive oils. In Finland a broad range of camelina oil products are already available in the largest retail chains.

During the last centuries plant breeders often selected against phytochemicals in which nutritionists are interested today. Negative effects on taste, flavour, texture and appearance were responsible for this endeavour. Therefore, *ex-situ* conservation of extensive collections of plant genetic resources and *in-situ* conservation of landraces and old varieties are important to provide the possibility to detect and exploit nutraceuticals in the future. Recently, the importance of a large genbank collection was impressively demonstrated in regard to food safety. US researchers identified 2 out of 16266 soybean accessions which do not express the immunodominant human allergen P34 of the cystein protease family. The allergen-null trait can now be introgressed into elite breeding lines by conventional breeding methods and provide food with low allergen content in the foreseeable future. Underutilized crops such as grain amaranth, quinoa and buckwheat are basic ingredients in gluten-free diets of coeliac disease-patients. Generally, food allergies are increasing rapidly in industrialized countries. A broad diversity in used edible plants can help to impair the risks.

As demonstrated by a few examples, a huge diversity in plant species can enrich our food culture in regard to both taste and health. In return, richness in food culture can have a major impact on the survival of plant species and landraces on farmers' fields.

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POLICY AND LEGAL INSTRUMENTS AND DEVELOPMENTS ON PLANT GENETIC RESOURCES IN EUROPE - AN OVERVIEW

Jozef Turok
Bioversity International, Via dei Tre Denari, 472A Maccarese, Italy, I-00057; (email: j.turok@cgiar.org)

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THE ESTABLISHMENT OF AN EUROPEAN GENEBANK INTEGRATED SYSTEM (AEGIS) AND IT'S RELATIONSHIP WITH PLANT BREEDING

Johannes M.M. Engels and Lorenzo Maggioni
Bioversity International, Via dei Tre Denari, 472/a, 00057 Maccarese, Rome, Italy; (email: j.engels@cgiar.org)

Within the framework of the European Cooperative Programme on Plant Genetic Resources (ECPGR) an initiative has been taken to establish a European Genebank Integrated System (AEGIS) through a participatory process. The goal of AEGIS is to create a rational and effective system for plant genetic resources for food and agriculture that is aimed at conserving accessions that are genetically unique and important. Such material will be safely conserved under conditions that ensure genetic integrity and viability in the long-term. The identified accessions of cultivated material and their wild relatives will be conserved in a dispersed manner at national and institutional genebanks that are committed to participate in AEGIS on the basis of a formal agreement with the respective governments. It is anticipated that the ECPGR Crop Working Groups are responsible for the coordination of the conservation action plans and that the ECPGR National Coordinators functions as a focal point for conservation activities at the national level. The ECPGR Steering Committee has the overall responsibility for the operation of the system whereas the AEGIS Advisory Committee, including a representative of the European Seed Association, provides supervision and guidance to the AEGIS coordination and its activities.

AEGIS will allow all germplasm accessions and their related information designated to AEGIS to be readily available and easily accessible to users. Ex situ conservation of germplasm will be carried out according to common, agreed quality standards, independently of where the germplasm is physically located and is expected to facilitate the use of and research on the conserved germplasm. A close involvement of plant breeders and other users of the germplasm will be essential to ensure that the use related activities meet their needs. On the policy-side, it is intended to develop AEGIS within the existing legal framework of the International Treaty and, where necessary, to extend its scope according to the spirit and intentions of the Treaty.

THERAPEUTIC POTENTIAL - NEW DIMENSION FOR EXPLOITATION OF PLANT GENETIC RESOURCES

Tibor Maliar[1], Ján Kraic[2], Andrea Sujová[1], Jarmila Drobná[2], Pavol Hauptvogel[2] and Martin Užík[2]
[1]University of SS. Cyril and Methodius, Námestie J. Herdu 2, 917 01 Trnava, Slovakia; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: tibor.maliar@ucm.sk)

Besides of traditional point of view focused on morphological, agronomical, qualitative, phytopathological, and other traits of maintained genetic resources there could be also embedded different usable biological and pharmacological properties related to preventive effects and curative impacts in humans and animals in maintained plant accessions. Account on this selected accessions from collections of *Triticum* sp., *Triticosecale* sp., *Secale* sp., *Hordeum* sp., *Amaranthus* sp., *Fagopyrum* sp., *Avena* sp., *Panicum* sp., *Glycine* sp., *Cicer* sp., *Lupinus* sp., *Lathyrus* sp., *Medicago* sp., *Trifolium* sp., *Anthyllis* sp., *Astragalus* sp., *Coronilla* sp., *Lotus* sp., *Melilotus* sp., and *Onobrychis* sp. were tested by simple biological assays *in vitro* to reveal prospective therapeutic potential against different considerable disorders of organisms - pancreatitis, arthritic disorders, pathophysiological disbalance of the coagulation system, metastasis processes of malignant oncological diseases, degenerative diseases, infections caused by bacterial and fungal attacks, etc. All observed biological effects were compared with effect of two standard substances - synthetic and natural. Present pilot study reveals interesting and unmapped potential of genetic resources maintained in plant genetic resource collections. Indication of thermostability, acidic, and alkalic stability of screened extracts from biological materials is also drafted.

WILD GATHERED FOOD PLANTS AND PLANT DOMESTICATION - CASE STUDIES OF TWO DISTANT AREAS (ITALY AND KOREA)

Karl Hammer[1], Jung-Hoon Kang[2] and Gaetano Laghetti[3]
[1]Institute of Crop Science, University of Kassel, Witzenhausen, Germany; [2]Genebank, Suwon, Republik of Korea; [3]CNR - Institute of Plant Genetics, Bari, Italy

In the last decennia, the Mediterranean diet became famous because of its positive health effects. These effects largely derive from the consumption of wild gathered food plants. As a continuous spectrum between wild and domesticated species exists, it was interesting to study the interaction of the primitive gathering process (in relation to the evolution of mankind) with the advanced domestication process. Many of the plants in South Italy are gathered from the wild, at the same time more or less domesticated races of the same species are grown. The evolution of the crop plants may have occurred some centuries ago, as in Arbutus unedo, Beta vulgaris ssp. maritima, Borago officinalis, Cichorium intybus, Ficus carica, Foeniculum vulgare, Portulaca oleracea and Scolymus hispanicus, or the shift from wild to cultivated species happened only recently, as in Diplotaxis tenuifolia, Muscari comosum, Papaver rhoeas and Silene vulgaris. Domestication and genetic introgression between wild, weedy and cultivated races are typical for the ongoing evolutionary process.The collection of wild plants is a part of the Mediterranean agriculturists' traditional knowledge and stimulates also agri- and horticulture. An intensive use of wild gathered food plants can also be observed in Korea. Like in Italy also many plants have been transferred to cultivation, initiating the domestication process as in Adenophora triphylla, Apacynum lancifolium, Codonopsis lanceolata, Ixeris dentata, Ligularia fischeri, Pleurospermum camtschaticum and Youngia sonchifolia. Also in Korea the use of wild plants leads to new cultivated species.The comparison of both areas helps to understand the process of domestication.

ORAL PRESENTATIONS

Session 1

Plant genetic resources conservation and use: an overview

CROP WILD RELATIVES AT THE GENEBANK OF CNR, BARI, ITALY

Pietro Perrino[1], Valeria Tomaselli[1], Massimo Terzi[1], Giulio Sarli[1], Gina Maruca[1], Lorenza Mallardi[1], Italo Scarascia[1], Marisa Scarascia[1], Pasquale Cataldo[1], Karl Hammer[2] and Domenico Lafiandra[3]
[1]CNR, Plant Genetic Institute - Germplasm Institute, via G. Amendola 165/A, 70126 Bari, Italy; [2]University of Kassel, Germany; [3]University of Tuscia, Viterbo, Italy

The Italian Gene Bank of the National Research Council (CNR) at Bari, started to collect crop wild relatives (cwr), together with threatened crops in 1970. At the beginning cwr did not receive much attention, as it was later on, in collaboration with FAO, IPGRI, ICARDA, IPK (Germany), Institute of Agrobotany (Hungary), University of Tuscia (Italy), and others. Germplasma, gathered in all the Mediterranean Countries, including Italy, Ethiopia, South Africa, Middle East, etc., were shared with national institutions and in some occasions were duplicated to IPK gene bank. The most important collected cwr concern species related to wheat, barley, oat, rye, pea, bean, cabbage, cowpea, lentil, sugar beet, meadow grass, white clover, lettuce, sage, crambe and others. They are preserved *ex situ* at 0°C and 35% of R.H (short and medium term) and at –20°C (long term). A database of the collection by genera and species has been created. A part from the research carried out in other centers on the material provided to them, for which, unfortunately, there is no feedback, a lot of research has been carried out at Bari in collaboration with other Italian and foreign researchers. From 1988 to 2000 the Italian Gene Bank of Bari coordinated a national project of CNR on plant, animal and microbial biodiversity, including cwr, with the aim to improve *in situ* and *ex situ* conservation and utilization of genetic resources. From 2002 to 2005, the Gene Bank, in collaboration with the Ministry of Environment, the Regional Council of Basilicata and the University of Bari, has also realized in Basilicata (at Policoro, PZ) a Thematic Center for the Safeguard and Protection of Mediterranean Plant Biodiversity, including cwr and endemic species of naturalistic importance. Data and information concerning genera and specie of cwr collected, preserved and studied at the Bari Gene Bank for utilization will be presented.

GENETIC EROSION OF LAND RACES OBSERVED DURING THE JOINT CZECH, SLOVAK AND POLISH EXPEDITIONS

Vojtěch Holubec[1], Pavol Hauptvogel[2] and Wieslaw Podyma[3]
[1]Gene Bank, Crop Research Institute, Praha Ruzyně, Czech Republic; [2]SARC - Research Institute of Plant Production Piešťany, Piešťany, Slovakia; [3]Department of Plant Breeding and Plant Protection, Ministry of Agriculture and Rural Development, Poland

During the period 1990 to present many joint or individual expeditions for collecting of genetic resources have been undertaken. Most of them (12) were joint missions organized by the Czech Republic, Slovakia and Poland, mainly in border region but also inland. The main share of collected samples is represented by wild plants (4296 accessions) with agricultural and horticultural use. Out of them 40 % were grasses and 25 % fodder legumes. Land races were of primary attention, but their availability differed according to region and time. While in the Czech territory only a very low number of landraces were found, in Slovakia their cultivation was kept traditionally till now. We were able to collect about 80 % of the land races in Slovakia. Similarly, we collected valuable land races in Beskyd Orawski in Poland. Altogether 168 accessions were collected, out of them cereals were prevailing. From other crops beans were often found in home gardens together with herbs and spices. The most important findings of field and horticultural landraces are discussed with notes on their cultivation and use. Among them were three findings of emmer, *Lathyrus sativus*, dark compact *Sorghum bicolor*, black form of *Pisum sativum*, various landraces of poppy – *Papaver somniferum*, lettuce – *Lactuca sativa* and ornamentals. It is obvious, the land race availability decreases very rapidly from early ninetieths and at present any finding is very rare. A comparison to the land races availability in 70 and 80 have been done on the base of results of German-Czechoslovakian collections leaded by Kühn, Hammer, Hanelt, Pistrick and others and Germen-Polish collections leaded by Kulpa, Góski, Jastrzebski, Hammer, Hanelt and others.

Acknowledgments: This work was supported by Grant numbers: QC0063, 1G46066 and Science and Technology Assistance Agency under the contract APVT- 27-028704.

SCOTTISH LANDRACES: OCCURRENCE, RESEARCH AND *EX SITU* CONSERVATION

Maria Scholten, Niall Green, Nigel Maxted and Brian Ford-Lloyd
University of Birmingham UK, Scottish Agricultural Science Agency, UK

The 2003 UK National Inventory of Plant Genetic Resources for Food and Agriculture commissioned by the Department of Environment, Food and Rural Affairs (DEFRA) identified a number of threatened cereal and fodder landraces, many of which are endemic to Scotland. A brief overview of Scottish landraces, their geographic spread and research projects associated with these crops is provided. The majority of these landraces are found on the Scottish Islands of Orkney, Shetland and Fair Isle in the North, and the Hebrides in the West. Three unique cereal landraces, bere barley, Hebridean and Shetland oat (*Avena strigosa* Schreb.) and a rye landrace (*Secale cereale* L.) are still present. Potato landraces can also be found. Some of the problems associated with UK landrace maintenance are illustrated by the example of Shetland cabbage (*Brassica oleracea* L.) which has been grown on the Shetland Islands for centuries but is now in serious decline. Details of a collecting mission to sample these landraces for *ex situ* conservation is provided and a new *ex situ* conservation maintenance system, the Scottish Landrace Protection Scheme, developed for the protection of Scottish landraces, is explained.

LINGUISTIC ISLANDS AND PLANT GENETIC RESOURCES - THE CASE OF GERMAN SPEAKING VILLAGES IN NORTHERN ITALY

Karl Hammer[1], Salvatore Cifarelli[2] and Gaetano Laghetti[2]
[1]Institute of Crop Science, University of Kassel, Witzenhausen, Germany; [2]CNR - Institute of Plant Genetics, Bari, Italy

Missions for collecting plant genetic resources in northern Italy proved the fast proceeding genetic erosion. Relatively well preserved landraces could be found in an isolated village in the mountains of northern Italy in 2001. This was confirmed in 2003. Further isolated linguistic communities in five additional areas have been visited in 2006. The outcome of the mission showed that there is a positive correlation between the landraces still available in an area and its cultural and linguistic integrity. But the evolution of plant genetic resources is also influenced by the surrounding pressures from Italian agriculturists. Linguistic studies can help in the collection of traditional landraces and in the interpretation of evolutionary pathways.Collecting of folk names is an important feature of ethnobotany and completes the information about plant genetic resources. The material collected includes rye, oats, peas, beans but also very rare crops like poppies and buckwheat. Material has been taken for conservation in the Bari genebank and for further characterization and evaluation.

DIVERSEEDS: NETWORKING ON CONSERVATION AND USE OF PLANT GENETIC RESOURCES IN EUROPE AND ASIA

Markus Schmidt[1], Karl Hammer[2], Poramate Banterng[3], Jan Engels[4], Brian Ford-Lloyd[5], Gregor Giersch[1], Ralph Gretzmacher[6], Rivka Hadas[7], Veronika Hager[6], Zhou Hai-Fei[8], Korous Khoshbakht[2], Qiu Lijuan[9], Nigel Maxted[5], Aung Naing Oo[3,10], Than Lam Nguyen[11], Anan Polthanee[3], Wei Wei[8] And Zhang Zengyan[9]
[1]Organisation for International Dialogue and Conflic Management; [2] University of Kassel, Institute of Crop Science, Department for Agrobiodiversity; [3]Khon Kaen University, Faculty of Agriculture, Department of Agronomy; [4]Bioversity International; [5]University of Birmingham, School of Biosciences; [6]University of Natural Resources and Applied Life Sciences Vienna; [7]Israeli Gene Bank for Agricultural Crops, ARO Volcani Center, Bet Dagan; [8]Institute of Botany, Chinese Academy of Sciences; [9]Chinese Academy of Agricultural Sciences; [10]Yezin Agricultural University, Department of Agricultural Chemistry; [11]Hanoi Agricultural University, Department of Agroecology and Environmental Science

Conservation and sustainable use of plant genetic resources (PGR) is vital in meeting the world's future development needs. Traditional crop varieties and crop wild relatives are often highly

endemic, ecologically rare, and most of them still survive in vulnerable ecosystems in developing countries. Given the importance of genetic resources for food safety, and the fact that centres of origin are mainly located in developing countries, we are convinced that it is absolutely necessary to link European researchers with scientists from these world regions that otherwise do have little or no resources to exchange their research results. Our two year project DIVERSEEDS aims to open European research networks to Asian research colleagues, to establish a communication platform, and to promote knowledge exchange on PGR and its management, taking existing initiatives into account. Participating researchers come from the European Union, Israel, China, Cambodia, Myanmar, Vietnam, and Thailand. The main objective of this project is – guided by the International Treaty of Plant Genetic Resources - to jointly elaborate a list of important PGR issues and recommendations for conservation and sustainable use of plant genetic resources in Europe and Asia. These recommendations will be published and made avaliable to researchers, policy makers, farmers and the general public. Diverseeds is an initiative that promotes international dialogue and cooperation between researchers working on PGR and agricultural biodiversity. – At the EUCARPIA section meeting, we will start with a brief presentation of DIVERSEEDS and will then use most of the time for an interactive workshop with meeting participants to discuss PGR issues of mutual interest to European and Asian colleagues, and possible ways to further promote cooperation and dialogue between PGR experts from these regions.
www.diverseeds.eu

MANAGEMANT AND EVALUATION OF EX SITU COLLECTIONS - THE GATERSLEBEN GENEBANK

Andreas Börner
Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Corrensstraße 3, D-06466 Gatersleben, Germany

World-wide more than 6 million accessions have been accumulated in ex situ genebanks. One of the four largest global collections, housing 150,000 accessions belonging to 890 genera and 3,032 species is maintained at the Leibnitz Institute for Plant Genetics and Crop Plant Research in Gatersleben. This presentation highlights activities of the IPK genebank on management improvement and evaluation of genebank material.

Studies on the genetic integrity after 50 years of maintenance were performed for self-pollinating (wheat) and out-pollinating (rye) crops applying DNA fingerprinting techniques. For wheat a high degree of identity was revealed, which underlines the efficiency of the precautions taken by the IPK genebank to preserve the genetic integrity. In contrast, the out-pollinating accessions revealed extensive shifts in allele frequencies. The extent of changes observed was related to the number of multiplication cycles. Strategies of maintenance and management germplasm collections are discussed.

With respect to the evaluation activities, data from sixty years disease resistance screening of Gatersleben genebank accessions (wheat) will be presented. In total nearly 150,000 tests against different diseases were performed at seedling and adult plant stages. The screening comprised 10,348 accessions belonging to 21 species of the genus *Triticum* as well as 489 randomly selected accessions belonging to 20 species of the genus *Aegilops*. Most of the investigated accessions were hexaploids (8,725), although also tetraploid (1,339) and diploid (127) wheats were included. The probability for finding resistant material was shown to be highest in *Aegilops* and within the diploid species of the genus *Triticum*. Within the genus *Triticum* the percentage of highly resistant accessions decreased with increasing ploidy level.

STATE OF ART OF GRAIN LEGUME MANAGEMENT IN GENE BANKS: RESULTS OF AN INTERNATIONAL SURVEY

María José Suso[1], Margarita Vishnyakova[2], Álvaro Ramos[3], Gérard Duc[4] and Mike Ambrose[5]
[1]IAS-CSIC, Apdo 4084, 14080 Córdoba, Spain; [2]Vavilov Institute of Plant Industry, 190 000, B. Morskaya str. 42, St-Peterburg, Russia; [3]Consejería de Agricultura y Ganadería. Rigoberto Cortejoso 14 2ª planta .47014 Valladolid, Spain; [4]INRA-URLEBP 86510, 21065 Dijon Cédex, France; [5]Department of Applied Genetics, John Innes Centre, Norwich, United Kingdom; (email: ge1susom@uco.es)

An online survey addressed to members listed in the European Cooperative Program for Crop Genetic Resources Networks Working Group on Grain Legumes and Grain Legumes (GL) germplasm managers and breeders was carried out to pinpoint the current problems in the management of GL germplasm, to work out the criteria and decisions involved in the implementation of regeneration procedures and to identify strategic areas where further research is required.

The presentation is based on the online responses and it is the product of author thoughts. Thus, colleagues from around the world who responded to the survey contributed to this presentation that attempts to highlight the main issues concerning the ongoing management and regeneration practices in GL collections.

The survey was divided into three sections: 1) germplasm collection details and current status of the regeneration needs; 2) Assessment over the understanding of basic information required to carry out appropriate regeneration procedures such as the breeding systems, the pollination requirements and pollinating agents, the isolation techniques, etc.. and regeneration facilities; and 3) Assessment of different options, in addition to *ex situ*, such as “in situ” and “on farm” conservation.

Obtaining, collating and analysing different kinds of existing data on mating system of GL species, effective pollination control methods and isolation facilities by species and location is one example of priority issue. In addition, the GL community has made clear in the survey for greater support for development of well-designed methodologies of regeneration that maintain the genetic structure of population. Regarding that the optimum regeneration strategy is more probably to be achieved integrating pollinators with the regeneration procedures. A major concern of GL community is the lack of empirical scientific information on the most suitable pollinator agents. The consequences of *on farm* and *ex situ* conservation strategies have not been well studied and resolved but also the method of researching, understanding and quantifying the complementary role of these strategies have not been well developed. Encouraged by the outcome of the survey authors are eager to support an ecosystem approach to the maintenance of GL germoplasm that consider the four way-interaction between plant, pollinator, environment and farmer and promote the linkage of sustainable use of germplasm with related efforts such as pollinator conservation and farmer participatory breeding.

Acknowledgement: The survey was hosted by ECP/GR secretariat and IPGRI website.

INTEGRATING GENEBANKS INTO BIODIVERSITY INFORMATION NETWORKS

Helmut Knüpffer[1], Dag Terje Filip Endresen[2] and Samy Gaiji[3]
[1]Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany; [2]Nordic Gene Bank, POB 41, SE-230 53 Alnarp, Sweden; [3]Bioversity International, Via dei Tre Denari 472/a, I-00057 Maccarese, Rome, Italy; (email: knupffer@ipk-gatersleben.de)

As called by the International treaty on PGRFA (Article 17), existing information systems should collaborate to form a global information network. According to the Food and Agriculture Organization of the United Nations (FAO), there are more than six million *ex situ* germplasm accessions of agricultural and horticultural crops conserved by genebanks worldwide. Many genebanks have computerised their information, but the database software and data models implemented may differ substantially between genebanks. Under the coordination of Bioversity International (formerly IPGRI), standards for the exchange and integration of germplasm information were developed and adopted by many genebanks.

Today there is no single point of access to all genebank collections worldwide at the accession level, but germplasm data portals such as the EURISCO (European search portal), numerous Central Crop Databases (CCDBs), the Nordic Genebank (NGB, Northern Europe), and the CGIAR’s System-wide Information Network for Genetic Resources (SINGER) among others, show that distributed data on genebank accessions can be accessed from global and regional as well as crop-specific data portals, implemented as classical data warehouses.

The Global Biodiversity Information Facility (GBIF) promotes the exchange of biodiversity related information using a new information technology called web services. Such technology deployed at the level of data providers offers the opportunity to tap remotely into the “living” database. Germplasm collections are very similar information-wise to other biodiversity collections, such as natural history museums, botanical gardens or herbaria. Initiated by Bioversity, GBIF data exchange technology was further developed to suit the needs of the PGR community.

From 2004 on, several genebanks became GBIF data providers, the first being NGB, IHAR (Poland) and IPK (Germany), followed by USDA-GRIN (USA) and CGN (Netherlands). Bioversity joined GBIF in 2006, bringing in SINGER and EURISCO. Thus, with two million accessions, one-third of the world’s germplasm holdings are presently searchable via GBIF. The wide adoption of GBIF technology for PGR information exchange would facilitate an alliance of distributed germplasm information systems. Already, Bioversity International has undertaken a feasibility study for such a global system comprising more than 2.3 million accessions.

A QUALITY MANAGEMENT SYSTEM FOR OPTIMISING THE CONSERVATION AND UTILISATION OF PLANT GENETIC RESOURCES

Ulrike Lohwasser, Andreas Graner and Andreas Börner
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Correnstrasse 3, D-06466 Gatersleben, Germany, (email: lohwasse@ipk-gatersleben.de)

A quality management (QM) system is the documented classification system of a given institution. All relevant key processes are visualized by procedure instructions and described in detail by working instructions. The establishment of a QM system is a measure to increase the satisfaction of the stakeholders (service quality) and to improve the internal genebank management. Moreover, the documentation of the individual processes is a key issue to perpetuate the long standing experience of the employees and their knowledge for a sustainable continuation of the conservation of genetic resources at the Federal *ex situ* Genebank in Gatersleben, Germany.

Three different process types are essential for a successful QM system of the genebank. Service processes to fulfil the customer requirements and to enhance the customer satisfaction, management processes to define the responsibilities and authorities, and supporting processes to assist with all necessary help for a smooth accomplishment of the service processes. Four main service processes for the German genebank have been defined: 1. To provide excellent seed and plant material. 2. To provide scientific knowledge, e.g. by publications or by resources such as the herbarium. 3. To perform research projects to further improve the conservation efforts and the utilisation of genetic resources. 4. To generate the human resources required for the future work on plant genetic resources. The implementation of these four service processes needs governance (management processes) and administrative support (supporting processes). Altogether, this results in a continual improvement of the QM system and in an optimal conservation and utilisation of plant genetic resources.

EVALUATION OF THE INRA BREAD WHEAT (*TRITICUM AESTIVUM L.*) COLLECTION FOR AGROMORPHOLOGICAL, TECHNOLOGICAL AND MOLECULAR TRAITS; BUILDING A CORE COLLECTION FOR CARRYING OUT A MORE COMPLETE EVALUATION

Jean Koenig, Jacques Bordes, Audrey Didier and Francois Balfourier
INRA, UMR 1095 INRA, Université Blaise Pascal 234 avenue du Brézet 63100, Clermont-Ferrand, FRANCE

INRA cereal collections have been grouped in one site at Clermont-Ferrand to optimize the management of these collections. New facilities have been built and an evaluation has been carried out on bread wheat collection of about 10000 accessions. We evaluated agronomical traits: heading date, height, and tolerance to diseases, to frost in field conditions. We described morphological traits: colour of ear and grain, awnedness, compacity, Thousand Grain Weight (TGW). Technological values were estimated through NIRS diagrams while genetic diversity was analysed with microsatellites markers. Diversity within and among different geographical origins or periods of cultivation has been described and a core collection of 372 accessions has been built in order to carry out a deeper evaluation of traits of agronomic interest in wheat germplasm.

UK NATIONAL FRUIT COLLECTIONS APPLE MORPHOMETRIC DATA ANALYSIS

Ruth Howell, Emma-Jane Allen and Mike Jeger
Imperial College, Wye Campus, Wye, Ashford, Kent TN25 5AH, United Kingdom; (email: m.jeger@imperial.ac.uk)

Multivariate methods were used to study the structure of morphological variability within the UK apple cultivar collection and to investigate the applicability of these methods to apple germplasm management. Characterisation data was collected from 164 accessions. Twenty-three characters were scored, comprising 10 quantitative and 13 qualitative traits. Ten sets of quantitative scores were recorded per variety.

Principle Components Analysis (PCA) of the quantitative traits visualised the apple varieties as a single continuous group and accounted for their diversity well. PCA, Canonical Variates Analysis (CVA) and ANOVA from the k-cluster analysis all indicated that the 10 quantitative traits significantly contribute to distinguishing between the apple varieties. Similarly, factor analysis of the 13 qualitative traits using CatPCA (Categorical PCA) produced a single group qualitative model of apple diversity. It also showed that fruit colour traits are both important differentially and are correlated.

The absence of identifiable groups of apple varieties was confirmed by cluster analysis. Various Hierarchical Cluster Analysis procedures were applied to the quantitative data, while the 2step method was used to analyse quantitative and qualitative data together. The results were inconsistent across clustering methods and subsequent CVA of the results showed poorly defined groups with considerable overlapping of group members.

Most previous large scale taxonomic studies of apple varieties have failed to identify groups. This is because, like other perennial out-breeding species, most variation is present within apple populations. Small scale investigations often appear to identify groups, and in this study when a randomly selected subset of 4 varieties was analysed by CVA the results were highly significant and the varieties clearly distinguished. Selection of a ‘core collection’ helps to target genebank resources. The generally accepted method for identifying representative accessions depends on the presence of genetically differentiated subgroups. Given that no such subgroups of apple cultivars exist, a different method is required, possibly based on parentage.

EVALUATION OF ADAPTIVE POTENTIAL OF WILD WHEAT SPECIES AND THEIR USE IN BREEDING OF EMMER WHEAT

Alvina Avagyan
Laboratory of Plants Gene Pool and Breeding, Armenian State Agrarian University, Teryan Str. 74, Yerevan 375009, Armenia; (email: alvinaav@mail.ru)

Having a wide spectrum of adaptation to unfavorable environment conditions wild wheat relatives represent a valuable source of genetic variation for improvement of abiotic stress tolerance in cultivated wheat. New variety of emmer wheat has been created based on crossing of wild two-grain wheat (*T. dicoccoides*) with new form of hard cultivated two-grained wheat.

The evaluation of adaptability and plasticity degree of parental forms with the purpose of appropriate initial material selection has been done based on auxanography method of plants linear growth study. Daily periodicity of linear growth of wild wheat has been studied in the field conditions in pre-mountainous zone of Armenia. Hourly observations for linear growth have been carried out twenty-four hours a day from the first leaves appearance to termination of flowering stage. The daily periodicity of growth has been investigated depending on endogenous and exogenous factors (air temperature, relative humidity, solar radiance duration, organogenesis stages). Several valuable characteristics for breeding have been revealed, such as high adaptation to changing factors of environment including low temperature of air, intensive influence of light flow and solar radiation, low humidity of air.

The data obtained have been used in selection of parental forms for crossings wild and cultivated wheat species. As a result of interspecific artificial hybridization the new variety of emmer wheat Zvartnotc (*T.durum conv. echinoramosum* X *T.dicoccoides*) has been created. Selected variety of emmer wheat combines the adaptive features of wild wheat and productivity characteristics of cultivated emmer variety, and distinguished by stability to stress exogenous factors fluctuations. The new variety has been submitted for state variety testing.

LANDRACES ARE STRUCTURED POPULATION AND SHOULD BE MAINTAINED ON FARM

Valeria Negri, Gildo Castellini, Barbara Tiranti, Renzo Torricelli, Nicola Tosti and Mario Falcinelli
Dipartimento di Biologia Vegetale e Biotecnologie Agro-ambientali e Zootecniche (DBVBAZ), Università degli Studi di Perugia, Borgo XX Giugno 74, 060121 Perugia, Italy; (email: vnegri@unipg.it)

Knowledge of the landrace (LR) levels of diversity is fundamental for LR use in breeding, as well as for planning in situ (on-farm) conservation activities. If genetically similar populations of a certain LR exist in an area, a single farm could carry out the conservation activity. If, however, the populations are different, several farms would need to be involved in their preservation. The level of variation within a population is also important because it affects the persistence of the population over time. Assessing the level of variation also provides the possibility of monitoring population changes and verify conservation effectiveness which is an essential step.

In order to define an appropriate on farm conservation strategy for LRs under threat which can serve as a model for other threatened populations, we studied a cowpea (Vigna unguiculata L.), a common bean (Phaseolus vulgaris L.) and celery (Apium graveolens L.) LR coming from different areas of Italy. The formers are autogamous species, the latter is an allogamous species. Each LR is cultivated in very restricted area (a few hectares). Different samples of each LR were collected from different farmers. In each LR overall and within population variation for several morpho-physiological and genetic traits (by using AFLP; SAMPL and SSR molecular markers) was assessed.

Each LR studied is structured as a metapopulation with a substantial genetic differentiation of subpopulations (i.e. farmer populations) which increases its effective size and consequently its chances of survival. Local extinction of a single subpopulation would reduce the overall amount of variation and should therefore be prevented.

Consequently, the best strategy for preserving the diversity of LRs, even in a restricted area, would be to maintain the entire metapopulation on-farm. This means that each farmer should receive appropriate advice and support to maintain his own population.

GENETIC RESOURCES OF VEGETABLE AND MAPS IN THE CZECH REPUBLIC

Karel Dušek, Kateřina Karlová, Elena Dušková, Helena Stavělíková, Věra Chytilová and Jan Losík
Research Institute of Crop Production, Dept. of vegetables and special crops Olomouc, Šlechtitelů 11, 783 71 Olomouc, Czech Republic; (email: Dusek@genobanka.cz)

Genetic resources of vegetables and medicinal, aromatic and culinary plants (MAPs) are maintained in the Olomouc workplace since 1953. These collections are incorporated in “National Programme for Plant Genetic Resources Conservation and Utilisation” which was accepted in 2002 and whose activities are focused on the protection, conservation and utilisation of plant resources of culture plants. At this time 8985 accessions of vegetables and 619 accessions of MAPs are collected in Olomouc.

Seed propagation as one of the most important tasks of genetic resources conservation is one of the biggest pride of Olomouc workplace. The system and type of isolation cages as well as an ideal insect pollination conditions is an outcome of long-standing optimization of this process. Regeneration of cross-pollinated plants is performed in the conditions almost identical to their natural environment. The airy mobile cages with netting cover are used to discriminate unfavourable hybridisation and bees, bumble-bees and syrphidflies (*Eristalis arbustorum*) are used to improve seed production.

The passport, characterization and evaluation data of accessions (values in scale 1 - 9, estimated on the base of national descriptor lists, which are presently available for the most important and numerous crops) and documentation of seed store in the Gene Bank are summarized to the national documentation system EVIGEZ. The passport data and short information about availability for users are on line on view at http://genbank.vurv.cz/genetic/resources.

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ANNUAL FORAGE LEGUMES COLLECTION (AFLC) IN NOVI SAD, SERBIA

Vojislav Mihailović[1A], Aleksandar Mikić[1A], Branko Ćupina[2], Sanja Vasiljević[1A] and Mirjana Vasić[1B]
[1A]Institute of Field and Vegetable Crops, Forage Crops Department, Maksima Gorkog 30, 21000 Novi Sad, Serbia; [1B]Institute of Field and Vegetable Crops, Vegetable Crops Department, Maksima Gorkog 30, 21000 Novi Sad, Serbia; [2]University of Novi Sad, Faculty of Agriculture, Department of Field and Vegetable Crops, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia; (email: mikic@ifvcns.ns.ac.yu)

Institute of Field and Vegetable Crops in Novi Sad is one of the leading institutions in Serbia in breeding various annual legumes, such as soya bean (*Glycine max* (L.) Merr.), beans (*Phaseolus* spp.), vegetable and field peas (*Pisum sativum* L.) and vetches (*Vicia* spp.). During the last decade of the last century, collecting of accessions of annual forage legumes, undertaken by Forage Crops Department of Institute of Field and Vegetable Crops and Faculty of Agriculture of University of Novi Sad, led to the establishment of Annual Forage Legumes Collection (AFLC) in 2001. The largest part of the collection are accessions either exchanged or donated, with ICARDA as the greatest donor, while others are wild and local populations, collected in various parts of Serbia, new genetic variability, developed within diverse breeding programmes, and cultivars purchased at local markets and healthy food shops. Today, the collection contains 1,460 accessions of 16 genera and 67 species, with 22 species of *Vicia* L., and 16 species of *Lathyrus* L. and with with 555 accessions of pea and 287 accessions of common vetch (*Vicia sativa* L.). Nearly one half of the accessions are advanced cultivars, about 300 accessions are traditional cultivars or landraces and more than 200 each are wild populations and breeders lines. The collection is maintained as a field collection at the Experimental Field of Institute of Field and Vegetable Crops at Rimski Šančevi, near Novi Sad, on a slightly carbonated chernozem soil. The collection passport database contains all relevant data according to Grain Legume Passport Descriptors. All activities related to the sustainable utilisation of the collection are based upon characterisation of its accessions for the most important morphological characteristics, as well as upon their evaluation for yields and chemical composition of forage and grain and tolerance of abiotic and biotic stress.

THE CZECH CORE COLLECTION OF ALFALFA MATERIALS

Tomáš Vymyslický, Jan Pelikán, Pavlína Gottwaldová and Jan Nedělník
Agricultural research, Ltd., Zahradní 1, 664 41, Troubsko, Czech Republic; (email: pelikan@vupt.cz)

Altogether 53 characters were evaluated in the set of 457 materials (varieties, newly bred varieties and wild forms collected in the nature) of the world collection of the alfalfa (*Medicago sativa, Medicago x varia* and *Medicago falcata*). Thirty plants of each origin were planted at the field, ten of them were evaluated in the years 2005 and 2006. All the evaluated characters were included into the analyses. Missing values were replaced by mean value. Cluster analysis was performed in the software Statistica for Windows for all the materials together. Complete linkage method was used for clustering and Euclidean distance as the measure of distance.

GENEPOOL OF UNTRADITIONAL HORTICULTURAL PLANTS OF NATIONAL BOTANICAL GARDENS IN KYIV

Svetlana Klymenko
[1]M.M. Gryshko National Botanical Gardens, National Academy of Sciences of Ukraine, Kyiv, Timiriazevskaja 1, 01014, Kyiv, Ukraine; (email: kvsvkiev@yahoo.com)

About 400 species of fruit and berry plants in Ukraine were introduced. From 50 genus only for two monotype species – *Cydonia* Mill. and *Mespilus* L. was appeared specific reserve by exhausted one, while for most species he remained considerable. The collection of department of acclimatization is represented more than by 120 species and forms of growing wild and 2000 sorts of cultural plants; among them are: *Actinidia* Lindl., *Amelanchier* Medic., *Aronia* Pers., *Chaenomeles* Lindl., *Cornus* L., *Crataegus* L., *Cydonia* Mill., *Cynoxylon* Nakai., *Diospyros* L., *Elaeagnus* L., *Hippophae* L., *Mespilus* L., *Morus* L., *Shepherdia* Nutt., *Sorbus* L., *Shizandra* Michx., *Zizyphus* Mill., *Viburnum* L. and etc. The long-term work showed possibility of the wide use of material of a different botanical-geographical origin for introduction. The best sorts have been incorporated in the "Register of Plants Varieties of Ukraine".

ON THE IMPACT OF CRYOPRESERVATION ON GENETIC RESOURCES CONSERVATION OF THE TWO MOST ADVANCED TEMPERATE CROPS - POTATO AND GARLIC

E. R. Joachim Keller[1], Anja Kaczmarczyk[1] and Klaus J. Dehmer[2]
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK); [1]Correns str. 3, D-06466 Gatersleben, Germany; [2]Parkweg 3a, 18190 Gross Luesewitz, Germany; (email: keller@ipk-gatersleben.de)

Genebanks counteract genetic erosion by various preservation methods. Usually seed storage is the most efficient way. Vegetatively propagated crops require more efforts. Cryopreservation is most efficient for these crops. Despite the potentially similarly high importance for all such material, some crops are more advanced. In Germany, these are potato and garlic. Regarding potato, activities started 1992 in Braunschweig and 1997 at IPK Gatersleben. Since 2004, IPK hosts the central German potato genebank. The droplet cryopreservation method is based on shoot tips cooled in DMSO droplets and fixed on aluminium foil. During the merging process of both German cryocollections, the power of this method was demonstrated using a second re-warming check. The mean regeneration rate of 968 accessions did not change significantly from 40% to 47%. As consequence, IPK follows a combined strategy of field, in vitro and cryopreservation at Gatersleben (cryo) and Gross Luesewitz (field, in vitro). Presently, 9.5% of 3057 accessions are exclusively cryopreserved, while 25% are maintained by an additional method. Efficiency considerations are conducted assessing cryopreservation reliability for different material. Further improvement is expected from research on influence of cold preculture, carbohydrates, amino acids, and phytohormones. The analyses of the methods comprise metabolic and expression studies and visualization of freezing and morphogenesis by electron microscopy. Garlic is maintained by vitrifcation of shoot tips from in vitro plantlets. Cold preculture and plantlet quality are important. The present mean of regeneration capacity is 36%. For further extension of cryopreservation a European GenRes project, starting recently, is used. Organizational structures are established for a tripartite cryobank including safety duplication.

TAXONOMIC DETERMINATION OF PLANT GENETIC RESOURCES - IMPACT AND CONSEQUENCES: CASE STUDY OF *LACTUCA* SPP.

Aleš Lebeda, Ivana Doležalová, Eva Křístková and Alžběta Novotná
Palacký University in Olomouc, Faculty of Science, Department of Botany, Šlechtitelů 11, 783 71 Olomouc-Holice, Czech Republic; (email: ales.lebeda@upol.cz)

The set of 95 *Lactuca* spp. accessions, provided by gene banks in Olomouc (Czech Republic), Gatersleben (Germany), Wageningen (Netherlands), Wellesbourne (Great Britain), Pullman and Salinas (USA), included 12 *Lactuca* species (*L. aculeata, L. altaica, L. dentata, L.*

dregeana, L. indica, L. livida, L. perennis, L. quercina, L. saligna, L. serriola, L. tatarica and *L. virosa*) grouped into 34 duplicate groups on the base of passport data. Plants were grown in the greenhouse and assessed for morphological traits and developmental stages following to the descriptor list (Doležalová et al., 2003). The aim of this work was to verify the taxonomic status of accessions and to define morphologic similarities within duplicate groups. The taxonomic status of 37 accessions was re-determined on the level of species and/or of the lower taxonomic units. Some accessions expressed a hybrid character. The whole set was clustered into five main categories: 1. taxonomic status of 20 accessions from 8 duplicate groups was re-determined, and accessions were morphologically different within the groups; 2. taxonomic status of seven accessions from four duplicate groups was confirmed, and accessions were morphologically different within the groups; 3. taxonomic status of 13 accessions from two duplicate groups was either re-determined, and/or either confirmed, accessions formed subgroups, and they were morphologically similar within subgroups; 4. taxonomic status of 29 accessions from ten duplicate groups was re-determined, and accessions were morphologically similar within groups; 5. taxonomic status of 26 accessions from 10 duplicate groups was confirmed, and accessions were morphologically similar within groups. Taxonomic status of wild *Lactuca* spp. accessions, as declared by holding gene banks, is not always correct and should be verified. The attention should be paid to the passport data of accessions, to identify the original holding institution of accessions and ways of their distribution. Knowledge of correct taxonomic ranging should be a base of all operations with plant material in gene banks, to prevent any genetic pollution and lost. The taxonomic status of germplasm material should be verified before starting of research work with this material, to avoid any confusing interpretation of the results. Morphological assessment should be a starting point and a base of identification of duplicates by other more sophisticated procedures, e.g. by mean of protein and molecular markers (Dziechciarková et al., 2004).

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EVOLUTION OF CHICKPEA FROM *CICER RETICULATUM* LADIZ. TO KABULI TYPES

Cengiz Toker, Huseyin Canci, Nisa Ertoy Inci, Fatma Oncu Ceylan and Serap Melike Icoz
Department of Field Crops, Faculty of Agriculture, Akdeniz University, TR-07058 Antalya, Turkey (email: toker@akdeniz.edu.tr)

Chickpea, *Cicer arietinum* L., (Leguminosae-Papilionoideae) belongs to tribe Cicereae Alef (Kupicha, 1977; Nozzolillo, 1981; van der Maesen, 1987; Ladizinsky, 1995). The genus *Cicer* L. contains 43 species which are mostly perennial and nine species including cultivated chickpea are annual (van der Maesen, 1987). The cultivated chickpea, *C. arietinum* L., is easily crossed with *C. reticulatum* Ladiz., which was discovered in 1974 in south-east Turkey (Ladizinsky and Adler, 1976). Morphological, cytological, biochemical and molecular studies between the wild form and the cultivated form and also their easily crossability relations indicated that *C. reticulatum* Ladiz. is considered the wild progenitor of the cultivated forms (van der Maesen, 1987; Ladizinsky, 1995). As a result of different ecological pressures and selection for agricultural traits by humankind, two types of cultivated chickpea have emerged. The first one, which is referred to as the *desi* characterized by blue-violet flower color and small, dark colored seeds with pigmentation on plants, looks like the progenitor. The other type is referred as *kabuli* type characterized by white flower and large, cream colored seeds without pigmentation on plants.

A total of 1500 seeds of *C. reticulatum* Ladiz. (AWC 611), i.e. 500 seeds each dose, was irradiated with 200, 300 and 400 Gy of gamma rays from a ^{60}Co source in TAEK (Turkish Atomic Energy Agency), Ankara, Turkey. M_1 plants were grown at Antalya location and harvested individually. M_2 generation was raised in separate rows at Antalya location. After germination, treated plants were carefully observed for all viable mutations throughout the life period. A mutant with white flower color was isolated in M_2 generation. Mutation frequency of this was estimated approximately 1/30000 on the basis of M_2 plant progenies. This mutant has white flower color with pigmentation on plant. Flower color (blue, violet/pink and white) in chickpea is controlled by three factors; B, P and C (Muehlbauer and Singh, 1987; Salimath et al., 1996; Kumar et al., 2000).

This results relieved that kabuli types were selected from mutant which were white flowers, thick and cream seed coat color of *C. reticulatum* mutant The result clarified that mutations was one of the factors affecting evolution of chickpea.

FRUIT GERMPLASM IN REPUBLIKA SRPSKA: INVENTORY, COLLECTION AND CONSERVATION

Gordana Đurić, Lidija Tomić, Boris Pašalić, Ljubomir Radoš and Nikola Mićić
Faculty of Agriculture, University of Banjaluka, Bulevar Vojvode Petra Bojovića 1A, 78 000 Banjaluka, Republika Srpska, Bosnia and Herzegovina; (email: lidijatomic@hotmail.com)

Republika Srpska is placed in the northern and eastern part of Bosnia and Herzegovina. Owing to its geographical position in Republika Srpska there are two types of climate: continental in the north and mediterranean in the south. Republika Srpska was exposed to the different civilizations and culture influences through the history. Ottoman Empire ruled until 1878 (1372 - 1878) when Austrio-Hungarians' took a domain.

In time Republika Srpska (Bosnia and Herzegovina) became very rich in biological diversity as the civilizations and climates mixed here.

Fruit genetic resources inventory, collection and documentation in Republika Srpska started during 1989 - 1991 within the project Plant Gene Bank of Yugoslavia. According to the saved documentation there has been inventoried and documented with MCPD details next accessions: *Malus* × *domestica* (11), *Prunus domestica* (6), *Pyrus communis* (11), *Prunus avium* (4), *Prunus cerasus* (2), *Prunus persica* (2), *Prunus armeniaca* (1), *Prunus cerasifera* (6) and *Juglans regia* (4).

Because of known reasons these activities were stopped and enabled to start again through the project »South Eastern European Network on Plant Genetic Resources 2004 - 2014 «. Focal points for SEEDNet implementation in Republika Srpska is Faculty of Agriculture, University of Banjaluka. This project enforced renovation of inventory and collecting activities and supported capacity buildings in order to establish Gene Bank. Inventory and collecting is directed through the Working Group for Fruits and *Vitis* established according to the project proposal. Since 2004 next accessions have been either inventoried or collected: *Malus* × *domestica* (28) and *Pyrus communis* (17). These accessions are documented with collection form and MCPD. Conservation is done *ex-situ* in collection orchard 20 km south from Banjaluka.

SELECTION OF DONORS FOR FRUIT QUALITY AND THEIR UTILIZATION IN BREEDING OF APRICOTS

Krška B., Vachůn Z. and Nečas T.
Mendel University of Agriculture and Forestry in Brno, Department of Fruit Growing, Horticulture Faculty in Lednice, Czech Republic

We have been study of the inheritance in apricot progenies of some parent cultivar from different eco-geographic group. The research of inheritance of the main pomological traits into progenies proved that the easily persistant heritage characters (cases when over 50 % of individuals inherited the value of trait identical to their parents or in between them) include: fruit firmness, flesh colour, skin overcolour, time of ripenning, fruit shape, pit adhesion. On the contrary, variable heritage characters (the value of traits inherited from parents dropped under 50 %) include: fruit taste and fruit size.

ORAL PRESENTATIONS

Session 2

Plant genetic resources enhancement for breeding

EXPLOITATION OF LANDRACES AND WILD BARLEYS IN BREEDING PROGRAMMES

Henryk J. Czembor and Jerzy H. Czembor
Plant Breeding and Acclimatization Institute – IHAR, Plant Breeding and Genetics Department, Laboratory of Applied Genetics, Radzikow, 05-870 Blonie, Poland

Cultivated barley, *Hordeum vulgare* L., is one of the main cereals. It is a founder crop of Old World Neolithic food production and one of the earliest crops domesticated. It is an important crop, ranking fifth in world crop production. In order of importance barley is used for: animal feed; brewing malts; and human food. Barley is a short season, early maturing grain with a high yield potential and may be found on the fringes of agriculture, in widely varying environments, including extremes of latitude and altitude where other crops are not adapted. It extends far into the Arctic, reaching the upper limit of cultivation in high mountains; it grows in desert oases and desert fringes, where it is more salt-and drought-tolerant than other cereals.

However, in modern cultivars of barley, available sources of diverse characteristics is very limited. Consequently, barley breeders are still looking for new genes which can be introduced into existing cultivars. Breeding companies very often cooperate with scientists in evaluation of gene banks large collections of landraces and wild barleys in order to select and create prebreeding material.

Authors participate in several such programmes for creation of prebreeding material which is used by breeding companies in Poland. Major goals of this research programmes are: (1) improve grain quality with high yield, (2) breed new varieties with high adaptability and stable, good quality, (3) breed disease-resistant varieties under different conditions. These goals are connected with current challenges and opportunities for genetic resources of barley. These challenges and opportunities include: (1) nutritional value of feed barley, (2) malting quality, (3) diversity of food products, (3) sustainable agriculture, (4) disease and pest resistance (new sources, multiple resistance), (5) resistance to abiotic stresses.

Barley is the second largest crop represented in the world gene banks. However, there are three major obstacles for an optimal utilization of barley germplasm stored in gene banks: (1) duplications and accessions without adequate passport data, (2) the scarcity of evaluation data on gene bank material, (3) increasing gap between gene banks and practical breeding (long-term breeding or prebreeding is often decreased when breeding is transferred from public to private sector).

Authors will discuss all mentioned above aspects concerning exploitation of landraces and wild barleys in breeding programmes.

LEAF RUST RESISTANCE OF *AEGILOPS MARKGRAFII* GERMPLASM: GEOGRAPHICAL VARIABILITY AND THE USE FOR BREEDING PURPOSES

Annette Weidner[1], Veit Schubert[1], Firdissa Eticha[2], Nayyer Iqbal[3], Elena K. Klestkina[4], Marion S. Röder[1] and Andreas Börner[1]
[1]Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstraße 3, 06466, Germany; [2]Bako Agricultural Research Center, P.O. Box 3, W. Shewa, Ethiopia; [3]Nuclear Institute for Agriculture and Biology (NIAB), Jhang Road, Faisalabad, Pakistan; [4]Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Lavrentyeva ave. 10, Novosibirsk, 630090, Russia; (email: weidner@ipk-gatersleben.de)

Leaf rust resistance of 169 *Aegilops markgrafii* (Greuter) Hammer accessions covering the whole area of distribution was analysed at the seedling stage. Most accessions (66.9%) showed complete resistance. Exclusively resistant accessions originate from the centre of distribution (around Ankara, Turkey). At the periphery in addition heterogeneous and susceptible accessions were found. Crosses of the resistant accession ‘S740-69’ with several susceptible accessions and vice versa revealed one dominant gene and some minor factors responsible for the leaf rust resistance.

From the cross of *Triticum aestivum* L. cv. ‘Alcedo’ x *Ae. markgrafii* (accession ‘S740-69’) different leaf rust resistant euploid introgression lines showing morphological variability were selected. This variability has been caused by the spontaneous integration of *Ae. markgrafii* chromatin into the wheat background. Using microsatellites the *Ae. markgrafii* chromatin was identified on the wheat chromosome arms 2AS, 2BS, 3BL, 4AL and 6DL. In addition, a QTL for the *Ae. markgrafii* leaf rust resistance was mapped to a distal segment of 2AS in a study of an F_2 population developed from a cross between a resistant introgression line with a wheat-like growth habit and the susceptible wheat cultivar ‘Borenos’.

Electron and fluorescence microscopical studies revealed that the resistance is mainly based on a hypersensitive reaction.

COMPARISON OF SELECTION METHODS ON ‘PIGARRO’, A PORTUGUESE IMPROVED MAIZE POPULATION WITH FASCIATION

Pedro M.R.Mendes Moreira[1], Silas E. Pêgo[2], Carlota Vaz Patto[3] and Arnel R. Hallauer[4]
[1]Escola Superior Agrária de Coimbra. Departamento de Fitotecnia. Sector de Protecção Vegetal.; [2]Instituto Nacional de Investigação Agrária; [3]Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa; [4]Maize breeder and Distinguished Professor in Agronomy, 1505 Agronomy Hall, Iowa State University, Ames, IA 50010; (email: pmoreira@esac.pt)

During 20 years of participatory plant breeding at Sousa Valley, mass selection and recurrent selection were applied on ‘Pigarro’, a maize landrace from the Sousa Valley Region, Portugal. To increase the knowledge on the genetic potential of this landrace, an evaluation of the yield gain and plant performance was conducted in Portugal (3 locations in 2 years) and in the USA (4 locations in one year). Results on ANOVA comparison of selection cycles between and within breeding approaches, and regression analyses on the rate of direct response to selection will be discussed.

GENE MINING AND USE IN IMPROVING YIELD, RESISTANCE TO STRESSES AND QUALITY IN LENTIL

Ashutosh Sarker, Bonnie Furman and William Erskine
International Center for Agricultural Research in the Dry Areas (ICARDA), P. O. Box 5466, Aleppo, Syria

Lentil (*Lens culinaris* Medikus subsp. *culinaris*) is an annual diploid species (2n = 14), grown as a pulse crop predominantly in Asia and Africa. It is one of the early-domesticated crops of the Fertile Crescent of the Near East and plays an important role in human, animal and soil health improvement. Its seed is a rich source of protein, minerals (K, P, Fe and Zn) and vitamins that contribute to nutritional security to the poor in many developing countries. The International Center for Agricultural Research in the Dry Areas (ICARDA) is situated in the Center of Origin of lentil and has a global mandate for its improvement. Since its inception, the Center participated in many collection missions in the countries of its Center of Diversity and in many lentil-growing countries. In this endeavor, ICARDA has assembled 11,125 cultivated and 583 wild accessions of lentil, the largest collection in the world. Of these, 7624 cultivated and 375 wild accessions have been characterized, searched for desirable traits and utilized to develop new genetic stocks and improved cultivars. The germplasm accessions possess marked genetic variation for agro-morphological, phenological, biotic and abiotic stress resistance and quality traits, the basis for its improvement. Using early-maturing germplasm, new transgressive segregants with extra-earliness have been developed for short-season environments of southerly latitude countries to fit in various cropping system niches. Genotypes with high level of resistance to key diseases (Ascochyta blight, rust, vascular wilt and Stemphylium blight diseases), drought and winter-hardiness have been developed and shared with national programs. Cultivars with suitability to machine harvest have been developed for West Asia and North Africa. Construction of improved genotypes with high concentration of iron and zinc are underway and some micronutrient-dense cultivars are already under fast tracking. To date, more than 100 lentil varieties have been released by various national programs, which emanated from ICARDA-supplied germplasm. New germplasm are being collected mainly from the Central Asia and the Caucasus region and through incorporation of new genes improved breeding lines are being developed as international public goods.

DISCRIMINATE FUNCTION – APPLICATION FOR DETERMINATION OF OIL AND FIBER FLAX *LINUM USITATISSIMUM* L. CULTIVARS BY QUANTITATIVE CHARACTERS

Beáta Stehlíková[1], Janka Nôžková[2] and Ján Brindza[3]
[1]Department of statistics and operation research, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic; [2]Institute of Biodiversity Conservation and Biosafety, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic; [3]Department of genetics and plant breeding, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic; (email: janka.nozkova@uniag.sk)

The aim of our research was to look for the suitable method for distinguishing of flax genotypes according to their economic use on fiber and oil types. For experimental work was used the set of 265 genotypes of flax; the data were obtained in the years 2000 – 2003. Complete data for 23 traits were obtained from the set of 252 genotypes. Biological material was obtained from Slovak National Gene Bank, RIPP Piešťany (139 genotypes) and from research and breeding institute Agritec Ltd. Šumperk (113 genotypes) from Czech Republic. Economic use was known in the case of set of 113 genotypes from Agritec Ltd.. At our disposal were 86 fiber and 27 oil types of flax. For verification of experimental set (265 genotypes) normal distribution were applied three tests of goodness-of-fit (Kolmogorov-Smirnov, Cramer-von Mises and Anderson-Darling tests). The H0 hypothesis on the level of 95 % significance was rejected. According to results of normal distribution was confirmed that the experimental set consisted from oil and fiber types of flax. By the application of kernel density function was confirmed an unambiguous distribution of 113 genotypes from Agritec Ltd. on two types according to two traits - Z2 – technical length of stem (mm) and Z61 – weight of thousand seeds (g). Consecutively was confirmed the normal distribution by the Kolmogorov-Smirnov test for both subsets and two selected traits. These results were affirmed by discriminate analysis in the experimental set of 113 genotypes. The discriminate analysis correctly classified 104 genotypes i.e. 92% in the consistency with known economic use of 113 genotypes with use of traits (Z2, Z61). Obtained discriminate functions were used for separation of 139 genotypes, which economic use was not known. The results are obtained by support of the project no. aAV/1121/2004 Department of education of the Slovak Republic.

USE OF *BRASSICA RAPA* GENETIC RESOURCES FOR BIOMASS PRODUCTION: HETEROSIS IN INTER - AND INTRA - POPULATION CROSSES

Atta Ofori and Heiko C. Becker
Department of Crop Sciences, Georg August University Göttingen, Von Siebold Str. 8, 37075 Göttingen, Germany

The use of plant biomass for biogas in Europe and other parts of the world has presently received much attention. Cultivation of biomass crops has therefore become a major agricultural alternative. Winter *B. rapa* is a potential biomass crop, mainly because of its high early biomass production. It could be used as a pre-crop harvested early in the year followed by a second crop. For use as oilseed, low erucic acid and low glucosinolate content is required, a seed quality that is hardly available in winter *B. rapa* accessions from genebanks. However for biomass breeding, old cultivars with high erucic acid and glucosinolate can be used. This study was therefore conducted to estimate inter- and intra-population heterosis in three cultivars; Largo (modern cultivar), Rex (older forage type) and Steinacher (old oilseed cultivars).

Twenty seven full-sibs (FS) with 9 each coming from the three possible combinations, 3 intra-populations FS, 3 parental populations and 3 composites formed from both inter and intra population crosses were evaluated at two locations in Germany. Data were recorded on days to flowering (DTF), fresh biomass yield (FBY), dry matter content (DMC), and dry biomass yield (DBY).

Most FS performed better than their mid-parent. Analysis of variance (ANOVA) showed significant differences among locations and entries x locations for most of the trait studied. On average, relative mid-parent heterosis (RMPH) of DBY across locations for inter population crosses were 21.60 for Rex x Largo, 11.67 for Rex x Steinacher and 10.00 for Largo x Steinacher whiles that of intra-population crosses were 11.28 for Rex x Rex, 13.30 for Largo x Largo and 8.28 for Steinacher x Steinacher. The mean RMPH recorded for the composites were 22.56 for composite Rex x Largo, 7.85 for composite Rex x Steinacher and 14.84 for composite Largo x Steinacher. In conclusion, the smaller differences between inter and intra population heterosis observed in this study was in agreement with our earlier work on within and between genetic diversity assessed by molecular markers.

EXPLOITING UNTAPPED WILD GENETIC DIVERSITY FOR CIMMYT WHEAT IMPROVEMENT

Maria Zaharieva[1], Susanne Dreisigacker[1], Claudia Bedoya[1], Masahiro Kishii[1], Abdul Mujeeb-Kazi[1], Thomas Payne[1] and Marilyn Warburton[1]

[1]International Maize and Wheat Improvement Center (CIMMYT), Apdo Postal 6-641, 06600 Mexico, D.F., Mexico; (email: m.zaharieva@cgiar.org)

Over the past century, the development and successful application of plant breeding methodologies has produced high-yielding wheat varieties. However, many potentially beneficial alleles have been lost due to bottlenecks imposed by the domestication of wheat coupled with intensive selection in modern breeding. Allelic variations of genes present in wild relatives can be recovered only by going back to the ancestors of cultivated wheat. One way to do this is the reconstitution of hexaploid wheat by interspecific crosses. Since the early 1990s, the International Maize and Wheat Improvement Center (CIMMYT) has focused largely on the creation of synthetic hexaploid wheats and backcrossing them to elite bread wheat cultivars producing synthetic derived lines that incorporate new, useful alleles. To date, CIMMYT has produced more than 1,000 synthetic hexaploid wheats using various durum wheat (AB genome) and *Aegilops tauschii* (D genome) resources. At the molecular level these synthetic hexaploid wheats and their derivatives are genetically diverse and distant from traditional bread wheat cultivars. Other wheat relatives can also be used as AB genome donors to generate new synthetics, thus providing access to new sources of diversity, alleles and traits. Diversity within AB genome species was analysed using microsatellite markers (SSRs), which showed that durum wheat accessions cluster together and are closely related to most of the *Triticum turgidum* subsp. *polonicum* and subsp. *turgidum* accessions. *Triticum turgidum* subsp *dicoccum* and subsp. *dicoccoides* accessions are less related to durum wheat and possessed higher genetic diversity and allelic richness. The use of *T. turgidum* subsp. *dicoccum* and subsp. *dicoccoides* accessions to develop new synthetic hexaploid wheats may better exploit the untapped genetic diversity of wild species for wheat improvement.

DEVELOPMENT AND MOLECULAR CYTOGENETIC ANALYSIS OF NEW WHEAT/WINTER BARLEY ADDITION LINES

Márta Molnár-Láng, Éva Szakács and Gabriella Linc

Agricultural Research Institute of the Hungarian Academy of Sciences, H-2462, Martonvásár, P.O. Box 19, Hungary; (email: molnarm@mail.mgki.hu)

The introgressive hybridization of barley to wheat makes it possible to transfer useful characters such as earliness, drought and soil salinity tolerance, and various traits for specific nutrition quality. Since the production of the first set of Chinese Spring/Betzes spring wheat/spring barley addition lines in 1981 only two new 5H and 6H addition lines from a hybrid between the wheat cultivar Shinchunaga and the barley cultivar Nyugoruden have been developed. It will be necessary to develop addition lines using different barley genotypes with great genetic variability for agronomic traits (two or six-row, winter or spring habit, biotic and abiotic resistance, etc.) if favourable characters from this cereal are to be mapped and transferred.

New disomic (2H, 3H, 4H, 1HS) and monosomic (2H, 3H, 6H, 7H) wheat/barley (*Triticum aestivum/Hordeum vulgare*) addition lines have been developed from hybrids produced in Martonvásár using the German two-rowed winter barley cultivar 'Igri' and the Ukrainan six-rowed winter barley cultivar 'Manas'. The addition lines were identified using genomic *in situ* hybridization (GISH) and two-colour fluorescent *in situ* hybridization (FISH) with the probes GAA, pAs1, HvT01, Afa family and pTa71 and with SSR markers. Combinations of four probes (HvT01-GAA, HvT01-pTa71, HvT01-Afa family) in FISH made it possible to identify all the barley chromosomes.

The 'Mv9kr1'/'Igri' and 'Asakaze komugi'/'Manas' disomic addition lines and the translocation lines originating from these additions may provide important additional information on barley genetics, as the barley genotypes are of the winter type and carry different genes (e.g. vernalization, frost resistance) compared to the spring type Chinese Spring/Betzes addition lines reported previously. From the point of view of wheat breeding these addition lines are potential sources of abiotic stress resistance, particularly for drought and salt tolerance.

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THE EXPLOITATION OF 1EBN *SOLANUM* SPECIES FOR POTATO PRE-BREEDING AND BREEDING RESEARCH

Ramona Thieme[1], Elena Rakosy-Tican[2], Tatjana Gavrilenko[3], Olga Antonova[3], Marion Nachtigall[4], Jörg Schubert[4], Udo Heimbach[5] and Thomas Thieme[6]
[1]Federal Centre for Breeding Research on Cultivated Plants, Institute of Agricultural Crops, Rudolf-Schick-Platz 3a, 18190 Groß Lüsewitz, Germany; [2]Babeş-Bolyai University, Clinicilor str. 5-7, 3400 Cluj-Napoca, Romania; [3]N.I. Vavilov Institute of Plant Industry, B. Morskaya Str. 42, 190000 St. Petersburg, Russia; [4]Federal Centre for Breeding Research on Cultivated Plants, Institute of Resistance Research and Pathogen Diagnostics, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany; [5]Federal Biological Research Centre for Agriculture and Forestry, Institute for Plant Protection in Field Crops and Grassland, Messeweg 11/12, 38104 Braunschweig, Germany; [6]BTL Bio-Test Lab GmbH Sagerheide, Birkenallee 19, 18184 Sagerheide, Germany; (email: r.thieme@bafz.de)

The cultivated potato is a major crop with complex quality requirements. For breeding of new varieties germplasm resources are essential in order to transfer genes for valuable production, quality and more importantly resistance traits to pathogens and pests. Wild *Solanum* relatives provide genetic diversity, but there are crossing barriers between the majority of the 200 wild species in *Solanum* section *Petota* and cultivated potato (Spooner et al. 2004) because of differences in Endosperm Balance Number (EBN). In addition, to overcoming hybridization barriers by ploidy manipulations, bridge and reciprocal crosses, mentor pollination, hormone treatments, embryo rescue there is another attractive tool, somatic hybridization by cell fusion.

Using protoplast electrofusion fertile interspecific somatic hybrids were obtained between wild species of the Series *Etuberosa*, *Bulbocastana*, *Pinnatisecta*, *Commersoniana* and potato varieties and breeding clones. Backcross progenies were produced by crossing with cultivated potato. Plants of wild species from genebank accessions, somatic hybrids and backcross progenies were characterized morphologically and for resistance to virus diseases (*Potato virus Y*, *Potato leafroll virus*), aphids, foliage and tuber blight caused by the oomycete *Phytophthora infestans* (Mont.) de Bary and the Colorado Potato Beetle ((*Leptinotarsa decemlineata* (Say)).

Results of the integration of this germplasm into pre-breeding and breeding research in potato are presented.

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SOMATIC HYBRIDS BETWEEN POTATO AND *SOLANUM CHACOENSE* ACCESSIONS HIGHLY RESISTANT TO COLORADO POTATO BEETLE

Elena Rakosy-Tican[1], Adriana Aurori[1], Ramona Thieme[2], Thomas Thieme[3], Radu Grumeza[4], Ivan Famelaer[4], Jan De Riek[5] and Geert Angenon[4]
[1]Plant Genetic Engineering Group, Faculty of Biology, Babes-Bolyai University, Clinicilor 5-7, Cluj-Napoca 400006, ROMANIA; [2]Federal Center for Breeding Research on Cultivated Plants, Institute of Agricultural Crops, Rudolf-Schick-Platz 3a, D-18190, Groß Lüsewitz Germany; [3]BTL Bio-Test Lab GmbH Sagerheide, Birkenallee 19, 18184 Sagerheide, Germany; [4]Laboratory of Plant Genetics, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Cedex, Belgium; [5]CLO, Department of Plant Genetics, Caritasstraat 21, 9090 Melle, Belgium, (email: arina5744@yahoo.com)

Somatic hybrids were produced by electrofusion of selected potato cvs. and *Solanum chacoense* (*S. chc*), which is highly resistant to Colorado potato beetle (CPB). Pre-evaluation resistance tests based on survival and increase in weight of larvae of CPB after feeding on leaves of different wild species showed that the two *S. chc* accessions are the most resistant to CPB. Different strategies were used in the somatic hybridization experiments. In the first, transgenic *S. chc* carrying *gfp* reporter gene, obtained by *Agrobacterium tumefaciens* mediated transformation (plasmid pHB2892) of stem segments, was used to select putative hybrid callus. The results based on *gfp* visual screening proved that vigorous growth is a good criterion for selection as *S. chc* protoplasts did not regenerate callus in the culture conditions employed. The second strategy was to produce somatic hybrids between the economically important potato cvs.: Agave, Baltica, Delikat and Rasant and two accessions of *S. chc*: GLKS 138 (Groß Lüsewitz – Gene Bank) and PI 4583101974 (high leptine producer – Sturgeon Bay Wisconsin). In total 84 putative hybrid clones were characterised by flow cytometry, chromosome counts, SSR and AFLP markers, evaluated in a greenhouse for male and female fertility, and backcrossed (BC_1) with the cultivars. Resistance to CPB of the somatic hybrids and BC_1 progeny is currently being determined. The third strategy involved somatic hybridization of transgenic mismatch repair (MMR) defficient *S. chc* (high leptine producer), carrying *msh2* antisense or dominant competitive gene, with cv. Delikat. The regeneration of a high number of putative hybrid plants and selection based on vigorous growth and flow cytometry, makes it possible to identify hybrids with new characters useful for potato breeding. MMR deficiency is expected to induce a high frequency of homeologous recombination during mitosis and meiosis, and to increase introgression of multiple genes into the potato gene pool.

ORAL PRESENTATIONS

Session 3

Molecular and information technologies for plant genetic resources – challenges and opportunities

UNRAVELLING UNANTICIPATED CONSEQUENCES IN TRANSGENIC PLANTS: WHAT CAN WE LEARN?

Jonathan Latham and Allison Wilson
Bioscience Resource Project, PO Box 66, Ledbury, HR8 9AE, UK; (email: jrlatham@bioscienceresource.org)

Plant transformation is frequently considered to be a predictable and straightforward method for introducing single traits into plant species. An alternative view is that plants are complex systems which, for various reasons, respond unpredictably to plant transformation. In an attempt to distinguish between these views, which have important implications for practical plant biotechnology and also biosafety, we have surveyed the peer-reviewed plant biology literature for studies evaluating the phenotypic consequences of plant transformation. Our purpose was to attempt to answer the following questions: 1) How common are unanticipated consequences of plant transformation? 2) What is the phenotypic spectrum of unanticipated consequences? 3) What mechanisms are responsible for unanticipated consequences?

So far, we have found numerous examples of heritable unanticipated consequences in transgenic plants. These include unanticipated phenotypes with morphological, reproductive, ecological, nutritional and toxicological deviations from the parental phenotype.

Because these phenotypes must have some underlying molecular basis we have organised the examples to clarify what that might be. In many cases the specific introduced transgene is clearly the cause since multiple independent lines show the same, or a similar, phenotype. In many instances however, the transgene *per se* appears not to be responsible and this finding implicates a change to the plant associated with the method of plant transformation. Unanticipated consequences falling into this latter category are associated with both *Agrobacterium*-mediated transformation and particle bombardment transformation methods.

CZECH WINTER WHEAT COLLECTION- ITS PROFILE AND “CORE” FORMATION

Ladislav Dotlačil, Zdeněk Stehno, Leona Lejšová, Iva Faberová and Václav Dvořáček
Crop Research Institute, 161 06 Praha 6 – Ruzyně 507, Czech Republic

The study aims to increase users´ value and improvement of study and management methods in winter wheat collection, which is the largest collection of genetic resources (GR) in the Czech Republic. Genetic variability was evaluated in model collection of winter wheat which represents diverse types and origin. The cultivars were sown and evaluated in field trials, and characterized using storage proteins (HMW Glutenins) and DNA markers (SSR). On the base of gained data, we calculated genetic distances among cultivars using cluster analyses. Representatives of homogenous clusters and genetically distant cultivars were selected as items of the “core” collection. We carried out analyses of all available pedigrees of winter wheat cvs and identified cultivars, which represent particular clusters and often occur in pedigree patterns. On the base of all this information we have created “core” collection of winter wheat.

Model collection (436 cvs.) became a base for creation of “core” collection. Using 40 SSR markers genetic diversity was estimated and we were able to eliminate 74 cvs. of high similarity. Similarity analyses based on morphological and agronomical data could identify only 34 identical cvs. by comparable similarity level. As a next step, we studied diversity of HMW –Glu subunit patterns as diversity markers. After all, Glu –alleles showed too low diversity to distinguish cvs. satisfactorily; occasionally we could use rare alleles as diversity markers. As a result, 353 accessions were chosen to the “core” set.

Using pedigree analyses another set of 541 accessions from the entire collection could be selected (original accessions, cluster representatives) without significant diversity decrease within the set. These cvs. should be further characterized and selected accessions added to the “core”. Pedigree analyses can be helpful in first steps of “core” creation, as an added tool to morphological and DNA markers. The procedures used can be applied in large collections of other crops. Jointly with the experimental work, characterization and evaluation data on wheat genetic resources have been significantly extended and valuable donors were identified.

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EVALUATION OF GENETIC RESOURCES AT THE GENE BANK AT THE AGRICULTURAL INSTITUTE OF SLOVENIA (USING MOLECULAR, BIOCHEMICAL AND MORPHOLOGICAL MARKERS)

Vladimir Meglič
Agricultural Institute of Slovenia, Hacquetova 17, 1000 Ljubljana, Slovenia; (email: vladimir.meglic@kis.si)

Early projects to collect Slovenian autochthonous populations, ecotypes and landraces of agricultural species were initiated about 50 years ago. Phytogeographic and historical background has supported the development of the national programme and through that conservation of plant genetic resources in Slovenia. The primary goal of the Slovene Plant Genetic Resources Programme for Food and Agriculture, where three istitutions are involved (Agronomy Dept. at the Biotechnical faculty of the University of Ljubljana, Institute for Hop Research and Brewing of Slovenia, Žalec and Agricultural Institute of Slovenia, Ljubljana), is to maintain, evaluate, regenerate and preserve Slovenian autochtonous species, ecotypes, populations and landraces of agricultural, medicinal and aromatic plants. All three institutions are housing more than 5000 accessions. Germplasm collection at the Agricultural Institute of Slovenia houses among other, more than 3000 accessions of grain legumes, *Allium, Solanum tuberosum*, *Triticum*, *Brassica*, *Lactuca*, forage crops, *Rubus* and *Vitis*.

The gene bank at the AIS holds an extensive *ex situ* collection of more than 1000 bean (*Phaseolus vulgaris* L.) accessions collected from various parts of Slovenia. In a more comprehensive analysis the genetic variation and relationships among and within accessions were described using molecular (AFLP, SSR, RAPD), biochemical (seed proteins) and morphological markers. In a similar way collection of lettuce (AFLP, SSR, morphological), corn landraces (MITE, IEF, morphological), cabbage (SSR) and potato (SSR) was evaluated and described. The *Phleum pratense* and *Trifolium pratense* germplasm collections were evaluated using morphological and chemical characteristics and assessement of the net lactacion energy and yield.

During the past few years, the Agricultural Institute of Slovenia put the emphasis on collecting activities, broadening of the collection with autochtonous material, and central crop database activities. In addition to the ex situ conservation, the material is available as well for breeding and potentially for use within the National Rural Development Programme.

CHARACTERIZATION OF GENETIC DIVERSITY AND STRUCTURE ANALYSIS WITHIN PEA (*PISUM SATIVUM* L.) GERMPLASM AT AGRITEC LTD. COLLECTION

Petr Smýkal[1], Jiří Jarkovský[2], Jukka Corander[3] and Miroslav Hýbl[1]
Agritec Plant Research Ltd., Plant Biotechnology Department, Zemědělská 2520/16, CZ-787 01 Šumperk, Czech Republic; Department of Mathematics and Statistics P.O. Box 68 ,FIN-00014, University of Helsinki, Finland; Institute of Biostatistics and Analysis, Masaryk University, Kamenice 3, CZ625 00 Brno, Czech Republic

A large collection, 1 244 accessions, of the *Pisum* genus is conserved and maintained at AGRITEC Ltd. Šumperk. To facilitate the management and increase efficiency of the use, a core collection is being currently developed. Also for breeding it is important to know the genetic basis of cultivars, especially to see if it has not become too narrow to render crops more vulnerable to diseases or pests. Additionally accessions which display DNA profiles most distinct from others are likely to contain the greatest number of novel alleles, which can be exploited in breeding.

The 164 accessions representing Czech and Slovak varieties bred over last 50 years were selected for evaluation of genetic diversity in this study. These were characterized by 42 morphological descriptors in two growth seasons, and DNA of bulk made from 10 plants per accession was investigated by several molecular markers, including microsatellite SSR and retrotransposon-based markers. The emphasis was put on easily scorable co-dominat RBIP (Retrotransposon-Based Insertion Polymorphism) markers based on the *PDR-1 Ty1-copia* element and microsatellite loci. Additionally, high copy *Ty3-gypsy* type elements, *Ogre* and *Cyclop* were successfully applied in multiplex IRAP-PCR (Inter-Retrotransposon Amplified Polymorphism) format (Smýkal 2006).

In total, 12 selected SSRs, 25 RBIP markers and 2 IRAP markers produced altogether 56 scorable polymorphic data points for each accession. Molecular data were subjected to genetic distance analysis by NTSYS-pc software. Calculated genetic distance of investigated set ranged from 0.5 to 0.96 of Jaccard Coefficient. Cluster analysis by Ward method has yielded 6 to 7 clusters both for SSR and RBIP data. Euclidean distance clustering of morphological characters structured set into 5 to 7 clusters. To enable integration and evaluation of all data in one analysis, Bayesian method using BAPS software was applied. The most informative and the best corresponding to pedigree showed the consecutive calculation first by morphological follow by molecular data. Based on morphology the best clustering by log of marginal likelihood was achieved for 3 or 6 clusters, with clear separation of fodder, dry seed and *afila* types of pea. The correspondence with Principle Component Analysis was performed. Clusters were further refined by DNA data into 12,17 a 4 sub-clusters demonstrating structuring of investigated set. The most informative ordination method for molecular data showed to be Multidimensional Scaling.

Division into 3 distinct breeding periods (prior to 1960, 1960-75, 1975 till recent) has revealed significant decrease in genetic diversity over time by all markers investigated by PopGene. Analysis of 10 individual plants for given accessions demonstrated heterogenity/ composed nature rather then residual heterozygosity. Close investigation of 5 selected accessions has revealed the possibility of genetic drift over period of germplasm maintenance. All these results are used in further work aiming at core collection development.

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GENETIC RESOURCES OF BARLEY AND OAT CHARACTERISED BY MICROSATELLITES

Leona Leišová and L. Kučera
Crop Research Institute, Drnovska 507, 161 06 Prague, Czech Republic; (email: leisova@vurv.cz)

Barley *(Hordeum vulgare* L.) and oat (*Avena sativa* L.) are important crop species. 1865 accessions of winter barley, 2707 accessions of spring barley and 1998 accessions of oat are hold in RICP Gene bank. Core collection is used to be established as tool for germplasm study, conservation of genetic variability and for the identification of useful genes. This information is valuable for breeders when a source of new alleles is needed.

This study examines the use of neutral genetic markers to guide sampling from a large germplasm collection with the objective of establishing from it a smaller, but genetically representative sample. Genetic variation of 176 barley accessions were analysed using 26 microsatellite loci, covering all 6 chromosomes. 330 oat accessions were analysed using 26 microsatellite loci that are mapped only into linkage groups. The cultivars of the both crops are originated from countries all over the world. For 26 barley microsatellite loci, 328 alleles were detected. The average number of alleles per locus was 12.6; it is lower than in bread wheat in previous work. In oat, analyses showed even lower level of the diversity than in barley. The comparison between wheat, barley and oat level of genetic diversity and its possible causes are discussed.

Cluster analyses based on microsatellites data showed that diversity in studied files of barley and oat accessions are not randomly distributed. It can be explained mainly by temporal impact to the breeding processes in different countries during last century. Accessing diversity at molecular level using microsatellite analysis gave us valuable information on the genetic structure of cereal core collections and provided new insights on genetic diversity of important crop genetic resources.

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GENETIC DIVERSITY AND ORGANIZATION OF A REPRESENTATIVE *PHASEOLUS VULGARIS* GERMPLASM COLLECTION FROM BULGARIA

Nasya Tomlekova[1], Jean-Pierre Baudoin[2], Ivan Poryazov[1] and Lilia Krasteva[3]
[1]Maritsa Vegetable Crops Research Institute, 4003 Plovdiv, Bulgaria; [2]Faculté Universitaire des Sciences Agronomiques de Gembloux, Gembloux, Belgique; [3]Institute of Introduction and Plant Genetic Resources "K. Malkov", 4122 Sadovo, Bulgaria; (email: nasia.tomlekova@gmail.com)

Evaluation of the Bulgarian *Phaseolus vulgaris* L. germplasm collection has been undertaken in order to constitute a representative "core collection" on the basis of various important characters.

Investigation on present genetic diversity in local common bean accessions and breeding forms has been carried out through 1D-SDS-PAGE and a densitometry of bands from proteinograms. Four phaseolin types: "T", "Ca", "C' and "S" have been distinguished indicating a low level of genetic diversity in comparison with the level occurring in origin centres of this neotropical species. As a highly conservative marker, the phaseolin type is helpful to characterize the primary gene pool of the accessions grown and maintained in a secondary domestication region, as Bulgaria became more than 300 years ago. In Bulgaria, representatives of the two known common bean gene pools have been identified, with a predominance of the Andean over the meso-American one. Most local accessions share the "T" phaseolin type, while the "Ca" type predominates among the breeding lines and varieties. Collection diversity on the basis of total seed storage protein patterns is greater than diversity based on phaseolin types. In 362 analysed accessions 114 distinguished proteinograms have been revealed.

MOLECULAR CHARACTERIZATION OF DUTCH APPLE COLLECTIONS

Robbert van Treuren
Centre for Genetic Resources, P.O.Box 16 Wageningen, Netherlands 6700 AA; (email: robbert.vantreuren@wur.nl)

The Centre for Genetic Resources, the Netherlands (CGN) maintains an *in vivo* apple collection of 151 accessions. In addition, several NGOs are actively involved in the conservation of apple genetic resources in the Netherlands. In 2005, a project was started to characterize about 700 Dutch apple accessions with 16 microsatellite markers. Objectives of the study were: 1) to improve the insight in the diversity of genetic resources of apple in the Netherlands; 2) to determine the degree of representation of CGN's collection; 3) to investigate possibilities for a more efficient conservation; and 4) to increase the interest for genetic resources to the user community. The project results obtained so far indicated that 1) considerable overlap in diversity occurs both within and between the investigated collections; 2) the passport data need re-examination; 3) no single collection covers the total diversity well; and 4) the efficiency of conservation can be substantially improved through cooperation between the collections. In cooperation with the NGOs, follow-up activities include detailed examination of the observed duplication groups and passport data and the development of a common database. In addition, the data are currently being investigated to identify potentially interesting material for the user community.

METAMORPHOSES IN BARLEY GENETIC RESOURCES EVALUATED BY MOLECULAR TOOLS

Ján Kraic[1,2] and Michaela Benková[1]
[1]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [2]Constantine the Philosopher University, Faculty of Natural Sciences, Trieda Andreja Hlinku 1, 94974 Nitra, Slovak Republic; (email: kraic@vurv.sk)

Genetic variation within barley (*Hordeum vulgare* L.) at the molecular level does not need to catch common known trends, i.e. decreasing of genetic variation detected in morphological, agronomical, and other phenotype traits. Molecular diversity at selected loci, also at the microsatellite loci, can also be increased by new alleles or allele combinations occurrence. This was also hypothesis of our study.

We analyzed development and changes in molecular variation at the microsatellite loci of barleys originated or cultivated in territory of Slovakia in last one hundred years. Based on our results we can conclude that there have been occurred quantitative and qualitative changes in the Slovak, Czech, and Czechoslovak barleys during this era. The absolute value and mainly also trend in total number of microsatellite alleles indicates that total number of alleles and genetic diversity range were increased from the begin of seventies of 20th century, after their depression in period 1944-1971. Average number of alleles per locus also increased from the year 1970. On the other hand trend curve for number of microsatellite alleles per one accession (genotype, cultivar, landrace) declined in time. It declares high heterogeneity in old cultivars and landraces and principal increasing of homogeneity of modern cultivars. So-called "time-specific" alleles, i.e. alleles specific for certain period of development were also detected. Total genetic diversity contained in barley originated from separate periods of development was changed, culminated in period 1930-1940, decreased in next 55 years, and again increased from the year 1985.

TARGETED MUTATION BREEDING AS A TOOL FOR TOBACCO CROP IMPROVEMENT

Aurélia Luciani[1], Emilie Julio[1], Frédéric Laporte[2], Stéphanie Reis[1], Christophe Rothan[2] and François Dorlhac de Borne[1]
[1]Altadis - Institut du Tabac, Domaine de la Tour, 769 route de Sainte-Alvère, 24100 Bergerac, France; [2]UMR Physiologie et Biotechnologie Végétales, IBV1-INRA Bordeaux, 33883 Villenave d'Ornon Cedex, France; (email: aurelia.luciani@altadis.com)

Nicotiana tabacum is a model widely used in functional genomics with transgenesis; however, genetically modified organisms are not accepted by consumers in Europe. Targeted mutagenesis as a non transgenic approach was assessed on a demonstration gene involved in alkaloid metabolism. A population of 4.000 EMS-mutagenized M2 families was created. Single Strand Conformation Polymorphism (SSCP) was used to target mutations. Eleven putative mutants were identified by screening 1344 M2 families. Mutations identified in DNA pools were validated by sequencing. Individual plants carrying missense or truncation mutations were studied for their phenotype. Homozygous plants for one truncation were identified, and the expected phenotype was observed in the field. These plants have been used as genitors to introduce this mutation into elite lines. Backcrosses are being performed to recover the elite line background in combination with SSCP analysis to track the mutation. The amphidiploid nature of tobacco avoids problems related to fertility. Efficiency of this method to create novel genetic variation and to develop cultivars has been demonstrated for the first time in tobacco.

USE OF GENETIC METHODS AND BIOTECHNOLOGY FOR DEVELOPMENT OF NEW PLANT GENETIC RESOURCES IN BELARUS

Alexander Kilchevsky, Lyubov Khotyleva, Nikolay Kartel, Valentina Lemesh and Sergey Malyshev
Institute of Genetics and Cytology, Akademicheskaya st.,27, Minsk 220072, Belarus; (email: Kilchevsky@igc.bas-net.by)

The Institute of Genetics and Cytology used the classical and molecular methods of genetics and biotechnology for development and study of the genetic collection of cereals, potato, sugar beet, flax, tomato, pepper and sunflower.

This collection includes:

- self-fertile lines of diploid and tetraploid winter rye. Some of them have marker genes of white grain (Vi) and short-stalk (Hl);
- monosomic and disomic lines of spring wheat with cytoplasms of Opal and Chinese Spring developed on the basis of the standard series of Chinese Spring monosomics;
- different kinds of alloplasmic and isoplasmic wheat lines;
- alloplasmic and chromosome-substitution lines of triticale and secalotriticum;
- primary potato dihaploids;
- di-, tri- and tetraploid forms of sugar beet;
- flax collection.

Primitive flax accessions (landraces) cultivated for a long time in certain regions and thereby having specific co-adaptive gene complexes can be a source of desirable genes for increasing gene pool. Parameters of growth and structure of yield were estimated in Belarusan flax accessions for selecting promising forms, which may be used in breeding. Comparative analysis was carried out in terms of RAPD and SSR data in the collection of Belarusan landraces, collected in the twenties-fifties. The possibility to define the status of accessions and to reveal duplicate accessions was shown.

Genetic diversity among breeding lines and cultivars is fundamental for further progress in hybrid breeding of tomato. Microsatellite markers for tomato have become available in increasing numbers and are a potentially useful system for the construction of large molecular-marker databases for tomato varieties. In this study we analysed a sample of 27 varieties and lines of tomato originating mainly from Belarus, Russia and Poland with a set of 15 microsatellite markers covering all chromosomes. The results obtained provide new information about the relationships between the varieties analysed.

GENETIC DIVERSITY OF TOMATO (*LYCOPERSICON ESCULENTUM* MILL.) LANDRACES USING MORPHOLOGICAL AND ISSR DATA

Panayiotis J. Terzopoulos and Penelope J. Bebeli
Agricultural University of Athens, Department of Plant Breeding and Biometry, Iera Odos 75, Athens, Greece, 11855; (email: bebeli@aua.gr)

The purpose of the present study was the characterization of 34 tomato landraces using 36 morphological traits and the estimation of their phenotypic diversity. The discrimination of the landraces, three tomato cultivars, three tomato hybrids and two L. pimpinelifolium accessions was attempted using the ISSR technique. Nei's genetic diversity statistics were applied on morphological data while Unweighted Pair-Group Method (UPGMA) based on Jaccard's coefficient was used for the molecular markers. A wide variation within the traits appeared in the whole collection. The mean value of the proportion of phenotypic diversity among populations (G_{ST}) was 0.21 with plant traits having the highest value. The populations had similar mean phenotypic diversity that ranged from 0.24 to 0.52. The heterogeneity of each population could be mainly attributed to various fruit traits. The most homogeneous traits within each population were plant traits that were common for most of the landraces. The ISSR primers did not show high degree of polymorphism (63.6%) and most of the accessions had high levels of genetic similarity. However, with the usage of the ISSR technique, all the samples were discriminated from each other. Conclusively, the under study landraces could be used for future breeding schemes, particularly for quality traits improvement due to many types of size, shape and color of their fruits. Furthermore, the ISSR technique is efficient for tomato genotypes discrimination.

VARIATION IN HIGH MOLECULAR WEIGHT GLUTENIN SUBUNITS OF SLOVAKIAN WHEAT VARIETIES AND THEIR *GLU-1* QUALITY SCORE

Edita Gregová[1], Daniel Mihálik[1], Svetlana Šliková[1], Pavol Hauptvogel[1] and Zuzana Šimová[2]
[1]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [2]Constantine the Philosopher University in Nitra, Trieda A. Hlinku 1, 949 01 Nitra; Slovak Republic; (email: gregova@vurv.sk)

Genomes of wheat varieties provide an available and highly efficient polymorphic system of genetic markers. Suitable protein markers in wheat are endosperm storage proteins – gliadins and glutenins. HMW-GS are encoded by alleles of *Glu-1* loci located on the long arms of the group 1 homoeologous chromosomes (*Glu-1A, Glu-1B, Glu-1D*). High molecular weight glutenin employing the standard sodium dodecylsulphate (SDS-PAGE) polyacrylamide gel electrophoresis methods were classified in 26 Slovak wheat landraces and 43 modern cultivars growed in Slovakia at present. Some of the HMW-GS subunits pairs 3+12 and 17+18 are present in old wheats missing in modern cultivars utilized in Slovakia nowadays. *Modern cultivars:* The most frequent HMW-GS genotype was – 0, 7+9, 5+10. The above-mentioned HMW-GS composition was found in 48.8 % of all genotypes analyzed. We found altogether 10 different combinations of HMW-GS genotypes occurring at various frequencies. The *Glu-1A* 1 allelic block occurring in 9 genotypes was combined

with *Glu-1D* 5+10 in all cases. Most genotypes (72 %) had the 0 subunit at the *Glu-1A* locus, which has no relevance to monitoring superior bread-making quality. *Landraces:* Total number of 8 alleles was detected at all *Glu-1* loci in landraces and old cultivars. The most frequent HMW-GS alleles were "Null" for *Glu-1A*, 7+9 for *Glu-1B* and 2+12 for *Glu-1D*, respectively. We found altogether 17 different combinations of HMW-GS genotypes and phenotypes occurring at various frequencies. High polymorphism was observed at the locus *Glu-1B* where alleles 20, 7+9, 17+18, 6+8 and 7+8 were found. For the *Glu-1B* locus the allele 7+9 was the most frequent (73 %) among the evaluated lines of wheat landraces and presence of this allele is associated with a good bread-making quality. Another allele associated with good quality found with a relatively high frequency was 5+10 at the *Glu-1D* locus (59 %).

In the whole view, there is difference on the genetic allelic richness between the landrace and the modern variety at *Glu-1*, which are 17 different combinations in landraces and only 10 different combinations in modern cultivars, respectively.

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INTERSPECIFIC GENETIC DIVERSITY AS DETECTED BY INTER-SIMPLE SEQUENCES REPEATS MARKERS IN *HEDYSARUM* GENUS

Houda Chennaoui-Kourda, Sonia Marghali, Mohamed Marrakchi and Neila Trifi-Farah
Laboratoire de Génétique Moléculaire, Immunologie et Biotechnologie, Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar, Tunis, Tunisie; (email: neila.trifi@fst.rnu.tn)

A better knowledge of forage legume genetic diversity is necessary to exploit their potential in the amelioration program and for a profitable management of the crop. In this context, the genetic diversity in Mediterranean *Hedysarum* species was examined by the help of inter-simple sequences repeats (ISSR). 96 polymorphic ISSR markers were generated using 8 primers. These markers were considered to estimate the genetic distance among species and to draw phylogenetic trees. Or data provide evidence of a high degree of genetic diversity in analysed species. We note particularly, the obvious distinction of the two species *H. aculeolatum* and *H. membranaceum* from the others ones. In addition, it's worth noting that *H. spinosissimum* L. subspecies (subsp. *capitatum* and subsp. *spinosissimum*) were clearly diverged on two different clusters and were distinctively as any others considered species. Therefore, the two subspecies would rather support their being raised to the rank of species. Moreover, this result concurs with previous data based on allozyme variation, molecular markers and recently, on generic morphological characters. Furthermore, a great similarity exhibited throughout ISSR markers between *H. coronarium*, the only cultivated *Hedysarum* species, and *H. flexuosum* that submitted at severe genetic erosion. Hence, these results can provide an alternative phytogenetic support suitable in a selection program to improve the Tunisia grasslands.

GENETIC RELATIONSHIP AND DIVERSITY IN OPIUM POPPY (*PAPAVER SOMNIFERUM* L.) LANDRACES COLLECTION USING AMPLIFIED FRAGMENT LENGTH POLYMORPHISM (AFLP)

Martin Kolník[1], Ján Brindza[1] and Zuzana Miklošíková[2]
[1]Institute of Biodiversity Conservation and Biosafety, Faculty of Agrobiology and Food Resources, Slovak Agricultural University in Nitra, Tr. A. Hlinku 2, SK-949 76 Nitra, Slovak Republic; [2]Department of Botany, Faculty of Agrobiology and Food Resources, Slovak Agricultural University in Nitra, Tr. A. Hlinku 2, SK-949 76 Nitra, Slovak Republic; (email: martin.kolnik@savba.sk)

Amplified fragment length polymorphism (AFLP) DNA analysis was performed on leaf samples and pollen grains of 46 accessions of opium poppy (*Papaver somniferum* L.) landraces from own collection held in Slovakia. A total of 683 scorable bands were amplified with following four different fluorescently labelled primer pairs (ACT-CAG, ACC-CAA, AAC-CTT, ACG-CTA), 566 (82.86 %) of them were polymorphic. 506 (74.08 %) bands were shared with 2 or more samples, and thus were potentially informative. A neighbour-joining tree based on Nei & Li genetic distance and bootstrap option with 5000 replicates was produced on the basis of the analysis of all AFLP bands that ranged between 50 and 500 base pairs generated by sequencer. It was necessary to use more than one primer pair to resolve clearly the genetic relationship between the closely related plants described in this study. The application of AFLP DNA analysis for cultivar identification represents an efficient, reliable procedure for identifying opium poppy landraces in a definitive manner. Opium poppy samples sharing common parental lines could be distinguished unambiguously from opium poppy samples of more distant genetic background. The banding patterns were reproducible, consistent within a genotype, and the DNA polymorphisms was frequent enough to be useful in characterizing genetic diversity in even closely related breeding lines.

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GENETICAL CHARACTERIZATION OF AUTOCHTHONOUS GENE POOLS OF FIG WITH MOLECULAR MARKERS

Semina Hadžiabulić[1], Lejla Kapur[2], Naris Pojskić[2], Mirsad Kurtović[3]
[1]Agromediterranean faculty, Mostar; [2]Institute for Genetic Engineering and Biotechnology, Sarajevo; [3]Faculty of Agriculture, Sarajevo

Microsatelite method was used for genetical characterization of autochthonous fig gene pools. Determined variaties of allels and frequencies of analized microsatelite loci of autochtonous fig cultivars are representing characteristics of indivudal cultivars. Frequencies of allels were calculated from determined genotypes in every set using direct counting. Genotype frequencies have also been calculated using direct counting of genotypes in the sample.

Samples autochthonous fig cultivars were collected from five different locations in the area of Herzegovina: Mostar, Ljubuški, Stolac, Počitelj and Čitluk. Three autochthonous genotypes have been present in all the locations tenica, petrovača bijela and crnica divlja.

Combining several mikrosatelite markers (loci) it is possible to get patterns which are characteristic (authentic) for some cultivars, population or tacsonomic category, therfore based upon that it s possible to continue with genethical characterization. For examination of polimorphism and intergroup differencies between the mentioned fig cultivars, microsatelite developed from 14 fig cultivars and two French wild-growing populations of F.carica. (Khadari et al., 2001.).

APRICOT GENETIC RESOURCES: CHARACTERISATION AND CONSERVATION

Lamia Krichen[1], Neila Trifi-Farah[1], Jean Marc Audergon[2] and Mohamed Marrakchi[1]
[1]Laboratoire de Génétique Moléculaire, Immunologie et Biotechnologie. Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar Tunis, Tunisie; [2]INRA, Unité de Génétique et Amélioration des Fruits et Légumes, INRA Montfavet, France; (email: neila.trifii@fst.rnu.tn)

In Tunisia, apricot culture is present in several areas all over the country, where it is usually propagated by grafting, except for the trees grown in the oases, which are multiplied by seed and are called ‘Bargoug’. Variability in apricot has been assessed by molecular studies: AFLPs and simple-sequence repeat (SSR) markers. Molecular polymorphism analysis revealed a small range of variation in 54 of Tunisian cultivars which can be attributed to a bottleneck caused by the use of only a few genotypes as parents in reproduced populations. The actual diversity of Tunisian apricots reflects the exchanges of plant material between regions over time. The polymorphic molecular markers are used to characterize and discriminate among all cultivars. In addition, results permitted the elucidation of homonyms and synonyms cases.

ORAL PRESENTATIONS

Session 4

Plant genetic resources in context of climatic changes

ASSOCIATION MAPPING – A NEW TOOL TO DETECT QTL FOR DROUGHT TOLERANCE IN BARLEY GERMPLASM

Kerstin Neumann[1], Andras F. Balint[2], Rajeev K. Varshney[3] and Andreas Börner[1]
[1]Leibniz Institute of Plant Genetics and Crop Plant Research, Corrensstrasse 3, 06466 Gatersleben, Germany, [2]Agricultural Research Institute of the Hungarian Academy of Sciences, H-2462 Martonvásár, Brunszvik street 2, Hungary; [3]International Crop Research Institute for the Semi-Arid Tropics , Patancheru 502 324, Andhra Pradesh, India; (email: neumannk@ipk-gatersleben.de)

Due to the global warming and the predicted increase of phases with little or no rainfall, breeding for drought tolerant crops is one of the main challenges for the future agriculture. Until today the success is only marginal. The search for quantitative trait loci (QTL) in a mapping population developed by a cross of two genotypes has a big disadvantage – the results are mostly only representative for that single cross. Association mapping coming from human genetics is a possibility to detect QTL in populations with a lot of different genotypes which makes the findings more powerful and hopefully better applicable for breeding.

Drought tolerance at germination stage was screened in a barley collection kindly provided by the International Center for Agricultural Research in the Dry Areas (ICARDA). It consists of 227 different barley genotypes including cultivars and landraces from 30 countries of four continents (Asia, Africa, Europe, and Australia) but also wild barley material (*Hordeum vulgare* ssp. s*pontaneum* L.).

Water stress was imposed by moistening filter paper with polyethylene glycol. Root and shoot length of the seedlings were measured after eight days of growth under controlled conditions in a climate chamber.

We will compare the obtained results with our earlier investigations in the 'Steptoe' x 'Morex' (SM) and the Oregon Wolfe barley population (OWB), both developed by the US Barley Genome Project. A stable QTL region controlling the growth and explaining up to 40% of the phenotypic variation was found on 5HL close to the centromere in the SM. In the OWB there is also a QTL on 5HL but with only small influence. A stronger QTL is here located on the short arm of 5H. Additional QTL in the SM and OWB are located on 1H, 4H and 7H but again their position is different in the two populations. The association mapping data can be used to detect the appropriate genotypes in the existing germplasm to be included in the breeding process.

INCREASE OF KNOWLEDGE ON THE PHYSIOLOGICAL RESPONSE OF MODEL *LOTUS* AND ITS AGRICULTURALLY IMPORTANT CULTIVARS TO STRESS CONDITIONS

Peter Paľove-Balang, Igor Mistrík, Ján Pavlovkin and Ladislav Tamás
Institute of Botany SAS, Dúbravská cesta 14, SK-84523 Bratislava, Slovakia

In South America, livestock feeding rely manly on grazing systems, and therefore grassland productivity determines livestock production. The pastures have low fertility and are lots of them are exposed to continuous low pH and Al stresses, especially in south part of Brazil and Chile. Among legumes, forage *Lotus* species have greater potential for adaptation to enviromentally-constained areas of Latin America.

Our project is integrating partners from EU and Latin America to help increase the Lotus productivity and nutritional value for livestock production. The main objectivities of the project are to generate new and important knowledge on the molecular biology, physiology and metabolism on the model and cultivated Lotus species under stress conditions, collect and test the available plant material and its nitrogen-fixing symbiont, find the phenotypes with contrasting tolerance to abiotic stresses and use them for breeding.

The characterisation of Lotus response to Al stress started with the analysis of the growth response. It was found, that the *Lotus corniculatus* cv. St. Gabriel (U) and *Lotus corniculatus* cv. Draco are more sensitive, than cv. St. Gabriel (B) and UFRGS, which are used in Brazil. The comparison of model plant (*L. japonicus* cv. Gifu), two sensitive and two putative tolerant cv. showed, that both tolerant cultivars have not only better growth at low pH but also significantly higher resting membrane potential in root cortical cells. We also characterised the inhibition of uptake of some ions and activities of enzymes involved in nitrate metabolism and oxidative stress (mainly peroxydases) in model plant, *Lotus japonicus*.

NON TRANSGENIC APPROACHES TO MAIZE DROUGHT TOLERANCE

Marcelo J. Carena
North Dakota State University

Maize (*Zea mays* L.) has a wide range of adaptation. As a consequence, the Corn Belt keeps moving north and west within the U.S. North Central Region. Genetic improvement is the main reason maize is becoming adapted to these once considered marginal areas. However, even though the ethanol industry is expanding in these areas maize is still limited in its extension to the west due to significant environmental challenges mainly drought. The goal of this project is to develop new lines and populations for improved drought stress tolerance. The NDSU corn breeding program is well prepared to conduct basic research and to apply it into the development of new products and releases as well as training new scientists in plant breeding. The approach is complementary to the one being performed by industry since it is a non-transgenic approach with no limits of improvement and impact considering drought tolerance is a very complex trait with several genes controlling the expression. Public efforts understanding the mechanisms of polygenic effects involved in drought tolerance have no limit to genetically improve corn in marginal areas where there is more need to solve important problems. The results of this study would significantly enhance our ability to improve corn in the next decades by increasing the availability of quality food, feed, and fuel as well as a better corn-ethanol relationship. Without harvestable good products efficient ethanol production will continue to be only a potential.

PHYSIOLOGICAL CRITERIA OF TOLERANCE TO DROUGHT AND HIGH TEMPERATURE IN WINTER WHEAT

Marek Živčák[1,2], Marián Brestič[1], Katarína Olšovská[1], Peter Ferus[1] and Jana Repková[1]
[1]Department of Plant Physiology, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia; [2]Botanical Garden SAU Nitra, (email: marek.zivcak@uniag.sk)

Application of physiological criteria in screening process is very helpful for improvement of wheat breeding efficiency. Assessment of several traits and methods for drought tolerance screening was the aim of our vegetation pot trials with seven winter bread wheat genotypes of different provenance performed in seasons 2003-2005. The water deficit was induced by withholding of irrigation after anthesis. In control and water stress variants several parameters of net photosynthesis, stomatal conductance, fast chlorophyll *a* fluorescence kinetics, leaf water status, osmotic adjustment, growth, phenology and yield were determined. We analyzed also mutual relationships among parameters and their correlations with yield. Drought stress influenced the grain yield of wheat cultivars in all observed years through reduction in number of kernels per spike and grain mass. The phenology was a trait well correlated with yield reduction caused by drought stress. The varieties differed also in sensitivity of stomatal closure and hence similar trend was observed in measurements of net assimilation rate, too. Delayed stomatal closure with higher values of net assimilation was correlated with higher performance in drought conditions. Similarly, non-stressed values of stomatal conductance of observed varieties, trait associated with level of water use efficiency (WUE) and transpiration efficiency, was also connected with better drought tolerance. Other promising traits observed were capacity for osmotic adjustment and free proline content in leaves. Fast chlorophyll *a* fluorescence kinetics measurements appeared as useful tool for monitoring of drought and heat stress effects on photosynthesis with Performance Index (PI) as the most sensitive fluorescence parameter recording drought stress effects and genotypic differences in drought susceptibility.

UTILISING PLANT GENETIC RESOURCES FOR ALUMINIUM TOLERANCE STUDIES

Sheeba Navakode, Ulrike Lohwasser, Marion S. Röder, Annette Weidner and Andreas Börner
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstrasse 3, D-06466 Gatersleben, Germany; (email: navakode@ipk-gatersleben.de)

Acidity and associated aluminium (Al) toxicity is a major constraint for crop yield in many parts of the world. In order to keep up with the population growth and ever increasing demand for food, a need to bring the marginal areas under cultivation gains attention. Since aluminium tolerant cultivars proves to be the most efficient solution for such areas, a need for utilising our plant genetic resources is very essential. The main focus of our study is to use our genebank collections for screening for Al-tolerant varieties and also for genetic studies applying molecular markers. Several wheat varieties including hexaploid, tetraploid and wild relatives were investigated, mainly from the problematic regions. A set of Wheat / *Aegilops tauschii* Coss. introgression lines was tested for mapping the Quantitative Trait Loci (QTL) involved. Microsatellite markers were used to map the loci, which could be efficiently used for Marker Assisted Selection (MAS) of Al-tolerant cultivars and also for marker assisted introgression of specific chromosome segments. Several cytogenetic stocks including `Chinese Spring´ substitution lines and single chromosome recombinant doubled haploids lines developed from them will also be investigated to get a more comprehensive picture of the genetics of aluminium tolerance in wheat.

SELECTION OF STRESS TOLERANT GENOTYPES IN CLONAL PROPAGATED SPECIES

Olga M. Jandurová
Crop Research Instituten, Research Station of Viticulture Karlštejn 98, 267 18 Czech Republic; (email: jandurova@vurv.cz)

Clonal selection is an breeding method used routinely for selection of vegetative propagated plants. The advantage of this method is the maintaining of the main character of the variety with improving of the specific desirable trait. In viticulture the breeding programmes based on clonal selection started in Europe in second half of the 19th century and due to that the signicicant progress was achieved in healthy status and performance in main commercially planted varieties. Our experimental material represent clonal progenies of five wine varieties, selected in most severe conditions for wine production in Czech republic. Initial preselected vines were chosen for individual selection in 1972-75, and after their evaluation the best of them were registered for commercial planting in years 1989-90. All our clones are planted in the same conditions in one vineyard. The age of vines is 25-27, minimum of plants per clone is 40. The results presented here came from individual evaluation of performance and yield in years 1999, 2000, 2001, 2003, 2004, 2005 and 2006 with respect to climatic condition in these seasons. The main agrometeorological characteristics showed no significant differences in averages of annual temperatures and average rainfalls in years 1999-2001, but the radical shortage of water with the average temperature increasing started in 2002 and was permanently present up to 2004. Different adaptibility to the long lasting drought condition was observed not only among varieties and clones, but also among individuals of the same clone. The average yield in 2004 was less than half of average from 1999-2001, but individually, there were also vines with weak increasing of yield in dry seasons. The ANOVA analysis of variance show highest individual variability in years effected with drought stress and help to identify individual plants with lowest variability in yield, most probably tolerant to drought conditions.

POSTER PRESENTATIONS

Session 1

Plant genetic resources conservation and use: an overview

EVALUATION OF SPANISH TRADITIONAL VARIETIES OF TOMATO FOR THEIR ANTIOXIDANT CONTENT

Adalid A.M.[1], Roselló S.[2] and Nuez F.[1]
[1]COMAV, Polytechnic University of Valencia, Cno Vera s/n, 46022 Valencia, Spain; [2]CAMN Dept, Vegetable Crops, Jaume I University, Campus de Riu Sec, 12071 Castellón, Spain; (email: rosello@camn.uji.es)

Tomato landraces are highly prized in the Mediterranean basin because of their excellent taste. However, in the last decades they have been replaced by new hybrids with higher yield, fruit uniformity and disease resistance, but with a reduced organoleptic quality compared to landraces. As a result, most of the traditional varieties in Spain are disappearing together with their valuable genetic diversity, a heritage which is the result of hundreds of years of cultivation, breeding and adaptation to different environmental conditions. In addition, some of these varieties are really interesting not only for their excellent taste, but also for content in antioxidants (mainly carotenoids and vitamin C), which have an important key role against certain cancer and cardiovascular diseases. Therefore, these varieties have their opportunity in those markets where consumers are ready to pay more for foods that are more nutritive and tastier. During hundreds of years, these landraces have only been selected by their taste and fruit colour and, therefore, selection of these varieties with high nutritional qualities is necessary to relaunch their use. In this work we have characterized forty-five *S. lycopersicum* Spanish landraces for their carotenoid and vitamin C content, including three *S. lycopersicum* var *cerasiforme* (cherry fruit type). In order to have comparisons with different tomato types, a highly consumed traditional variety (cv. ‘Canario’), two accessions of cherry fruit type from Amsterdan and Praga, and three accesions of *S. pimpinellifolium* with high antioxidant content were used as controls. All the accessions showed a vitamin C content lower than *S. pimpinellifolium* controls, although in general traditional varieties tested had medium vitamin C content. However, we have selected four Spanish tomato landraces with high contents of lycopene and -carotene. BGV005659, BGV000965, BGV005582 and BGV002125 showed lycopene and -carotene contents between 25 and 50% higher than those of cv. ‘Canario’. -carotene content in these accessions was similar to the best *S. pimpinellifolium* accession and higher than the rest of tomato controls. For lycopene content, only *S. pimpinellifolium* accession BGV006195 showed similar values than the selected landraces. These results and the excellent organoleptic quality strengthen the huge potential of traditional varieties and their use *per se* in specific uses (organic farming or gourmet products).

CULTIVAR DIVERSITY IN A COLLECTION OF SOYBEAN (*GLYCINE MAX.* L. MERR.) IN THE SLOVAK GENEBANK

Gabriela Antalíková and Mária Žáková
SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 921 68 Piešťany, Slovak Republic; (email: antalikova@vurv.sk)

Fifty accessions of soybean maintained in the Genebank in Slovak Republic were selected. The evaluations were conducted during 2003 and 2004 growing seasons in Slovakia. The experiment was a randomized complete-block design, with each accession replicated two times. Morphological, evaluation and agronomic characters according to Descriptors for soybean were determined: plant height, plant height of the lowest pod setting, number of plant branch, number of internodes, number of nodes, 1000 seed weight, yield seed, crude protein content and vegetation period emergence to maturity. The data were analysed statistically using methods such as correlations, analysis of variance and cluster analysis. Analysis of variance ANOVA was used to determine the relative magnitude of sums of squares attributable to cultivar and year. Hierarchical cluster analysis was applied on means across blocks and years via Ward´s clustering algorithm and squared Euclidian distance as a measure of dissimilarity. Results of collection’s evaluation will be useful in further breeding and research programmes.

PGR PROGRAMME IN FINLAND: FROM ENHANCEMENT OF ON FARM CONSERVATION TO CRYO PRESERVATION AND MARKER TECHNOLOGIES

Kristiina Antonius[1] and Merja Veteläinen[2]
[1]Mtt Agrifood Research Finland, Biotechnology And Food Research, Myllytie 10, Fin-31600 Jokioinen, Finland; [2]Mtt Agrifood Research Finland, Biotechnology And Food Research, Tutkimusasemantie 15, Fin-92400 Ruukki, Finland

The Finnish national PGR programme was established in 2003 and from the beginning the most important activity has been to secure the national conservation of the vegetatively propagated crop species in a rational way in field gene banks and laboratories. The Finnish seed propagated crops and their wild relatives are maintained in the Nordic Gene Bank. However, enhancement of *on farm* conservation of landraces is an essential part of the national programme at the moment. Research activities have in recent years focused on development of long-term cryopreservation and DNA marker technologies for clonally propagated plants, particularly fruits and berries.

On-farm conservation project of landraces in Finland through an agronomic and sociological-historical approach was launched in the beginning of this year. Identification of socio-economic, agronomic and policy factors affecting on-farm conservation is an essential part of the project, as well as collection of the landraces. Establishment of a conservation network will be one of the outcomes of the project.

Cryo-preservation techniques were introduced at MTT in year 2004, as the only unit in the Nordic countries exploiting this method for plant material. The practical preservation, as well as research, is mainly located at MTT Laukaa Research and Elite Plant Station. Long-term preservation has started first with *Humulus*, *Prunus* and *Rubus* materials. In addition to optimising methods for particular species and genotypes, research is conducted on various types of preserved plant material (buds, shoot tips, somatic embryos). Furthermore, we are continuously monitoring the additional beneficial effects like virus elimination and enhancement of plant regeneration capacity.

DNA profiles are mainly produced with PCR-based microsatellite markers. In addition, we have developed new type of markers, which are based on retrotransposon sequences. They are now available for apples and some other fruit and berry species. These markers are utilized to complement microsatellite analysis, especially in the identification of mutant clones.

PHENOTYPE CHARACTERISTIC VARIABILITY OF GENOTYPES THE OILY SQUASH POPULATIONS (*CUCURBITA PEPO* VAR. *STYRIACA*)

Zdenka Balatova[1], Jan Brindza[1], Jana Nozkova[2], Jan Popik[3] and Dezider Toth[1]
[1]Department of genetics and plant breeding, Faculty of Agrobiology and Food Resources, Slovak Agricultural University in Nitra, Tr. Andreja Hlinku 2, 949 76, Nitra, Slovakia; [2]Institute of Biodiversity Conservation and Biosafety, Slovak Agricultural University in Nitra, Tr. Andreja Hlinku 2, 949 76, Nitra, Slovakia; [3]University Pharm Kolíňany, 949 01, Nitra; (email: zdenka.balatova@uniag.sk)

The Oily squash (*Cucurbita pepo* L. var. *styriaca* Grebenšč.) belongs to the most important alternative plant species for different uses. All around the world and also in Slovakia is cultivated as a fruit, fodder, medicinal, melliferous and specially oil plant. Due to this fact the aim of this experimental study is determined variability of flowers, fruits and seeds in the Oily squash population. In the experimental study was tested 699 plants of 4 cultivars the oily squash population. The following measures was defined from the characters obtained from assurance by flowers: petals length 25-134 mm, petals width 10-100 mm, length of anthers 5-24 mm; by fruit: fruit weight 170-1760 g, fruit length 90-124 mm, fruit width 94-187 mm, number of evolved seeds in fruit 68-211 pcs, number of undeveloped seeds in fruit 4-250 pcs and by seeds: seeds weight 4.11-116.51 g, seeds length 13.19-21.53 mm, seeds width 6.44-11.21 mm and seeds thickness 0.87-3.52 mm. Also particular plant parts were used for image recording to document the traits variability.

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SOME NOTES TO OCCURENCE OF SOME TAXA THE GENUS *PRUNUS* IN PANONIAN REGION

Tibor Baranec[1], Pavol Hauptvogel[2], Gábor Vörösváry[3] and Gábor Csizmadia[3]
[1]Slovak University of Agriculture in Nitra, Department of Botany, Tr. A. Hlinku 2, 949 01 Nitra, Slovak Republic; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 92168 Piešťany, Slovak Republic; [3]Research Center for Agrobotany, Tapioszele, Hungary; (email: Tibor.Baranec@uniag.sk)

Diversity of autochthonous plum species (*Prunus* L.) on the territory of Great Hungarian Plain - Carpathian basin, two species *P. spinosa* L. and *P. dasyphylla* Schur are presented. Taxonomical diversity of the some local populations of both species in four large regions were studed: The Őrség region- south-western part of the Great Hungarian Plain near to the Austrian border - (Bajánsenye, Kondorfa, Magyarszombatfa, Nagyrákos, Őriszentpéter). Hortobágy region - north-eastern part of the Great Hungarian Plain near to the Romanian border: Dévaványa, Kunmadaras; Balaton region- W side: Tihany, Aszófő, Cserszegtomaj. Ipeľsko-rimavská vrchovina - northern part of the Great Hungarian Plain: Chľaba, Šahy, Vinica, Čebovce, Želovce, Tomášovce, Fiľakovo, Šitorská Bukovinka. The result of hybridization with cultivated taxa of genus *Prunus (P. domestica, P. insititia, P. cerassifera)* in our field study of mixed spontaneous plum shrubs population i.e. *P.* x *dominii* Baranec , *P.* x *fruticans* Weihe, *P. x schurii* Baranec were confirmed. The expected taxa *P.* x *fletcheri* Domin was not found on studied localities. *Prunus dasyphylla* Schur is a relatively rare species on the territory of Carpathian basin with large affinity to hybridisation.

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EVALUATION OF EUROPEAN PRUNUS DATABASE IN SLOVAK REPUBLIC

Daniela Benedikova
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: benedikova@vurv.sk)

All activities with conservation of plant genetic resources in Slovak Republic are coordinated by the RIPP Piestany, within the framework of the National program for conservation of plant genetic resources for Food and Agriculture. This Programme is fully funded by the Ministry of Agriculture.

Slovak collections of fruit trees are at present on three places within the framework National Programme. Total number 5 176 fruit accessions included cultivars, hybrids, local varieties, wild, inter-specific hybrids and rootstocks of apples, pears, sweet cherry, sour cherry, peach, plums, strawberry, currant and other species. All are held on different sites and kept like field collections which are well organized, with computerized lists of accessions, passport data and some with descriptions data. Coordination of Plant Genetic Resources in Europe is undertaken by Bioversity International in ECPGR. During their Networks and Working Groups collate national inventories of European cultivar accessions. Collections of *Prunus* genetic resources are at present created by 886 accessions: apricot 341, peach 237, almond 35, cherry 163 and plum 110. In the European Prunus Database we have included 123 accessions originated in the Slovak Republic.

NATIONAL PROGRAM FOR CONSERVATION PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE IN SLOVAK REPUBLIC

Daniela Benediková, Michaela Benková, Pavol Hauptvogel, Mária Žáková, Jarmila Drobná, René Hauptvogel, Iveta Čicová, Gabriela Antalíkova, Lubomír Mendel
SARC-Research Institute of Plant Production, Bratislavska 122, 921 68 Piestany, Slovak Republic; (email: benedikova@vurv.sk)

Conservation of plant genetic resources in Slovakia is provided through National Program for conservation plant genetic resources for food and agriculture, which was amendment and published in Official publication MA SR in March 2005. National Program recording 28,758 accessions of genetic resources, problematic which is solving on the SARC-RIPP Piestany and another 18 co-solving institutions. Methods of maintenance are different, there are *ex situ*, *in situ* and *in vitro*. Gene bank SR stored in active collection 13,944 accessions and in base collection 3,337 accessions. Vegetative multiplying species are maintenance in the field collection - repositories. According to restricted treaty National program recording in 5 repositories 40, 58 ha surface.

In the fiftieth years many landraces of some species were collected. During expeditions from 1987 till 2006 we have collected more then 5000 samples including fodder crops, cereals, grain legumes, grasses, vegetables, popies, aromatically and medicinal plants.

The wheat collection is organized according to the growth habit of the accessions in sub-collections of winter and spring wheat. It currently includes 4711 accessions: 623 of basic collection and 4160 of active collections.

The most common species of aromatic plants in the Slovakia are agrimony, chamomile, marigold, milfoil, ribwort, sage. In the Gene bank SR are 156 accession medicinal and aromatic plants in the base, active and working collection. To the collection of the pseudocereals belong: *Fagopyrum, Panicum, Setaria, Sorghum, Amaranthus, Chenopodium*. There are about 300 accessions of the pseudocereals in the SARC-RIPP Piestany. The collections of forage genetic resources consist of 1153 accessions representing 50 different species of *Fabaceae* family. Activities of forage genetic resources collections include and utilization of *Medicago, Trifolium, Lotus, Onobrychis, Anthyllis, Melilotus, Coronilla* and *Astragalus* species.

The accessions of plant genetic resources are evaluated under field conditions on the SARC-RIPP experimental fields. The aims are collecting, conservation and evaluation for all selected aspects (morphological characteristics, phenological stages, evaluation of yield characters, disease resistance and post harvest quality analyses) according to the descriptor list for each species, developed on the basis of UPOV, IPGRI and EVIGEZ Descriptor Lists.

International co-operation is very active there is membership in the Commission FAO for genetic resources, activity in VII. Phase ECPGR under the coordination Bioversity International Rome. The Slovak representing researchers are very active and working in 13 working groups.

THE STUDY OF VARIABILITY ON AGRO-MORPHOLOGICAL CHARACTERISTICS OF SPRING BARLEY DEVELOPED FROM 1900-2003 MAINTAINED IN SLOVAK GENEBANK

Michaela Benková, Mária Žáková, Ján Kraic and Daniela Mikulíková
SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, Piešťany, Slovak Republic; (email: benkova@vurv.sk)

A set of 106 spring barley accessions of Slovak origin and former Czechoslovakia origin, developed from 1900 to 2003, was studied in 2004-2005. The study was conducted to assess the impact of breeding on nine agro-morphological traits of barley cultivars.

The obtained data were analysed statistically using basic statistic characteristics, analysis of variance (ANOVA), correlation analysis and principal component analysis (PCA). An analysis of variance revealed strong influences of year and genotype on traits of study. Significant breeding progress was observed for plant height, 1000-grain weight, spike per m^2, spike density, length of spike, grain yield, resistance to lodging, resistance to powdery mildew, total starch and protein contents. PCA based on agro-morphological traits divided the whole collection in the two groups corresponding to the two different periods (1900-1971 and 1972-2003). The data analysis confirmed that the development and successful breeding during the last 50 years produced high yielding modern varieties.

SURVEY OF MEDICINAL AND AROMATIC PLANTS IN ANTALYA – TURKEY

Mehmet Bilgen[1], Yasar Ozyigit[1] and Ozkan Eren[2]
[1]Faculty of Agriculture, University of Akdeniz, Antalya-Turkey; [2]Faculty of Science, University of Adnan Menderes, Aydin-Turkey; (email: bilgen@akdeniz.edu.tr)

There is a rising demand in connection with request for medicinal and aromatical plants which are used in medicine, spice, cosmetic, parfume industries and in making the relaxing and therapeutical herbal teas in the world. In this research, medical and aromatic plants species are searched in west Antalya (Central Antalya, Korkuteli, Elmalı, Kemer, Kumluca, Kaş ve Finike) in Turkey and 549 plant materials in 61 plant families which have different origins were collected and were made theirs herbarium. As research results, determined 143 plat species which have 34 families in research area. Results of the study showed that for *Lamiacea* family was 59 species, for *Fabacea* family was 13 species and other families was 71 species found.

EVALUATION AND USE OF SPRING BARLEY WORKING COLLECTION IN BREEDING AT THE STATE STENDE CEREALS BREEDING INSTITUTE

Mara Bleidere
State Stende Cereals breeding institute, LV-3258, p.Dizstende, Talsi regio.; (email: maara.bleidere@gmail.com)

In Latvia spring barley (*Hordeum vulgare L.)* is the second most important cereal species. Plant breeders traditionally base breeding programmes on working or breeders' collections of carefully selected genotypes that possess useful traits for incorporation into an adapted variety. Collecting, evaluation and using of genetic resources in the plant breeding process started since foundation of State Stende cereals breeding institute in 1922. During this period 11 spring barley varieties are created in Stende. Knowledge about the variation available may help barley breeders develop strategies for varieties improvement. Working collection tends to be dynamic and is modified according to aims of breeding program. Currently the total number of samples in the spring barley working collections is 560 accessions from 33 countries – modern varieties and breeding lines (two-row, six-row, hulled, hulless). One of the tasks is detailed investigation of those genotypes to find initial material with valuable traits that provide their suitability to local agro climatic conditions. The evaluation criteria are productivity traits, agronomic performance, and disease resistance. As barley in Latvia mainly is used as a source of energy and concentrated nutrients for all classes of livestock, high attention is paid to evaluation of specific grain quality traits – β-glucan, ADF, NDF, protein digestibility, content of mineral nutrients as well as amino acid composition. Often the result of selection are breeding lines not contain full complex of valuable traits therefore not registered as a new variety but the same time they are genetically valuable material according to separate traits. There are 57 such breeding lines in the working collection. They are the valuable donors for creation of the new varieties suitable for local conditions. In the program of spring barley these lines are included in the further hybridisation as one of the parents and such kind of combinations compile more than one third from total number. Such kind of approach is used already many of years and has result. For creation of the newest spring barley varieties 'Sencis 'and 'Kristaps' one of the parents were Stende breeding lines $7542_{77\text{-}27}$ (76-17/Ofir) and $9023_{83\text{-}48}$ (Francegold/He-R-54) created in 1977 and 1982 respectively characterized with complex resistance to diseases.

STUDY OF GENETIC SOURCES OF FRUIT SPECIES IN THE REGION OF BÍLÉ KARPATY IN THE CZECH REPUBLIC

Stanislav Boček[1] and Václav Tetera[2]
[1]Mendel University of Agriculture and Forestry Brno, Zemědělská 1, 61300, Brno, Czech Republic; [2]Czech Union for Nature Conservation – Basic Organisation 58/06 Bílé Karpaty, Bartolomějské náměstí 47, 69801, Veselí nad Moravou, Czech Republic; (email: bocek@mendelu.cz)

During the period 2003–2006 the systematic mapping of old and local fruit varieties was carried out in the area of Protected Landscape Area of Bílé Karpaty. The aim of the project (VaV/620/10/03, supported by the Ministry of Environment of the Czech Republic) was to find and rescue traditional old and local-indigenous fruit varieties for keeping and restoration of landscape character and for biodiversity preservation. Mapping and collecting expeditions took place in 35 land registers of the area of Bílé Karpaty. Occurrence of extensive orchards and significant old trees was recorded in orthophotomaps (1:5000) and GIS with attributes such as ownership, orchard management, plant diversity, age of tree, biometrical data and health condition. Altogether 180 orchards, more then 2200 trees and 220 varieties or landraces of apple trees, pear trees, plum and prune trees, sweet cherries, sour cherries and whitty pears were localized and described. Pomological description of local varieties, not yet described, was made. Interesting local varieties were found, mainly plums with yellow or green skin: ´Bílá slíva´, ´Bílá trnka´, ´Zelená slíva´, ´Zelená švestka´, ´Žlutá durancie´ and pear trees with red flesh (´Krvavka´) or striped skin (´Oharkula´). Scion material was taken and propagated in two new regional nurseries specialized on production of local varieties. Finally two mixed gene bank orchards were established in Rokytnice and Bojkovice on the area of 2.5 ha and 3.0 ha, respectively.The meaningful local and rare varieties grafted on seedling rootstocks are planted there. The orchard management is traditional, extensive and it fulfils the conception of on farm genetic resources conservation with the emphasis of economic fruit utilisation by certification in organic production system. The plant material situated in both germplasms is available for scientific research and breeding. It practically represents the scion source for nursery utilisation.

HEDYSARUM CORONARIUM IN TUNISIA: 30 YEARS OF CONSERVATION EFFECT ON GERMINATION POTENTIALITY AND ISSR GENETIC DIVERSITY

Hédia Bourguiba, Houda Chennaoui-Kourda, Mohamed Marrakchi, Sonia Marghali and Neila Trifi-Farah
Laboratoire de Génétique Moléculaire, Immunologie et Biotechnologie, Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar, Tunis, Tunisia; (email: neila.trifi@fst.rnu.tn)

Hedysarum coronarium L. (Sulla), considered as an excellent forage, is exploited for alternative uses such as environmental protection, landscape enhancement and high quality honey production. As many other forage legumes, *H. coronarium* is submitted to severe genetic erosion. Therefore, the conservation of these phytogenetic resources is established by the construction of a “genetic reserve” including seeds of 200 accessions of local *Hedysarum* spontaneous populations, collected from 1976 to 2005. In order to estimate the impact of such conservation, 6 accessions belonging to two populations of *H. coronarium*: Tunis and Jebel Zit are tested for their germinative power and ISSR genetic diversity evolution during 30 years of conservation. A decrease of germination rate is observed: 20% and 28% respectively in Tunis and Jebel Zit populations. In order to precise the influence of the genetic diversity conservation, the Inter-Simple Sequence Repeats (ISSR) is exploited. Three 3’anchored ISSR primers and two unanchored ones are generated a total of 48 and 62 polymorphic markers respectively in Tunis and Jebel Zit populations. Results are discussed in term of genetic diversity and adequate conservation.

INNOVATIVE USAGE OF THE SPRING BARLEY GENE RESOURCES

Natálie Březinová Belcredi[1], Jiří Kopáček[1], Jaroslav Prýma[2], Jaroslava Marková[1], Ivana Paulíčková[3] and Jaroslava Ehrenbergerová[1]
[1]Mendel University of Agriculture and Forestry in Brno, Zemědělská 1, Brno, Czech Republic; [2]Research Institute of Brewing and Malting, PLC, Malting Institute Brno, Mostecká 7, Brno, Czech Republic; [3]Food Research Institute Prague, Radiova 7, Praha 10, Czech Republic; (email: belcr@centrum.cz)

Today high quality of food and input materials has been required. People return to nature and green malt is used as an important source of fiber, vitamins, mineral substances, enzymes and chlorophyll. We followed significant antioxidants (enzymes superoxide dismutase and catalase, vitamin E), which can catch reactive radicals in the live organism, inhibit their creation and digest lipid hydroperoxides.

The selected antioxidants were determined in the biomass of spring barley (Malz, KM 1910, Sebastian,) in two growing phases (DC29, DC31) from two localities (Žabčice, Kroměříž – CZ). In 2006 juice was made from the biomass of the variety Sebastian (DC31, Žabčice). The highest activity of superoxide dismutase (SOD) was determined with the Ransod set in the variety Sebastian. Higher mean SOD activity was determined in the locality Žabčice versus the locality Kroměříž. Content of vitamin E was assessed using HPLC with fluorescent detection. Higher vitamin E activity was calculated in the samples of green biomass grown in Kroměříž. The mean vitamin E activity was the highest in the growing phase DC29. The higher mean value of the catalase activity (on the mean of all varieties) was in the first growing phase in both the localities. Statistically significantly higher values were determined in the samples from the locality Žabčice. The highest activity was determined in the variety Sebastian in the first sampling. Treatment with high pressure and freezing was the most considerate way of processing of the obtained products (juice) from the aspect of antioxidative and enzyme activity, fluid drying was the least considerate. Lyophilisation for preserving vitamin E activity and content of its isomers appeared to be the most appropriate, treatment with high pressure and freezing was the least suitable.

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THE USE OF NATIVE SPECIES FOR PHYTOREMEDIATION PURPOSES

Simonetta Bullitta[1], Giovanna Piluzza[1], Vera Safronova[2], Mario Deroma[3] and Filippo Virdis[4]
[1]ISPAAM-CNR, Sezione Pascoli Mediterranei, Via Enrico de Nicola 1, 07100 Sassari, Italy; [2]ARRIAM, Podbelskogo Sh.3, St. Petersburg-Pushkin 196608, Russia; [3]Dipartimento Ingegneria del Territorio, sez. Geopedologia, Via de Nicola, 07100 Sassari (I); [4]DESA, Università di Sassari, Via de Nicola 1, 07100 Sassari, Italy; (email: bullitta@cspm.ss.cnr.it)

The use of native species in phytoremediation combines the soil remediation with the restoring of biodiversity, habitat enhancement and conservation. The use on a large scale of native species for phytoremediation purposes in heavy metal polluted areas, requires that species combine high biomass yield and metal tolerance and accumulation. Also, high seed production is important for the spreading of species in contaminated areas.

Seeds were collected from plant populations of several native species growing in heavy metal (HM) contaminated areas of the minerary region of Iglesias (SW Sardinia-Italy). Although the investigated area was highly contamined due to the past extraction activities, more than 300 taxonomic units are capable to survive in such environments. In order to identify genotypes combining high heavy metal tolerance and accumulation and high biomass and seed yield, the species *Chrysanthemum coronarium*, *Lolium rigidum*, *Scorpiurus muricatus*, *Hedysarum coronarium*, *Pisum sativum*, *Lotus ornithopodioides* and *Lotus edulis* were chosen to perform a field experiment in a mine waste area of the Iglesias region, having the following soil concentration ranges of heavy metals: Zn (900-51748 mg kg^{-1}), Pb (709-13675 mg kg^{-1}), Cd (6-280 mg kg^{-1}). Plant development and seed and biomass production were recorded. Content of nutrient elements and heavy metals in plant tissues were determined by means of an atomic absorption spectrometer. A high variability was found among and within species for heavy metal tolerance and accumulation. Among the tested species, *Chrysanthemum coronarium* showed appreciable biomass production matched with the ability to tolerate and accumulate HMs, suggesting interesting perspectives for the selection of genotypes to be used for phytoremediation purposes in HM polluted areas.

DOMESTIC CABBAGE (*BRASSICA OLERACEA* VAR. *CAPITATA* L.) POPULATIONS FROM VOJVODINA

Červenski Janko, Djuro Gvozdenović, Jelica Gvozdanović-Varga, Maksimović Livija and Milić Stanko
Scientific Institute of field and vegetable crops Novi Sad, Maksima Gorkog 30, Novi Sad, Serbia; (email: jankic@ifvcns.ns.ac.yu)

Breeding success depends largely on the potential for broadening the genetic variability of the species concerned. One of the ways in which said variability can be widened in cabbage is by introducing new populations into the process of selection and production. In the previous period, we were able to augment this species with two new domesticated populations and one cultivar. The populations were collected in the areas of the towns of Čurug and Deronja. The new cultivar had been developed from the selection materials of the Institute of Field and Vegetable Crops in Novi Sad. The two populations are late-maturing white cabbages suitable for fresh consumption and pickling. The newly developed cultivar is a medium late, slightly red genotype and is also intended for fresh consumption and sauerkraut making.

EVALUATION VARIABILITY OF MORPHOLOGICAL TRAITS OF *PANICUM MILIACEUM* L.

Iveta Čičová

SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: cicova@vurv.sk)

Millet (*Panicum miliaceum* L.) belongs to the oldest cereals that are used by men. The aim of this study was to determine the variability of morphological traits of the common millet, and to evaluate differences among different varieties. In the years 2005 – 2006 twenty- four genetic resources of millet were cultivated in RIPP Piešťany. They were evaluated per Deskriptors for *Panicum miliaceum* and *P.sumatrense* IBPGR 1985. Measured and evaluated were these traits: plant height, number of basal tillers, blade length of flag leaf, blade width of flag leaf, sheath length of flag leaf, number of primary inflorescence branches, length of peduncle, peduncle exsertion, and length of inflorescence.

Significant differences in morphological traits were found in plant height, blade length of flag leaf, blade width of flag leaf, number of primary inflorescence branches, length of peduncle, peduncle exsertion, and length of inflorescence, which prove also measured minimal and maximal values for individual parameters in the years 2006: plant height 870 – 1403 mm, blade length of flag leaf 188,15 - 346,65 mm, blade width of flag leaf 12,6 - 20,9 mm, length of inflorescence 128,6 - 357,75 mm, number of primary inflorescence branches 7,1 - 11,1, length of peduncle 125,95 – 270,85 mm, peduncle exsertion 31,3 – 186,85 mm. In the year 2005 the situation was another one, according to other climatic conditions, there were measured the values as follows: plant height 815 – 1538 mm, blade length of flag leaf 182,15 – 255,5 mm, blade width of flag leaf 13,7 - 20,6 mm, length of inflorescence 152,6 - 362,75 mm, number of primary inflorescence branches 8,9 - 19,3, length of peduncle 125,95 – 270,85 mm, peduncle exsertion 45,1 – 166,7 mm.

The varieties PAN 27/81, IHAR 6 and IHAR 8 were most different from the other varieties in plant height. The varieties POLNAR 99-38 and IHAR 4 were most different from the peduncle exsertion. The longest inflorescence had these evaluated genetic resources: Kijevskoe and Iljicevskoe.

STUDY OF THE MOLECULAR WORLDWIDE VARIABILITY OF *SOLANUM LYCOPERSICUM* VAR. *CERASIFORME*

Laura Cordero, María José Diez and Fernando Nuez
Institute of the Conservation and Improvement of the Valentian Agrodiversity (COMAV), Polytechnic University of Valencia, Camino de Vera, s/n, 46022 Valencia, Spain, (email: fnuez@btc.upv.es)

S. lycopersicum var. *cerasiforme* (Dunal) Spooner, Anderson, and Jansen is considered to be the ancestor of the cultivated tomato. This variety together with the cultivated species has spread from its center of origin in Peru all over the world. From Peru it spread to Mexico, where the domestication of tomato took place; later, it was taken to the rest of continents. This study was performed to assess the molecular variability existing in *S. lycopersicum* var. *cerasiforme*. One hundred and eighty five accessions were studied, 31 from Peru, 54 from Ecuador, 21 from the rest of South America, 24 from Mexico, 20 from the rest of Central America, 5 from North America, 10 from Europe, 13 from Asia and 7 from Africa. Morphological characterization was performed in order to identify and assess the membership of the accessions to this botanical variety. Many of these accessions showed the typical characteristics of this variety, bearing small rounded fruits and with 7 to 9 flowers per inflorescence. Some other accessions had bigger, ribbed and flattened fruits. These accessions come mainly from Ecuador and Peru and were similar to the ones described by Rick and Holle (1990). Accessions were collected by our team or requested to other genebanks. Eleven microsatellite markers were used in this study. These markers were previously selected as highly polymorphic in *S. lycopersicum*. The number of alleles per loci of each microsatellite varied between 4 and 18. Factorial Correspondence Analysis and Principal Coordinate Analysis were performed. The main part of the accessions grouped forming a medium density group. The accessions from Mexico grouped a side from the main group. Others coming from the Department of Napo in Ecuador showed more differences with the rest of accessions and were located apart from the others studied in this work. These accessions had flat and ribbed fruits, although other accessions with the same morphology were included in the bigger group, together with the main part of the accessions. Implications of these results on the spreading and diversification of *S. lycopersicum* var. *cerasiforme* is discussed.

References: Rich, C.M.; Holle, M. 1990. Andean *Lycopersicon esculentum* var. *cerasiforme*: genetic variation and its evolutionary significance. Economic Botany 44: 69-78.

THE USING OF THE ELECTRO-MAGNETIC FIELD OF THE MILLIMETRE DIAPASON FOR INCREASING OF SEEDS VIABILITY UNDER THE *EX SITU* CONSERVATION

Liudmila Corlateanu
Centre for Plant Genetic Resources of Moldova, Republic of Moldova; (email: lcorlateanu@yahoo.com)

The influence of the millimeter irradiation as the factor of stimulation of the initial metabolism processes in small seeded crops was studied with the aim to increase their viability under *ex situ* conservation. When the seeds of some cultural plants with the low initial germination were exposed to the millimeter irradiation (MMI) with the wavelength 5,6 mm and different strength of power (from 2,4 to10,4 mWt/sm^2), the significant increase in germination was attained under the initial (2 min) and terminal (8 and 10 min) exposures of this influence. The non-linear resonant character of the curve “exposure of irradiation – germination of seed” was revealed. Irradiation of seeds with the definite doses (exposures) of MMI in continuous regime of introduction of this factor was more effective than in an interrupted regime. After irradiation of dry and soaked seeds it was revealed that the resonant character of the “dose – effect” curve was more pronounced in the variant of soaked seeds. Quantitatively the effects were approximately similar.

A CORE COLLECTION OF *CUCURBITA PEPO* SPANISH LANDRACES

Belén Picó, María José Diez, and Fernando Nuez
Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV), Camino de Vera, 14, 46022, Valencia, Spain

The genus *Cucurbita* is native to North America. Spain served as a bridge between Latin America and Europe for the exchange of these vegetables. *C. pepo* is today the most economically important species. It includes eight horticultural groups in two main subspecies, *pepo* and *ovifera*. The *C. pepo* collection at the Genebank of the COMAV began in the eighties as a part of a program aimed to avoid the genetic erosion of Spanish *Cucurbita* landraces. Today is one of the most important collections in Europe, including about 400 accessions, most of which are landraces that are still cultivated under traditional cropping systems for self-consumption or sale in local markets (Ferriol *et al.*, 2003). Most of the landraces belongs to the subspecies *pepo*, which is consistent with the lack of traditional consumption of the cultivar-groups of the subspecies *ovifera*. In order to develop a core collection of *Cucurbita* Spanish landraces, accessions were grouped on the basis of seed characterization, as seed traits are highly correlated with fruit traits. A sub-sample of accessions representing the maximum diversity in seed traits, origin, and other passport data were selected for further characterization. Different situations were found in Spanish areas with different agro-climatic conditions and traditional cultural practices. In the north of Spain, we find a high diversity of Pumpkins, with primitive characteristics, used in a traditional way for human and/or cattle consumption. In Central Spain, there still exists a high variability for primitive Vegetable Marrow and Pumpkin types. In contrast, in the Mediterranean area, where most of the intensive vegetable production is concentrated, the elongated types with modern characteristics are mostly represented, and displacement of landraces by new breeding cultivars is observed. A core collection consisting of about 20% of the whole collection has been established. It represents the genetic diversity of Spanish *C. pepo* germplasm, optimizing its conservation and use by breeders. The molecular diversity of this collection will be studied.

References: Ferriol M., Picó B. y Nuez, F. 2003. Genetic diversity of a germplasm collection of *Cucurbita* pepo using SRAP and AFLP markers. Theor. Appl. Genet. 107(2): 271-82.

CHANGES IN PLANT GENETIC RESOURCES OF LUBELSZCZYZNA (SOUTH EAST REGION OF POLAND) FROM 1980S TO 2006

Denise F. Dostatny[1], Dorota Nowosielska[1] and Anna Seroczyńska[2]
[1]Instytut Hodowli i Aklimatyzacji Roślin, Krajowe Centrum Roślinnych Zasobów Genowych, Radzików, 05-870 Błonie; [2]Wydział Ogrodniczy, Katedra Genetyki, Hodowli i Biotechnologii Roślin i Architektury Krajobrazu, Szkoła Główna Gospodarstwa Wiejskiego, ul. Nowoursynowska, 166 02-766 Warszawa; (email: d.dostatny@ihar.edu.pl)

The flora of Poland includes more than 2500 species of vascular plants. Approximately 400 species are plants with potential functional meaning. The area of Lublin is still one of the Poland's regions richest in local, old varieties of cereal and vegetable plants, as well as rare weed species. According to the assessment of genetic erosion of functional plants performed throughout the last 20 years by the National Centre for Plant Genetic Resources, the pace of vanishing of traditional cultivations and old varieties of crop plants is dramatically high; consequently also accompanying plants vanish. They are being replaced by ever new weed varieties resistant to herbicides.

In order to establish the range of genetic erosion that has occurred in the recent years in the formerly abundant region of southeast Poland, three expeditions were organised in the years 2005 – 2006 to collect material and compare it with the material collected during expeditions held in the 1980s. During these expeditions in the 1980s over 130 seed samples were collected. They were mainly cereals and papilionaceous but also vegetables, medicinal plants, fodder, and weeds. The expeditions of the years 2005 – 2006 resulted in about 300 samples of crop and relative plants, herbs and weeds. This means that the region, inhabited by people traditionally involved in seed production, remains extremely abundant in local plant populations, particularly of vegetables. One of the curiosities of the region is a farming specialisation of some of the villages, where almost all people seed their fields with herbs. However, old cereal and lentil varieties have vanished. The conclusion is that the species plant composition of the area has slightly changed. The share of cereal plants has dropped while the share of vegetables and herbs has grown. On limestone soils in the vicinity of Lublin and Chełm we may also observe rare species of weeds of the *Caucalido-Scandicetum* association that is endangered due to herbicide use.

The area of the former Lublin voivodship is extremely interesting and valuable in terms of finding samples of old crop plant varieties and wild weeds. In some of the areas extensive farming is still exercised, which favours preservation of old varieties and weeds. There is a tradition followed by elderly farmers of growing vegetables from seeds produced personally in home gardens. Occurrence of rare rendzina soils also favours preservation of weed species connected with this type of soil. It seems logical to continue the expedition research in Lublin area to protect its valuable genetic resources both in *in situ* and *ex situ* as soon as possible, as the collection of plants stored in the Gene Bank forms a cultural and scientific achievement of each state and we are responsible for its conservation.

CURRENT STATUS OF GENETIC RESOURCES OF MEDICINAL, AROMATICAL AND CULINARY PLANTS COLLECTION IN THE CZECH REPUBLIC

Elena Dušková and Karel Dušek
Crop Research Institute, Dept. of vegetables and special crops Olomouc, Šlechtitelů 11, 783 71 Olomouc, Czech Republic; (email: Duskova@genobanka.cz)

Collections of medicinal, aromatical and culinary plants (MAPs) are in Czech Gene Bank carried out *ex situ* (field collections and gene bank seed collections) and it is represented by 619 accessions distributed in 71 species. The highest species diversity is found in the families *Lamiaceae, Apiaceae* and *Asteraceae*. The wild species from both the Czech Republic and abroad areas and also some regional and restricted varieties are included in collections. Most of this species are in collections represented also by Czech origin cultivars.

Complex evaluation of biological, morphological and economic characteristics is obvious part of work. Evaluation data (values in scale 1 - 9, estimated on the base of national descriptor lists, which are presently available for 27 MAPs) are obtained during regeneration and also some research projects. A special attention is given to study of propagation abilities of species difficult to propagate and to biochemical testing of essential oil content. Huge parts of *Lavandula, Carum* and *Calamus* collections have been studied for their diversity in pharmaceutically active substances content in collaboration with Mendel University of Agriculture and Forestry Brno and under supporting by national grant organisations. Another species (*Agrimonia, Betonica, Hypericum, Origanum, Plantago* and *Salvia*) forms a part of research project studying florid meadows re-creation at 5 protected landscape areas around all the country. The main goal of this project is to ascertain if these species are genetically almost identical at all localities or if there are any importantly different populations according their pharmaceutically effective substances content.

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COLLECTING OF OLD CULTIVARS, WILD SPECIES AND PRIMITIVE FORMS OF GENUS *MALUS* MILL. IN THE BOTANICAL GARDEN – CBDC OF THE PAS IN WARSAW

Marta Dziubiak
Botanical Garden – Center for Biological Diversity Conservation, Prawdziwka 2, 02 – 973 Warsaw, POLAND, Phone: +48 22 648 38 56; (email: marta.dziubiak@wp.pl)

Collecting and protecting of plant genetic resources is very important task. The necessity of protection of cultivated plants was noticed in eighties of the 20th century. Governments of 168 countries, Poland among them, ratified the Convention on Biodiversity from Rio de Janeiro (1992). Since then many projects on collecting, evaluating and different methods of storing of cultivated plants has been undertaken.

The most important genus of cultivated fruit-trees in Poland is an apple-tree (*Malus* Mill.). Old cultivars, primitive forms and species of apple-tree as wild relatives of cultivars and potential donors of valuable features for breeding have been collected in the Botanical Garden – Center for Biological Diversity Conservation of the Polish Academy of Sciences in Warsaw since 1987. Firstly, the accessions from pomological collections at scientific institutions like Institutes for Fruit Growing in Skierniewice, Dresden, Ujfehértó and Universities of Agriculture in Warsaw and Lublin were taken in order to collect them in one place and get with them familiar. Next, since 1995 local expeditions to old traditional orchards in Poland and neighboring countries were organized. Up to now 823 different taxa from genus *Malus* was collected in the Botanical Garden - CBDC of the PAS in Warsaw, to this number 772 old cultivars and primitive forms (identified or not) and 51 wild species and crossings. 794 old cultivars were brought as scions to grafting in years 1987 – 1995 and 227 in years 1996 – 2006. From all 1011 old cultivars brought to the Botanical Garden during these 19 years 76% of the collected materials remains today. An interesting division of *Malus* collection is the collection of *Malus sieversii* (Ledeb.) M. Roem seedlings coming from natural stands in Kazakhstan (100 genotypes). Collecting of genus *Malus* Mill. in Botanical Garden of PAS in Warsaw is a part of the national program of Plant Genetic Resources Conservation.

References: Dziubiak M. 2004. Collection of the genus *Malus* Mill. in the Botanical Garden of the Polish Academy of Sciences in Warsaw. Journal of Fruit and Ornamental Plant Research, Special ed., 12: 121-128.

DATABASES AS TOOLS FOR ENHANCED UTILIZATION OF CROP COLLECTIONS

Iva Faberová and Ivan Hon
Crop Research Institute, Drnovská 507, 161 06 Praha-Ruzyně, Czech Republic

Activities in Plant Genetic Resources for Food and Agriculture (PGRFA) documentation are directed to management of information on immense number of ex situ samples collected and gathered mainly in genebanks and research institutions. All maintained PGRFA are documented mostly as databases and major part of this information is available on the Internet.

While the first step was devoted to gathering samples and information the consequent activities are directed particularly to utilization of collections. Well designed databases and documentation systems offer an easy orientation in rising amount of information, which couldn't be effectively processed by any other classical method. At the beginning many separate information systems have arisen, later on effort was focused on regional centralization and recently comprehensive and large information systems prevail.

The most important international documentation systems and standards for PGRFA purposes were developed by FAO, CGIAR (Consultative Group on International Agricultural Research) centers and by the USDA (US Department of Agriculture). The FAO information and early warning system WIEWS is offering meta data mainly (important documents and links, directories of institutions including their activities, monitoring of GPA activities). The CGIAR system SINGER is presenting data on samples kept in all CGIAR collections going to the accession level of information (passport, characterization/evaluation, geographical distribution). The ECPGR system for European region as part of CGIAR includes European Crop Databases and the multi-crop EURISCO catalogue, important links and publications. The USDA National Plant Germplasm System (NPGS) GRIN is a comprehensive platform on accession level of information comprising passport, characterization/evaluation data, images, bibliography, taxonomical part and meta data.

Recently developed the Global Biodiversity Information Facility (GBIF) portal becomes the most important global router to all biodiversity related data. It was designed to enable the use of biodiversity and other databases by facilitating "data-mining" from distributed data sources and from different disciplines via one entry point.

DETECTION OF LATENT BACTERIAL ENDOCONTAMINANTS IN SYMPTOMLESS HOP (*HUMULUS LUPULUS* L.) SHOOT CULTURES

Juraj Faragó[1], Natália Faragová[1] and Barbora Vidová[2]
[1]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [2]University of SS Cyril and Methodius, Dept. of Biotechnology, Nám. Jozefa Herdu 2, 917 01 Trnava, Slovak Republic; (email: farago@vurv.sk)

In vitro storage of plant genetic resources can be accomplished by cultivating different types of explants (growth-tips, nodal explants, calli, somatic embryos) on defined media in culture vessels in *in vitro* conditions. One of the principal requirements of successful *in vitro* culturing of plant material is high sterility during all the steps of the culture protocol. In our laboratory at RIPP Piešťany, we store more than one hundred accessions of predominantly (94 clones) meristem culture-derived clones of 10 cultivars of hops (*Humulus lupulus* L.). Eight clones were introduced into *in vitro* culture in 1994, 94 clones in 1996, and 11 clones in the year 2000. The subculture interval of cultures, maintained in slow growth conditions, ranges from 12-18 weeks, so the oldest cultures were subcultured 53-54 times, and the youngest cultures 19-times from their establishment in *in vitro* culture. Our aim in this study was to monitor the potential occurence of latent endocontaminating bacteria in these long-term stored cultures using two microbial indexing media, i.e. Thornton's agar (ThA) and Medium 523 (M523). Of the 885 explants tested, 5.9% explants showed bacterial endocontamination on ThA, and 9.6% on M523, respectively. Of the two indexing media, M523 proved to have higher sensitivity in detecting latent endocontaminants, as 20 explants negative on ThA was positive on M523, while 1 explant only negative on M523 was positive on ThA. Our results suggest, that both the indexing media are effective in detecting latent bacterial endocontaminants in long-term stored shoot cultures of hop, i.e. M523 especially for faster-growing bacteria, and ThA for slower-groving bacteria. Our system of latent bacterial endocontaminants indexing is used in our laboratory for maintenance of high phytosanitary conditions of long-term stored *in vitro* cultures of virus-free germplasm of hop.

IN VITRO STORAGE OF MERISTEM CULTURE-DERIVED HOP (*HUMULUS LUPULUS* L.) GERMPLASMS

Juraj Faragó[1], Martina Hudcovicová[1] and Petra Vojteková[2]
[1]SARC-Research Institute of Plant Production Piešťany; Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [2]Constantine The Philosopher University, Trieda A. Hlinku 1, 949 01 Nitra, Slovak Republic; (email: farago@vurv.sk)

Maintenance of plant material in *in vitro* culture provides an effective system for establishment of both active and base level germplasm collections, especially for the conservation of those plant species that can not be stored as true seed. We established an effective protocol for maintenance of meristem culture-derived virus-free stocks of hop (*Humulus lupulus* L.) in *in vitro* conditions. Several approaches have been tried to optimise the storage system based on the slow growth method, including media modifications (mineral contents, sugar content and type of solidifying agent), cold storage (25/20°C, 15/10°C, and 5±2°C) and the use of plant growth retardants (ancymidol and paclobutrazol at 0, 1, 2.5, 5, and 10 µM; mannitol and sorbitol at 0, 10, 20, 30 and 40 $mg.l^{-1}$). Comparison of different concentrations of minerals (full-strength, 1/2-strength, and 1/4-strength), different sugars (sucrose, glucose) and solidifying agents (Phytagel, agar) resulted in the development of optimised maintenance medium containing full-strenth MS minerals, 20 $g.l^{-1}$ glucose and 7 $g.l^{-1}$ agar, without growth regulators. Maintenance of hop shoot cultures at 5±2°C prolonged the subculture interval to 10 months at high survival rate (>90%) and quality parameters (plant height, shoot number, node number, root length and number, fresh weight of roots, stems and leaves). Of the growth retardants used, sorbitol at 40 $g.l^{-1}$ concentration showed the best results regarding high survival (>91,7%), growth rate (50% less than in the control) and acceptable physiological state of explants. The genetic stability of *in vitro* stored plant material was studied by molecular analysis of microsatellite markers. The use of primer pairs 7a82, 3a88, 5-2, HlGA3, and HlGA4 (Brady et al.: Euphytica, 91: 277-284, 1996) in 111 samples of selected genotypes indicated occurence of no somaclonal variation after two years of *in vitro* storage of hop shoot cultures.

THE ITALIAN MINISTRY OF AGRICULTURE’S PROGRAMME FOR THE IMPLEMENTATION OF THE FAO INTERNATIONAL TREATY ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE (ITPGRFA)

Carlo Fideghelli and Petra Engel
CRA- Istituto Sperimentale per la Frutticoltura, Via di Fioranello 52, 00134 Rome, Italy

In 2004, the Italian Ministry of Policies on Agriculture, Alimentation and Forestery (MiPAAF), in response to the Italian ratification of the ITPGRFA, launched a Research Programme specifically targeted at the implementation of the objectives outlined in the Treaty. This Project is coordinated by the CRA-Istituto Sperimentale per la Frutticoltura in Rome and involves 16 Agricultural Research Institutions belonging to the MiPAAF and one Institute of the National Research Council. Research activities are aimed at the collection, conservation, characterization, evaluation, documentation and utilization of more than 70 crops strategic for the Italian agriculture (cereals, fruits, vegetables, olive, grapevine, citrus, fodder and forage crops, as well as forest species, industrial crops, medicinal and ornamental plants and tobacco), 26 of which are currently included in the Multilateral System of the ITPGRFA.

During the first triennium (2004-2006), activities were largely focussed on broadening the genetic base of the crops in the respective collections; the recovery of autocthonous material was a central item, but attention was also put on the collection/ acquisition of material from abroad. As a result, more than 2.000 new accessions were recorded throughout the involved Institutes. The second triennium (2007-2009) focuses mainly on the sustainable utilization of the material in collection; related activities include the re-introduction of old authocthonous varieties to the markets and the promotion of local products.

Concerning the evaluation of the conserved material, attention is given to agronomical, qualitative, technological, ecological and ornamental aspects as well as to the development of methodologies for sustainable cultivation systems. Characterization is not only done agronomically and morphologically, but most Institutes also perform biochemical and molecular analyses of their accessions in order to enhance transparency of the collections and to identify the genetic origin of the material they conserve. A central aim of the ITPGRFA is facilitating access to the material and to related information; to this end, the National Inventory on PGRFA has been established, an interactive on-line catalogue on PGR conserved *ex situ* throughout the country which allows the consultation of updated information on currently more than 26.000 accessions.

CONSERVATION OF PLANT GENETIC RESOURCES IN LITHUANIA

Bronislovas Gelvonauskis
Plant gene bank, Stoties 2, Akademija, Kedainiai distr. Lithuania; (email: b.gelvonauskis@agb.lt)

A National Plant genetic resources (PGR) Coordinating centre was established at the Institute of Agriculture in 1993 for coordination activities on PGR investigation at different research institutions. The Baltic - Nordic PGR project was initiated by Nordic Gene Bank (NGB) in 1994. It promoted eight Lithuanian research institutes to consolidate their efforts to start development of the national PGR conservation system. In 2001 the law on National Plant Genetic Resources was enacted by the Parliament of Lithuania. The Government of the Republic of Lithuania enacted the decision to establish Plant gene bank since the 1st of January 2004. Its main functions are to co-ordinate the collection, research, conservation and use of the national plant genetic resources in Lithuania and keep the genetic material in long term storage. In the PGR network five institutions are involved, which are responsible for collection, research and conservation of plant genetic resources according to different plant groups (agricultural crops, horticultural plants, forest trees, medical and aromatic plants and ornamental plants). In long-term storage at temperature -18° C are kept seeds of near 2000 accessions. The long-term seed storage is annually supplemented by new accessions. Accessions representing 115 plant species have been put for the long-term preservation. Old landraces and varieties of agricultural crops, advanced varieties and valuable breeding material, as well distinguished populations of wild relatives of cultivated plants and forest trees have already been stored in the long-term seed storage at Plant gene bank. Vegetatively propagated plants are maintained in field collections at research institutes, universities and botanical gardens.

CARROT GENETIC RESOURCES MANAGEMENT BY NETWORK IN FRANCE

Emmanuel Geoffriau[1], Anita Suel[1], Valérie Le Clerc[1], Jacky Granger[1], Cécile Dubois[1], Didier Peltier[2] and Mathilde Briard[1]
[1]Institut National d'Horticulture UMR 1259 GenHort, 2 rue Le Nôtre 49045 Angers, France; [2]Université d'Angers UMR 1259 GenHort, 2 bd Lavoisier 49045 Angers, France; (email: Emmanuel.Geoffriau@inh.fr)

The number of varietal carrot types, cultivated and therefore consumed in France as in Europe, has dramatically decreased in the past century, due to the needs for more homogeneous, easy to harvest and prepare products, along with a good shelf presentation. A great diversity for root color, morphology, adaptation characteristics still exists but is threatened. In order to preserve the French genetic patrimony and anticipate new breeding or growers needs, actions of conservation of genetic resources are implemented in France through a specific organization in networks for plant and animal species and also micro-organisms. The network "Carrot and other *Daucus*" was created in 1996, under the coordination of the Office of Genetic Resources (BRG), and involves research institutes, seed companies, experimental and technical agencies as well as botanical gardens or amateurs, all experts of the carrot species. The purpose of the network is to inventory, collect, characterize and evaluate accessions in order to regenerate, store and distribute authenticated carrot accessions in the national collection, corresponding to the French patrimony. More diverse carrot accessions of cultivated or wild *Daucus* are also conserved and studied for breeding or research purposes. In relation with the network, research is conducted on genetic diversity in order to understand its organization and evolution, and help manage carrot genetic resources.

CHEMICAL VARIABILITY OF *ARTEMISIA ABSINTHIUM* L. GROWING WILD IN POLAND

Anna Geszprych
Department of Vegetable and Medicinal Plants, Warsaw Agricultural University, Nowoursynowska 159, 02-776 Warsaw, Poland; (email: anna_geszprych@sggw.pl)

Wormwood (*Artemisia absinthium* L., *Asteraceae*) is a perennial growing wild in ruderal communities, at roadsides and waste lands. Its herb is used as a medicinal and flavouring raw material. It improves appetite and digestion, and reveals antihelminthic and antimicrobial activity. The most important groups of its active compounds are bitter principles and essential oil.

The aim of the study was to compare the content and composition of essential oil and phenolic compounds in wormwood growing wild in Poland. In mid August wormwood herb was collected from sixteen natural sites in the central and north-eastern area of Poland. At each site the herb was harvested separately from the plants being at vegetative and generative stage of development. In the air-dry raw material the content of essential oil, flavonoids and phenolic acids was determined. The qualitative analysis of essential oil was carried out by gas chromatography. The content of essential oil in the herb of plants being at vegetative stage of development ranged from 0,63 to 1,17%, whereas in the herb of flowering plants – from 0,31 to 1,35%. The dominant constituent of essential oil was sabinyl acetate (11 populations), β-thujone (2 populations) and chrysanthenyl acetate (3 populations). The content of flavonoids in wormwood herb ranged from 0,17 to 0,54%, and phenolic acids from 0,26 to 0,75%. There was no clear relation between the stage of plant development and the content of the investigated compounds in the herb.

STUDY OF THE WITHIN-VARIETIES VARIABILITY IN THE ASSORTMENT OF ALFALFA MATERIALS

Pavlína Gottwaldová, Jan Pelikán and Tomáš Vymyslický
Agricultural research, Ltd., Zahradní 1, 664 41, Troubsko, Czech Republic; (email: pelikan@vupt.cz)

In the set of 457 origins (varieties, newly bred materials and wild materials) of the Medicago (*Medicago sativa, Medicago x varia* and *Medicago falcata*) 20 characters were evaluated (measured, weighted, counted). The traits were found out on individual plants grown in the field outplanting. For each origin and each character the variation coefficients were estimated from the observed values. These coefficients were used as the measure of within-varieties variability. The biggest average variability reached the following traits: height at the beginning of flowering, length of terminal leaflet, width of terminal leaflet and number of pods per 100 flowers. The origins with the biggest and the lowest values of the variation coefficients were chosen.

RECOVERING OF THE RED AND ASLIKE CLOVER GENETIC RESOURCES OF THE LATVIAN ORIGIN BY PLANT TISSUE CULTURE

Dace Grauda and Isaak Rashal
Institute of Biology, University of Latvia, Miera Street 3, Salaspils, LV-2169, Latvia; (email: dace@email.lubi.edu.lv)

Red and (*Trifolium pratense*) and aslike (*Trifolium hybridum*) clover are popular folder legumes suitable for growing in ecological conditions of Latvia. Many varieties bred in Latvia as well as landraces and local wild or semiwild forms were stored only in the N. Vavilov All-Russian Institute of Plant Industry, VIR. Recently, several accessions of the Latvian origin were repatriated from the VIR. Seeds in the VIR collections were kept in the room temperature. Most of repatriated genotypes were reproduced more than 20 years ago and seeds did not germinate in soil at all. Therefore our goal was to elaborate *in vitro* method of germination of old aged seeds of red and aslike clover and consequent plant multiplication. Ten repatriated clover accessions (four of red clover and six of aslike clover) were selected for germination *in vitro.* We got germination of all tested accessions, even in the case when seeds are older then 30 years and all time were kept in the room temperature. The percent of germinated seeds differed among accessions and correlated with age of seeds. Pre-treatment with potassium permanganate, which we found earlier as effective for the cereal seeds, was effective also in clover both for seed sterilisation and germination stimulation. Most germinated seeds formed phenotypically normal seedlings with all organs. Before multiplication seedlings were cultivated on the basal MS medium for a month. Micropropagation was done on the basal MS medium. Best results were achieved by micropropagation of the stem segments approximately 2 mm in length. In a month of cultivation plantlets were ready for the planting in the soil or for a new cycle of multiplication. Number of finally obtained plants is depended not only from seed germination ability, but as well from micropropagation ability, showed high genotype dependence, and from acclimatization success in soil after *in vitro* cultivation. Elaborated method can be used in plant genetic resources programmes for restoring of bad kept accessions.

TOKAY VINE CULTIVARS (*VITIS* SPP.) GENETIC RESOURCES REVITALIZATION IN SLOVAKIA

Diana Gregusová and Jan Brindza
[1]*Department of genetics and plant breeding, Faculty of Agrobiology and food Resources, Slovak Agricultural University in Nitra, Tr. Andreja Hlinku 2, 949 76, Nitra, Slovakia; (email: diana.gregusova@uniag.sk)*

Tokay viticulture and enology is one of the old traditional agrosystems in Slovakia and also in Europe. The three legislative sufferable vine varieties – Furmint (F), Lipovina (L) a Muškát žltý (YM) has been grown for almost for 400 years in the small microregion. Cultivation the vine varieties conditioned a high stage of genetic erosion, because it is cultivated on the same locality for more than 300 years. Due to this fact has been assign the experimentally revitalization of genetic resources the Tokay vine varieties. The file 315 genotypes, was used for testing. By morphometrical analysis were the selected genotypes evaluated by traits on the level of leafs and bunches. By the leaf was defined: length shape 70–158 mm (F), 52–157 mm (L), 60–210 mm (YM), shape width 65–218 mm (F), 104-201 mm (L), 90 – 214 mm (YM). On bunches are assessed bunch length 56–250 mm (F), 63–323 mm (L), 60–210 mm (YM), bunch width 40–148 mm (F), 40–130 mm (L), 32–140 mm (YM), bunch weight 16.3–264.2 g (F), 16.5–320.4 (L), 16.5–320.4 (YM), berry length 7.8–19.07 mm (F), 9.6–17.69 mm (L), 10.48–18.95 mm (YM) and berry width 5.7–17.82 mm (F), 8.99–19.76 mm (L),10.3–18.53 mm (YM). Selected genotypes will be used as genetic resources for sustenaible breeding of the Tokay vine varieties.

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PHENOTYPIC CHARACTERISTICS OF *DIOSPYROS LOTUS* L. GENOTYPE USED IN BREEDING PROCESS

Olga Grygorieva[1], Svetlana Klimenko[1], Jan Brindza[2], Dezider Toth D.[2] and Vasilij N. Derevjanko[1]
[1]M.M. Gryshko National Botanical Gardens, National Academy of Sciences of Ukraine, Kyiv, Timiriazevskaja 1, 01014, Kyiv, Ukraine; [2]Institute of Biodiversity Conservation and Biosafety, Slovak Agricultural University in Nitra, Tr. A. Hlinku 2, SK-949 76 Nitra, Slovak Republic; (email: ogrygorieva@mail.ru)

Experimentally were verified the introduction, adaptability, variability degree of economically important traits and the potential to use of date plum (*Diospyros lotus* L.) in conditions in the Forest–Steppe of Ukraine. The experimental study has been oriented on selected individuals – genotypes growing in Ukraine (Kiew and Novaja Kachovka), in Slovakia (Mlyňany and Bratislava) and in Hungary (Budapest). With the tested genotypes has been determined the weight ranges of fruits growing in Ukraine (U) from 1.9 to 4.5 g, on Slovakia (S) from 3.4 to 5.3 g and in Hungary (H) from 2.12 to 4.59 g. Fruit length has been found for the relevant localities in ranges 12.34–15.98 mm (U), 16.57–19.53 mm (S) and 12.41–17.79 mm (H). Fruit width was in Ukraine from 14.7 to 19.53 mm, in Slovakia from 16.06 to 20.11 mm and in Hungary from 14.65 to 21.41 mm. Weight of thousand seeds achieved in Ukraine values from to 140 g, in Slovakia from 214 g and in Hungary from 193 g. Seeds length in Ukraine was from 8.17 to 10.94 mm, in Slovakia from 10.40 to 13.10 mm and in Hungary from 8.98 to10.70 mm. Seeds width was in Ukraine from 4.45 to 6.46 mm, in Slovakia from 5.17 to 6.17 mm and in Hungary from 5.75 to 7.26 mm. The localities exerted significant differences between the fruit, calyx and other traits shapes. With the tested genotypes has been found a tolerance against low temperatures and adaptability on different cultivation conditions.

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THE ROOT MORPHOLOGY OF NEW CZECH LUCERNE CANDIVAR IN RELATION TO STAND DENSITY

Josef Hakl, Jaromír Šantrůček, Daniela Kocourková and Pavel Fuksa
Department of Forage Crops and Grassland Management, Faculty of Agrobiology, Food and Natural Resources, Czech University of Agriculture Prague, Kamýcká 129, 16521, Prague 6-Suchdol, Czech Republic; (email: hakl@af.czu.cz)

The root system morphology of alfalfa is in the relation with plant persistency as well as yield and quality of dry matter. The aim of this study was compare the tap-root diameter and ratio of plants with branching root system among five new Czech alfalfa candivars and control variety Jarka. In spring 2003, the plot experiment with evaluated candivars was established in the field of the Czech University of Agriculture Prague in Suchdol in complete randomized blocks. In 2003 – 2006, the samples of plants were taken in each autumn from squares 30 x 30 cm with four replications per each alfalfa entries. The plants number, tap-root diameter, and ratio of root branching plants were assessed by each sample. Stand density decreased from 650 pcs.m^{-2} in 2003 to 100 pcs.m^{-2} in 2006. Tap-root diameter was significantly positively correlated with root branching and negatively with stand density. When effect of density was excluded as covariate, the highest taproot diameter provided Jarka and candivar ŽE XLV, the lowest the candivar ŽE XLII. The highest differences among alfalfa entries in this value were observed in the last year 2006. As regards root branching plants, the high initial stand density eliminated branching of root on the level around 5 % within three years period. In last year 2006, the ratio of branching plants over 20 % provided candivars ŽE XLV and XLII. Other evaluated candivars did not exceed 10 % level. The control variety Jarka provided ratio around 15 %. The differences among evaluated alfalfa candivar could be detect but stand density strongly modified these parameters thus must be take in the account. This research was supported by Research Project of Ministry of Education, Youth and Sports of Czech Republic No. 6046070901.

INFORMATION SYSTEMS ON PLANT GENETIC RESOURCES IN GERMANY – A NATIONAL APPROACH IN AN INTERNATIONAL CONTEXT

Siegfried Harrer[1], Frank Begemann[1], Lothar Frese[2], Dr. Christoph Germeier[2] and Michaela Haverkamp[1]
[1]Federal Agency for Agriculture and Food (BLE), Div. 513 - Information and Coordination Centre for Biological Diversity, Deichmanns Aue 29, D-53179 Bonn, Germany; [2]Federal Centre for Breeding Research on Cultivated Plants (BAZ), Erwin-Baur-Str. 27, D-06484 Quedlinburg, Germany; (email: siegfried.harrer@ble.de)

It is expected that by 2030 the world will have to feed an extra 2 billion people, of whom 90 % will live in developing countries. Food production and security for this increasing world population will highly depend on the conservation and sustainable use of agricultural biodiversity and genetic resources. Crops and their wild relatives thereafter referred as plant genetic resources for food and agriculture (PGRFA) provide the raw material that researchers and plant breeders use to improve the quality and productivity of crops, in order to respond to environmental and demographic changes. There is a high international interdependence with regard to crops and the genetic diversity within these crops. PGRFA are mainly maintained *ex situ* in worldwide 1.500 genebanks conserving approx. 6 million accessions. The future of agriculture therefore depends on international cooperation and on an open exchange not only of these resources but also of information related to these PGFRA.

The National Inventory PGRDEU (www.genres.de/pgrdeu) is the central documentation of plant genetic resources in Germany. It contains data of the genebanks of the Institute of Plant Genetics and Crop Plant Research (IPK) and the Federal Centre for Breeding Research on Cultivated Plants (BAZ) as well as other specialised collections of public and private stakeholders. PGRDEU provides interfaces for further national and international information systems like EURISCO (http://eurisco.ecpgr.org/). For the use of PGRFA in breeding comprehensive information about their traits is essential. To address these needs the Information System for Evaluation Data of Plant Genetic Resources EVA (www.genres.de/eva) was developed as a prototype. Now, the EVA-system serves as a platform for a Public Private Partnership for evaluation and as a future platform for the further development of a comprehensive National information system on evaluation and characterisation data. Information requirements on genetic resources are included *inter alia* in the Convention on Biological Diversity (CBD) as well as in the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), which entered into force in June 2004. In the presentation, the potential contribution of the different information systems to the monitoring of the genetic resources, to plant breeding and to breeding research will be demonstrated by examples taking into account the national and international framework for conservation, sustainable use and to the fair and equitable sharing of benefits arising out of their use.

THE POSSIBILITIES OF USE OF AEGILOPS SPECIES IN WHEAT BREEDING

Margarita Harutyunyan
Laboratory of Plants Gene Pool and Breeding, Armenian State Agrarian University, Teryan Str. 74, Yerevan 375009, Armenia; (email: pgr_lab@mail.ru)

Breeding of high quality varieties of soft wheat based on combination of different genomes of wheat and *Aegilops* L. species is one of priority directions of modern wheat improvement programmes. *Aegilops* species are distinguished by high content of protein in grains. Each species and interspecific form has a great reserve of potentially useful information for restoration of quality and productivity of cultivated varieties. *Aegilops tauschii* Coss. *ssp.strangulata* /Eig/ Tzvel. is the donor of D genome of hexaploid wheat. This genome provides characteristics of flour and pastry which are necessary for bread making.

Nine *Aegilops* species are growing in Armenia. The spontaneous crossings between aegilops and wheat species usually take place in the wheat fields. The numerous spikes of wheat-aegilopes hybrids have been collected. Basically, they are sterile, but we have selected 56 kernels out of about 1000 hybrid spikes. The several generations of plants grown from these kernels have been investigated. Sterile, semi-fertile, fertile, intermediate sterile and particularly sterile plants looking as Aegilops are been grown. The interested forms distinguished by the complex of features and characteristics have been revealed. The repeat back pollination with wheat pollen has been done, versatile and thorough research and selection have been carried out. This is an important initial material for wheat breeding for drought resistance. By the use of *Aegilops* species the intergeneric hybrids A.tauschii x T.urartu, T.boeoticum x A.tauschii, which are also a good initial breeding material have been created in the Laboratory. Due to the crossings between *A.tauschii* and *T.aestivum* the new wheat variety "Voskeask" (Gold Spike) has been obtained. This new variety has been released in the Republic.

SOME FACTS REGARDING MAIZE GERMPLASM IN ROMANIA

Ioan Has[1], Voichita Has[1] and Silvia Străjeru[2]
[1]Agricultural Research Station, Turda, Romania; [2]Gene Bank, Suceava, Romania

Romania is one of the great maize cultivating countries in Europe. The yearly maize cultivated areas are around 3 million hectares. The great number of farmers, the conspicuous climate and land differences, as well as the germplasm sources from Turkey and Italy, in the XVIIth and XVIIIth centuries, as well as those which came directly from America in the early XXth century, caused the differentiation of a very great number of local populations, with a vegetation period from FAO 180 to FAO 700, from indurata to dentiformis convariety.

In Romania, the up - to - date maize breeding started at the beginning of 1957s, when five research stations were set up at: Fundulea, Turda, Lovrin Şimnic and Podu-Iloaie. All these centers had as an immediate target the production of maize hybrids, out of public foreign inbred lines, but at the same time, during 1957-1962 an ample work for collecting, studying and preserving the old landraces and local populations throughout Romania was performed. To such an effort the Research Station of Suceava also contributed, starting with 1958, where later in 1982 the Gene Bank was set up. After studying the landraces and local populations on the "per se" value, and in some cases, the combining ability, too, inbred lines were obtained and synthetic populations were constituted as well, on the basis of phenotypical similarities and origin area. Such synthetically populations were also obtained at Turda and Fundulea. More substantial research funds were allocated for these maize germplasm breeding stations for a longer time budget. Composites and synthetically populations were constituted at Turda and Fundulea on the basis of similar genetic basis inbred lines, also starting with full – sib and half – sib reciprocal recurrent selection programs. After 1990, the funds allocated for agricultural research have been reduced, the budgetary allocations for the study and maintenance of maize germplasm have been much diminished. That is why some germplasm sources have been deposited at the Gene Bank, the other sources being kept at the breeding stations, thus existing the danger to lose them.

HOME GARDENS AND CROFTS IN *ON FARM* CONSERVATION OF AGRO-BIODIVERSITY IN SLOVAKIA

René Hauptvogel
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: r.hauptvogel@vurv.sk)

On-farm conservation is considered to be the sustainable management of genetic diversity of locally developed traditional crop varieties and forms by farmers within traditional agricultural and horticultural cultivation systems. The Slovak Republic has always paid and still pays a close attention to the conservation of cultural plants gene pool. The collecting expeditions perform the essential task in the preservation and conservation of landraces and originally grown cultural species. In several areas of Slovakia old varieties can be found, which can enrich our gene pool collections. During exploration in the north area of Slovakia in region Orava, in the year 2006, were collected local landraces of *Brassica oleracea* L. "Oravská". That samples was found by home gardens and crofts in Orava and are generally small in size (0.01 ha). Data were collected on the farm, farm management, agronomic, including information related to the use, traditions and social context. As regards vegetable, it has ever been cabbage that was cultivated in Slovakia and that was an important food component mainly of rural population. In the period of intense development in agriculture it has not been incorporated into large-scale production systems. Until the 1960s the managed mosaic of a typical farm in north Slovakia consisted of the herbal garden; a small extensive pasture; plots close to the homestead for vegetables, fibre crops, cereals for human consumption and fodder. This paper presents traditional knowledge on the management of home gardens.

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DIVERSITY IN WINTER WHEAT LANDRACES AND OBSOLETE CULTIVARS

Jiří Herrmuth, Ladislav Dotlačil and Zdeněk Stehno
Crop Research Institute, Drnovská 507, 161 06 Prague -Ruzyně, Czech Republic

Two sets (122 and 101 cultivars respectively) of European winter wheat landraces and obsolete cultivars were evaluated in successive 3-years field trials. Clustering according to the country of origin enabled only very rough differentiation in few characters (earliness, spike productivity). Old cvs had in average by 2–3% higher crude protein content than modern ones, however, genotypes showing 18% protein content were found (Bergland, Ukrajinka, Sippbachzeller, Innichen Nr. 25001, Barbu du Finistre). Spike productivity characters, except of TGW, were in negative correlation with protein content. Donors of earliness and longer grain filling period were identified, as well. High protein content and relatively good spike productivity and/or long grain filling period or earliness were found in cvs Visperterminen 640 E, Hatvan, Szekacz 1242, Berchtesgardener Vogel, Ble du Lot and Barbu du Finistere.

Diversity of HMW *Glu* -subunits has been analyzed by means of SDS-PAGE in the set 1 (n=122). Relatively rare were alleles 2* at 1A and 3+ 12 at 1D as well as alleles 8, 6, 9, 7, 13+16 and 17+ 18 at 1B. Glutenin patterns themselves were not sufficient for geographic characterization of cultivars, however, significant changes in incidence of particular alleles in different European regions were observed. At 1 A chromosome, absence of *HMW –Glu* subunit was very frequent in West- and North-West Europe and strongly decreased in Middle and especially East Europe whereas allele 1 has higher incidence in East Europe. Tendency of decreasing incidence of 2+12 alleles from west (82%) to east (17%) and opposite tendency of 5+10 alleles is noticeable for 1 D chromosome. At 1 B chromosome, increasing incidence from west (16 %) to east (60 %) has been found for alleles 7+9; an inverse trend has been found in allele 20.

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DETECTION AND SELECTION OF INTRODUCTED AND WIDESPREAD GENOTYPES OF BLACK MULBERRY (*MORUS NIGRA* L.) POPULATION IN THE SLOVAKIA FOR THE PLANT BREEDING

Jana Holecyova[1], Jan Brindza[1], Zdenka Balatova[1] and Radovan Ostrovsky[2]
Slovak Agricultural University in Nitra, Faculty of Agrobiology and Food Resources, Tr. A. Hlinku 2, 949 01 Nitra, Slovakia; [1]Department of Genetics and Plant Breeding; [2]Institut of biodiversity and biological safety; (email: jana.holecyova@uniag.sk)

In the Slovak area is occurring only in limited numbers, in total nearing to 1000 individuals. For experimental study were selected 954 genotypes of mulberry population. Geographical distribution of mulberry trees was registered by the GPS equipment and is documenting the population occurrence at altitudes between 146 and 517 m. The prevailing numbers of these trees are localized in a village Pukanec, where are presently available around 500 producing trees. Many trees are aged from 200 to 300 years and some are in a very bad condition. There is an extended problem with reproduction of this tree, thence the genetics erosion of black mulberry is showing an increasing trend. Fruits ripes gradually from July to August, what gives assumption for direct consumption of fresh fruits. Morphometric analyses expressing distict differences between the selected genotypes in fruit length (10.7 – 27.2 mm), fruit width (9.2 -16.3 mm), fruit weight (0.62 – 6.78 g). On the basic of statistical analyses, we determined four genotypes (M113, M476, M393, M498), which are potentially suitable as genetic resources and an introductory plant material for breeding of new races.

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THE BREEDING VALUE OF VARIETY SAMPLES OF HARD WHEAT AS A RAW MATERIAL OF MACARONI PRODUCTION

Marina Hovhanisyan
Laboratory of Plants Gene Pool and Breeding, Armenian State Agrarian University, Teryan Str. 74, Yerevan 375009, Armenia; (email: pgr_lab@mail.ru)

Hard wheat is considered as an initial product for macaroni production, due to the less content of starch in comparison with soft wheat and more content of protein. Hard wheat grains are more valuable in quality, more stable to pest and diseases, in case of application of appropriate agrotechnical measures varieties of hard wheat may provide high and stable yields. The area of hard wheat cultivation in the Republic of Armenia is not large. Because of climatic and soil factors hard wheat varieties are cultivated only in separate farms. The works on new varieties breeding, propagation and extension are carried out in the Laboratory of Plants Gene Pool and Breeding. Due to collaborative research and breeding programmes with ICARDA 50 variety samples of hard wheat were received. All theses samples have been tested in the valley and pre-mountainous conditions of the Republic as winter crops.

According to the three years data under the low altitude conditions the most prospective variety sample has been selected as a result of phonological, phytopathological explorations, filed observations and individual artificial selection. This cultivar is distinguished by the short stem (90 sm), high productivity (one spike weight is 2,5 g in average), large grains (1000 grains weight is 62.5 g), high protein content (16.5%), high degree of resistance to pest and diseases. The selected variety sample at present is propagating with the purpose of submitting for state variety testing. After, it is planned to suggest new hard wheat variety to farmers for cultivation in valley and pre-mountainous zones of the Republic.

SEED COLLECTIONS IN LONG-TERM STORAGE AT NATIONAL CENTRE FOR PLANT GENETIC RESOURCES IN POLAND

Mariusz Chojnowski
National Centre for Plant Genetic Resources, Plant Breeding and Acclimatization Institute, Radzików, 05-870 Błonie, POLAND; (email: m.chojnowski@ihar.edu.pl)

Long term seed storage facility at Plant Breeding and Acclimatization Institute in Radzików, Poland was established in 1981. At present over 65 000 accessions are stored in base collections in Long-Term Seed Storage Laboratory at National Centre for Plant Genetic Resources. The seeds are stored at -20°C (base collection) and 0°C (active collection). The drying and storage protocols follow international standards for gene banks. The collected seeds belong to 226 genera and 520 species. The most frequently represented genera are: *Triticum* – 11 262 accessions, *Hordeum* – 6080 accessions, *Dactylis* – 5542 accessions, *Festuca* – 4528 accessions, *Pisum* – 2443 accessions, *Phleum* – 2397 accessions, *Secale* – 2225 accessions, *Avena* – 2223 accessions and *Triticale* 2049 accessions. The structure of the collections preserved in long-term storage is as follows: cereal crops – 42%, grasses – 26%, vegetables – 12%, crop legumes – 11%, industrial crops – 6% and other collections including medicinal, flower and rare plants – 3%. About 50% of accessions (mainly cereals) are also stored as samples in active collection, which are immediately ready for distribution. Other crops are multiplied to create an active sample according to demand frequency and multiplication possibility. In the past the only random samples were evaluated to verify seed viability. Actually, program concerning evaluating all accession stored under long term conditions is introduced. Both, standard and biochemical methods of seed vigour estimation are introduced in seed viability testing. For seeds with decreasing viability and vigour, methods of seed invigoration before regeneration of accessions are investigated.

COLLECTION AND EVALUATION OF GENETIC RESOURCES OF FORAGE GRASSES AND LEGUMES IN LATVIA WILD

Biruta Jansone and Aldis Jansons
Agency of LUA Research Institute of Agriculture, Skriveri-1, Aizkraukle district, LV 5126, Latvia; (email: szc@inbox.lv)

The nature of Latvia is comparatively rich in forage grasses and legumes. Grassland areas occupy approximately 23% of farming lands, whereas wild grasslands (meadows and pasture-lands) – only 0,4% (~25,6 thous.ha). In the course of time, large areas of wild grasslands become overgrown and are transformed into arable land. Therefore, the spread of various species of plants is endangered, as well as the decrease of biological variety is taking place.

Our state has joined the programme of preserving of international genetic resources. For this reason, since 2000, the breeders of grasses of the Research Institute of Agriculture together with the scientists of the LU Institute of Biology have been arranging research expeditions. 13 expeditions of this kind have taken place, in the course of which, a great amount of species of perennial forage grasses has been collected, which is used for the formation of collections, as well as for the preservation in Gene Bank. 3 international expeditions have been arranged, where breeders of forage grasses of 3 Baltic states have taken part.

The most widely spread species of legumes, which were collected during the expeditions, were the following: *Trifolium pratense*; *Trifolium hibridum*; *Trifolium hibridum* ; *Medicago sativa* ; M*edicago falcata; Medicago lupulina; Lathyrus pratensis; Vicia cracca; Lotus corniculatus; Melilotus albus; Astragalus glycyphyllus; Lathyrus tuberosus.* Various species of forage grasses in wild grasslands can be found in especially large amounts. This is the most important group of grasses, because, in the meadows and pastures they form more than 50% of the total herbage. (Strazdina E., 2000). It was possible to collected *Alopecurus pratensis*, *Phalaris arundenacea*, *Festuca arundenacea*, *Arrhenatherum elatius*, *Bromus inermis*, *Agrostis alba* in Latvia wild. In order to evaluate and describe the collected patterns, they are sowed out in the experimental plots and compared with each other. The most valuable properties are noted. The most perspective patterns are chosen for selection work. A perspective species of *Alopecurus pratensis* and *Phalaris arundenacea* have been formed from the selected material in wild.

References: Strazdina E. (2000) Dabas daudzveidibas saglabasana lauku ainava. Latvijas dabas fonds.

YIELDING CHARACTERISTIC OF SIX CLONES OF GIANT GRASSES FROM GENUS *MISCANTHUS* AT EARLY DEVELOPMENT STAGES

Stanisław Jeżowski and Katarzyna Głowacka
Institute of Plant Genetics Polish Academy of Sciences, Strzeszyńska 34, 64-479 Poznań, Poland; (email: Ajez@igr.poznan.pl)

The study presents results of investigations concerning variation in characters of biomass (dry matter) weight yields in selected six clones of giant grasses from genus *Miscanthus*. The experiments involved clones of the best hybrid plants generated within species *Miscanthus sinensis* (clones MS/3, MS/4, MS/5 and MS/6), as well as clones generated from interspecific hybrids *Miscanthus sinensis* x *Miscanthus sacchariflorus* (clones MG/1 and MG/2). Investigations were conducted on the basis of a 3-year field experiment taking into consideration early stages of plant development, i.e. from planting until full yielding was reached in the third year of cultivation. The field experiment was established in a random block design with three replications. Planting was performed using root rhizomes at planting density of 1 plant per 1m^2, which is equal to 10 000 plants per 1 ha. Analysis of variance for analyzed *Miscanthus* clones in terms of characters of biomass yield structure (plant height, tillering, tuft diameter and shoot diameter), taking into consideration all the years, showed that a significant variation between analyzed clones begins as early as the second year of plant vegetation. Calculated correlations showed that yields of biomass (dry matter) of analyzed clones were affected first of all by the number of shoots, followed by tuft diameter, shoot diameter and finally by plant height.

CURRENT STATUS OF GENETIC RESOURCES OF *CUCURBITACEAE* VEGETABLES AND *LACTUCA* COLLECTION IN THE CZECH REPUBLIC

Kateřina Karlová
Crop Research Institute, Dept. of vegetables and special crops Olomouc, Šlechtitelů 11, 783 71 Olomouc, Czech Republic; (email: Karlova@genobanka.cz)

Collection of vegetables of *Cucurbitaceae* family is currently represented by 1802 accessions distributed in 45 species in Czech Gene Bank. The biggest part of collection shapes (according to field production in the Czech Republic) *Cucumis sativus* L. (801 accessions) and *Cucurbita* sp. (755 accessions) whereas also some "exotic" species as *Lagenaria, Luffa, Momordica, Trichosanthes* and *Echinocystis* are also inset. The main goal of the work with these species is its regeneration because only 53% of cucumbers and 20% of pumpkins is already regenerated and a lot of accessions will lose germination in a few years. These species are regenerated in isolation cages and a good fruitfulness is got with insect pollinators (honey bee). A big trouble brings on a low quality of original seeds – many accessions presented as a variety are not uniform and they produce highly heterogeneous plants and seeds. Collection of *Lactuca* consists of two big parts – culture genus *Lactuca sativa* L. (839 accessions) and wild species (*L. altaica, L. quercina* etc.) or species relative to *Lactuca* genus (*Mycelis, Sonchus*) which should furnish some genes of plant diseases resistance. This part of collection matches 604 accessions and include among 19 species. More than 80% of *Lactuca sativa* accessions are already regenerated but unfortunately there are a lot of duplications presented. To eliminate these duplications of both Czech and also abroad origin varieties is a main goal for early future work.

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MALUS GENETIC RESOURCES IN BELARUS

Zoya A. Kazlouskaya
Belarusian Research Institute for Fruit Growing, Samokhvalovitchy, Minsk reg., 223013 Belarus; (email: zoya-kozlovskaya@tut.by)

The aim of the Belarusian genetic resources programm for apple is to collect, preserve, evaluate and make available national and international cultivated and local varieties and wild species of apples for breeding, genetics and pomological studies. At present our genebank of *Malus* comprises 1114 accesses including 802 varieties and hybrids of *M. domestica*, 72 – *M.X atrosanguinea*, 3 - *M. baccata,* 12 - *M.coronaria,* 164 - *M.Xfloribunda,* 2 – *M.Xpurpurea,* 6 - *M.Xprunifolia,* 1 - *M.Xrobusta,* 1 - *M.sargentii,* 21 - *M.sieboldii,* 1 - *M.sikkimensis,* 3 - *M. sieversii var. Niedzwetzkyana,* 1 - *M.sylvestris,* 3 - *M.Xzumi* and 23 interspecific hybrids. The apple collection has been investigated for potential use in breeding and enlarged with genotypes obtained from interspecific crosses. One of the aims of our breeding program is to create new original breeding population with combined multiple resistance to the most important diseases and damaging factors in our climate. Many accessions from the collection were included into hybridization. The innovation of work is the assessment of the breeding value of parents and cross combinations. Interesting sources of durable resistance are selections of cv. Kola (F_1 *M.coronaria*), *M. sieboldii, M. Xsargentii, M.Xzumi.*

RARE MORPHS INTO POPULATION *IN VITRO* PLANTS DEVELOPED FROM THE WILD GRAPE ENBRYOS

Viktor Klymenko and Irene Pavlova
National Institute of Vine & Wine "Magarach", 31 Kirov St., 98600 Yalta, Crimea, Ukraine; (email: elena@magarach.crimea.ua)

The plants from the embryos of *Vitis vinifera* L. *subsp.silvestris* Gmel. are got *in vitro*. A total of 87 viable plants were the objects for investigation. There were lethal cases in ontogenesis. The analysis on frequency of rare morphs in the population of juvenile plants was carried out.

The got results show that total frequency of rare morphs made 0,388, which is the ever-higher index of presence of anomalies in the hybrid progeny. The morphs of characters "quantity of cotyledons" and "knitness of cotyledons" not found out. The morphs of apical dominance are observed relative frequently. The morph rosette (presence of branches at plantlets) was the most frequent. Frequency of violations of apical dominance far excels frequency of anomalies, usually looked after both in nurseries of seedlings *in vivo* and in the populations of plants *in vitro*. It should be noted that cotyledons had more frequent everything the elongated form. The plants were characterized mainly by very large cotyledons and long ramified roots. Frequency of vigorous, well developed plants was 0,322.

Thus, research of population *in vitro* of the plants, got from the embryos of wild grape, allowed to expose the following characteristic features: elongated form of cotyledons, plant vigor, high-frequency of rare morphs, especially morphs of apical dominance. The results of observations may be used on genetics, botany and physiology, for *in vivo*, *in vitro* and *in ovulo* experiments also.

USE OF *BROMUS MARGINATUS* AND *BROMUS INERMIS* FOR ENERGY PURPOSES

Daniela Kocourková, Josef Hakl, Pavel Fuksa and Jiří Mrkvička
Department of Forage Crops and Grassland Management, Czech University of Agriculture in Prague, Kamýcká 129, 165 21, Prague 6-Suchdol, Czech Republic; (email: kocourkova@af.czu.cz)

The aim of this study was to evaluate *Bromus marginatus* Nees ex Steud. and *Bromus inermis* Leyss. under different stand management as the possible energy crops for production of biomass for direct combustion. The studied traits were biomass yield, moisture, ash and nitrogen content and calorific value. The experiment was established in Prague in 2002. The studied treatments were: two cuts with fertilisation (100 kg N ha^{-1}), two cuts without fertilisation, one cut at the end of growing season without fertilisation and a delayed harvest in spring without fertilisation. Higher biomass yield was achieved in *B. inermis* 5,53 t.ha^{-1} than in *B. marginatus* plots 4,36 t.ha^{-1} ($P<0,0001$). The effect of fertilisation on biomass yield was higher in *B. inermis.* The calorific value of the biomass of observed grass species ranged from 17,47 MJ.kg^{-1} (in *B.inermis* biomass harvested in spring) to 18,81 MJ.kg^{-1} (in *B.inermis* biomass from the second cut on fertilised plots). There were no significant differences in moisture, ash and nitrogen content between the species. One cut treatments provided biomass of better values of qualitative parameters but higher yield was achieved in two cut treatments, especially when the fertilisation was used. *B. inermis* is more suitable for energy biomass production than *B. marginatus* because the quality of biomass of studied grass species is comparable and the biomass yield is higher in *B. inermis*. This research was supported by Research Project of Ministry of Education, Youth and Sports of Czech Republic No. 6046070901.

THE VARIABILITY OF MORPHOLOGICAL TRAITS OF CARROT GERMPLASM

Teresa Kotlińska[1], Alina Zabagło[2] and Ewa Żukowska[2]
[1]Plant Genetic Resources Lab., Research Institute of Vegetable Crops, Konstytucji 3 Maja 1/3, 96-100 Skierniewice, Poland; [2]Production and Breeding of Horticultural Plants Ltd., Żbicka 32, 32-065 Krzeszowice, Poland; (email: tkotlin@inwarz.skierniewice.pl)

The collection of genus *Daucus* includes 636 accessions. Each year the valorisation of morphological and economic traits of selected number of carrot genotypes from gene bank is carried out. The results of investigations obtained on the carrot landraces during 2005-2006 are presented. In the trials eighteen carrot accessions originated from Estonia, Georgia, The Netherlands, Russia and Poland for 25 traits selected from IPGRI descriptor list were characterised. These traits included: leaf colour, root diameter 1 cm above root tip/end (cm), root tip/end shape, root surface, green colouration of interior of the top, root type grouping, root shoulder shape, root length, root and core diameter, root weight, colour, yield, and structure. The chemical composition of roots (dry matter, sugar content, carotene and nitrate) was also determined. The results confirm a great variability of traits of examined carrot accessions. The characterisation of collected material from various origins allow to find the traits useful in breeding works.

GENETIC RESOURCES OF *LACTUCA SALIGNA* AND THEIR MORPHOLOGICAL ASSESSMENT

Eva Křístková, Aleš Lebeda and Ivana Doležalová
Palacký University in Olomouc, Faculty of Science, Department of Botany, Šlechtitelů 11, 783 71 Olomouc - Holice, Czech Republic; (email: ales.lebeda@upol.cz)

A total of 74 seed samples of *L. saligna* L. were acquired during collecting missions in Northern Italy (Po river lowland, Liguria, Riviera, Torino) and South-Eastern France (Hautes Alpes) in 1998 and 1999 (Lebeda et al., 2001). In 2002 and 2003 plants were regenerated in greenhouse and assessed for 36 morphologic traits according to the descriptor list (Doležalová et al., 2002) The aim of this study was to verify the taxonomic status of seed samples collected in natural habitats, and to describe the level of variation of some morphological traits. Eight samples did not germinate, twenty one samples were determined as *L. serriola* and 45 samples were determined as *L. saligna*. The set of morphological traits can clearly distinguish the species *L. saligna* from *L. serriola*. Type of composed inflorescence (spike-like panicle of heads), type of branching from the base and along the whole main stem, acute-subacute shape of apex of stem leaves, number of ligules in a head not higher than 16, dark coloration of anther tube caused by the presence of anthocyanine, and composition of cells in pappus in one row, are traits attributed to *L. saligna*. Shape of rosette and stem leaves expressed high variability within a set and have led to distinguish two varieties of the species. *L. saligna* var. *saligna* was identified on four locations in Italy and one location in France. *L. saligna* var. *runcinata* was identified on 16 locations in Italy and one location in France. Plants from one location in France were represented by mixture of both varieties, and moreover stem leaves of var. *runcinata* were double lobed. No clear relation between leaf shape (character of lobes) and presence of trichomes on midrib of stem leaves were found on both forms. Samples with similar double lobed leaves from two different locations strictly differed by number of ligules in heads; they had either high number of up to 16 ligules in heads, either 9 ligules only.

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NEW MUTANT FORM IN TRITICALE

Kishtili U. Kurkiev
Dagestan Experimental station of Vavilov Institute of Plant Industry, Russia, Derbent; (email: kkish@mail.ru)

Studying hexaploid triticale collection we found 1 plant differing in phenotype from all known triticale forms. It has the next characteristics: plant height 43 cm, length of upper internode 18 cm, spike length 5.5 cm, spikelets number 32, spike density 58.2, number of seeds per spike 30, weight of seeds in spike 1.1 g and weight of 1000 seeds 36.7. In progeny of this plant 3 different phenotypes were found. Plants of 1st type were semidwarf (plant height 15-20 cm), of the 2nd one – semitall (35-60 cm) and that of 3rd type were tall (110-120 cm). Therefore the initial plant was heterozygote. The first type has specifific morphological plant structure different from all all known triticale forms. Plant height is much less than in the most semidwarf sample of hexaploid triticale sample (5cm) from Vavilov Institute of Plant Industry collection. Plant have up to 7 internodes, upper two having distinct development (5-10 cm). Other internodes develop rarely and their length can be 0.1-0.8 cm. In most cases lower internodes possess are of overall length 1-1.5 cm. Each tiller has 5-7 well developed leaves lower leaves growing as from rosette. Flag-leaves lengths and widths are 20-25 and 1.5 cm respectively. Sheathes of all leaves overgrow corresponding internodes by 5-20 cm. The number of tillers per plant is 1-7. Spike of plants is short (4-6 cm) with many spikelets (25-35). Width of the spike is 1.5-2 cm. Spike density increases significantle in upper part. Awns length is 2-3 cm; number of seeds per spike is 5-20 grain being small and unplumped. This form of hexaploid triticale is likely natural mutant. There is no segregation in progeny of plants of 1st type. We proposed term Rosellate Leaf Mutant Dwarf (RLMD). Plants of 2nd type are in phenotype closer to initial plant. They are taller than plants of the 1st type. Spike is longer and seed quality is better. These plants are heterozygotes. In their progeny plants of all 3 types are observed. Third type does not differ from usual hexaploid triticale forms.

MONITORING THE LAST AUTOCHTHONOUS HULLED WHEATS IN CENTRAL SOUTHERN ITALY

Gaetano Laghetti[1], Domenico Pignone[1], Salvatore Cifarelli[1] and Karl Hammer[2]
[1]CNR – Institute of Plant Genetics, Bari, Italy; [2]Institute of Crop Science, University of Kassel, Witzenhausen, Germany

About 30 years ago it was thought that two species of 'farro', namely *Triticum dicoccon* Schrank and *T. monococcum* L., were no longer grown in Italy, but, in 1981 three and four accessions of these species respectively were discovered in a mountain area of the Appennino Sannita (central southern Italy). In 2006/07 some monitoring missions were carried out to check the current situation of these ancient hulled wheats, specifically in the same area where they were collected in 1981. The same zones were also investigated by both paleo-archeobotany and agrobiodiversity points of view. The results of this research have shown that nowadays *T. monococcum* seems to be completely extinct while *T. dicoccon* is still cultivated in very few traditional farms, mainly as a fodder crop. Few spikelets resembling *T. monococcum* were found in the farmers seed stocks, which are currently being investigated for chromosome number, a definitive method to asses the pertinence of seeds to one species or the other. A strong genetic erosion was detected for *T. dicoccon* and several nowadays samples were contaminated by seeds of modern spelt varieties (*T. spelta* L.). In the present study the causes of this genetic erosion and which safeguarding actions to undertake are presented and discussed.

GERMPLASM COLLECTIONS OF CROP WILD RELATIVES – RESEARCH, STUDY AND USE ON THE DEPARTMENT OF BOTANY, PALACKÝ UNIVERSITY IN OLOMOUC (CZECH REPUBLIC)

Aleš Lebeda, Ivana Doležalová, Eva Křístková, Barbora Mieslerová, Miloslav Kitner, Božena Navrátilová, Martin Duchoslav, Pavel Havránek and Drahomíra Vondráková
Palacký University, Faculty of Science, Department of Botany, Šlechtitelů 11, 783 71 Olomouc-Holice, Czech Republic; (email: ales.lebeda@upol.cz)

Germplasm collections of crop wild relatives are in the centre of scientific interest on the Department of Botany. All collections are used for educational and research purposes. Overview of research activities and publications are available on the web site (http:// botany.upol.cz). The collection of wild cucurbitaceous species includes 50 accessions of seven genera (*Benincasa, Citrullus, Cucumis, Cucurbita, Lagenaria, Luffa, Momordica*). Research is focused at study of their morphological variation, interspecific hybridization, embryo-rescue and protoplast cultures, and plant interactions with pathogens and pests (Lebeda et al., 2007). The collection of wild *Lactuca* species includes about 700 accessions of 18 wild species. The research is aimed at a study of eco-geography, biodiversity in natural habitats, collecting, studies of taxonomy, morphology, anatomy, karyology, molecular variation and interaction with lettuce downy and powdery mildews (Lebeda et al., 2007). The collection of the genus *Lycopersicon* with about 120 accessions of nine species is studied for response to tomato powdery mildew on the level of intact plants, leaf discs, cell structures and enzyme activities. The collection of the genus *Allium* includes about 500 populations representing various natural habitats of Europe. The research is aimed at a study of incidence, geography, ecology and reproductive biology of the polyploid complexes. A collection of 12 accessions of chive, collected in natural habitat from near Praha-Zbraslav on Vltava riverbank, contain unique genotypes useful in breeding programmes. Original locality was destroyed during the flooding in August 2002. The collection can be re-introduced to original habitats.

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PLANT GENETIC RESOURCES OF OAT FOR FOND

Igor G Loskutov
N.I. Vavilov Insitute of Plant Industry, 190000, B. Morskaya str., 44, St. Petersburg, Russia; (email: i.loskutov@vir.nw.ru)

Presently, identification of oat genetic diversity requires studying all the characteristics of this crop, demanding improvement by breeding. The most important ones are qualitative traits of oat grain, as they manifest great variability depending on the genotype of a cultivar and environmental conditions. Oat is now used for food and feed, being a source of high protein and lysine content. Besides, high-quality oat grain, with its increased content of oil and antioxidants, has recently been utilized for dietary purposes.

N.I. Vavilov Institute of Plant Industry (VIR) holds an oat germplasm collection, which is considered one of the largest in the world and unmatched in Europe (over 12,000 accessions). It represents virtually the whole global genetic diversity of this crop with an exceptionally broad range of variability in major plant characters, including breeding ones. This is very helpful for identification of genotypes meeting diverse demands of breeders. The most important biochemical components capable of raising oat’s nutritional value in addition to protein also include oil, ß-glucans, sterols, tocopherols and other antioxidants. Biochemical parameters were studied in a set of oat accessions representing the cultivated *Avena sativa* and all wild species of oat with different ploidy levels stored in the VIR collection. Selected for protein were the accessions of wild species with more than 20 % of protein content and well-balanced amino acid composition, while for oil content in caryopsis both cultivated and wild oat accessions were identified, with over 9-10 % of oil and well-balanced fat acid composition. The content of ß-glucans in the studied accessions varied from 3.3 % to 6.2 %. The highest content (over 5 %) was found in the cultivars Kirovets, Argamak, Sprint 2 (Russia), Aslak (Finland) and Belinda (Sweden). Also identified as potential sources of ß-glucans were VIR´s accessions: Teremok, Amursky Utyos (Russia), Sinelnikovsky 28 (Ukraine), Holden, Spear and Wright (USA). According to the preliminary data, total tocopherol content in the studied naked oat varieties was 2 to 3.5 times higher than in filmy forms. It was also observed that in different varieties the content of the α isomer amounted to 53-55 % of the total number of tocopherols, the sum of ß+γ made 32-40 %, while δ could reach 15 %. Lines with high oil content manifested close correlation between the content of ά-tocotrienols and the amount of oil. Preliminary results of the analysis performed on the limited set of cultivated oat forms showed that the total sterol content in filmy cultivars can be 1.7-2.4 %, while in naked ones this parameter amounted to 2.3-2.6 %. The study of VIR´s oat collection in search for donors of the above-mentioned biochemical components is currently underway. This work is targeted at selection and utilization of source materials for breeding high-quality oat cultivars, both filmy and naked, with increased content of oil, ß-glucans and antioxidants, thus contributing to a greater diversity of dietary products.

EVALUATION OF MORPHOLOGICAL VARIATION IN COLLECTION OF RYE LOCAL LANDRACES FROM TURKEY

Wiesław Łuczak, Jerzy Puchalski and Anna Martyniszyn
Botanical Garden-Center for Biological Diversity Conservation of the Polish Academy of Science, Prawdziwka St. 2, 02-973 Warsaw, Poland; (email: wluczak@obpan.neostrada.pl)

Botanical Garden-Center for Biological Conservation of the Polish Academy of Sciences started the program on conservation of genus *Secale* genetic resources in 1974. Up till now more than 2000 rye accessions have been collected. The rye collection is represented by modern varieties, local landraces and wild *Secale* species. In 1980 we started the cooperation on rye genetic resources conservation and evaluations with the USDA research institutions and we received ca. 700 accessions of unique rye germplasm collected in Turkey.

The aim of these studies was to evaluate one part of the joint Polish-American rye germplasm collection from Western Turkey represented by 250 local landraces collected in provinces Manisa, Balikesir, Denizli Izmir and Bilecik. 8 morphological and phenological characters in three year field observations were estimated according to standard variety Dańkowskie Złote. Resistance to 5 fungal diseases was observed. Analyzed data of selected morphological and phenological characters did not show the significant differences between average values for observed characters in subsequent year. Presented data showed also a similar distribution of deviations from standard variety in these three vegetation seasons. It seems that evaluated group of the Turkish rye local landraces showed high repeatability of morphological data during three years observation cycle. However, influence of weather conditions during vegetation periods was observed. Evaluated local landraces were higher than standard cultivar, with longer spike but smaller number of kernels per spike as well as lower thousand kernel weight. The evaluated Turkish local landraces shoved significant variability of deviation from standard, when were compared on the basis of collection site locality. The altitude of these localities differed from 121 to 858 meters above see level. High variation coefficient for disease resistance showed the selection possibility for higher resistance or tolerance among investigated local landraces.

MORPHOLOGICAL TRAITS AND SEED PRODUCTION POTENTIAL OF SOME WILD *TRIFOLIUM* SPECIES IN SERBIA

Zoran Lugic, Jasmina Radovic, Dejan Sokolovic, Rade Stanisavljevic and Goran Jevtic
Institute for forage crops, Trg kosturnice 50, 37000 Krusevac, Serbia; (email: zoran.lugic@ikbks.com)

Thanks to high climate variability and different soil conditions there are many plant species existing in various plant associations in Serbia. Leguminous species, especially over 50 species from genus Trifolium, are very important either from aspect of biodiversity or for improving of meadow and pasture quality. Introducing of their morphological and biological traits is the first step in their conservation and utilization. This examination includes five widespread *Trifolium* species (*T. montanum, T. alpestre, T. hybridum, T. prataense and T. pannonicum*) collected from three different sites from 500 to 1100m above see level. In the beginning of flowering ten individual plants of every species are collected. The next morphological traits are observed: plant height (cm), number of tillers, green mass yield and leaf size. In seed maturity phase from the same sites ten individual plants of every species are collected and analyzed for seed yield components (number of bloom per plant, number of florets in bloom, total seed number per plant and weight of 1000 seeds). The highest plants and green matter yield per plant are obtained in *T. pratense* and *T. pannonicum* genotypes (40-65cm and 125-210 gplant^{-1}), while the smallest plants are present in *T. montanum* species (20-40 cm; 40-80 gplant^{-1}). Great variability of individual plants is recorded both among and within localities. The similar variability in individual plants, species and localities is obtained for all seed yield components. The highest number of bloom per plant is obtained in *T. hybridum* (40-95) and the lowest in *T. montanum* (3-8). The highest flower number per bloom had *T. montanum* (60,80-188,60) while *T. hybridum* (49,80-59,60) had the lowest flower number per bloom. *T. hybridum* and *T. pretense* had the highest seed yield potential, while the species *T. pannonicum* and *T. alpestre* had low values for this trait.

EVALUATION OF MORPHOLOGICAL AND PRODUCTION TRAITS AT GENETIC RESOURCES OF GRASSES AND LEGUMES

Jana Martincová[1], Miriam Kizeková[1] and Jarmila Drobná[2]
[1]SARC-Grassland and Mountain Agriculture Research Institute, Mládežnícka 36, 974 21 Banská Bystrica, Slovak Republic; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: jmartin@vutphp.sk)

A research trial was conducted with wild ecotypes and with a range of cultivars of grasses and legumes, respectively, at Banská Bystrica site over 2005 – 2006, in the 1st and 2nd harvest years. Morphological, biological and economic parameters were investigated, namely: plant height, ear length, flag leaf length and width, spring growth intensity, regrowth rate and dry matter (DM) production. The research trial comprised 18 accessions of 8 grass species (*Festuca rubra, Festuca valesiaca, Poa pratensis, Trisetum flavescens, Phleum pratense, Phleum phleoides, Bromus erectus, Bromus inermis*) and 14 accessions of 6 legume species *(Anthyllis vulneraria, Coronilla varia, Onobrychis viciifolia, Lotus corniculatus, Medicago lupulina, Trifolium repens*). The tallest plant was recorded at *Onobrychis viciifolia* cv. Taja (833.9 mm) among the legumes and at *Bromus inermis* cv. Tabrom (965.6 mm) among the grasses. A positive correlation was found between the plant height and the ear length. The longest inflorescence and flag leaf, respectively, were found at *Bromus inermis* cv. Tabrom. Total DM production ranged between 2.85 and 10.20 t ha^{-1} at grasses (the highest DM yield was recorded at *Bromus inermis* cv. Tabrom) and from 0.59 to 15.57 t ha^{-1} at legumes (the highest DM yield was found with *Onobrychis viciifolia* cv. Taja). Dry matter production was significantly higher at the cultivars than at the ecotypes.

A NEW ATTEMPT TO USE MINORITY CROPS IN THE FUNCTIONAL FOOD DEVELOPMENT

Ľubomír Mendel, Jarmila Drobná and Iveta Čičová
SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 920 01 Piešťany, Slovak Republic; (email: mendel@vurv.sk)

The aim of the study was to determine the bread-making performance of blends of the flours from minority crops at 10, 15, 20 % levels to wheat bread and to investigate the effect of the blends on the chemical characteristics, rheological characteristics and sensory quality of bread. All flours samples added to the blends were analyzed for crude protein, protein, wet gluten, starch, fat, crude fiber, dietary fiber, macro nutrients and ash contents. The farinograph characteristics of composite flour (water absorption, dough development time, dough stability) were determined. Breads prepared from the blends were evaluated for physical characteristics (bread volume, high, width and spread ratio) and sensory characteristics (color of crust, color of crumb, crumb texture, flavor, taste and total sensory score was calculated). The flour blends had higher protein, fat, crude fiber, dietary fiber and ash contents than wheat flour. The level of these nutrients was improved with increased amounts of the blends. The protein content of the composite flour breads was higher than that of the wheat flour bread. Water absorption capacities of the flour blends increased, while the dough development decreased with increased level of blends. The dough stability decreased with increased amounts of the blends. Bread volume and spread ratio decreased significantly with increased addition of all blends except addition of oat. Sensory scores differed significantly amongst them color, flavor and overall acceptability.

THE DIVERSITY OF GERMPLASM OF TRITICALE IN SLOVAKIA

Ľubomír Mendel
SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 920 01 Piešťany, Slovak Republic; (email: mendel@vurv.sk)

The aim of the work is to characterize quantitative traits of accessions of triticale germplasm, from either Slovakian or foreign countries. Significant differences among entries were estimated for all traits and accessions were classified into similar genetic groups. Principal component and

hierarchical cluster analyses produced five different groups. In particular, the absence of a strong association among the investigated traits and their dominant independent roles in each separate principal component allows the achievement of a useful recombinant in breeding work. An interpretation of each cluster, based on the data obtained from the accessions, provides practical information to establish a subset of triticale collection for further activities.

GENETIC SOURCES OF HEALTH-PROMOTING FOODS

Daniela Mikulíková, Pavol Hauptvogel, Ľubomír Mendel, Iveta Čičová, Michaela Benková, Gabriela Antalíková and Ján Kraic
SARC-Research Institute of Plant Production Piešťany, 921 68 Piešťany, Bratislavská 122, Slovak Republic; (email: mikulikova@vurv.sk)

Currently, attention is being paid to foods that improve wellness. In effort to prevent the civilization diseases, increased attention has been given to functional foods. There are foods to which a component has been added for a resultant positive effect or eliminated due to a deleterious effect on health.

One of components of functional foods is resistant starch (RS). Due to its beneficial effects on digestive physiology, resistant starch is regarded as a prebiotic among the new generation of dietary fibre. Many well-known corporations (Cerestar, American Maize, OJI Starch, Avebe) produce functional foods enriched with resistant starch. Production methods use either chemically modified type RS_4 or type RS_2 obtained from genetically modified corn or barley cultivars. At this time in Slovakia, such foods as well as resistant starch as nutritional supplement are not available. The aim of this study was to screen for natural sources of RS_3 (arising during cooking, baking and freezing) in cereals, pseudocereals and legumes. The evaluated set contained seed samples from 248 cultivars from 18 plant crops: 26 wheat cultivars, 31 barley, 11 rye, 13 triticale, 9 tritordeum, 12 oat, 15 buckwheat, 18 millet, 10 foxtail millet, 6 sorghum, 2 quinoa, 25 amaranth, 20 pea, 11 lentil, 14 kidney bean, 5 faba bean, 16 chickpea and 8 soya bean. Significant differences in RS_3 were demonstrated within individual plant-crops and their cultivars. On the basis of the obtained results, 9 crops were identified as being very suitable natural sources of RS_3 and at the same time, whose cultivation is possible in our climatic conditions. Based on the legal cultivars registered in the Slovak Republic, we recommend the following cultivars as natural sources of health-promoting RS_3 resistant starch: triticale (cultivars Kendo, Pinokio, Presto, Tricolor), rye (Dankowskie Nove, Esprit), wheat (Boka), buckwheat (Pyra), chickpea (Alfa), kidney bean (Fabia, Ultima), pea (Elkan, Gloriosa, Zázrak z Kelvedonu), faba bean (Omar) and lentil (Renka).

VARIABILITY OF SELECTED QUALITATIVE TRAITS OF MATURE LEAF IN GERMPLASM OF GRAPEVINE (*VITIS* SPP.)

Katarína Popiková Mitická and Ján Brindza
Institute of Biodiversity Conservation and Biosafety, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 9494 76 Nitra, Slovak Republic; (email: katarina.miticka@uniag.sk)

Variability of qualitative traits was evaluated on land races of grapevine (*Vitis* spp.) in clonal repository in the locality Sebechleby – Stara Hora. During the year 2006 were tested 28 genotypes of grapevine. The experimental set of genotypes was evaluated on selected traits of mature leaf: shape of blade, number of lobes, anthocyanin colouration on main veins on upper side of blade, blistering of blade upper surface, shape of teeth on main lobe. Internationally used lists of descriptors for *Vitis* spp. (IPGRI and OIV) were applied for genotypes classification and description. Between the tested genotypes 73 % had leaves wits 5 lobes. More than 7 lobes had 3 % of samples. The most genotypes were represented by wedge-shaped leaf blade (45%), and the less of genotypes (7%) had leaf with cordate shape. Presence of anthocyanin colouration of main veins on upper side of leaf blade was found out on the 4 tested genotypes. Blistering of leaf blade upper surface was not presented at 62% of samples. Very weak blistering was found out at 10% and weak blistering at 28% of samples. All tested samples had open shape of teeth of main lobe. The results obtained from evaluation of qualitative traits will be used for basic description of vine land races conserved in clonally repository. Simultaneously the results will be used for development of information system GENOTYPDATA *VITIS*.

MANTAINING TRADICIONAL AGRICULTURAL SYSTEMS – THE LAST REDOUBT OF LONG TERM *IN SITU* CONSERVATION

Pedro M.R.Mendes Moreira[1], Nuno Queiroz[1], Nuno Teixeira[1], Daniela Santos [2],Carlota Vaz Patto[3], João P. Santos[1], Liliana Morgado[1], João P. Santos[1], Carlos Santos[1], Rui Soares[1], Vitor Carvalho[4] and Silas E. Pêgo[5]
[1]Escola Superior Agrária de Coimbra (ESAC), Departamento de Fitotecnia, Sector de Protecção Vegetal.; [2]ESAC. Dep. de Ciências Exactas e do Ambiente, Sector de Mesologia, Topografia e Hidráulica; [3]Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa; [4]ESAC. Dep. de Ciências Exactas e do Ambiente, Sector de Biologia; [5]Instituto Nacional de Investigação Agrária; (email: pmoreira@esac.pt)

In Northern and Central regions of Portugal traditional polycrop farming systems are generally characterized by small farms (considered in some cases as homegardens), old farmers, mountain areas and secular water systems. These farmers were, for centuries, the guardians of the long term germplasm *in situ* conservation (e.g. of maize, with its important role on the farming systems structure) and the enduring reservoirs of empirical knowledge. Nevertheless, during the 80's and 90's, considerable farmers migration occurred, jeopardizing future knowledge transmission, since the farmer traditional activities are endangered. This "farmer erosion" will continue unless adequate political measures are urgently taken.

During 2005 a collecting mission took place with three main targets: 1) Collecting the germplasm of the traditional polycroping systems; 2) Gathering information from the farmer linked with the management of his traditional polycroping systems; 3) Collecting information on traditional food products. The collected information together with the results obtained in 2005 and 2006 field trials revealed that traditional polycroping systems could be of major importance for: participatory maize breeding programs, *in situ* conservation and participatory polycroping systems breeding.

A case study of a particular traditional system of Northern Central Region is presented.

PORTUGUESE *IN SITU/ON FARM* CONSERVATION THE ROLE OF ONG'S

Pedro M.R.M. Moreira[1], Miguel Malta[2], Carlota Vaz Patto[3] and Manuela Veloso[4]
[1]Escola Superior Agrária de Coimbra (ESAC). Departamento de Fitotecnia. Sector de Protecção Vegetal.; [2]ESAC Dep. de Ciências Sociais e Humanas; [3]Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa; [4]Estação Agronómica Nacional, Departamento de Recursos Genéticos e Melhoramento; (email: pmoreira@esac.pt)

The natural conditions (e.g. landscape and climatic diversity), farming systems and well-timed collecting missions (Vaz Patto et al. 2006), explain why Portugal still represents a genetic resources sanctuary for some species (e.g. maize, common bean). But this sanctuary is threatened by the replacement of landraces by widely adapted improved varieties and hybrids, by habitat destruction and especially by "farmer erosion", *i.e.* farmers are getting old without possibility of passing on their knowledge and germplasm to the next generation. This means that the traditional systems are being lost. These traditional systems are characterised by sustainability, environmental friendship and quality orientation. Conservation *ex situ*, is a help, but several limitations are pointed out (*e.g.* the processes of diversification and co-evolution stops). So it is urgent to support rural communities to preserve and promote *on farm* conservation. This paper summarizes some of the work done by Portuguese ONG's that are supporting *on farm* conservation of locally adapted landraces.

EVALUATION AND USING OLD AND MARGINAL VARIETIES OF PLUMS IN PROGRAMME EU POLITICS OF QUALITY

Valéria Müllerová[1], Ján Brindza[1] and Pavol Tóth[2]
[1]Department of genetics and plant breeding, Faculty of Agrobiology and Food Resources, Slovak Agricultural University in Nitra, Tr. Andreja Hlinku 2, 949 76, Nitra, Slovakia; [2]Department of Animal Husbandry and Food Production, Faculty of Agricultural Engineering, Slovak Agricultural University in Nitra, Tr. Andreja Hlinku 2, 949 76, Nitra, Slovakia; (email: valeria.mullerova@uniag.sk)

Plum (*Prunus domestica* L.) is a species adapted on Slovakia conditions. Fruit has been used especially for production of food products and liquors. Because of plum pox virus (PPV) distribution, the fruit production was markedly reduced. Some of the primal distributed populations are characterized by high tolerance to PPV. For this reason the marginal population of “Gemerská” plum in the region of Novohrad is experimentally verified. In the first stage 55 genotypes were chosen. 12 quantitative traits were evaluated. By fruit was determined: weight 7.6-24.0 g, length 27.5-44.6 mm, width 20.1-35.3 mm and thickness 17.4-31.6 mm. On the stones were determined weight (0.5-1.3 g), length (16.8-28.0 mm), width (8.0-16.8 mm) and thickness (5.2-9.1 mm). The length of leafs blade was 20.0-110.0 mm, the width 13.0-65.0 mm. The mellow fruits were used for production of damson cheese by traditional technology. During the production was defined temperature on the top (80-85 °C) and inside (90-95 °C). The average content of solids was 29.6-38.6 %. Following the chemical, sensorial, microbiological and technological analyses will be prepared a proposal for using damson cheese as the traditional product of guaranteed quality.

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CHARACTERISATION OF THE GENETIC OAT RESOURCES OF DOMESTIC ORIGIN BY ELECTROPHORETIC SEPARATION OF STORAGE PROTEINS

Lenka Nedomová[1], Edita Gregová[2], Ivana Polišenská[1] and Tomáš Vyhnánek[3]
[1]Agricultural Research Institute Kroměříž, Ltd., Havlíčkova 2787/121, Kroměříž, CZ-767 01, Czech Republic; [2]Slovak Agricultural Research Centre - Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [3]Mendel University of Agriculture and Forestry in Brno, Zemědělská 1, Brno, CZ- 613 00, Czech Republic; (email: nedomova@vukrom.cz)

Profiles of individual oat (*Avena sativa* L.) genotypes bred in the territory of the Czech and also former Czechoslovak Republic were characterised using analyses of seed storage proteins. The use of both avenin and globulin fractions polymorphism was verified. Avenins were separated by acid polyacrylamide gel electrophoresis (A-PAGE) and globulins by SDS-PAGE. The genotypes were compared among one another based for the presence of particular protein fractions. The level of polymorphism of avenin protein fractions was higher than that of globulin protein fractions. The two methods, particularly in combination, showed to be appropriate for identification of oat cultivars. All genotypes of analysed cultivars were unambiguously distinguished. The results are assumed to be used for completing descriptor data on resources with electrophoretic patterns of proteins as well as for breeders´ utilization in a breeding process.

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THE EFFECT OF HEAD-SPACE GASES ON VIABILITY OF HERMETICALY STORED SEED SAMPLES OF RYE, WHEAT AND TRITICALE

Maciej Niedzielski and Jerzy Puchalski
Botanical Garden-Center for Biological Diversity Conservation of the Polish Academy of Science, Prawdziwka St. 2, 02-973 Warsaw, Poland; (email: mniedz@ob.neostrada.pl)

Seed banks, besides plant living collections, are the main *ex situ* preservation method for plant genetic diversity conservation. According to the IPGRI recommendations for orthodox seed, dried samples are stored in hermetic containers at ca -25^{0}C. It helps to prolong their life-span for long time. However, aging processes are not stopped completely. Important role in aging of dry seed play oxidative reactions of lipids due to free radicals activity or autooxidative processes. End products of these reactions-low molecular volatiles, could be accumulated in hermetic storage containers. Head space gases contain high amount of alcohols, aldehydes and ketons. Due to their chemical activity, they may react with proteins and nucleic acids negatively affecting seed viability (Zhang at all 1993).

The aim of this experiment was to analyze the head space gases contents in sealed aluminum foil packages with seed samples. Rye, wheat and triticale seed samples representing totally six cultivars were stored at 35^{0}C at three levels of moisture content 0,06 gH_2O/gdm, 0,08 gH_2O/gdm and 0,12 gH_2O/gdm. Content of gaseous environment inside of containers was analyzed using gas chromatography. Seed viability as germination ability was tested according to ISTA method. Seed viability and moisture content have been compared to the same seed subsamples stored over saturated salt solutions in glass desiccators, periodically ventilated as a control. The experiment is still in progress. Preliminary results of viability evaluation in relation to head space gases revealed significant differences among samples stored in hermetic packages and desiccators.

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POTENTIAL USABILITY OF POLLEN FROM MOUNTAIN RYE *SECALE STRICTUM* (C. PRESL.) C. PRESL.

Janka Nôžková, Oľga Urbanovičová, Martin Kolník and Radovan Ostrovský
Institute of Biodiversity Conservation and Biosafety, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic; (email: olga.kunova@uniag.sk)

During the years 2005 and 2006 there were realized analyses on the mountain rye *Secale strictum* (C. Presl.) C. Presl.. Plots were based on classical agro technical principles for cereals on the fields of Slovak Agriculture University in the locality of Nitra - Malanta. There was studied the morphological variability of ears and their parts during the flowering. From 50 randomly selected ears there were made detail digital records of spike, anther and feathery stigma. The length of anther was evaluated; the range was from 5.3 mm to 11.1 mm. The size and shape of pollen grains was evaluated on the 12 selected plants. From each plant there was took away 30 pollen grains randomly and their size were measured. Mean length of equatorial axis was 58.88 µm and mean length of polar axis was 35.42 µm. Also digital records of the pollen grains were documented. The image records of pollen grains were made by light microscope Zeiss Axiostar plus, and details of ear parts by macroscope Zeiss Stemi 2000. During the years 2005 and 2006 the flower pollen of mountain rye was harvested. The methodology of harvesting of the largest amount of pollen was formed. The best period of plant harvesting was closely after beginning of flowering, when the first anthers from upper third of ear are taken out. The gathered plants were put to the jars with water and consecutively dried in the indoor conditions. Obtained biological material of pollen and flower parts was sieved through a special uhelon sieve with the pore size of 139 µm. This method brought enough flower pollen, approximately 192.7 g. The important content elements will be determined in the flower pollen by selected chemical and biochemical analyses.

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A GROWER-POMOLOGICAL EVALUATION OF SOME PEACH AND NECTARINE CULTIVARS IN GENE-POOL COLLECTION ON HORTICULTURE FACULTY IN LEDNICE

Ivo Ondrášek and Ivan Oukropec
Mendel University of Agriculture and Forestry in Brno, Department of Fruit Growing, Horticulture Faculty in Lednice, Czech Republic; (email: ondrasek@zf.mendelu.cz)

In accordance with a perennial evaluation of peach and nectarine cultivars from gene-pool collection in Lednice is composed following grown and pomological distribution. From blooming time point of view belongs among early blossom cultivars for expamle varieties Siberian C and Nataly. Late flowering are Catharina and Nectadiofik. According to ripening time belongs to early group cultivars Maycrest, Starkcrest, Earlycrest and Wang 2. To the late ripening group of cultivars belongs Lucia, Orion, Venus and Sandra. From a frost hardiness point of view belong among hardy cultivars Miss Italia, Flamingo, Fenix, Elegant Lady, Envoy, Harbelle and Maria Marta. Such as less frost hardiness cultivars are denoted varieties Armking, Rich Lady or Aurelia. Thanks to evalutaion of taste quality and growing demands is possible support following perspective cultivars – Maycrest, Royal Glory, Miss Italia, Symphonie, Springbelle, Delice, Ruby Prince, Supercrimson, Harko, Flavortop, Big Top, Orion and Venus.

UTILIZATION OF GEOGRAPHICAL INFORMATION SYSTEMS IN *IN SITU* PLANT GENETIC RESOURCES PRESERVATION

Radovan Ostrovský[1], Ján Brindza[2], Jana Holecyová[2] and Jana Červeňáková[2]
[1]Institute of Biodiversity Conservation and Biosafety, Slovak University Of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia; [2]Department of genetics and plant breeding, Faculty of Agrobiology and Food Resources, Slovak University Of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia; (email: Radovan.Ostrovsky@uniag.sk)

Development of technical and research areas led to utilization of Geographical information systems (GIS) technology in process of *in situ* plant genetic resources preservation. Partial regional information system in GIS environment present effective tool for localizing of genotypes, it offers possibilities for data browsing and classifying, spatial analysis and map sets creation.

Three model regions were selected in Slovak republic. In partial regional information system, there were recorded 480 genotypes of black mulberry (*Morus nigra* L.) in Pukanec region; there were localized 54 genotypes of service tree (*Sorbus domestica* L.) in Sobotište region and 691 genotypes of fruit species in Haluzice region.

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PASSPORT AND SPECIAL DESCRIPTORS AS WELL AS IMAGE ANALYSIS USE IN FLAX GENETIC RESOURCES (*LINUM USITATISSIMUM* L.) EVALUATION AND CHARACTERIZATION

Martin Pavelek, Petra Vinlárková and Bohumila Matysová
AGRITEC Plant Research Ltd., Šumperk, Czech Republic

Czech Flax National Collection (*Linum usitatissimum* L.) belongs to the biggest European one (Pavelek, 2002). 2056 accessions are maintained in the collection at the end 2006. Since 2003 the collection has been systematically analysed from the point of passport and special descriptors view. Since 2004 image analysis has been used in order to receive initial input data for collection rationalisation, detection of duplicates and core collection of 10 % previous collection size creation conserving the original range of genetic variability. The first set of 350 accessions (X13 – contemporary modern varieties) have been studied by passport and special descriptors analysis as well as molecular method use. The genetic diversity of morphological traits has been found, the individual genotypes have been divided into the respective 40 clusters and these ones have been evaluated and characterized (Pavelek, Smýkal, Horáček, 2006). In this work the possibilities of image analysis use have been studied not only for the documentation system EVIGEZ but also to get the knowledge whether the traditional system of evaluation by passport and special descritors can be replaced by image analysis and to be used in flower morphology evaluation and duplicates detection especially. Set of further 151 X13 accessions has been evaluated by passport descriptors, and image analysis of 19 flower, boll and seed traits. These ones have been retrospectively converted into the classification system according to the National Descriptor List (Pavelek, Faberova, in press) and by image analysis parameters (area, length, width, Max Feret, Min Feret, circularity, elongation) utilization the duplicates were detected and analysed in order to evaluate similarity or distinquish respectivelly.

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“BLITO” (*AMARANTHUS* SPP.): A GREEK TRADITIONAL NEGLECTED CROP

Domenico Pignone[1], Gaetano Laghetti[1], Karl Hammer[2], Eleni Psarra[3] and Stelios Samaras[3]
[1]CNR – Institute of Plant Genetics, Bari, Italy; [2]Institute of Crop Science, University of Kassel, Witsenhausen, Germany; [3]Greek Gene Bank, Thessaloniki, Greece

During germplasm collecting missions carried out in Greece in 2005 and 2006 it has often been noticed that in local markets young plants of *Amaranthus* spp. were sold as a green vegetable under the name of Blito (Βλιτο). Local sellers indicated that this vegetable was not collected from the wild. Only few fields were found devoted to the production of Blito for the local markets in Crete, Lefkada, Ithaki and Kefallonia, but many family gardens often showed the presence of small lots of Blito at different growing stages.

The identification of *Amaranthus* species is not always simple, but at least two species were present in family fields, namely, *Amaranthus lividus* L. (syn. *A. blitum* L. subsp. *oleraceus* (L.) Costea), the cultivated form generally sold in markets, and *A. retroflexus* L., a wild species, largely present in the area. Interviews with farmers indicated that the wild form was originally a weed not eliminated from the filed, but later seeds of *A. retroflexus* were collected from the most vigorous plants. No major difference in flavour was reported for the two species. Other species were also present at a lesser extent (e.g. *A. paniculatus* L. syn. *A. cruentus* L.) and were cultivated as ornamentals. A search for traditional food has demonstrated that also in some areas of Italy *Amaranthus* species are cultivated on a small scale with different names, one of them being Blito. It is interesting to observe that this practice is more diffused in the North-East of Italy, close to the region of Venice. Venice dominated the Mediterranean in the 15th -18th century, particularly in the islands explored. A confirmation of the interchange of genetic resources also comes from local names of grapes (e.g. moscatello) or tomatoes (comidori, from the Italian pomidori). It is interesting to notice that, similarly to what observed in other rural traditional areas (e.g. in Calabria or in Sardinia, Italy), when plants are grown for self consumption, farmers tend to experiment new cultivations and often attempt domestication of wild plants, sometimes with a good success.

CONSERVATION AND USE OF GRAPE GENETIC RESOURCES IN UKRAINE

Alla Poluliakh, Vladimir Volynkin and Irina Vasylyk
National Institute for Vine and Wine “Magarach”, 31 Kirov St., Yalta, Crimea, 98600, Ukraine; (email: select_magarach@ukr.net)

Collecting, conservation and use of grape genetic resources are of great importance for modern Ukraine and the international community in general since these activities contribute to the national and global food security. Today genetic homogeneity of commercial grape plantings is increasing, and this makes them more vulnerable to biotic and abiotic environmental factors.

The grapevine collection of the Institute “Magarach” which has been granted national status was established in 1814. It grows grape accessions from 41 countries of the world’s different regions of grape and wine growing. The *Vitaceae* Lindley family is represented by three genera of which: the genus *Ampelopsis* Michaux. contains three species: *Ampelopsis aconitifolia* Lavallée, *Ampelopsis cordata* Michaux. and *Ampelopsis serjanieafolia* Regel.; the genus *Parthenocissus* Planch. contains two species: *Parthenocissus inserta* Fritch. and *Parthenocissus quinquefolia* Planch.; and the genus *Vitis* Linn. contains 23 species. The species *Vitis vinifera* L. is represented by two subspecies, *Vitis vinifera silvestris* Gmel. and *Vitis vinifera sativa* D.C. The subspecies *Vitis vinifera sativa* D.C. contains a total of 29 forms of the wild-growing grape, 1432 local and autochthonous varieties (including 249 of *convar. pontica* Negr., 101 *convar. occidentalis* Negr., 407 *convar. orientalis* Negr.) and 730 newly-bred varieties obtained via crossing within the species *Vitis vinifera* L. (including 261 new varieties released in Ukraine). The collection also grows a total of 860 varieties of interspecific origin of which 263 are interspecific hybrids, 82 are hybrids of *Vitis amurensis* Rupr., 28 are hybrids of *Vitis labrusca* L., 6 are hybrids of *Vitis riparia* Michx., and one is a hybrid of *Vitis rupestris* Scheele.

Research into the intravarieties variation is underway, aimed at selection and conservation of valuable clones. The grapevine collection of the Institute has always been an instrument of selection and development of new genotypes. The varieties

Bastardo magarachskii, Podarok Magaracha, Tsitronnyi Magaracha, Pamiati Golodrigi cultivated both in Ukraine and other countries may enter as examples of these activities. The hereditary basis of valuable traits inherent in accessions maintained in the Institute's grapevine collection serves as a source of initial material for creation of new generations of grape varieties.

WILD POPULATIONS OF BIRDSFOOT TREFOIL (*LOTUS CORNICULATUS* L.) - GREAT SOURCE OF VARIABILITY

Jasmina Radović, Zoran Lugić, Dejan Sokolović, Rade Stanisavljević and Tanja Vasić
Institute for forage crops, Trg kosturnice 50, 37 000 Krusevac, Serbia; (email: jasmina.radovic@ikbks.com)

Birdsfoot trefoil is a widely distributed old-world species that is adapted to a broad range of environments. This species is a widely spread in nature pastures in Serbia and it's a regular component of a numerous association in wild flora. Birdsfoot trefoil is very important fodder leguminous plant in hilly-mountainous region of Serbia, because it is providing the protein component in forage on the low quality soils which is not suitable for alfalfa and red clover. One of the conditions for a faster expansion of this species is a continual improvement of available varieties. A common problem with the genetic improvement of many forage species has been the limited genetic base used for the cultivar development. Wild populations of birdsfoot trefoil in Serbia represent great source of initial selection material for obtaining of high productive and persistent genotypes.

The aim of this paper was to determine the productivity and morphological traits of wild populations of birdsfoot trefoil collected from different locations in Central Serbia in order to find the genotypes with good agronomical traits. The populations were investigated in second and third year of exploitation. Morphological analyses of agronomic important traits were made in second cut. Investigated material has demonstrated high variability in regard to monitored parameters between and among populations. Intra population variability was very high for dry matter yield (CV 21-57%), as for number of steam per plant (CV 21-54%). Variability for those traits between populations was lower (CV 20-32%). For other monitored traits coefficient of variability between populations (CV 10 %) and among populations (CV 6-24%) were lower, too. Recorded differences among, as well as high variability of individual plants within populations, indicate that wild populations of birdsfoot trefoil are rich source of variability for creation of new varieties of this species for different purpose.

PRESERVATION OF IN VITRO FRUIT PLANTS IN COLD STORAGE

Jiri Sedlak and Frantisek Paprstein
Research and Breeding Institute of Pomology Holovousy, 508 01 Horice v Podkrkonosi, Czech Republic; (email: sedlak@vsuo.cz)

Studies on in vitro cold storage of selected genotypes of sweet cherry rootstocks ´P-HL-A´, ´P-HL-C´ and strawberry cultivars ´Korona´, ´Elvira´, ´Redgauntlet´ were carried out to verify the suitability of this method for duplicate conservation of fruit germplasm in RBIP Holovousy. Shoots were multiplied on MS medium with 1 mg · l^{-1} BAP. The cultures were then stored on the same multiplication medium at 4 0.5 °C in cooler. The viability of in vitro cold-stored plants was monthly evaluated for the period of 15 months. The best results were achieved for sweet cherry rootstock ´P-HL-A´, where 33 % of plants survived and developed new shoots after 15 months of storage at 4 °C. On the contrary all in vitro plants of genotype ´P-HL-C´ died within 7 months after the beginning of cold storage. Three strawberry cultivars had intermediate results. Survival rates of strawberry in vitro plants after 12 months at 4 °C were 15 % for Corona, 3 % for Elvira and 2 % for Redgauntlet. The storage of in vitro cultures at 4 °C appears to be promising technique for medium-term conservation of fruit germplasm.

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CHARACTERISATION OF MORPHOLOGICAL AND ECONOMIC TRAITS OF HOP GERMPLASM

Urszula Skomra
Institute of Soil Science and Plant Cultivation – State Research Institute, Czartoryskich 8, 24-100 Pulawy, Poland

The collection of hop cultivars held at the Institute of Soil Science and Plant Cultivation – State Research Institute in Puławy was established in 1972. At present the collection includes 224 cultivars which represent hops cultivated in the whole world. Genetic resources of hop are maintained in the field. Evaluation of accessions covered morphological characteristics and economic traits.

In the years 2004-2006 the 35 hop cultivars representing aroma and bitter types were evaluated. The examined accessions were characterized by a great variation of morphological traits, like the length of internodes and lateral shoots, the height of attachment of the first cone-bearing shoots and the coiling index, which determines an easiness of shoots for training onto the twines. Alpha acid content which is most important characteristic for brewing industry, fluctuated between 2,1% and 10,5% in aroma cultivars and between 5,3% and 14,0% in bitter hops.

Gathered genotypes are potential source of different genes determinative valuable economic traits which can be used by breeders to release new selections with good yield quality and also well adapted to our climate and soil conditions.

EVALUATING AND BROADENING OF MEADOW FESCUE AND ORCHARDGRASS AUTOCHTHONOUS POPULATIONS COLLECTION IN SERBIA

Dejan Soković, Jasmina Radović, Zoran Lugić, Aleksandar Simić and Snežana Babić
Institute for forage crops, Trg kosturnice 50, Kruševac, Serbia; (email: dejan.sokolovic@ikbks.com)

Meadow fescue (*Festuca pratensis* Huds.) and cocksfoot (*Dactylis glomerata* L.) are very important perennial fodder grasses with multiple purposes for animal feed production on grasslands and pastures. In Serbia they are caenobionts of plant associations from the class *Molinio-Arrhenatheretae*, from lowlands to valleys in hilly areas. *Festuca pratensis* Huds. is mostly frequent in associations *Cynosuretum cristati*, *Festucetum pratensis* and anthropogenic association *Arrhenatheretum elatioris*. *Dactylis glomerata* L. is characteristic species of grasslands from alliance *Arrhenatherion elatioris* with different presence and covering. In hilly region it is mostly present on moderately moist soil and mezoxerofile woods and on some habitats over 1000m a.s.l., too. Collecting of those perennial grass species was conducted in order to find prosperous genotypes which are acclimatized on ecological conditions in Serbia and to incorporate them in breeding as initial breeding material. Also determining sites and associations, and preserving genotypes of those grasses *in situ* should protect genetic resources and variability of mentioned species.

Seed collection of 16 meadow fescue, 24 seed and 46 green plant cocksfoot accessions from 16 different localities across Serbia has been formed earlier. All seed and few promising green plant accessions are incorporated in pre-breeding process in spaced plant nursery with 20 plants per population. During two years nine traits of cocksfoot were investigated and variability within and between populations were obtained. Also several traits were observed in first year of meadow fescue nursery.

Collecting in 2006 was carried out across Central Serbia according to IBPGR descriptor for fodder grass plants. All accessions were gathered as seed, after *in situ* observation, representing material with great potential for selection. Meadow fescue was collected from various habitats with focus on resistance, whereas late maturing was favorable trait in cocksfoot. Seed are harvested in diameter of 15-20 m for each location with 50 genotypes (plants) per population at least. Ten samples of meadow fescue and 21 samples of cocksfoot were collected from 18 localities on 14 areas across Central Serbia. All samples were collected from hilly habitats from 200 to 1100 m above sea level. Those samples will be incorporated in characterization and evaluating trial in next year.

MISCANTHUS GENOTYPES AS A SOURCE OF BIOMASS AND THEIR SELECTED UTILIZABLE FEATURES

Mieczysław Stasiak
IUNG-PIB, Institute of Soil Science and Plant Cultivation – State Research Institute, Puławy, Department of Breeding and Production of Special Plant, Al. Czartoryskich 8, 24-100 Puławy; (e-mail: stamie@poczta.fm)

Utilizable features of Miscanthus genotypes were defined in order to choose the most appropriate genotypes for the production of biomass in Poland. Seven genotypes of *Miscanthus* species from TINPLANT Laboratory in Magdeburg were investigated. There are as follow: *Miscanthus sinensis* (40,07,105), *Miscanthus Robustus* (115,114), *Miscanthus giganteus* and its related 117 Genotype. The plants were planted in 0,85 x 0,80m spacing (14 705 plants ha^{-1}). Directly before the harvest in January 2005, height of five plants of each of genotypes and diameter of their shoots were measured. The shoots were also counted. Giganteus and 117 Genotype were characterised by the highest height, diameter and yield. Statistically there was no-significant difference between yields of the investigated Miscanthus genotypes.

BIOMASS YIELD OF SHORT ROTATION WILLOW CLONES IN RELATION TO CUTTING FREQUENCY

Mieczysław Stasiak and Robert Borek
IUNG-PIB, Institute of Soil Science and Plant Cultivation – State Research Institute, Puławy, Poland, Department of Breeding and Production of Special Plant, Department of Agrometeorology and Applied Informatics, Al. Czartoryskich 8, 24-100 Puławy; (email: rborek@iung.pulawy.pl)

The scope of the two factorial experiment was productivity of four willow clones (1023, 1047, 1052, 1054) in three cutting cycles: one year, two or three. Field trials was conducted on soil classified to weak rye complex localized in the Grabow Experimental Station IUNG-PIB Pulawy in 2003 year. Cutting were planted at the density of 40 000 plants ha^{-1} in rows 0,75 apart at with distance in row 0,33 m. Results were obtained during three years of experiment. Harvests were performed on December 2004 (one year old shoots), 2005 (one and two year old shoots) and 2006 (one, two and three year old shoots). It was found that there were not statistically significant differences between clones. The highest yield of wood dry matter i.e. 43,2 t ha^{-1} year^{-1} was obtained in three years cutting cycle. Wood obtained in one year cycle showed the highest water content (50,4 %), water contents in two and three year old shoots were lower and its average was close to 46 %.

CURRENT STATUS OF THE *SOLANACEAE* AND *ALLIUM* COLLECTIONS IN THE CZECH REPUBLIC

Helena Stavělíková and Jan Losík
Crop Research Institute, Department of vegetables and special crops Olomouc, Šlechtitelů 11, 783 71 Olomouc, Czech Republic; (email: stavelikova@genobanka.cz)

Genetic resources of vegetable crops from genus *Allium* - garlic, shallot and onion, leek and Welsh onion are maintained by Research Institute of Crop Production Prague), genebank, Olomouc station. This workplace maintains the collection of tomato, pepper, eggplant and Physalis.

Workplace Olomouc holds the international field gene bank for vegetatively propagated *Allium* sp. of long- day type. The collection of garlic consists of 624 the accessions. The accessions come from the whole world mainly from Czechoslovakia and Soviet Union. The collection is divided to three parts according to ability to produce the scape: part with the scape 310 accessions, part without scape 206 accessions and the part of accessions has the topset in the different part of the pseudostem 108 acc. Collection of shallot consists of 121 acc. Main part of this collection is formed by material of Scandinavia. 22 accessions are representing onion collection. We have the Czech material only one accession is from Poland. The collection of pepper includes 514 accessions. The large part of collection represents by old open pollinated varieties from Czechoslovakia, Hungary and Soviet Union. During multiplication we have used two system of forestall the outcrossing. The first: plants were grown in plastic tunnels. These were isolated by special bags before flowering.

After three weeks the bags were removed and the small fruits were tagged by cotton thread. The seeds were taken from tagged fruits. The second: The plants are grown in the isolation cages. Maintaing collection of tomato has 1593 accessions. It includes both indeterminate (1034 acc.) and determinate (559 acc.) plant growth types. The old open – pollinated varieties from Czechoslovakia USA and the Soviet Union are basis of the collection. The tomato accessions are multiplied in the field condition. All accessions are described according relevant international descriptor lists.

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REPATRIATION OF GERMPLASM ACCESSIONS OF CZECH/SLOVAK LOST GRASS VARIETIES

Magdalena Ševčíková and Helena Marková
OSEVA PRO Ltd., Grassland Research Station Rožnov-Zubří, Hamerská 698, 756 54 Zubří, Czech Republic; (email: markova@oseva.cz)

Landraces and cultivars belong to the cultural heritage of every country. In the former Czechoslovakia, grass breeding in the 1920's was based on selection from local ecotypes in the three distinct regions of Southern Bohemia, Northern Moravia and later Slovakia. This resulted in the development and cultivation of 45 varieties of 17 grass species.

The oldest varieties were never tested or registered. It was 1937 before the first varieties were registered, namely Táborský (-á) and Větrovský (-á) which originated in Bohemia, and then varieties Rožnovský (-á) from Moravia which were registered in 1940 followed by Slovakian varieties Levočský (-á) in 1949-1950. Seed multiplication, a new branch of agriculture, played an important role in the improvement of grassland and increased the incomes of the farmers involved, especially in the economic poor mountainous and sub-mountainous regions. Unfortunately, most of these "historical" varieties were not preserved in a germplasm collection before the systematic work on plant genetic resources took place in research institutes. The national inventory showed that the number of missing accessions amounted to 27 of 34 deleted varieties, although four of them have since been regenerated from seed found at local breeders.

Using the European Central Crop Databases at first and later the EURISCO web catalogue which provides access to all the *ex situ* plant genetic resources information in Europe, other European genebanks were identified as the holders of nine accessions of Czech and/or Slovak origin. These institutes, namely IPK Malchow, RAC Tápiószele, IGER Aberystwyth and VIR St. Petersburg, were asked for their repatriation. Seed samples of eight accessions were received from three institutes while a request to VIR has so far been unsuccessful. The regeneration process was successful in seven of the accessions and thereby, thanks to the international co-operation, seven "lost" varieties have been rescued for the Czech germplasm collection.

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GENETIC DIVERSITY IN A COMMON BEAN (*PHASEOLUS VULGARIS* L.) *EX SITU* COLLECTION OF ITALIAN LANDRACES

Barbara Tiranti[1], Leonardo Macaluso[2], Pierluigi Spagnoletti Zeuli[2] and Valeria Negri[1]
[1]Dipartimento di Biologia Vegetale e Biotecnologie Agroambientali e Zootecniche (DBVBAZ), Università di Perugia, Borgo XX giugno 74, 060121 Perugia (Italy); [2]Dipartimento di Biologia, Difesa e Biotecnologie Agro-Forestali, Università degli Studi della Basilicata, Viale dell'Ateneo Lucano 10, 85100 Potenza (Italy); (email: vnegri@unipg.it)

Landraces (LRs) are vital genetic resources for breeding purposes, diversification of production, developing new farming systems and new quality products. The extent and distribution of the genetic diversity in a crop depends on its breeding system, geographical, ecological and human factors. Conservation of genetic variability is essential for present and future human well-being.

To date, the *in situ* or *ex situ* conservation strategies have been applied with little information on the genetic diversity that was being conserved. In order to improve conserved germplasm management, it is necessary to understand the genetic diversity that is present in collections. Common bean LRs have been obtained from Italian farms and local markets, mostly located in Central Italy, and their seeds samples were used to establish an *ex situ* collection at DBVBAZ. In this study the amount of genetic diversity and its distribution in 159 Italian LRs were assessed using different approaches that included morphological (international descriptors), biochemical (phaseolin seed proteins) and molecular analysis (*Simple Sequence Repeats* markers). Results obtained showed a wide variation overall morphological traits, especially seed characters. The three major phaseolin types were found, 'C' (38.9%), 'S' (33.1%) and 'T' (28.0%) types. Nine of ten loci analysed were polymorphic and 82 different alleles were detected overall SSR loci.

Our findings on the extent and distribution of different aspects of genetic diversity in this Italian common bean LRs collection is an essential prerequisite to determinate what to conserve and how to conserve it. In addiction all the information collected will offer the opportunity to rationalize the collection, to develop a core collection and to exploit these resources for valuable traits.

NATIONAL AMPELOGRAPHIC COLLECTION OF RUSSIA: CREATION AND USE

Leonid Troshin[1], Vasilii Nosulchak[2] and Alexandr Smurygin[2]
[1]Kuban State University of Agriculture, 350044 Krasnodar, Russia; [2]Experimental Breeding Station of Krymsk, 353384 Krymsk, Russia; (email: lptroshin@mail.ru)

The necessity of making NACR are caused under the circumstances of absence in the time of USSR and available big collections in Ukraine (3220 samples) and Moldova (2750).

Since 1995 year were introducted 3920 original samples. The gene pool of grape engaged in from 30 ampelografic collections of 14 countries. From described 276 aboriginal Russian varieties in ampelografic books we collected 104 samples. However in collection we don't have now the representatives by wild-growing grape from 15 centers its growing on Northern Caucasus (in found places were rated 66 wild-growing grapes). The geographical origins on countries were determined for 90% varieties. It show that the gene pool is from 41 countries of the world. There is predominate varieties (88%) on ampelografic status, hybrids forms are 3,9%, clones – 2,5%, rootstock - 1,3%. The forms of wild species *Vitis (Tournef.) L.* formed 2,3% from the hole gene pool. The varieties of *V. vinifera L*. are dominated on kind's composition: 3/4 gene pool, from them 2/3 varieties are local and 1/3 – hybrids, interspecies varieties 23,8%.

From Coast territory are 60 forms of *V. amurensis Rupr*. 67 samples of species of kind *Vitis L., Ampelopsis Michx., Parthenocissus Planch*. were taking: from them choose *V. riparia Michx., V. rupestris Scheele, V. candicans Engelm., V. aestivalis Michx.*, introduced from USA. The varieties another species of kind *Vitis L.* formed in gene pool all 2%, from which 2/3 - *V. labrusca L.* The main value present without seeds varieties, which are have the higher demand. In our gene pool 110 without seeds varieties. As the result of long learning bearing varieties of grape were chosen on complex signs Arkadia, Novoukraine earlier, Caberne Myshako, Cabernek, Krymchanin, Merlo Gramotenko, Merlok, Muscat Odesskii, Rislinalk, Risling Dzhemete, Rkatsiteli Magarach, Tavkveri Magarach, Citronnyi Magarach and another, which were selected in State list of Russian selection attainment or given on State test. As in our state ampelografic bank of dates till that moment are absent we decide the problem of its making and filling it professional information .
(http://www.vitis.ru/)

GENETIC RESOURCES OF ORNAMENTAL PLANTS AND THEIR EVALUATION PROBLEMS: CHINA ASTER

Jiří Uher
Mendel University of Agriculture in Brno, Faculty of Horticulture, 69144 Lednice na Moravě, Czech Republic; (email: uher@zf.mendelu.cz)

Despite to long tradition of breeding and evaluation of China aster (*Callistephus* NEES.) in Czech Republic, there are no descriptors to map the high variability within the genus and hundreds of hybrids, and number of evaluated characters in a wide range of cultivars some Czech and German research stations do not suffice for the evaluation of genepool and breeding applicability. Therefore, classification schedule were proposed to evaluation of China aster genepool considerating a coordination, facilitation and support the collecting, breeding and exchange of information and central documentation of *Callistephus* in relations to other therophytic genera of *Asteraceae* family. Classification schedule contain 20 morphological and 10 phenological descriptors, and 16 descriptors for evaluation of sensitivity of China aster cultivars to diseases and pests (passport data were published separately). Accordingly to proposed descriptors, 52 inland and foreign varieties of Chinese asters were in the 2000-2005 collected and evaluated in twenty morphological characters (plant height and branching, stem and leaf color, leaf morphology, head number, morphology, size and color) for screening of varieties with high ornamental value. Evaluation of flower heads morphology is difficult of appreciation and were based on slightly modificated Maatsch & Schultze classification. Height of plants, as well as branching density and position were dependent at variety, but seems to be essentially influenced by planting dates, temperature and water availability. Only few of the characters does appear linked: most notable seems correlations within plant height and branching length / position, and within head size and head type. No significant correlations between plant height and days to flowering were recorded.

GENETIC RESOURCES OF ORNAMENTAL PLANTS AND THEIR EVALUATION PROBLEMS: CANNA SPECIES AND HYBRIDS.

Jiří Uher
Mendel University of Agriculture in Brno, Faculty of Horticulture, 69144 Lednice na Moravě, Czech Republic; (email: uher@zf.mendelu.cz)

Despite to increasing importance of Canna lilies (*Canna* L.) in floriculture, there are no descriptors to map the high variability within the genus and hundreds of hybrids, and number of evaluated attributes in a wide range of cultivars in RHS and some research stations do not suffice for the evaluation of genepool and breeding applicability. Therefore, classification schedule for Canna lilies were proposed for evaluation of *Cann*a genepool considerating a co-ordination, facilitation and support the collecting, breeding and exchange of information and documentation of Canna lilies. Classification schedule contain a lot of morphological descriptors, some phenological descriptors, and descriptors for evaluation of sensitivity of *Canna* cultivars to diseases, pests and other stress factors. Accordingly to proposed descriptors, twenty hybrid varieties of Canna lilies and some native species (*C. iridiflora* Ruiz.& Pav., *C. compacta* Roscoe and *C. indica* L. in three native varieties) were evaluated in forty morphological characters. Height of plants, suckers production, leaf number, as well as stem and leaf morphology were dependent at variety, but can be essentially influenced by planting dates, temperature, water availability and stage of plant development. In other traits, such as rhachis position or spathe and petals wax cuticle, were not recorded any significant differences between varieties and/or native species evaluated as far. Dependent at varieties, but imponderably influenced by climatic conditions seems to be (beside leaf shape and color) flower characteristics only. Some varieties seems to be identical with some other in the monitored characters, and verification of their authenticity (e.g. through molecular data survey) appear to be necessary.

COMPARISON OF EFFECTIVENESS OF RANDOMIZED COMPLETE BLOCK DESIGN, ALPHA DESIGN AND AUGMENTED DESIGN FOR EVALUATION ACCESSIONS

Martin Užík, Pavol Hauptvogel and Alžbeta Žofajová
SCAR – Research Institute of Plant Production Piešťany, Bratislavská 122, 92168 Piešťany, Slovak Republic; (email: uzik@vurv.sk)

The aims of experiments with winter wheat accessions established in 2004/05 and 2005/06 were: to compare effectiveness of randomised complete block design (RCBD) to α-design, for augmented design to evaluate effectiveness of adjustment of observed data by linear interpolation or by average value of 4 control cultivars included in superblocks. The experimental field was divided into 8 rows, each one consisted of 32 plots, (4 plots of column check cultivars, 4 plots of block check cultivars and 24 accessions). The first 4 rows created 1-th replication and the 5-8 rows created the 2-nd replication. According to α-design 96 accessions were grouped in 12 blocks (3 blocks in each row). For considered augmented design, in which repeated accessions in the 2-nd replication were considered as the other accessions, 2 types of check cultivars, a column check cultivar, respectively block one were used for adjustment of observed values. 4 column plots were included vertically on the over 8 rows – the 1-th plot at the head row, the 2-nd and 3-rd as 11–th eventually as 22-nd plot in order within row, and the 4 plots at the end of the each row. On the column plots cultivar Ilona was sown and data were used for linear interpolation. Blocks in 4 rows created superblock, each contained besides accessions also the check cultivars. Total 6 superblocks were formed in experiment. From column check cultivar data, predicted value XP_{ij} for each plot by linear interpolation were counted, from which coefficient of adjustment ap_{ij} for each plot as the difference between XP_{ij} and average XP. were estimated. Adjusted value for each accession XA_{ij} were determined as sum observed value (X_{ij}) and ap_{ij}. From average value of block check cultivars XK_j (j =1–6 block) and average of all block check cultivars in experiment (XK.), coefficient of adjustment ab_j was accounted for each block. Adjusted value for accessions XB_{ij} were sum of observed value accessions Xij and ab_j. Experimental error of observed data of incomplete block design, (α-design) was lower (79 %) in the year 2005 or 57 % in the year 2006 in comparison RCBD. Evaluation of adjusted data by analyses of variance (incorrect way) was effective only by RCBD, but by GLM analyses the experimental errors were the same as of observed data. The ratios of MS among sources of analysis of variance were changed by adjustment methods and by the way of analysis (RCBD, GLM). MS of genotypes were not or only a little changed but MS of replications were significantly decreased by block adjustment and on the contrary MS of replication was increased by linear adjustment. The correlation coefficients among replications were considered as the efficiency factor of adjustment. Correlation coefficients between 1-st a 2-nd replication of adjusted values were not stronger in comparison to the observed ones, that means, the identical accession could be considered with the same probability as different one in another block of experiment.

DIVERSITY IN TURKISH SESAME COLLECTION FOR FAT AND FATTY ACID COMPOSITIONS

Bülent Uzun, Cigdem Arslan and Seymus Furat
Department of Field Crops, Faculty of Agriculture, Akdeniz University, TR 07059, Antalya, Turkey; (email: bulentuzun@akdeniz.edu.tr)

The genetic diversity of Turkish sesame collection was investigated for oil content, oil yield and fatty acid composition. A total of 103 sesame accessions grown in different ecological conditions were collected from 18 provinces of Turkey. The oil content and oil yield varied between 41.3 to 62.7% and 72.6 to 647.8 kg/ha, respectively. The % content of oleic, linoleic, palmitic and stearic acid in the seed oil ranged between 29.3 to 41.4%, 40.7 to 49.3%, 8.0 to 10.3% and 0.09 to 4.8%, respectively. Linolenic and arachidic acids were the minor constituents of the seed oil of the collection with a range of 0.06 to 0.75% and 0.01 to 0.31%, respectively. Multivariate analysis of the collection revealed that first three PC axes gave Eigen-values > 1.0 and cumulatively explained 67.4% of the total multivariate variation. The first PC axes separated stearic, oleic, and linoleic acids while the second PC axes separated oil yield, arachidic and linolenic acids. The third PC was mainly associated with oil content. The hierarchical classification separated the 103 accessions into eight homogeneous diversity groups. The results obtained in this study provide useful background information for developing new cultivars with high oil content and different fatty acid compositions.

CURRENT STATUS OF THE *TRIFOLIUM PRATENSE* COLLECTION IN NOVI SAD, SERBIA

Sanja Vasiljevic, Aleksandar Mikic, Slobodan Katic, Vojislav Mihailovic and Branko Cupina
Institute of Field and Vegetable Crops, Maksima Gorkog 30, Novi Sad, 21000Serbia; (email: sanjava@ifvcns.ns.ac.yu)

Red clover (*Trifolium pratense* L.) is the second most important perennial forage legume in Serbia, where it is planted on about 120,000 ha. It is grown the most in the hilly and mountainous parts of central Serbia with an acid soil reaction and humid climate. Twenty years ago, the Institute of Field and Vegetable Crops began a concentrated effort on the collection of red clover in order to obtain as much genetic variability as possible for the subsequent breeding of this crop. Domestic local populations from Serbia and the Republic of Srpska were collected first. More recently, the Institute's red clover collection has been significantly enlarged through international collaborations with the world's leading gene banks and institutes maintaining reference collections (GKI - Szeged, Hungary; OKI – Szarvas, Hungary, Freudenberger KG, Deutschlang; Department plantengenetica en Veredeling, Belgie; Federal Centre for Breeding Research on Cultivated Plants-Braunschweig; Nordic Gene Bank; Plant Research International, Vageningen, the Netherlands; National Center for Plant Genetic Resources, Ukraine; Vsjesajuznij institut kormov (VIK); Australian Medicago Genetic Resource Centre - South Australia, Banca de Resurse Genetice Vegetale – Suceava; Jogeva Plant Breeding Institute – Estonia, Universidad Mayor de san Simon, Facultad de Sciencias Agricolas -Bolivia, International Center for Agricultural Research in the Dry Areas – Syria; National Agricultural Research Foundation Fodder Crops and Pastures Institute - Greece). The Institute's red clover collection currently has 350 accessions.

CHARACTERIZATION OF THE PBAI (IHAR) GENE BANK DATABASE CONTENT

Marcin Zaczyński
Plant Breeding and Acclimatization Institute, National Centre for Plant Genetic Resources, Radzików, Poland

Poster represents information about interesting genetic resources gathered in PBAI gene bank. The charts represents general structure of gene bank collections and acquisition of accessions collected in years 2000 to 2006 with details about most interesting data.

It represents details (amount, region of origin and species, number of gathered landraces in every years 2000 to 2006) about valuable landraces. PBAI gene bank have large number of traditional cultivars which have great potential as a source of the resistance genes, which could be useful under extreme weather conditions and as a disease resistance. Second part contain similar data about advanced cultivars stored in gene bank seed stock.

CYTOGENETIC VARIATION AMONG *BRASSICA NAPUS* CULTIVARS AND THEIR HYBRIDS

Zahra Normohammadi[1] and Masoud Sheidai[2]
[1]Tabiat Modarres University, Tehran, Iran; [2]Shahid beheshti University, Tehran, Iran

Meiotic study was performed in 19 *Brassica napus* cultivars considering chiasma frequency and distribution, chromosomes pairing, as well as the occurrence of B-chromosomes and their effects on chiasma frequency. Such cytogenetic pairing, along with agronomic characteristics, may be used in planning hybridization among the *B. napus* cultivars. All cultivars studied possessed n=19 chromosome number (4x) and showed a deviant course of prophase-I meiosis with a synezetic knot and post pachytene diffuse stage. The cultivars studied differed significantly in chiasma frequency and distribution as well as bivalent formation, indicating their genomic differences. Cluster analysis and ordination based on principal components analysis grouped those cultivars showing meiosis similarities. Some of the cultivars showed the occurrence of B-chromosomes.

MANAGEMENT OF GENETIC RESOURCES OF MAIZE IN FRANCE

Anne Zanetto[1], Philippe Carre[2], Claude Tabel[2], Brigitte Gouesnard[1]
[1]UMR- DIAPC (Diversité et Adaptation des Plantes Cultivées), Institut national de la Recherche Agronomique, Domaine de Melgueil, 34130 MAUGUIO, France; [2]Pro-Maïs, 39 chemin Virebent, croix Daurade, 31200 TOULOUSE, France

The conservation of genetic resources in France is based on network organisations under the authority of the French National Board for genetic resources (BRG "Bureau des resources génétiques"). The Maize network comprises national and private partners, all involved in conservation and utilisation of Maize genetic resources. The objective of the network is to conserve, characterise, utilise and distribute the French national Maize genetic resources. All the partners contribute to the work necessary for conservation of good quality and traceability.

The whole collection of maize conserved includes over 5200 accessions: 1400 accessions are conserved by the network and the rest are scientific material. Within the French Maize network, a national collection of 558 freely available accessions has been defined and include 272 landraces populations, 65 synthetic, 74 composite and 115 tropical populations and 15 public inbred lines. The multiplications are carried out by the partner of the network. After drying them off, all the accessions are conserved in a cold chamber at INRA Montpellier, as the active bank and 2 other places are considered as saving and secondary bank in freezers. Those accessions are characterised with morphological and agronomical characters following the international descriptors (IPGRI and UPOV). Some characterisation has also been carried out with molecular markers in order to get a better pattern of the diversity of its collection and its position within the international diversity of maize around the world.

A RESGEN project, including 7 European countries has permitted to sort this material and to get out a European core collection of 96 accessions including 16 French accessions. Those descriptions are available in a database (http://www.montpellier.inra.fr/gap/resgen88/). A new database is under construction to make those data available via an Internet website. This database called SiReGal will be a common schema for different networks of genetic resources in France managed by INRA.

HARDSEEDEDNESS AND PATTERN OF HARD SEED BREAKDOWN UNDER FIELD CONDITIONS OF TWO ANNUAL PASTURE LEGUMES: *ASTRAGALUS HAMOSUS* L. AND *CORONILLA SCORPIOIDES* L. KOCH*.*

Aziza Zoghlami[1] and Mongi Zouaghi[2]
[1]Laboratoire de Productions Animales et Fourragères. Institut National de la Recherche Agronomique de Tunisie, Rue Hédi Karray, 2080-Ariana, Tunisia; [2]Laboratoire de Productions Fourragères et Pastorales. Institut National Agronomique de Tunisie, 43, Avenue Charles–Nicolles, 1082, Tunis Mahrajène, Tunisia; (email: zoghlami.aziza@iresa.agrinet.tn)

The hardseededness and the pattern of hard seed breakdown of 23 populations of *Astragalus hamosus* L*.* *(*Milkcicer vetch*)* and *Coronilla scorpioides* L Koch*.* *(Scorpion* vetch*)* collected from northern and central Tunisia were evaluated and compared with two annual medic species used as controls. The seeds from both species were produced under field conditions during two consecutive seasons (2000-2001) & (2001-2002) at Bouchrik's Agricultural College (45 km south east Tunis).

Progress of seed softening in the field within the first and the second summer after pod set was measured in samples taken at the end of May of each year at pod maturity and thereafter at four-week intervals until the end of the autumn. The experiment for both species was a completely randomised blocs design with 3 replications. Results showed that both species exhibited different patterns of seed softening. In 2001, initial hard seed was more than 90% for both species, while in 2002 it was more than 90% in *A. hamosus* L. and higher than 80% in *C. scorpioides* L Koch.

In 2001, significant seed softening occurred in *C. scorpioides* L. Koch. by August and continued into September to reach final hard seed percentage in October of 46%. By contrast, seeds of *A. hamosus* L. softened very slowly reaching a final level of 85%, significantly different only from the initial level. The seeds produced by A*. hamosus* L*.* were very hard compared to those of *C. scorpioides* L Koch. and those of the Australian check 'Paraggio' of *M. truncatula*. For this cultivar's, softening was extended over a long period and occurred before than that of the local check '204' of *M. minima*. Our results showed that the potential of these species is important either for improving pasture productivity or increasing the pasture sustainability.

POSTER PRESENTATIONS

Session 2

Plant genetic resources enhancement for breeding

YIELD POTENTIAL AND HERBAGE QUALITY OF ESTONIAN NATURAL ALFALFA POPULATIONS

Ants Bender and Külli Annamaa
Jõgeva Plant Breeding Institute, Aamisepa 1, Jõgeva 48309, Estonia; (email: ants.bender@jpbi.ee)

Estonia is one of the northernmost countries in Europe where alfalfa is spread on semi-natural grasslands. Alfalfa has turned out to be durable species under favorable growing conditions of Estonia, even during irregular grazing. There are regions in Estonia where alfalfa has grown continuously without reseeding for more than 100 years.

The genebank and fodder crops department of the Jõgeva Plant Breeding Institute (Jõgeva PBI) carried out expeditions to the Estonian alfalfa habitats in 2001-2002. The seed was collected either from ecotypes or from the fields not cultivated for at least 15 years. In total 28 samples of alfalfa was collected. In order to determine yield potential and herbage quality of the 15 collected alfalfa populations, plot trial was established at the Jõgeva PBI in 2003. Estonian alfalfa varieties Jõgeva 118 (cutting type), Karlu (rhizomatous vegetatively spreading cutting and grazing type) and Juurlu (creeping-rooted grazing type) were included as standard varieties.

The trial was seeded in four replications with randomized complete bock design. Yield and its distribution across three harvests were determined. Botanical and leaf to stem analyses were carried out. Protein was determined by Kjeldhal method. Intake, digestibility and relative feed value were calculated on the basis of ADF and NDF. As an average of 2003-2005 varieties Jõgeva 118, Karlu and Juurlu produces nearly equal dry matter yield (DMY) (100%, 102,9% and 100,1% respectively). DMY of one population (collected from Reigi) significantly exceeded the standard varieties by 9,2%. According to the growth dynamics and DMY the other populations were divided into two groups: 1) populations with modest re-growth, prevalently yellow-flowered sickle medick (Medicago falcata L) type (DMY 44,9-53,2%); 2) hybrid alfalfa (M. varia Mart) populations with yellow or variegated flowers (DMY 70,5-95%). Population from Reigi attracts attention due to its high DMY potential. Natural populations with poor re-growth could be further bred for special landscaping purposes. In these circumstances durability and low maintenance costs unlike forage quality are of high priority.

THE CYTOPLASM OF *NICOTIANA BIGELOVII* (TORREY) WATSON – A NEW TYPE OF CYTOPLASMIC MALE STERILITY USED IN THE PRODUCTION OF COMMERCIAL TOBACCO (*N.TABACUM* L.) HYBRIDS

Apoloniusz Berbeć
Insitute of Soil Science and Plant Cultivation National Research Institute, Czartoryskich 8, 24-100 Puławy, Poland; (email: berbec@iung.pulawy.pl)

Although most of the known 25 or so alloplasmics of cultivated tobacco *Nicotiana tabacum* involving wild *Nicotianae* as cytoplasm donors are male sterile, few have been employed as the source of cytoplasmic male sterility (CMS) in commercial tobacco hybrids. Of those sources, *N.suaveolens* (*cms su*) is by far the most important, *N.glauca*-type (*cms gl*) and *N.undulata* (*cms und*) having also been used on some smaller scale. In this breeding unit, the cytoplasm of another *Nicotiana* species, *N. bigelovii* (*cms big*), was used to develop black root rot and PVY resistant CMS hybrids of flue-cured tobacco which have gained wide acceptance among tobacco growers in Poland. In a field trial which involved three alloplasmic variants of the hybrid VRG-2 (VRG-2 *cms gl*, VRG-2 *cms su*, VRG-2 *cms big*), the *cms big* hybrid compared well with both *cms su* and *cms gl*. *Cms su* was found superior to both *cms big* and *cms gl* for some biometrical traits (leaf dimensions). However, those differences were not reflected in recorded yields which were at a very similar level in *cms su* and *cms big* and slightly, but not significantly, lower in *cms gl*. Under heavy challenge of the necrotic strain of PVY, *cms su* was found to show a certain percentage of diseased plants whereas both *cms big* and *cms gl* remained disease free. Erratic expression of resistance to the common necrotic strain of PVY in *suaveolens*-type alloplasmics of flue-cured tobacco and a good yielding ability of cms *bigelovii* alloplasmics were the principal reason for chosing *N.bigelovii* as the cytoplasm donor in newly developed tobacco hybrid cultivars.

PARTNERSHIP OF GRASSES AND FUNGAL ENDOPHYTES AS AN OLD-NEW SOURCE OF BIODIVERSITY

Bohumír Cagaš, Magdalena Ševčíková and Helena Marková
OSEVA PRO Ltd., Grassland Research Station Rožnov-Zubří, Hamerská 698, 754 54 Zubří, Czech Republic; (email: cagas@oseva.cz)

The investigation of the partnership between fungal endophytes *Neotyphodium* spp. and some grass species is a relatively new problem. The analysis of the Czech assortment of registered grass varieties made since 1995 has produced the following results: the number of varieties of perennial ryegrass containing *Neotyphodium* has grown more than twice (26 % - mostly turf varieties), Italian ryegrass varieties with *Neotyphodium* make up 12 %, in meadow fescue they constitute nearly 64 %, in tall fescue more than 30 %, in sheep fescue almost one fourth and in red fescue 5 %. In other species no endophytes were found. The former investigation into the occurrence of *Neotyphodium* in ecotypes of perennial ryegrass revealed the distribution of host plants in all parts of the Czech Republic. The higher incidence of plants with endophytes was recorded on warmer and drier localities. The presence of *Neotyphodium* in 38 % of seed samples of ecotypes of perennial ryegrass (collected in different parts of Bohemia and Moravia in 1991 – 2006) was investigated. The infestation of E+ samples moved from 15 % to 90 %. The presence of endophytic hyphae in *Festuca arundinacea* (samples collected on Moravian localities in 1996 – 2004) varied from 45 % to 60 %. The incidence of E+ and E- plants within one genotype implies the extension of biodiversity (mostly in genera *Festuca* and *Lolium*). This phenomenon should be studied more intensively and useful host plants should be described and preserved for further utilization.

RESISTANCE OF SELECTED OAT GENETIC RESOURCES TO LEAF DISEASES

Viera Červená, Jozef Gubiš, Štefan Masár and Katarína Bojnanská
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: cervena@vurv.sk)

Oats (*Avena sativa* L.) are the third most grown cereal in the world after wheat and barley. In natural conditions, oats are affected by a variety of factors such as soil-climatic conditions or the occurrence of pathogen microorganisms. To the most important diseases attacking oats in the conditions of Slovakia belong the crown rust, leaf blotches (Helminthosporium leaf blotch and speckled blotch), powdery mildew and loose smut. The goal of our work was to evaluate the resistance of 20 oat genetic resources to the most important fungal diseases. The evaluation was done by means of the field trials conducted at two localities in Slovakia and laboratory tests using the populations of *P. aveane*, crown rust and powdery mildew. No symptoms of powdery mildew were visible in field trials at both experimental localities, however, when inoculating the leaf segments of the tested genotypes in laboratory conditions, no genotype was found to be resistant to the powdery mildew isolates used for the tests. According to the attacked area of leaf segments the oat genotypes showed moderate to strong attack of the pathogen in laboratory conditions. All genetic resources of the evaluated set were resistant to the leaf blotches complex despite of the higher attack of registered cultivars Avenuda and Euro. In the laboratory experiments for which the juvenile stage of the plants are used, the genotypes PS-119 (Valentín) and PS-121 showed resistance to *Pyrenophora avenae*. High level of resistance to crown rust in field conditions was detected in the genotypes Auron and Flämingsstern. Low levels of AUDPC were observed in the breeding materials PS-124 and PS-126.

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EXPLOITATION OF HORDEUM BULBOSUM AND HORDEUM SPONTANEUM IN BARLEY BREEDING FOR POWDERY MILDEW AND LEAF RUST RESISTANCE

Jerzy H. Czembor[1], Henryk J. Czembor[1] and Richard Pickering[2]
[1]Plant Breeding and Acclimatization Institute – IHAR, Plant Breeding and Genetics Department, Laboratory of Applied Genetics, Radzikow, 05-870 Blonie, Poland; [2]New Zealand Institute for Crop and Food Research Limited, Private Bag 4704 Christchurch, New Zealand

Twenty-four recombinant lines derived from crosses between barley (*Hordeum vulgare*) and bulbous barley grass (*H. bulbosum*) were tested in IHAR Radzikow greenhouse for resistance to leaf rust (*Puccinia hordei*) and powdery mildew (*Blumeria graminis* f. sp. *hordei*). These recombinant lines were obtained in New Zealand Institute for Crop and Food Research Limited, Christchurch, New Zealand. Eight differential isolates of *P. hordei* and 14 differential isolates of *B. graminis* f. sp. *hordei* were used.

In addition, 48 accessions of wild barley (*Hordeum spontaneum*) were screened for resistance to powdery mildew (*B. graminis* f.sp. *hordei*) under greenhouse conditions. These accessions originated from 6 countries: Syria - 15, Iran - 4, Iraq - 6, Turkey - 1, Lebanon - 7, Palestine - 15. These accessions were provided kindly by International Center for Agricultural Research in the Dry Areas – ICARDA, Aleppo, Syria. After preliminary screening 23 resistant single-plant lines were selected. These lines originated from 15 landraces (9 from Palestine, 3 from Iran, 2 from Iraq and 1 from Syria) and were tested with 20 differential isolates of *B. graminis* f. sp. *hordei*.

Obtained results showed that, 20 tested lines (83%) derived from crosses between barley (*H. vulgare*) and bulbous barley grass (*H. bulbosum*) showed resistance to *P. hordei*. Ten (42%) of these lines showed resistance to all eight differential isolates of *P. hordei* used. Among 24 of these tested lines 22 (92%) possessed genes for resistance to powdery mildew. In most of them (66%), the presence of gene *Mla12* was postulated. Among *H. spontaneum* lines about 61 % (14) were resistant to all isolates used. Remaining 9 of these lines were resistant to at least 80% isolates used. This study showed that recombinant lines derived from crosses between barley (*H. vulgare*) and bulbous barley grass (*H. bulbosum*) and *H. spontaneum* from Near East are very valuable source of resistance both to leaf rust and powdery mildew and should be used in barley breeding for disease resistance.

EXPLOITATION OF LINES WITH MLO GENE SELECTED FROM BARLEY LANDRACES COLLECTED IN YEMEN IN BARLEY BREEDING PROGRAMMES FOR DURABLE POWDERY MILDEW RESISTANCE

Jerzy H. Czembor and Henryk J. Czembor
Plant Breeding and Acclimatization Institute – IHAR, Plant Breedning and Genetics Department, Laboratory of Applied Genetics, Radzikow, 05-870 Blonie, Poland

Resistance to powdery mildew (*Blumeria graminis* f. sp. *hordei*) of 36 accessions of barley landraces collected from Yemen was investigated. These accessions were provided kindly by International Center for Agricultural Research in the Dry Areas – ICARDA, Aleppo, Syria. Seven (19%) tested landraces showed resistance after inoculation with powdery mildew. From these landraces 9 single plant lines were selected. These lines were tested with 20 differential isolates of powdery mildew. The isolates were chosen according to their virulence spectra, which were observed on the Pallas isolines differential set and 7 additional differential cultivars.

It was impossible to postulate which specific allele or alleles for resistance are present in 4 of the tested lines. However, in 2 lines the presence of Mlo resistance was postulated. This postulation was based on lack of visible signs of infection except for occasional infection type 4 (compatible) small mildew colonies [disease reaction 0(4)] and on investigations under microscope. This is first report about spontaneous presence of Mlo resistance in barley landraces originated from Yemen. These new sources of very effective Mlo resistance to powdery mildew should be used in barley breeding programmes.

AGRONOMIC AND FORAGE QUALITY TRAITS OF DOMESTIC AND FOREIGN RED CLOVER (*TRIFOLIUM PRATENSE* L.) VARIETIES

Jarmila Drobná and Martin Užík
SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 921 68 Piešťany, Slovak Republic; (email: drobna@vurv.sk)

Evaluation of germplasm collections under field conditions is obvious recognized as a general method to estimate genetic variability. The agronomic traits and forage qualitative parameters have been studied for a 3-year period with the aim to assess the productivity and forage quality of some foreign and domestic red clover varieties and to investigate the variability among twenty-one domestic and foreign diploid red clover varieties. The differences between varieties for all agronomic and forage quality traits were highly significant. Analyses of variance revealed highly significant differences between cuts and years with the highest green matter yield in the first cut and in the first productive year. Similarly the nutritive value of evaluated varieties was significantly affected by cut and by year. The variability of both agronomic and forage quality characters encourage the use of evaluated varieties as a genetic material in the research and breeding programmes.

NUTRITIOUS AND HEALTHILY PREVENTIVE VALUE OF NAKED OAT

Daniela Dvoncova and Peter Hozlar
SARC- Research and Breeding Station at Vígľaš-Pstruša, Slovak Republic

The collection of 43 naked oat genotypes was tested in 2004 and 2005 under conditions of potato growing area in the Research and Breeding Station Viglas-Pstrusa (VSS Viglas-Pstrusa) on chosen qualitative indicators and nutritious and healthily preventive substance content in a naked oat grain. Quite high variability of a grain content of individual naked oat genotypes has been found out and it has also been proved when compared with a grain content of three husked oat control genotypes. Unlike husked oats, naked oats have shown higher content of starch, proteins, fats, β-glucans and higher volume/capacity weight. Husked oats have demonstrated higher content of dietary fibre and 1000 grain weight. The naked oat genotype collection itself has shown variability of starch content 56,2-65,7%, of protein content 13,1-21,49%, of fat content 3,42-7,45%, of dietary fibre content 2,3-5,3% and of β-glucan content 2,68-4,64%. Based on the comparison of two pilot years we can claim that the highest year influence has been proved on the protein content, less on fat content. Significantly lower year influence has been shown in starch and dietary fibre contents.

MOLECULAR AND HISTOLOGICAL CHARACTERIZATION OF ENDOPHYTES IN TUNISIAN TALL FESCUE AND PERENNIAL RYEGRASS

Hanen Elazreg, Salma Ghariani, Nidhal Chtourou-Ghorbel, Mohamed Chakroun[1], Mohamed Marrakchi and Neila Trifi-Farah
Laboratoire de Génétique Moléculaire, Immunologie et Biotechnologie. Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar Tunis, Tunisie; [1]Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Rue Hédi Karray, 2049 Ariana, Tunisie; (email: neila.trifii@fst.rnu.tn)

The fungal *Neotyphodium lolii* and *Neotyphodium coenophialum* endophytes infecting respectively perennial ryegrass (*Lolium perenne* L.) and tall fescue (*Festuca arundinacea* Schreb.) are recognized as having impacts on the agronomic characteristics on host grasses and on performance of herbivores grazing pastures. In order to detect endophytes in Tunisian perennial ryegrass and tall fescue, molecular and histological studies are carried out. Histological study has been applied on leaf sheaths and seeds of 3 spontaneous populations of each host grasses. The intercellular hyphae of endophytes in tall fescue were detected only in seeds with low concentrations. Concerning Perennial ryegrass, any infected plant by endophytes was observed.

Molecular detection on total DNA cellular of leaves was employed. In tall fescue, using primers based on intron 1 and 3 of tubuline 2-4 gene, 444 bp amplification products was obtained reflecting plant infection rates between 80% and 100%. In the case of II-1/II-2 primers, the observed lower level of

1000 bp amplification products (3%) can be attributed to no specificity of the considered primers. Molecular analysis in perennial ryegrass confirms the absence of endophytes for all analysed populations. Results can be attributed especially to a long storage period that affects the high fungal endophyte viability in grass seeds.

GENETIC DIVERSITY FOR SOME BIO MORPHOLOGICAL PARAMETERS FOR THE MAIZE LANDRACES (*ZEA MAYS* L.) IN KOSOVA

Shukri Fetahu and Sali Aliu
The University of Prishtina , The Faculty of Agriculture , Str,Boulevard “Bill Clinton “ 10000 P.N. Kosova – UNMIK

Local genotypes for many time were exposed the complex interaction of different environment and human factors and as consequence of this is a source of diversity which has passed through natural selection process. The biodiversity of the maize local landraces are gen-founds in functionality of plant breeding.

The object in these research is to test local maize landraces in order to determine diversity and possibility to including in the programs of plant breeding for creating inbreed lines that can used as germplasm for making specification new maize hybrid formula in the region of Kosova. With research are identified two forms of landraces 1. Zea mays,var identata dhe 2.Zea mays ,var indurata L.The reaserch was developed in the Subregions : (Burim-Sbr 1,Drenas Sbr -2, Vushtrri Sbr-3, Besiane Sbr -4 and Sharri Sbr -5),with an area of 2.032 km ^{2} or 18.62 % of the territory of Kosova.The research combinatory was :Sub regions Sbr-5 x Parameters 3 x Repetitions 5 = 75 combinations .The experimental design :Split Plot “ ,while the results where calculated with different mathematical and statistical models (MMS).With research are achieved variability and diversity between landraces for the biomorphological quantitative parameters .The average of the Ear height (EH) for the landrace was μ = 41.73 cm , for the maximum height was ▲ 47.25 cm for the minimum ear height was ▼ 35.26 cm . The differences between landraces for the height of the ear were 11.99 cm or with variability of 34%. Was characterized with high significant differences for the probability $P<0.01$. For the height of the plant (PH) show that were differences for the investigated factors and their interaction in favor of one or other factor. For the maximal value for height of plant of the landraces was realized in Istogu Subregion xg = 179.93 cm , for the minimal value realized in Sharr xg =145.76 cm with differences d= 34.17 or with total variability of 22 %.For the minimal values of the leave area (LA) were realized landraces from Sharr ,xg= 271.80 cm ^{2} , or if comparing with total value μ =346.76 cm^2 lower for -74.96 m respectively -22%. The maximal surfaces were shown by the Subregions Istogu xg =462.057cm^2 or for + 115.29cm ^{2} , respectively +34 % higher from from total value n μ, respectively, that is significantly different for the probability P 0.05 and 0.01.Diversity and differences for the investigated factors in different subregions was indicated between intereaction by gentotyp and environment The coefficient of correlation between PH and LA was highly correlative r^2 =0.73* , for EH and PH .was 0.66.

Literatura: Fetahu Sh , Aliu S, Kaciu S.(2005) : Variability and genetic erosion of White landraces (Zea mays L.)in Kosova, 30 march -2 April 2005, XVII Eucarpia Genetic Resources Section Meeting , Castelsardo , Italy.

GENETIC RESOURCES STUDIES OF LOQUAT AND IT’S USE IN A BREEDING PROGRAME

Ana Delia Gisbert, Jose Martínez-Calvo, Carlos Romero, Jaime Prohens, Gerardo Llácer and Maria L. Badenes
Instituto Valenciano de Investigaciones Agrarias, Apartado oficial 46113 Moncada, Valencia, Spain

Loquat species (*Eriobotrya japonica* Lindl.) originated in China, later was introduced in Japan. However, introduction in Europe occurred much later, in eighteen century. Since then, the species was very well adapted to the Mediterranean climate, mainly in South East of Spain, where is located more than 50 % of total Mediterranean crop production.

In 1992 a genetic resources project funded a survey of loquat in Spain. The results allowed establishing the first loquat germplasm collection in Spain. In 1996, a European project titled ‘Conservation, evaluation and collection of underutilized fruit species' supported surveys and collection of plant material from these species in the Mediterranean basin countries. One of these surveys resulted in enlargement of the germplasm collection of loquat established at IVIA, Valencia, Spain, which became the loquat European germplasm collection. This collection is being extended with new accessions collected across the world, but currently is the richest in plant material from the Mediterranean countries. However, due to the recent introduction of the species in the Europe the diversity encountered is low. Recently, accessions from Asian countries have been introduced in terms of broader the collection. Studies of diversity based on pomological traits and molecular markers are under the way. In this paper SSRs molecular markers has been developed from loquat aimed at using them to study and compare the genetic diversity between the accessions from Mediterranean and Asian origin. Ten SSRs obtained have been tested in a set of potential genitors from both origins: European and Asian. Results demonstrated the usefulness of these markers for genetic diversity studies and pointed out the convenience of combining both gene pools for future breeding.

REVEALING OF CONNECTION OF FRUIT MATURING TERMS IN CULTIVARS AND HYBRIDS OF *P. CERASIFERA* EHRH. WITH THEIR BIOCHEMICAL FEATURES

Gorina M. Valenytana and Richter A.A.
Nikita Botanical Garden, Yalta, Crimea, Ukraine, 98648

The researches have been done on the plants from the collections of the Nikita Botanical Gardens on the South Coast of the Crimea in 1995-2005. The work has been done on plants of P.brigantiaca Vill., P. cerasifera Ehrh. and their hybrids (Gorina, Polyanichenko, 1996).

The aim of this work is to determine the influence of fruit maturing terms on the accumulation of dry substances, sugars, leucoanthocyanins and titratable acids in them.

Studying the rates of biological development of plants on the example of cherry-plum varieties and hybrids of P. brigantiaca with varieties of P. cerasifera we can mark that the date of fruit ripening, number of days after the full blossom are interconnected by direct correlation dependence (r = 0.23 – 0.98**), at the same time this connection is more close with the number of days after the blossom (r = 0.73** – 0.98**). The content of dry substances from one side and the date of fruit ripening, number of days after full blossom, number of days after the end of blossom of cherry-plum varieties and hybrids are connected by direct dependence (r = 0.38 – 0.56*). The date of ripening and the content of titratable acids are connected in many cases by direct correlation (r = 0.43* – 0.71**), and the reliable connection in ratio sugars/acids in fruits of cherry-plum varieties is absent. This connection in hybrids is negative (r = -0.41* - -0.51*).

In all cases it is marked the negative connection between the titratable acids of fruit and the ratio of dry substances to titratable acids (r = -0.73** - -0.81**) or the ratio of sugars to acids (r = -0.75** - -0.80**).

With the help of distant hybridization of P.brigabtiaca (period of ripening 02-08.09) with varieties of P. cerasifera (ripening period 01-16.07) some hybrids with quite wide period of ripening (03.07 – 26.08) have been obtained. The number of days after full blossom and the content of titratable acids in fruits of varieties didn't reveal the reliable correlation dependence (r = 0.27-0.41). The positive connection (r = 0.40*-0.77**) is marked in hybrids. At the same the number of days after the end of blossom and the content of sugars and leucoanthocyanins are not reliably connected. This tendency have been during all three years of work (1996, 1997, 1998).

The most hybrids of alpine plum with cherry-plum with late period of fruit ripening have the high content of organic acids in fruits (3-6%). So, as a result of interspecific combinations of crossing the hybrids with later period of fruit ripening have been obtained. Probably, further selection work with these forms allow to obtain fruits with more harmonious taste.

Obtaining varieties with long fruit forming period allow to do the selection on the high content of dry substances and sugars, suitable for different forms of proccessing.

REWIEV OF BASIC CHARACTEISTICS OF GENOTYPES IN ONION COLLECTION

Jelica Gvozdanovic-Varga, Mirjana Vasic and Janko Červenski
Institute of field and vegetable crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia; (email: jeca@ifvcns.ns.ac.yu)

The onion is a widely distributed vegetable crop, which takes an important place in the vegetable production in Serbia. The traditional planting method is the one from sets. Old cultivars and populations and, in recent years, foreign cultivars are grown. The large variety of genotypes, including both domestic populations and cultivars, comprises the significant gene fund of this region.

The onion collection of Institute of Field and Vegetable Crops in Novi Sad is based on the populations and cultivars from the territory of the former Yugoslavia. This paper reviews 30 onion genotypes for the basic IPGRI descriptors (ANNEX I). Variability of the reviewed characteristics was determined by the PCA analysis. High variability values have been established for bulb skin color, bulb flesh color, bulb hearting and bulb skin thickness. The genotypes varied in bulb skin color as well as in bulb flesh color from white to dark violet. These two characteristics had the largest impact on clustering, with a single genotype being heterogeneous exactly for these two characteristics.

MORPHOLOGICAL CHARACTERIZATION OF SPRING WHEAT MATERIAL IN ESTONIA

Merlin Haljak, Külli Annamaa and Anne Ingver
Jõgeva Plant Breeding Institute, Aamisepa 1, Jõgeva 48309, Estonia; (email: merlin.haljak@jpbi.ee)

Gene bank for long-term conservation of the seeds of agricultural crops was set up at the Jõgeva Plant Breeding Institute in 1999, because of this the need for the characterization of accessions raised up. In 2000 Estonia joined the International Union Of Protection Of New Varieties (UPOV) for what reason_requirements for the new varieties changed.

These changes caused necessity for investigation of varieties and breeds by the protocol of UPOV, which has been also the basement of ECPGR (European Cooperative Programme for Crop Genetic Resources Networks) descriptor lists. The department of homogeneity breeding was established at the Jõgeva Plant Breeding Institute in 2002. The basic purpose is investigation of morphological characteristics in homogeneity breeding. A new variety has to meet the requirements of distinctness, uniformity and stability (DUS).

In this study morphological characteristics of spring wheat material was tested in the period of 2002-2006. By the UPOV protocol there are 26 characteristics tested the both in the field and laboratory. For this article 12 the most distinctive ones were selected. The following features were estimated: the anthocyanin coloration of auricles of flag leaf, the hairiness of auricles of flag leaf, the glaucosity of sheath of flag leaf, the glaucosity of ear, the claucosity of neck of culm, the hairiness of upper node of culm, the ear shape in profile, the length of scurs, the ear density, the ear color, plant height and the grain coloration with phenol.

Results of the estimation of morphological characteristics can be used in: Breeding – a new variety candidate must pass through the DUS-test; Seed production – for field certification and Gene bank – characterization data provide additional value for accessions.

EVALUATION OF WINTER BREAD WHEAT GENETIC RESOURCES FROM COLLECTION OF THE GENE BANK OF SLOVAK REPUBLIC

Pavol Hauptvogel
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: hauptvogel@vurv.sk)

Plant genetic resources are important for breeding new varieties. SARC-RIPP Piešťany mainly manages collections bread wheat, durum wheat, spelt wheat and wheat wild relative's species. A large part of these resources is an integral part of European collections (coordinated by the Bioversity International) and is accessible to the international community and naturally of the domestic breeders companies. The aims of research in plant breeding and genetics are focused on finding genotypes which are well adapted to the environment and acceptable level of quality and productivity. Accent has been placed on evaluation agro-morphological, biological a technological characteristic. Field experiments were conducted in Slovakia during 2003-2006 to assess the suitability of winter wheat varieties from European and other countries for future breeding programmes. The interrelationships between domestic and foreign varieties of bread wheat are also discussed.

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SEARCHING FOR SUITABLE SOURCES OF TOTAL DIETARY FIBRE

Michaela Havrlentová[1], Magdaléna Bieliková[1], Pavol Hauptvogel[1], Gabriela Antalíková[1], Iveta Čičová[1], Peter Hozlár[2] and Michaela Benková[1]
[1]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [2]SARC-Research and Breeding Station Vígľaš – Pstruša, 962 02 Vígľaš - Pstruša, Slovak Republic

The aim of the submitted work was to measure the variation in total dietary fibre content among different primary food-stuffs. The amount of total dietary fibre was determined by using Total dietary fibre assay procedure (Megazyme International Ireland Ltd.). The total number of 84 samples (cereals: wheat, oats, barley, tritordeum, rye, and triticale; pseudocereals: buckwheat, millet, and amaranth; and legumes: chickpea, soybean, and lupine) was analyzed. Differences in measured parameter were found among the species. It was observed that legumes (with the mean value of 31.46% total dietary fibre) are the best sources of the monitoring health beneficial compound. The amount of total dietary fibre in pseudocereals ranged between 10.75% (amaranth) and 29.03% (buckwheat), with the mean of 18.56%. The mean value of total dietary fibre in cereal samples was 14.28% with the range 3.8% (triticale) and 34.94% (oats). The most suitable sources of the monitoring parameter - that positive influence functional properties of food-stuffs and in terminal affect the health state of consumers – were lupine, oats, soybean, and buckwheat.

GLYCINE COLLECTION IN THE CZECH REPUBLIC

Pavlína Hrstková
Mendel University of Agriculture and Forestry Brno, Dept. of Crop Science, Plant Breeding and Plant Medicine, Czech Republic; (email: hrstkova@mendelu.cz)

The soybean (*Glycine max* (L.) Merr.) germplasm collection is the part of the Czech National Grain Legume Collections maintained by AGRITEC, Ltd. Šumperk and the Crop Research Institute in Prague. From the year 2002 the accessions and new genotypes have been multiplied and characterised at the Field research station of the Mendel University of Agriculture and Forestry in Brno. Characterisation is done using the Czech descriptor for genus Glycine Willd. (Pastucha et al., 1987). Selected quantitative and qualitative variables are evaluated on randomly chosen plants during vegetative season (growth, leaf and flower characters) and after harvest (pod and seed characters). Multivariate statistical analyses were performed on the data obtained from 72 genotypes (including landraces, breeders lines and advanced cultivars) to detect structure in the relationships between variables (factor analysis) and to estimate differences between genotypes (cluster analysis). Multivariate exploratory techniques enabled assessment of variability in qualitative and quantitative characteristics and grouping of genotypes according to their similarity, therefore they can provide useful information for maintaining the collection and potential breeding work purposes.

BACTERIAL BLIGHT (*PSEUDOMONAS SYRINGAE* PV. *GLYCINEA*) ON SOYBEAN (*GLYCINE MAX*)

Pavlína Hrstková and Jana Víchová
Mendel University of Agriculture and Forestry Brno, Dept. of Crop Science, Plant Breeding and Plant Medicine, Czech Republic; (email: hrstkova@mendelu.cz)

Bacterial blight is one of the most common bacterial diseases of soybean (Glycine max (L.) Merr.). The disease is caused by Pseudomonas syringae pv. glycinea (Coeper) Young et.al. Although bacterial blight usually does not cause significant yield losses with the exception of seasons with excessive rains and cool temperatures during growing, the disease is seedborne and can affect seed quality.

In the year 2006 twelve lines of soybean, both commercial varieties and selected accessions from the gene bank collection (Crop Research Institute, Prague, CZ), were tested using casual agent of bacteria blight. The plants were grown in a glasshouse and in the growth stage of first two leaves infected with bacterium strain Psg A 055. The development of the disease was evaluated and the plants were classified according to the symptom occurrence. Significant differences in susceptibility to the disease were found among tested lines, the European landraces and the variety Rita, which originated from them, were identified as highly susceptible (98 % - 100 % of infected plants). On the contrary, the varieties developed in Canada (OAC Vision, Quito) showed the highest resistance against bacterial blight (72 and 53 % of infected plants, resp.).

EVALUATION OF RESISTANCE OF BARLEY AND WHEAT VARIETIES AND BREEDING LINES TO CZECH PAV ISOLATE OF BYDV

Jana Chrpová[1], Václav Šíp[1], Jiban Kumar Kundu[1], Taťána Sumíková[1], Ondřej Veškrna[2] and P. Horčička[2]
[1]Crop Research Institute, Department of Genetics and Plant Breeding, Drnovská 507, Praha 6, CZ-161 06, Czech Republic; [2]SELTON, Ltd., Sibřina, Czech Rep., 250 84; (e-mail: chrpova@vurv.cz)

Barley Yellow Dwarf Virus is transmitted by several species of aphids and causes probably the most important virus disease of cereals. Most spring and winter barley cultivars grown in Central Europe have been found susceptible or very susceptible to infection with PAV strain prevalent in this region. High resistance levels are associated with presence of Yd2 gene in spring and winter barley. PCR diagnostic markers Ylp is available for identification of this gene. Moderate resistance conferred by genes non allelic with Yd2 was detected in the winter cultivar Perry from the USA and cultivar Sigra from Germany. Some lines derived of variety Sigra reached good resistance and yielding level, but achievement of yield stability is more difficult.

In wheat wider choice of resistant genotypes still offer spring types. In RICP Prague-Ruzyně the materials obtained from ICARDA and CIMMYT programmes, Chile, Canada, USA and Poland have been tested for resistance to BYDV. It was found that either Bdv1 or Bdv2 need not guarantee obtaining desirable resistance level. more promising appeared to be some other materials obtained from Canada, Poland and Chile. Breeding lines Kivu-85, QG 2.1, QG 4.37 (Canada), the line SOA217/02 (Poland) and varieties Quino-Baes and Bárbaro-B from Chile were found tolerant or medium tolerant. Two years results showed high tolerance of winter wheat cultivars McCormic, Roane and Tribute (USA).

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UTILIZATION OF RHT GENES SOURCES IN WHEAT BREEDING

Jana Chrpová[1], Miroslav Škorpík[1], Václav Šíp[1], Alžběta Žofajová[2], Martin Užík[2], Daniel Mihálik[2] and Michal Šajgalík[2]
[1]Crop Research Institute, Drnovská 507, Praha 6, CZ-161 06, Czech Republic; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 921 68 Piešťany, Slovak Republic; (e-mail: chrpova@vurv.cz)

In wheat, two sources of semi-dwarfing genes have been successfully used by breeders. The Norin 10 dwarfing genes *Rht 1* (Rht-1B1b) and *Rht 2* (2Rht-D1b), that can be selected for their insensitivity to the applied gibberellic acid (GA), have been widely used to reduce the plant height and increase the grain yield. The second important source of dwarfing genes is Akakomugi. Unlike the genes *Rht 1* and *Rht 2* which can readily be detected by their insensitivity to GA, the responsive Akakomugi genes (*Rht 8, Rht 9*) are difficult to follow in any breeding programme. KORZUN et al., (1998) found out that microsatelite marker WMS-261 and its 192 basic allelic pairs are diagnostic for Rht 8 gene.

Insensitivity to applied gibberelic acid, indicated the presence of Norin 10 dwarfing genes, was detected in 30 of 70 (42,8 %) winter wheat varieties registered in the Czech Republic in 2006. The presence of Rht 1 or Rht 2 gene was detected in some varieties on the basis of hybrid analyses in F_2 generation. The presence of Rht 8 was detected with the use of molecular marker now in 4 winter wheat varieties registered in the Czech Republic.

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GENOTYPE VARIABILITY OF FATTY ACIDS IN *AMARANTHUS* GRAINS

Dalibor Ješko[1], Iveta Čičová[1] and Milan Čertík[2]
[1]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; [2]Faculty of Chemical and Food Technology, Slovak University of Technology, Radlinského 9, 812 37 Bratislava, Slovak Republic

Lipids are important parts of *Amaranthus* grains. Amaranth grains have been found as not only good source of linoleic acid but also they have been suggested as an alternative to marine animals as a natural source of squalene. Our study was focused on genotype variability of fatty acid profile in 9 amaranth species (20 varieties). Oil contents and squalene contents were determined as well. Substantial differences in total oil content and squalene content were found among the amaranth varieties. The major fatty acids of amaranth oil consisted of palmitic acid (9.5-20.3%), oleic acid (15.7-35.0%), and linoleic acid (37.1-57.5%). A high degree of unsaturation was detected in amaranth oils that varied between 1.11-1.44. Moreover, relationship between C18:1/C18:2 ratios and squalene amounts were observed. Thus, fatty acid composition and ratios of individual fatty acids offer additional taxonomic and physiologic information for classification of various *Amaranthus* grain varieties.

EFFECT OF ORGANIC AND CONVENTIONAL FARMING SYSTEM ON WEED SPECIES RICHNESS IN THE SPECIFIC CROP ROTATION

Marta Klimeková, Zuzana Lehocká and Štefan Žák
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: klimekova@vurv.sk)

Biodiversity is simply a term for the variety of life and the natural processes of which all living things are part off. In terms of weeds this means presence of more diverse range of species. Unfortunately most modern societies are putting high pressure on ecological systems and reducing biodiversity through the intensive use of natural resources.

Organic farming has recently become of great interest in Slovakia. For example, in 2003 share of organic managed land represented was only 2.25 % of total agricultural land while in year 2005 it raised to 4.62 %. This means an area growth of 37,712 ha in two years. The main reason for this interest is the endeavor to conserve old farming traditions, grow agricultural production without synthetic fertilizers and pesticides, conserve the environment and try to reduce production costs in order to sell more production on domestic and foreign markets. Organic farming systems can be hypothesized to support higher diversity of weed species than conventional farming systems. This fact had to be verified in the Central European conditions. The objective of our study was to investigate in year 2003-2005 the effect of organic and conventional farming systems on weed species richness using the following specific crop rotation: winter wheat, pea, winter wheat, potatoes, spring barley and alfalfa. The study was conducted in the fields of the experimental station established on degraded Chernozem on loess in a corn / barley growing region in south-west Slovakia (near Piešťany). The weed species were counted at the beginning of vegetation period (before the first chemical treatment in conventional farming system) and immediately before the harvest of the main crop.

The results have shown that the weed species diversity in winter wheat was higher in the organic farming system than in the conventional farming system. Higher weed species number was after alfalfa (fore-crop) than after pea in both farming systems. A 46 % of weed species reduction occurred after pea and about 25 % after alfalfa before winter wheat harvesting. In the conventional farming system where chemical treatment applications were used the weed species reduction in winter wheat stand after alfalfa and pea was 64.6 % and 60.9 % respectively. Weed species diversity in spring barley stand was about 40 % higher in the organic farming system compared to the conventional farming system. There was a reduction of 61.86 % of weed species in the conventional farming system and only 30.7 % in the organic farming when compared to the diversity of weeds at the beginning and at the end of vegetation periods. Since potato plant has better plant competitiveness to weed species than pea plant, the number of weed species was less in potatoes stand than in pea. In conclusion the study has shown that in all crops the weed species diversity in the organic system was higher than in the conventional farming system. While less weed species spectrum was determined in autumn than in spring periods in all crops.

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MULTIVARIATE ANALYSIS OF DIVERSITY AMONG POLISH MODERN CULTIVARS OF WINTER TRITICALE FOR AGRONOMIC TRAITS

Wanda Kociuba[1], Aneta Kramek[1], Wiesław Mądry[2], Krzysztof Ukalski[2] and Joanna Ukalska[2]
[1]Institute of Plant Genetics, Breeding and Biotechnology, University of Agriculture, Lublin, Poland; [2]Department of Biometry, Warsaw University of Life Science, Warsaw, Poland

A phenotypic diversity among 36 Polish cultivars of winter triticale for plant height (X_1), grain weight per main spike (X_2), number of grains per main spike (X_3), 1000 grains weight (X_4) and protein content in grain (X_5) was assessed. The studied cultivars have been developed by Polish breeders and released in the period from 1982 to 1999. Data were collected in an experiment conducted across three years, 2002-2004 at the Experimental Field Station near Lublin, Poland. In each year the experiment with the cultivars was carried out on one-plot replicates. Plant height was measured in three random places on plots. Weight and number of grains per spike and 1000 grains weight were determined on a sample of 50 spikes randomly taken from each plot. Protein content in grain was measured on a sample of grains from each plot using Kjel-Tec apparatus (N×5,7). Combined analyses of variance for each trait data according to the random model (both cultivars and years were assumed to be random factors) were done. Variance components were estimated for each trait separately using *REML* method. Coefficients of heritability (repeatability) of three-year phenotypic means were estimated on the basis of the variance components. Estimates of genotypic values were obtained using *the best linear unbiased predictor (BLUP)*. To analyze phenotypic diversity of the cultivar collection for the five agronomical traits, the pattern analysis was used. This methodology consisted of cluster analysis carried out by Ward's procedure in order to classify genotypes into homogenous groups (classification stage) and of principal component analysis to assess relations and similarities among the genotypes and clusters (ordination stage). The both procedures were used on the basis of the *BLUP's* for each trait. The genotypic variances were significant for all traits. The obtained heritability coefficients were quite high (above 0,6) except number of grains per main spike (0,49). The three first principal components accounted for 89% of the total variation between genotypes. The highest positive values of correlation coefficients were between the first principal component (PC1) and total grain weight per main spike (0,98), number of grains per main spike (0,73) and thousand grain weight (0,58). Then, these three traits of main spike had the relatively largest contribution to the overall (multivariate) variability of the cultivars. The second principal component (PC2) was strongly positively correlated with grain protein content (0,82) and plant height. The cultivars were grouped into five clusters on the basis of pseudo–t^2 statistic. The results of the studies indicate the presence of the substantial diversity among the Polish modern cultivars of winter triticale for the agronomic traits including mostly total grain weight per main spike and its components: number of grains per main spike and thousand grain weight. Multivariate description of this diversity could make easier the selection of the cultivars as pairs of parents in breeding programmes which maximize chance of obtaining new valuable recombinants in their offspring.

LOCAL GENETIC RESOURCES AND THEIR USE FOR SELECTION IN BULGARIA

Liliya Krasteva
Institite of Plant Genetic Resources ,,K.Malkov", 2 Drujba Str., 4122 Sadovo, Bulgaria; (email: krasteva_ipgr@abv.bg)

The Institute of Plant Genetic Resources "K.Malkov", Sadovo, Bulgaria is ratified as a national center responsible for the research work on organization, collection, research and use of the plant resources with local and foreign origin for the selection needs and direct introduction.

2157 accessions of green beans, tomatoes, eggplants, watermelon, melon and squash classified by families are collected as a result of the implemented 22 missions during the period of 1978 – 2006. The created collections are studied in accordance with the international descriptor list. They were established collections by characteristics for collection needs. We worked out international projects for collection and conservation of the local plant resources. The collected and studied local genetic resources take 42% of the national collection of the vegetable genetic resources in IPGR, Sadovo. 1050 accessions are stored for long-term conservation in the genebank of IPGR, Sadovo.

FINDING OF PPV RESISTANCE DONORS IN APRICOTS

Boris Krška[1], Jaroslav Salava[2] and Jaroslav Polák[2]
[1]Mendel University of Agriculture and Forestry in Brno, Faculty of Horticulture Lednice; [2]Division of Plant Health, Crop Research Institute, Prague - Czech Republic

In this study, we determined donors for resistance to *Plum pox virus* (PPV) in apricot. The tested genotypes were selected into some groups according to the presence of symptoms and results of ELISA test: Immune-Harlayne; Resistant-Leronda, Henderson, Stella, Stark Early Orange, Betinka (LE-3276) and LE-3241; Medium resistant-Harcot, Sundrop, Mari de Cenad, LE-3246, LE-2926, LE-3209, LE-3662 and Veecot; Medium susceptible-Harval, Lerosa, Goldrich, Dacia, Mai Chua Sin and Pentagonála. The apricot cultivars and selections Stark Early Orange (SEO), Harlayne, Betinka, LE-2926 and LE-3246 were used as the source of resistance to PPV. Several crosses between apricot cultivars and selections resistant and susceptible to PPV have been performed to study the inheritance of resistance to PPV. Various segregation ratios (1:3, 3:5, 1:7 and 7:9) were obtained. The Chi-square (χ^2) test was used to analyze the data. The possible contribution of these results for breeding of apricot to resistance to PPV will be discussed.

DEVELOPMENT OF TRITICALE LINES WITH HL GENE FOR SEMIDWARFNESS

Kishtili U. Kurkiev
Dagestan Experimental station of Vavilov Institute of Plant Industry, Russia, Derbent; (email: kkish@mail.ru)

The aim of the work was to improve triticale lines created on the basis of dominant gene HL for semidwarfness and selection of forms with good yield ability and seed quality. Sample of hexaploid triticale PRAG 199 created on the base of semidwarf line with dominant gene HL for semidwarfness was crossed with triticale forms with complex breeding valuable characters: tall PRAG 160 (Russia), semitall – Presto (Poland) and Kurskaia stepnaia (Russia), semidwarf AD 1422 (Ukraine). Samples Kurskaia stepnaia and AD 1422 possess 2R/6D substitution.

As a result of F_1 – F_5 study for plant height, length of spike-bearing internodes, spike length, spikelets number, spike density, number and weight of seeds from main tiller we selected more than 40 semidwarf lines with good traits of productivity and seed quality. These lines were studied for yield structure: number of seeds and their weight from area unit, diseases resistance and lodging tolerance. As a control commercial varieties of wheat (Nika Kubani) and triticale (Sojuz) were used. The best lines were selected in crosses PRAG 199 × PRAG 160, PRAG 199 × Presto and PRAG 199 × Kurskaia stepnaia. They significantly exceeded control varieties for crop capacity. Lines selected in cross PRAG 199 × Presto are of special interest; at significant decrease of the plant height (by 20-30 cm) yield ability and seed quality were at the level of tall form. Comparing with wheat standard all selected lines exceeded it for yield ability.

INTROGRESSION OF GENE RHT10 FOR SEMIDWARFNESS IN TRITICALE FROM WHEAT VARIETY AI-BIAN 1

Kishtili U. Kurkiev
Dagestan Experimental station of Vavilov Institute of Plant Industry, Russia, Derbent; (email: kkish@mail.ru)

In crosses of wheat variety Ai-bian 1 with rye seeds are formed very rarely and are not viable. To overcome non-crossability we crossed Ai-bian 1 with Chinese spring that is carrier of kr genes. Plants of F_1 and F_2 were pollinated with pollens of rye variety Saratovskaia 7. After pollination of 10 F_1 plants we did not obtained viable progeny. In F_2 we pollinated 65 semidwarf plants. Seed formation was from 0 to 75%. Most seeds were small and without endosperm. Taking into account dominant nature of kr genes we did not obtain expected number of F_2 CS × Ai-bian 1 plants having good crossability with rye that is possibly explained by effect of additional factors.

Amphidiploids (1-3) were obtained only from 6 plants F_2 Ai-bian1 × CS. At all we had 12 plants F_1 (F_2 Ai-bian1 × CS) × Saratovskaia 7. These hybrids did not differ in plant height (46-55 cm), internode length and number. Significant differences were revealed for spike length, spikelets number, spike density, number of seeds per spike and plant, number of tillers, length and width of flag-leaves. At isolation of F_1 (F_2 Ai-bian1 × CS) × Saratovskaia 7 spikes seeds were not formed so we worked with hybrids obtained after open pollination. Hexaploid triticale samples grown in nursery were a source of pollens. Even in this case fertility also was low but due to heterosis for vegetative traits (big tiller number, large spikes with many flowers) we obtained sufficient number of of hybrid seeds. Twelve plants F_1 (F_2 Ai-bian1 × CS) × Saratovskaia 7 produced viable progeny. Plant height in F_2 ranged from 40 to 90 cm. Length of upper internode and number of seeds in spike were intermediate, spike length was bigger and number of seeds in main spike was lower in comparison with parents. Number of seeds per spike was much bigger in F_2 (11.7-24.7) than in F_1. Possibly number of seeds per spike will increase in next generations. In phenotype most F_2 (F_2 Ai-bian 1 × CS) × Saratovskaia 7 plants are closer to octoploid triticale, but there are forms intermediate between octo- and hexa forms. All amphidiploids were obtained at open pollination and so are heterozygotes, so we expected segregation for many traits in their progeny. In next generations it is necessary to select stable triticale semidwarf lines with different levels of ploidy and good productivity.

THE POSSIBILITIES OF USE FOR BREEDING THE WILD SPECIES AND CULTIVATED FORMS OF THE GENUS *BETA*

Kamilla Kużdowicz
Plant Breeding and Acclimatization Institute, Al. Powstańców Wlkp.10, 85-090 Bydgoszcz, Poland; (email: k.kuzdowicz@ihar.bydgoszcz.pl)

The genetic variability of the plant material is necessary for breeding to create new cultivars. At present, there are more than 500 very morphological and genetically differential accessions of the genus *Beta* in the gene bank of the Polish National Centre for Plant Genetic Resources in Radzików. All collected materials have been obtained from national breeding institutions and from international expeditions mainly and have been evaluated according to the “Descriptors for *Beta*” (IPGRI 1996). The work is not simple because each plant have to be evaluated individually (ploidy level, sterility, multigermicity, etc).

Wild *Beta* species from *Beta, Corollinae* and *Procumbentes* sections are important as a natural source of resistant genes to diseases, pests and stress abiotic factors. So far, by traditional way of breeding transferred all of desired traits from wild beet species to cultivar beets was no successful. Fast progress of a tissue culture technique and genetic engineering has given a new chance for breeders. The most modern hybrid cultivars of sugar and fodder beet based on CMS lines have got a very narrow genepool in contrast with collected accessions. Utilization of these cultivated forms of the genus *Beta* is determined by the main trends of breeding and research. Population materials received from international expeditions are interesting in many respects, particularly as a new sources of resistance or tolerance to the important beet diseases.

For lasts years all of the received accessions have been evaluated for two main beet pathogens: *Aphanomyces cochlioides* Drechsler and *Cercospora beticola* Sacc.. Several tolerant populations of cultivated beets were found in these investigations and some of them can be used in breeding programs. Now, we try to select the genotypes tolerant to drought and salinity stress. On the base of the collected materials five hybrid fodder beet cultivars are obtained: Magdalena, Juta, Jarko, Jaspis and Jawor.

References: IPGRI.1996. Descriptors for *Beta* (*Beta* spp). International Board for Plant Genetic Resources, Rome, Italy.

POLISH HYBRIDS OF CULTIVATED OATS WITH *AVENA MACROSTACHYA*

Bogusław Łapiński[1] and Wiesław Podyma[2]
[1]Plant Breeding & Acclimatization Institute (IHAR) – Radzików, PL-05-870 Błonie, Poland; [2]Department of Plant Breeding and Plant Protection, Ministry of Agriculture and Rural Development, Poland; (email: b.lapinski@ihar.edu.pl),

Avena macrostachya (Cosson et Durreu de Maisoneure) is the tetraploid most unique wild species of oat, because of its perenniality, self-incompatibility, winterhardiness and resistance to diseases and pests. Therefore, it has been considered a valuable source of genetic variation for breeding and used in some breeding programmes in UK and USA. Recent results of American scientists confirmed the expected improvement of oats resistance to low temperatures, powdery mildew and the SBMV virus.

Since 2002, a new crossing programme is carried out in the Plant Breeding & Acclimatization Institute (IHAR) in Radzików near Warsaw, based on foreign winter oats and own *A. macrostachya* accesions from a collecting mission to the Atlas Mountains. Three F1 genotypes were obtained using embryo rescue, next cloned, treated with colchicine and grown in vicinity of winter cultivated oats, which served as pollinators. Both primary synthetics and back-cross generations were derived from two F1 hybrids. Only three of the BC1 genotypes had the most expected chromosome number of 56, the remained 26 had 40-49 chromosomes and majority of them were highly sterile or weak. After their cloning and further back-crossing several families were selected, which showed the *A. macrostachya* high level of resistance to mildew and improved resistance to soil-borne diseases.

The decaploid primary synthetics (2n=10x=70) were most resistant to diseases and drought, but they were retarded in growth and showed decreased fertility. The octoploids (2n=8x=56), which contain half-reduced dose of the *macrostachya* genome, seem a much promising new species of winter-hardy oat, which combines high resistance to biotic and abiotic stresses with high vigour, large seed and acceptable level of fertility. Further crosses on the 8x ploidy level are continued in order to decrease plant hight, husk content and improve seed setting.

POLISH GERMPLASM COLLECTION OF *NICOTIANA TABACUM* L. AS THE BASIS OF TOBACCO BREEDING

Dorota Laskowska
Institute of Soil Science and Plant Cultivation-State Research Institute, ul. Czartoryskich 8, 24-100 Puławy, Poland; (email: Dorota.Laskowska@iung.pulawy.pl)

Nicotiana tabacum L. germplasm comprising 784 accessions are being maintained at the Institute of Soil Science and Plant Cultivation in Puławy, Poland. Cultivars were collected by acquisitions from over 30 foreign countries. 31 % of accessions come from polish breeding centers.

Cultivars are grouped into eight types: flue cured (265), basma (89), petiolate-oriental (52), semi-oriental (17), large-leaf cultivars (57), burley (68), cigar (92), dark air-cured (144). Of much interest are 17 alloplasmic lines derived either from cytoplasmic mutations or by breeding alien *Nicotiana* cytoplasms into cultivated tobacco. A genetic-cytoplasmic male sterility system is utilized for commercial hybrid production. Many cultivars have been acquired on account of their genetic resistance to major diseases of tobacco. Some accessions can be used as check or indicator plants. The cultivars vary for genetic potential to accumulate alkaloids from nicotine-free cultivars to cultivars of 5 % content of nicotine. Such a broad genetic variation holds the key to the successful breeding of improved tobacco cultivars.

GENETIC RESOURCES OF SPRING BARLEY: SCREENING FOR SUITABILITY TO ORGANIC BREEDING

Algė Leistrumaitė, Žilvinas Liatukas and Gražina Statkevičiūtė
Lithuanian Institute of Agriculture, Akademija, LT-58344 Kėdainiai, Lithuania; (email: alge@lzi.lt)

The steadily developing organic agriculture requires cultivars possessing a complex of special traits. Such cultivars have to be sufficiently tall (80-90 cm) in order to compete with weeds and be resistant to the main diseases. The spring barley genotypes tested were Lithuania-registered cultivars, genetic resources collection and new cultivars used for initial breeding. The main focus was placed on powdery mildew (PM) among all leaf diseases due to its harmfulness and the ability of its pathogen to adapt rapidly to the new powdery mildew resistance genes with the exception of *Mlo* genes. The old cultivars were sufficiently tall but very susceptible to PM (resistance score 6-9) during trial period. The cultivars developed more than ten years ago were shorter, more than half of them were too short in 2004 and only 2 among the 24 cultivars were tall enough (71-80 cm) in 2005. Only one cultivar was resistant among the tall genotypes in 2004. Modern resistant cultivars were tall enough (11 genotypes among 22) in 2004, but these cultivars were too short in 2005-2006. The resistance to powdery mildew highly correlated between years, the other traits did not correlate so highly. The *Mlo* gene was the most frequent (32 % of cultivars). Only *Mlo* and *1-B-53* genes conferred complete resistance to PM.

VITIS GENETIC RESOURCES IN CROATIA – PRESERVATION, EVALUATION AND REVITALIZATION OF GRAPEVINE VARIETIES

Edi Maletic, Ivan Pejic, Jasminka Karoglan Kontic, Darko Preiner and Silvio Šimon
Faculty of Agriculture, University of Zagreb, Svetosimunska 25, HR-10000 Zagreb, Croatia; (email: emaletic@agr.hr)

According some literature data, at the end of 19th and beginning of 20th century, there were more than 400 grape varieties in Croatia. Unfortunately, because of many reasons (introduced pests and pathogens, modern economic pressure and introduction of world well known cultivars), drastic erosion of autochthonous cultivars has occurred. In last decade, many efforts in the preservation of grapevine biodiversity in Croatia have undertaken. Detail inventarisation of vine-growing regions in Croatia has shown that lot of autochthonous cultivars still can be found, but many of them are endangered and for a long time neglected. To preserve them against the extinguishing, we have established since 2001 national *ex situ* collection at the Faculty of Agriculture in Zagreb, where we have collected 93 autochthonous accessions so far. Besides, we started to build few regional collections, to save duplicates and enable their economic evaluation in appropriate climatic conditions.

Along with the multiplication into collection, amphelographic description (OIV descriptors) and genetic analyses (at least 6 core SSR loci) of cultivars have been carrying out. So far, 62 cultivars have known genetic profile, and additional 20 are in the progress. Comparison of the microsatellite genotypes of the analyzed cultivars with international varieties shows that most of them has unique genotype which supports hypothesis they are Croatian autochthonous cultivars. In few cases microsatelites were also useful in clarification of synonym and homonym questions as well as parent/progeny relationships. All this data, along with photos from different plant parts, are supposed to be entered in the electronic database. We have observed a high quality potential in case of some neglected cultivars, and we started economic revitalization for few most promising. Along with that, we started their clonal and sanitary selection.

USE OF 1R CHROMOSOME TRANSLOCATIONS TO IMPROVE BREAD-MAKING QUALITY IN TRITICALE

Petr Martinek[1], Miroslava Vinterová[2], Kateřina Pajurková[2] and Martin Hromádko[3]
[1]Agrotest fyto, Ltd., Havlíčkova 2787, 767 01 Kroměříž, Czech Republic; [2]Mendel University of Agriculture and Forestry in Brno, Institute of Plant Biology, Zemědělská 1, 613 00 Brno, Czech Republic, [3]SELGEN Co. Ltd., Breeding station Úhřetice, 538 32 Úhřetice, Czech Republic; (email: martinek@vukrom.cz)

To improve bread-making quality of triticale (x *Triticosecale* Wittmack; 2n = 6x = 42, AABBRR), the glutenin allele *Glu-D1d* encoding HMW subunits *5+10* is used. *Glu-D1d* is on chromosome 1DL and positively affects bread-making quality in wheat. The two donor types of winter triticale with translocated chromosome 1R were used: Presto 1D.1R$_{5+10}$-2 and Presto Valdy. These were developed by Professor A.J. Lukaszewski from the University of California, USA. Single translocation 1R.1D$_{5+10}$-2 carries on the long arm of 1R the wheat segment from 1DL with the *Glu-D1d* replacing the secalin locus *Sec-3*, double translocation 'Valdy' carries on the long arm of 1R the translocation 1R.1D$_{5+10}$-2 and on the short arm a segment from 1DS with wheat loci *Gli-D1* and *Glu-D3*. Two sets of triticale donor lines derived from the cv. Presto with 1D.1R$_{5+10}$-2 and Valdy translocation were evaluated for agronomic and grain quality characteristics in 2002-2005. The dough was non-sticky in Valdy, slightly sticky in 1R.1D$_{5+10}$-2 and sticky in check cv. Presto. Both types of donor lines were crossed with selected triticale cultivars. The offsprings of F_2 – F_5 single plants were selected for the presence of *Glu-D1d* using DNA markers. In F_5 generation, lines homozygous in *Glu-D1d* and in some cases even in the whole spectrum of HMW proteins were found using polyacrylamide gel electrophoresis (SDS-PAGE) method. The triticale line M-4/2 (origin: Presto 1R.1D$_{5+10}$-2 linie 1 / Moreno) with substantially improved bread-making grain quality has been developed. The improvement of bread-making quality in triticale is limited by low values of Hagberg falling number (FN), which are usually markedly lower than those in wheat. It is necessary to combine suitable glutenin alleles with the genes controlling low α-amylase activity. The study was supported by the project MSM 2532885901.

AGRI GEN RES TARGETED ACTION: LEAFY VEGETABLES GERMPLASM, STIMULATING USE

Chris Kik[1]and Vladimir Meglič[2]
[1]Centre for Genetic Resources, the Netherlands (CGN), Wageningen University and Research Centre, Bornsesteeg 65, 7608 PD Wageningen, the Netherlands; [2]Agricultural Institute of Slovenia, Hacquetova 17, 1000 Ljubljana, Slovenia; (email: vladimir.meglic@kis.si)

The overall objective of the proposed action, which has started in Janauary 2007, is the establishment of a network of partners active in the conservation and utilisation of Plant Genetic Resources (PGR) of the leafy vegetables most important for Europe. These vegetables comprise lettuce (*Lactuca* spp.), spinach (*Spinacia* spp.) and chicory (*Cichorium* spp.), and also increasingly important minor crops like lamb's lettuce (*Valerianella locusta*) and rucola (*Eruca sativa* and *Diplotaxis* spp.).

During a four year period European databases of the target leafy vegetables will be developed, more than 1200 accessions of the different leafy vegetables will be characterized and regenerated and with that their conservation and availability for potential utilisation will be improved. Also important properties of almost 750 accessions will be evaluated, allowing breeders to utilize the most promising germplasm in their plant improvement programs. Furthermore marketing and utilisation activities of Non Governmental Organisations (NGO's) which participate in the project will contribute to an increased utilisation of the collections by farmers (incl. organic producers) and consumers and will stimulate the utilisation of selected material for restaurants, supermarkets, farmers markets, etc.

To meet the objectives of the Leafy Vegetables project, a consortium of fourteen European partners* was established, which covers all the necessary knowledge to make this project a success. Five workpackages, namely Documentation, Characterization & Regeneration, Evaluation, Utilization & Marketing and Coordination were developed. This major investment in EU Leafy Vegetable genetic resources will result in the upgrading of the EU leafy vegetable databases and will allow for a considerably improved utilization of collections by breeders and also by NGOs active in the area of promoting regionally produced products. Furthermore the improved databases will allow the EU leafy vegetable genebanks to analyse gaps in their collections and to safeguard them in a better way via the improvement of their safety duplications.

BIOLOGICAL PECULIARITIES OF NEW WINE VARIETIES OF GRAPEVINE RELEASED BY THE INSTITUTE "MAGARACH"

Misak Melkonian, Nathalia Studennikova and Olga Razgonova
National Institute for Vine and Wine "Magarach", 31 Kirov St., Yalta, Crimea, 98600, Ukraine; (email: Olga Razgonova@meta.ua)

Grape varieties with colored berries and juice with resistance to biotic and abiotic factors of the environment and not inferior quality of the fruit to *Vitis vinifera* have been created.

The parent forms Nerkarat and Megrabuir were used as donors of valuable traits, and their mid-to-late ripening crosses entered as objects of research: Ai-Petri (Nerkarat x Parvana), Kafa (Megrabuir x Doina), Fiolent (Megrabuir x Yerevani zheltyi), Prazdnichnyi Magaracha (Megrabuir x Tsvetochnyi). Mechanical properties and technological characteristics of the new varieties were studied. The qualitative and quantitative composition of biologically active substances present in the skin and in the pulp of the berry was determined, consisting of carbohydrates, phenolics, pigments, pectic substances and proteins. Other quality parameters envolved in the formation of palate and color of the desired wine were measured, such as relative density d^{20}_{4}, pH, etc. The study varieties are at least equal to the control Cabernet Sauvignon with refer to the overall quality or even superior to it in a number of parameters.

To further improve the breeding and selection process, nine model populations containing the variety Tsitronnyi Magaracha and the form Muscat Jim as parents were chosen on the South Coast of the Crimea to study heterosis, thus leading to 11 heterotic seedlings.

The following interesting forms were revealed in different study populations: the seedling N 31-96-33-16 (Tsitronnyi Magaracha x Zeitoun) with heterosis effects for weight of the cluster (+28.2%) and yield per vine (+18.5%); the seedlings N 32-96-13-24 and 32-96-31-14 (Tsitronnyi Magaracha x Nerkarat) with heterosis effects for weight of the cluster (+14.2% and +31.7, respectively) and yield per vine (+6.3% and +17.4%, respectively); the seedling N 223-96-28-6 (Tsitronnyi Magaracha x Spartanets Magaracha) with heterosis effect for weight of the cluster (+42.2%); the seedlings N 29-96-28-9 and N 29-96-28-10 (Tsitronnyi Magaracha x Megrabuir) with heterosis effects for sugar accumulation (+2.8%) and weight of the cluster (+20.6%) in the former and for weight of the cluster (+58%) and yield per vine (+110.8%) in the latter; the seedling N 66-96-13-11 (Muscat Jim x Tsitronnyi Magaracha) with heterosis effects for sugar accumulation (+1.9%) and weight of the cluster (+28.2%); 100% and 86% of the population (Muscat Jim x Assol) with heterosis effects for weight of the cluster and yield per vine, respectively, and the seedlings NN 64-96-9-11, 64-96-9-13, 64-96-9-14 and 64-96-9-15 with heterosis effects for sugar content of the must, weight of the cluster and yield per vine.

EVALUATION OF WILD SERBIAN POPULATIONS OF BLACK-POD VETCH (*VICIA SATIVA* SUBSP. *NIGRA* (L.) EHRH.) FOR FORAGE YIELDS

Vojislav Mihailović[1], Aleksandar Mikić[1], Branko Ćupina[2], Dragan Milić[1], Slobodan Katić[1] and Imre Pataki[1]
[1]Institute of Field and Vegetable Crops, Forage Crops Department, Maksima Gorkog 30, 21000 Novi Sad, Serbia; [2]University of Novi Sad, Faculty of Agriculture, Department of Field and Vegetable Crops, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia; (email: mikic@ifvcns.ns.ac.yu)

Commonly regarded as the most widely distributed of all common vetch subspecies, black-pod vetch (*Vicia sativa* subsp. *nigra* (L.) Ehrh.) is rather widespread all over Serbia. It is frequently found growing together with large-flowered vetch (*Vicia grandiflora* Scop.) and hairy vetch (*Vicia villosa* Roth) in diverse environments, including urban areas. Wild Serbian populations of black-pod vetch usually germinate during autumn, successfully survive winter conditions, and, due to indeterminate growth, have extended period of both flowering, beginning in late April and early May, and maturing, extending from late May throughout June and July. They also have an ability to regenerate after cutting and even to bear fruit more than once a year.

A small-plot trial was carried out in 2005 and 2006 at Rimski Šančevi Experimental Field of the Institute of Field and Vegetable Crops. It included six black-pod vetch wild populations from Annual Forage Legumes Collection (AFLC) of Forage Crops Department, collected at various sites in the region of Novi Sad. All six cultivars were sown in early October, with a rate of 180 viable seeds m^2, and cut in the stages of full flowering and formation of the first pods. There were monitored plant height (cm), number of stems and lateral branches (plant^{-1}), number of internodes (plant^{-1}), green forage yields (g plant^{-1} and t ha^{-1}), hay yields (g plant^{-1} and t ha^{-1}) and forage dry matter portion. Plant height varied between 33 cm in the population MM 05/08 and 74 cm in the population MM 03/08. The population MM 03/08 had the greatest number of stems and lateral branches (14.0 plant^{-1}) and number of internodes (185.7 plant^{-1}). The population MM 03/09 had the highest yields of both green forage (17.83 g plant^{-1} and 26.8 t ha^{-1}) and hay (4.35 g plant^{-1} and 6.5 t ha^{-1}). The population MM 04/03 had the smallest number of stems and lateral branches (5.3 plant^{-1}) and number of internodes (58.0 plant^{-1}), as well as the lowest yields of green forage (7.04 g plant^{-1} and 10.6 t ha^{-1}) and hay (2.77 g plant^{-1} and 4.2 t ha^{-1}). Portion of forage dry matter ranged from 0.23 in MM 03/17 to 0.40 in MM 04/03.

EVALUATION OF WILD SERBIAN POPULATIONS OF HAIRY VETCH (*VICIA VILLOSA* ROTH) FOR FORAGE YIELDS

Vojislav Mihailović[1], Aleksandar Mikić[1], Jorge Mosjidis[3], Thomas Devine[4], Đorđe Krstić[2] and Imre Pataki[1]

[1]Institute of Field and Vegetable Crops, Forage Crops Department, Maksima Gorkog 30, 21000 Novi Sad, Serbia; [2]University of Novi Sad, Faculty of Agriculture, Department of Field and Vegetable Crops, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia; [3]Auburn University, Dept. Agronomy and Soils, 202 Funchess Hall, Auburn AL 36849-5412, USA; [4]Beltsville Agricultural Research Center, Sustainable Agricultural Systems Laboratory, Building 001, BARC-West, 10300 Baltimore Ave., Beltsville MD 20705, USA; (email: mikic@ifvcns.ns.ac.yu)

Together with common vetch (*Vicia sativa* L.) and Hungarian vetch (*Vicia pannonica* Crantz), hairy vetch (*Vicia villosa* Roth) represents a traditional annual forage legume in both Serbia and the whole Balkan Peninsula. A recently renewed breeding programme on hairy vetch in Institute of Field and Vegetable Crops is aimed at the development of cultivars with high and quality yields of forage, suitable for green manure as well and with sufficient tolerance to low temperatures and more determinate growth. So far, it resulted in one cultivar on the Serbian national list, NS Violeta, and several newly developed lines in the process of testing and registration. On the other hand, hairy vetch is widely distributed in the form of wild populations across the whole country, often growing together with large-flowered vetch (*Vicia grandiflora* Scop.) and black-pod vetch (*Vicia sativa* subsp. *nigra* (L.) Ehrh.) in diverse environments, including urban areas. Wild Serbian populations of hairy vetch germinate during autumn, survive winter conditions, and have extremely extended period of both flowering, beginning in early May, and maturing, extending from late June throughout July and August. They also have an ability to regenerate after cutting and even to bear fruit more than once a year.

A small-plot trial was carried out in 2005 and 2006 at Rimski Šančevi Experimental Field of the Institute of Field and Vegetable Crops. It included four hairy vetch wild populations from Annual Forage Legumes Collection (AFLC) of Forage Crops Department, collected at various sites in the region of Belgrade and Novi Sad. All four cultivars were sown in early October, with a rate of 180 viable seeds m^2, and cut in the stages of full flowering and formation of the first pods. There were monitored plant height (cm), number of stems and lateral branches (plant^{-1}), number of internodes (plant^{-1}), green forage yields (g plant^{-1} and t ha^{-1}), hay yields (g plant^{-1} and t ha^{-1}) and forage dry matter portion.

Number of plants before cutting varied between 91 in the population MM 03/26 and 148 in the population MM 04/13, while plant height varied between 116 cm in the population MM 04/19 and 178 cm in the population MM 03/26. The population MM 03/26 had the greatest number of stems and lateral branches (10.0 plant^{-1}) and number of internodes (140.0 plant^{-1}), as well as the highest yields of both green forage (57.66 g plant^{-1} and 51.9 t ha^{-1}) and hay (9.02 g plant^{-1} and 9.6 t ha^{-1}). The population MM 04/13 had the smallest number of stems and lateral branches (4.0 plant^{-1}) and number of internodes (69.0 plant^{-1}), as well as the lowest yields of green forage (20.10 g plant^{-1} and 30.1 t ha^{-1}) and hay (4.00 g plant^{-1} and 6.0 t ha^{-1}). Portion of forage dry matter ranged from 0.21 in MM 03/26 and MM 04/19 to 0.24 in MM 04/13.

GENEALOGICAL ANALYSIS OF DIVERSITY IN SPRING BARLEY CULTIVARS OF THE CZECH REPUBLIC AND THE FORMER CZECHOSLOVAKIA

Jarmila Milotova[1], Katerina Vaculova[1], Sergey P. Martynov[2] and Tatyana V. Dobrotvorskaya[2]
[1]Agricultural Research Institute Kromeriz, Ltd., Havlickova 2787, 767 01 Kromeriz, Czech Republic; [2]Information and Computation Centre of Russian Academy of Agricultural Sciences, Tver, Russia; (email: milotova@vukrom.cz)

Successful selection of parents for new hybrid combinations depends on the knowledge of genetic diversity. The analysis of tendencies of genetic diversity change in sets of cultivars recommended for cultivation in different regions and years is useful for correction of breeding programmes and production strategy. The genealogical approach is considered equivalent to other methods for evaluation of genetic diversity in cultivars (Cox et al. 1985, Souza and Sorrells 1991).

Genealogical approach using the pedigree analysis was applied to study genetic diversity within a set of 137 spring barley (Hordeum vulgare L.) cultivars and breeding lines developed, grown and released in the territory of the Czech Republic (CZE) and the former Czechoslovakia (CSK) in 1900-1999. The pool of original ancestors comprised 80 landraces and old varieties, and 65 breeding lines with unknown origins. The proportion of local landraces and old varieties in the examined cultivars was higher than 62%.

The greatest contribution from the original ancestors was assessed in the variety Hanna (CSK). Relationships between original ancestors and various conditions of cultivation (regions of Bohemia, Moravia, and Slovakia), site of breeding (breeding station), and end use (malting x feed) were found. Contribution of principal ancestors to the pedigrees of the cultivars (genetic bases of the cultivars) developed by individual stations in the former Czechoslovakia were different, which confirms distinction of applied breeding programmes. In general, the number of original ancestors used in breeding has increased except of the period from the 1940s to 1980s. Genetic erosion of local materials was observed. Genetic diversity in 49 modern cultivars (developed in 1980-1999) was assessed using coefficients of parentage that divided the set into 14 different clusters.

References: Souza, E., Sorrells, M.E., 1991. Prediction of progeny variation in oat from parental genetic relationships. Theor. Appl. Genet. 82: 233-241.

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CHARACTERISATION OF *FUSARIUM* AND BYMV RESISTANCE IN CZECHS *TRIFOLIUM PRATENSE CORE*-COLLECTION

Moravcová H., Poláková M, and Nedělník J.
Agricultural research, LtD. Troubsko, Zahradní 1, 664 41 Troubsko, Czech Republic; (email: moravcova@vupt.cz)

The thesis is based on *Trifolium pratense* core-collection construction and some its characteristics evaluation. In framework of the core-collection were seventy-six items, which were consecutive tested to resistance against *Fusarium* spp. and the Bean yellow mosaic virus (BYMV). *Fusarium* spp. fungi are the most common red clovers pathogens, which are able to cause growth depression, reduction of the persistence and stress tolerance, even death. The tested plants were inoculated and their reaction was evaluated. BYMV is responsible for reducing seed, forage and hay yields. The leaves on infected plants may be crinkled, distorted, irregular in shape, and about half normal size, with yellow mottling and streaking. Very susceptible plants may be killed with BYMV. The virus can be transmitted from infected to healthy plant by aphid vectors or by mechanical means. The results of tests comparison was achieved.

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PRE-BREEDING ON PORTUGUESE MAIZE LANDRACES: SCREENING OF MAIZE GERMPLASM WITH POTENTIAL FOR PARTICIPATORY BREEDING.

Pedro M.R.Mendes Moreira[1], João P. P. Santos[1], Marisa Antunes[1], Carlota Vaz Patto[2] and Silas E. Pêgo[3]
[1]Escola Superior Agrária de Coimbra, Departamento de Fitotecnia. Sector de Protecção Vegetal.; [2]Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa; [3]Instituto Nacional de Investigação Agrária; (email: pmoreira@esac.pt)

Due to an enormous range of natural cultivation conditions (topography, microclimate, precocity, pest and disease resistance, etc) maize, after its introduction from America by Columbus, has evolved in Portugal into different landraces, i.e., genetic speciation under human selection. These mass reservoirs of genetic adaptability have also a valuable conservation function, justifying the existence of a participatory conservation program. In fact, genetic resources maintained in genebanks could be more usefully deployed in both plant breeding and in the farmers' fields.

With this study a pre evaluation of 51 maize landraces, collected in the Centre North of Portugal from February to April 2005, took place. The landraces were sowed during May 2005 in the fields of ESAC (Coimbra Superior School of Agriculture), and screened with the "HUNTERS" method; five representative ears from each population were also characterized. Data concerning disease and pest attack was also recorded.

A certain level of diversity was found in plant and ear morphology and pest resistance. Based on this study results on yield, root and stalk lodging allowed the selection of the best accessions and comparative field trials were implemented in three different locations. Evaluation results are discussed and potential landraces for participatory plant breeding programs presented.

INTERSPECIFIC HYBRIDIZATION AS A SOURCE OF THE ORIGINAL GENETIC VARIATION WITHIN *CAPSICUM* GENUS

Pawel Nowaczyk and Luboslawa Nowaczyk
University of Technology and Life Sciences, Department of Genetics and Plant Breeding, Bernardynska 6, 85-029 Bydgoszcz, Poland; (email: warz@utp.edu.pl)

The distant crossing make it possible to create the new genotypes combining the genetic information of different botanical taxons. Therefore, in the range limited to the existing genes interspecific hybridization seems to be an alternative for genetic plant modification. In our experiments, conducted since mid-nineties, three species of *Capsicum* genus were used. A lot of genetic stable, homozygous lines were obtained as a result of pedigree selection with the offspring valuation. Among of *Capsicum annuum* L. x *Capsicum chinense* Jacq. hybrids the forms characterized by an exceptionally technological performance of fruit are the most interesting. The feature mentioned above means the share of edible pericarp part in the total fruit weight. The maximum level of this trait exceeded 90 %. Among of *Capsicum frutescens* L. x *Capsicum annuum* L. offspring the phenotypes with soft-flesh fruit caught the attention. Such crop may be the raw material for biological active food or nutraceutics production. The soft tissue of pericarp, when fully matured, is mechanically separated from inedible fruit parts, like placenta and seeds as well as skin. The product retain all of the biological and taste properties. The lines we have obtained differ in terms of capsaicinoids content.

THE USE OF GENETIC RESOURCES FOR BREEDING GRAPE VARIETIES SUITED TO DEFINITE BIOTIC AND ABIOTIC FACTORS OF THE ENVIRONMENT

Nicholas Oleinikov, Vladimir Volynkin, Svetlana Levchenko and Nathalia Roshka
National Institute for Vine and Wine "Magarach", 31 Kirov St., Yalta, Crimea, 98600, Ukraine; (email: select_magarach@ukr.net)

A program for immunobreeding "Analog" was developed at the Institute "Magarach" and is currently underway. The program aims to improve efficiency of grape breeding and to achieve varieties whose characteristics are distinguished for genuine novelty. As envisaged by the program and in accordance with the breeding task, we concern ourselves with development of new grape varieties which would combine the multiple resistance to pests, diseases and unfavorable environmental factors quality of the fruit at the best levels found in their international counterparts. To achieve this, new initial material is searched for, accumulated in collections, studied and involved in generative hybridization.

A total of 105 initial forms were assessed for resistance to oidium, and a number of resistant ones were revealed. These are the varieties Aris, Venus, Antaeus magarachskii, Assol, Riesling Magaracha, Khajibei and Tsitronnyi Magaracha. Regularities governing the inheritance of resistance of the leaf apparatus to oidium were studied, leading to the determination of the average estimate of F_1, the breeding value of the study populations, the domination degree and heterosis. The inheritance of resistance to oidium was of intermediate nature and governed by gene additive effects. Hybrid depression, a bias toward the parent with higher susceptibility, a similar level of resistance in the parents and in the F_1 progeny and a bias toward the parent with higher resistance were observed in 17, 48, 7 and 28 per cent of the study populations, respectively. The level of phenolic substances and the presence of the muscat aroma were revealed in 11 parent forms and their hybrid progeny. The varieties Assol, Regent and Megrabuir were high in phenolic substances (292.6 mg/100g, 289.7 mg/100g and 276.3 mg/100g, respectively). The initial form Magarach N 31-77-10 was highly resistant to fungal diseases and its fruit contained high levels of phenolic substances and pigments (298.6 mg/100g and 10.6 mg/100g, respectively). The varieties Muscat Jim, Italy and Tsitronnyi Magaracha were high in terpenic alcohols responsible for the muscat aroma (0.78 mg/dm3 in the former two and 2.38 mg/dm^3 in the latter).

CORRELATIONS OF SOME TRAITS IN THE SET OF ALFALFA ORIGINS

Jan Pelikán, Tomáš Vymyslický and Pavlína Gottwaldová
Agricultural research, Ltd., Zahradní 1, 664 41, Troubsko, Czech Republic; (e-mail: pelikan@vupt.cz)

Within the set of 457 origins (varieties, newly bred varieties and wild forms) of alfalfa (*Medicago sativa, Medicago* x *varia* and *Medicago falcata*) of the world collection maintained in the Czech national gene bank 28 characters were evaluated. From the obtained mean values of particular weighted, measured and counted characters the estimations of correlation coefficients were calculated. The estimations were used as the extent of the tightness of linkage of measured traits. The results obtained are presented in the matrix and are commented.

THE NEW MARIGOLD VARIETY „*PLAMEN PLUS*“ – SELECTED YIELD CHARACTERISICS BEFORE SINGLE FLOWER HARVESTS DURING PRODUCTION SEASON

Andrea Plačková and Ivan Šalamon
Department of Ecology, Faculty of Humanities and Natural Sciences, Presov University, 17th November St., SK- 081 16 Presov, Slovakia; (email: plackova@fhpv.unipo.sk)

Photosynthesis process is dependent on photoreceptors, which are biosynthesized with chlorophylls and the additive plastid pigments: β-, α-carotenes and xanthophylls. Carotenoids are biosynthesized in some flowers with an orange color. The very important attribute of these compounds is their anti-oxidative activity; it is protection of organism against reactive oxygenic forms. The typical example is Marigold, *Calendula officinalis* L., which is one of the medicinal plants well-known for its wide therapeutic use. It is an annual plant which likes hot warm and dry climate with the lover moisture. In the last five years its cultivation, collection and the sale of dry flowers became favorite and profitable activity in the Estern parts of Slovak Republic. The new „*PLAMEN PLUS*“ variety was bred on plenty larger flower, the advantageof which is a bigger weight with high content of carotenoides. Our research work is investigated on carotenoid quantity of Marigold flowers, which were collected 6 times during production season. A year field experiment (2006) was initiated with this new variety in Presov – a mildly warm climatic sub-mountain region with neutral soil with very good fertility. Main component of Marigold flowers was isolated by extraction with methanol and the β–carotene quantity was determined by spectrophotometer. Plant production of biomass and bioactive compounds are most strongly influenced by genetics and the growing environment (dry or wet climate). A comparison of the flower yields from the single harvests indicates differences from 1.3 _ 0.3 to 3.6 _ 0.5 kg dry biomass pre 100 m^2. Total drug yield in 2006 was 15.2 kg dry flowers per 100 m^2. The carotenoid contents were changeable during production season and the % values varied from 0.100 to 0.145. The contribution reports above indicate that climate aridity has an important role as well. The varying soil – climatic conditions during production season provide heterogeneous of facilities to quantity of flower yield and carotene components.

CHARACTERIZATION, EVALUATION AND USE OF GENETIC RESOURCES IN EGGPLANT BREEDING

Jaime Prohens, Julio Ernesto Muñoz, Adrián Rodríguez-Burruezo, Santiago Vilanova and Fernando Nuez
Instituto de Conservación y Mejora de la Agrodiversidad Valenciana (COMAV), Universidad Politécnica de Valencia, Camino de Vera 14, 46022 Valencia, Spain

Most of the commercial production of eggplant (*Solanum melongena*) is based on a few commercial types that have a narrow genetic base. At this respect, local materials could contribute to the genetic improvement of eggplant. We have initiated an eggplant breeding programme based in the utilization of local varieties from the germplasm bank of COMAV (Spain). Although most of the materials from this collection are from Spain (secondary center of diversity for eggplant), there is also a representation of materials of other origins, mainly African, Asian and from the Mediterranean basin. Local materials contained in this collection display a wide diversity for many fruit traits of agronomic interest and also for other traits of relevance for eggplant breeding, like the presence of prickles in the plant or the number of flowers per inflorescence. Several agronomic performance trials, in which commercial hybrid and non-hybrid varieties have been compared with local materials have allowed the identification of some accessions that, under open field cultivation, have a yield similar or even greater than commercial varieties. An important part of the molecular diversity (estimated with AFLPs and microsatellites) contained in the local varieties is not present in modern commercial varieties. In addition, we have demonstrated that hybrids between local varieties situated at a great genetic distance are heterotic for yield. In this way, we have obtained high yielding hybrids between local varieties. Evaluation for content in antioxidant phenolics has allowed the identification of materials with contents much higher than those present in commercial varieties. These materials are being used in a breeding programme for improved nutritional quality. The results obtained so far indicate that the exploitation of local materials of eggplant can lead to significant gains in eggplant breeding.

LATVIAN FLAX GENETICS RESOURCES - REPATRIATION AND EVALUATION

Isaak Rashal[1], Dace Grauda[1,2] and Veneranda Stramkale[2]
[1]Institute of Biology, University of Latvia, Miera Street 3, Salaspils, LV-2169, Latvia; [2]Agricultural Science Centre of Latgale, Kulturas sq. 1, Vilani, Rezekne distr., LV-4650, Latvia; (email: izaks@email.lubi.edu.lv)

Flax breeding started in Latvia in 1923. At least 10 varieties and many breeding lines were created based on selection from the best local and Russian landraces till 1941. After the Second World War flax growing was not considered as an important task for the Latvia region. In 1970, flax breeding in Latvia was cancelled. Fibre flax breeding was started in the country again since

1992; oil flax growing and breeding has started in Latvia only recently. Currently there are no local flax varieties suitable for the changeable Latvian weather conditions. Therefore repatriation and investigation of the Latvian flax genetic resources became a very actual task. 78 flax accessions of the Latvian origin, created and collected before the Second World War were repatriated from the N. I. Vavilov Institute of Plant Industry (Russia), the Flax Research Institute of Russia, and the Institute of Plant Genetics and Crop Plant Research (Germany). Several repatriated varieties were evaluated and results of tree year's field trials were summarized. All investigated local genotypes shown good ecological plasticity. Some local genotypes were better in several agriculturally important traits in comparison with standard varieties. Best of them were used in the fibre and oil flax breeding program at the Agricultural Science Centre of Latgale. For the intensification of the breeding process we are looking for a possibility to apply biotechnology methods to create additional flax breeding initial material. Anther culture is used to obtaining DH lines from hybrids with good lodgings and disease resistance and other agronomically important traits. Conditions of embryo induction, as well as regeneration and rooting media were optimised for used hybrids. To increase available genetic variation somaclonal variation in calli culture were induced and investigated. For this optimal conditions of calli inducing from local breeding material were found.

MAIN BIOLOGICAL AND ECONOMIC TRAITS IN CORNELIAN CHERRY GERMPLASM

Vojtěch Řezníček
Dept. Breeding and propagation of horticultural crop, MZLU Brno, Czech Republic

We study some biological traits like vigorous, phenology age and productivity in Cornelian cherry germplasm collection. Different vigorous and crown volume were find, for example cultivar Fruchtal has low value, most intensive vigorous was appear at the cultivar Jaltsky. The differention between phenology age has also been detected. Among Cornelian cherry collection we have different genotypes on the base their fruit size and fruit quality.

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GRASS PEA (*LATHYRUS SATIVUS* L.), A PROTEIN – RICH PULSE WITH A MODERN FUTURE?

Wojciech Rybiński[1] and Michał Starzycki[2]
[1]Institute of Plant Genetics, Polish Academy of Sciences, Strzeszyńska 34, 60-479 Poznań (Poland); [2]Plant Breeding and Acclimatization Institute, Oil Crop Department, Strzeszyńska 36, 60-475 Poznań, Poland, (email: wryb@igr.poznan.pl)

Lathyrus sativus (grass pea) is a rich a protein pulse crop, that is easily grown on marginal land and under adverse environmental conditions and have great agronomic potential as grain and forage legume, especially in drought condition. Under these conditions grass pea is superior in yield, protein value, nitrogen fixation, and drought, flood and salinity tolerance than other legume crops. *Lathyrus* species have a considerable potential in crop rotation, improving soil physical conditions; reducing amount of disease and weed populations, with the overall reduction of production costs (Vaz Patto et al., 2006). From this point of view grass pea is a major crops in Bangladesh, China, India and Pakistan to the lesser extent in many countries in Europe, the Middle East, northern Africa as well as in Chile and Brasil in South America. Grass pea was already in use in Neolithic times, and presently is considered as a model crop for sustainable agriculture. In Poland *Lathyrus sativus* is one of the least common grain legumes and is grown on a small scale in eastern Poland. Grass pea was introduced to Poland (Podlasie Region) in the XVII century, probably with the settling of Tatars.

Apart from the unquestionable advantages mentioned above, grass pea is also characterized by a number of less favourable features. Hence, one of the conditions for broader introduction of the species in Polish agriculture is the genetic improvement of a number unfavourable characteristics. Beside effects of recombination, such possibility is offered by mutation induction through the introduction of additional variability of features, represented by mutants. The seeds of two cultivars, Derek and Krab, very good adapted for polish environmental condition, constituted initial material for mutation induction with use of chemomutagens. The goal of work was obtaining of mutants representing in comparison to initial forms increase of variability of traits. In result of this work were obtained the mutants with variation of plant habitat, reduced number of lateral branches, improved yield structure parameters, lodging resistance, shorter ripening time and better chemical composition of seeds (protein and fat content, fatty acid composition). Because of a narrow gene pool represented in Poland by not numerous landraces, increased variation of traits in mutants constituted an interesting initial materials for breeding purposes and increase a chance for introducing of improved grass pea cultivars to polish agriculture as a protein – rich pulse.

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RECENT ADVANCES IN PEAR BREEDING AT CLUJ-NAPOCA, ROMANIA

Radu Sestras[1], Adriana Sestras[2], Adrian Barbos[2] and Eugenia Harsan[2]
[1]University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Manastur St., Cluj-Napoca 400372, Romania; [2]Fruit Research Station, 3-5 Horticultorilor St., Cluj-Napoca 400454, Romania; (email: rsestras@usamvcluj.ro)

Pear breeding at Cluj-Napoca, Romania, started in 1953 when Fruit Research Station was founded. The most well-known and spread cultivars of pear created in Cluj-Napoca were ‘Napoca’ and ‘Doina’. In the last years there were homologated six new pear cultivars, as following: ‘Haydeea’ created by artificial hybridization between ‘Beurré Hardy’ x ‘Beurré Six’; ‘Ina Estival’ = [‘Napoca’ x (‘President Drouard’ x ‘Williams’)]; ‘Virgiliu Hibernal’ = ‘Passe Crassane’ x ‘Comtesse de Paris’; ‘Jubileu 50’ = ‘Napoca’ x ‘Beurré Precoce Morettini’; ‘Milenium’ = (‘Josephine de Malines’ x ‘Doctor Lucius’) x ‘Comtesse de Paris’; ‘Rosioara de Cluj’ = ‘Red Williams’ x ‘Beurré Giffard’. All of these cultivars have a good productivity, fruit quality and suitable adaptation for Romanian weather conditions. Among them, ‘Rosioara de Cluj’, ‘Ina Estival’, ‘Jubileu 50’, are early ripe (fruits of ‘Rosioara de Cluj’ ripen on middle July, meanwhile ‘Ina Estival’ and ‘Jubileu 50’ in August). ‘Haydeea’ is ripening in September, it has a high productivity and proved a good response to *Psylla* attack. ‘Milenium’ and ‘Virgiliu Hibernal’ are winter cultivars, with prolonged storing of fruits. The new cultivars created at Cluj-Napoca enrich Romanian assortment of cultivated pear and international germplasm repository. Also, these cultivars represent useful genetic resources and could become valuable as parent stocks in future pear improvement programs. One of the new cultivars obtained at Cluj-Napoca (‘Haydeea’) still gives birth to seedlings with valuable traits, therefore it prove a good capacity to transmit its valuable hereditary amount.

THE RESPONSE OF PEAR CULTIVARS TO ERWINIA AMYLOVORA ATTACK IN CENTRAL TRANSYLVANIA CONDITIONS, ROMANIA

Radu Sestras[1], Adriana Sestras[2] and Adrian Barbos[2]
[1]University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Manastur St., Cluj-Napoca 400372, Romania; [2]Fruit Research Station, 3-5 Horticultorilor St., Cluj-Napoca 400454, Romania; (email: rsestras@usamvcluj.ro)

Fire blight, caused by the bacterium *Erwinia amylovora*, is one of the most damaging diseases of pear in the world. In Cluj-Napoca area, situated in central Transylvania, Romania, fire blight was observed first in 1994, very late comparative with the other countries from occidental Europe. In the last ten years at Fruit Research Station Cluj-Napoca, the response of more than 15000 genotypes of pear to fire blight attack was analyzed, from among which 350 are cultivars and *Pyrus* species, more than 140 are clonal selections and the remainder of them seedlings. The response of the cultivars from National Pear Collection from Cluj-Napoca to fire blight attack, assessed in natural conditions of infection, range on a large scale of variability, which denotes a strong influence of the genotype in expression of resistance or sensitivity to disease. From all cultivars, about 25% have not presented symptoms of attack, among them being the following: ‘Blanquet precoce’, ‘Klementinka’, ‘Severianka’, ‘Beurré Bachelier’, ‘Kieffer Seedling’, ‘Er Shi Shinge’, ‘Beurré Amanlis’, ‘Bristol Cross’, ‘Beurré Liegel’, ‘Beurré de Lucon’, ‘Grand Champion’, ‘Magness’, ‘Mericourt’ etc. and several old autochthonous cultivars (‘Pere malaiete’, ‘De Zahar de Bihor', 'Cu Miez Rosu', 'Clopotele', 'Garoafa mare', 'Zaharoasa de Vara', 'Craiese', 'Para de apa'). Also, there were identified several species of *Pyrus* with no attack, as *P. ussuriensis*, *P. common pear*, *P. lindlezi*, *P. malifolia*, *P. persica*, *P. variolosa*. The remarked genotypes could be potential sources for further breeding programmes and increase the number of genotypes available for breeding new pear cultivars resistant to *Erwinia* attack.

HEREDITY OF NEW FEATURES *GLANDULARIA CANADENSIS* PLANTS, OBTAINED BY CHEMICAL MUTAGENESIS

Anna Shirokova
Main Botanical Garden, Russian Academy of Sciences, Botanicheskaya Str., 4, Moscow 127276 Russia; (email: glandularia@yahoo.com)

Glandularia canadensis is a little-known garden plant. However, this species is promise to use in summer borders and containers. It grows to 45 cm height with a spread shoots to 60 cm long. Its flowers are zygomorphic, magenta-rose. Chemical mutagenesis is widely used to produce primary material for selection. In our work, we utilized this technique to induce variability in *G.canadensis*. Its seeds were treated in the solutions of DES (diethylsulphate). The widest spectrum of variability was obtained in the variant with 0,05% DES. Variability of morphological traits — shape, size and color of flowers, size of spikes, shape, dividing and color of leaves, pubescence and habitus of plants were studied in eight generations. In the M_2 generation, the plants with traits being different from the wild type were selected. The traits to select were erect compact plant, humifuse plant, disk-like spikes with falciform flowers, near symmetrical flower limb, and lavender and violet-purple flowers. The study of divergence characters in M_3 has shown that the humifuse habitus appeared in the population with frequency 28-35% and the compact habitus (strong erect plants) with frequency15-18%. The plants with large pale lavender-pink fragrant flowers were found in M_2 population; on theirs base new breeding strain was selected. By hybridization of this strain and strains with small violet or lilac flowers plants with large lavender flowers were obtained. The effect of Heterosis (vigorous plants, abundant clusters, seed set) took place in F_1 progeny by crossing wild type of *G. canadensis* with prospective mutant strains.

Therefore strains of *G. canadensis* selected on the base of mutant forms may be useful source for future breeding programs.

INTROGRESSION OF RYE (*SECALE CEREALE* L.) CHROMOSOME SEGMENTS INTO CULTIVATED WHEAT (*TRITICUM AESTIVUM* L.)

Annamária Schneider, Éva Szakács and Márta Molnár-Láng
Agricultural Research Institute of the Hungarian Academy of Sciences, H-2462, Martonvásár, P.O. Box 19, Hungary; (email: schneidera@mail.mgki.hu)

Several hundreds of wheat cultivars (*Triticum aestivum* L.) worldwide contain the 1RS chromosome arm from rye (*Secale cereale* L.) all of which can be traced back to the same rye genotype 'Petkus'. The main objective of the present research is to replace it by other rye chromosome arms originating from genetically diverse rye genotypes.

Earlier studies demonstrated that when a wheat cultivar with the 1RS.1BL translocation was crossed with an octoploid triticale, trivalents arose in the course of meiosis in the F_1 hybrid and thus new wheat/rye recombinants developed in the 1RS arm. A new recipient wheat genotype was developed in which the crossability gene *kr1* is combined with the 1RS.1BL translocation. The Martonvásári 9 kr1 line was crossed with Martonvásár wheat cultivars carrying the 1RS.1BL translocation (Mv Magdaléna, Mv Béres). The genome composition of the F_1 hybrids was analysed using GISH to confirm the presence of one 1RS.1BL translocation in these plants. Plants with two 1RS.1BL translocations were selected, again using GISH, in the F_2 generation. Plants with the *kr1kr1* genotype (recessive homozygous) will be selected from the F_2 generation according to the seed set after pollinating with rye. More than 50 different rye genotypes of different geographical origin were collected from the genebanks in Gatersleben (Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany) and the USDA, ARS (National Small Grain Collection Aberdeen, Idaho, USA). The polymorphism of several different rye cultivars has been analysed with PCR-based molecular markers and using FISH with different repetitive probes (pSc119.2, Afa family, AAC, pSc200, pSc250).

Genotypes exhibiting polymorphism compared to the 1RS arm of Petkus origin will be selected for pollinating the new recipient wheat genotypes with *kr1kr1*, 1RS.1BL genome composition. Hopefully new recombinants will be produced, which can be used for wheat improvement with new resistance genes and diverse quality parameters.

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CHOICE OF VALUABLE DONORS FOR BREEDING AMONG WINTER WHEAT LANDRACES AND OBSOLETE CULTIVARS

Zdeněk Stehno[1], Jiří Hermuth[1], Ladislav Dotlačil[1], Václav Dvořáček[1] and Edita Gregová[2]
[1]Crop Research Institute, Drnovská 507. 161 06 Prague 6 – Ruzyně, Czech Republic; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic

Collection of wheat genetic resources in the Gene bank department of the Crop Research Institute (CRI) is regularly evaluated with the aim to select possible donors of grain quality or disease resistance. Promising sources of disease resistance (combined resistance in particular) are introduced into breeders' tests to evaluate them under different conditions.

Evaluation of wheat landraces and obsolete cultivars has been aimed mainly at grain quality parameters. The heterogeneous landraces and obsolete cultivars were divided according electrophoreses of gliadins and glutenins in Gli – Glu lines. Seventy HMW-Glu lines have been evaluated separately for three years (2003, 2004 and 2006) in Ruzyne locality (sugar beet growing area). Registered cultivars 'Samanta', 'Ilona' and 'Šarka' were used as check variants. Grain quality parameters as crude protein content, wet gluten content, proportion of gliadin, glutenin and albumin+globulin fractions, gluten index and Zeleny sedimentation have been measured. Crude protein content of the check cultivars varied from 14.3 to 14.5 %. The highest protein content (19.8 %) has been determined in the line from obsolete Hungarian cultivar 'Mindeszentpusztai', followed by lines from 'Szekacz 19 (19.2 %) and Austrian cultivar 'Bergland' (19.0 %). Also the highest wet gluten content (53.4 %) has been identified in 'Mindeszentpusztai'. Favourable values of Zeleny sedimentation (over 50 ml) showed lines from 'Fleishman 481', 'Szekacz' and 'Stepova'. Among other characteristics, the content of albumin+globulin fraction had the lowest genetic variability and consequently low correlation to the rest of parameters. On the other hand the results confirmed high correlation of crude protein content to its components as wet gluten content (r=0,80), content of glutenins (r=0.87) and gliadins (r=0.77) but low correlation to albumin + globulin fraction (r=0.39).

The most of selected lines with valuable quality parameters has been introduced into collection of wheat genetic resources in Czech gene bank and will be available for utilisation in breeding programmes.

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NON-SPECIFIC RESISTANCE AGAINST WHEAT POWDERY MILDEW IN *AEGILOPS SPELTOIDES* AND *AEGILOPS TAUSCHII* ACCESSIONS

Miroslav Švec[1], Peter Pančík[1] and Pavol Hauptvogel[2]
[1]Comenius University in Bratislava, Faculty of Natural Sciences, Department of Genetics, Mlynská dolina B1, 842 15 Bratislava, Slovak Republic; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 921 68 Piešťany, Slovak Republic; (email: msvec@fns.uniba.sk)

Non-specific resistance to powdery mildew (*Blumeria graminis* (DC.) E. O. Speer f.sp. *tritici* Em. Marchal) in 8 accessions of *Aegilops speltoides* Tausch and in 41 accessions of *Aegilops tauschii* Coss. was tested at the stage of primary and tertiary leaves in the laboratory conditions. Degree of reduction of infectious efficiency on tertiary leaf compared to the infectious efficiency on primary leaf was used as parameter of resistance. Hexaploid wheat variety Amigo served as resistance check and Chinese Aibian-1 variety as susceptible check. With exception of accession AE 413, all samples of *Aegilops speltoides* reached a level of resistance of Amigo wheat variety. Accession AE 413 coming from Israel had only 14 % of resistance value compared to Amigo. Fifteen genotypes of all tested accessions of *Aegilops tauschii* reduced infectious efficiency of pathogen to zero or less than one per cent. Any elongating secondary hyphae was scored in accessions CGN 1312 from Iran, AE 181 from Tadjikistan, AE 211 from Azerbaijan, AE 454 from Georgia and AE 1087 from Afghanistan at the stage of tertiary leaves. There is a supposition these accessions will have satisfactory adult plant resistance and so will be a suitable resource for non-specific resistance. Sixteen accessions of this species were characterized by moderate decrease of infectious efficiency on the third leaf (less than 50 %). For this reason these accessions will probably have a little potential for resistance breeding. Degree of resistance or susceptibility was not in relation with country origin of particular accessions.

THE PERFORMANCE OF LUCERNE ACCESSIONS COLLECTION FROM ESTONIA‘S ISLANDS IN LITHUANIA

Antanas Svirskis
Lithuanian Institute of Agriculture, University Šiauliai, Dotnuva-Akademija, Kėdainiai LT-58344, Lithuania; (email: antanas@lzi.lt)

Lucerne is the highest yielding and most valuable of all perennial legume species grown in Baltic countries on fertile calcareous soils. Lucerne breeding was started in Lithuania 85 years ago. Since the very beggining a special focus has been placed on winterhardiness and seed production improvement under country‘s conditions by using local initial material and promising varieties and accessions from various regions.

The Estonian natural lucerne populations growing on the northern and western coast and on islands Baltic sea has very good winterhardiness. In case of suitable growing place and utilisation regime, they stay in the stand for a long time. There are plants of these populations that have vegetative spreading ability. Two international expeditions were arranged in 2002 and 2003 where a collections of indigenous accessions of lucerne was gathered, which contains besides yellow-flowering lucerne, several interesting and valuable accessions of blue-flowering lucerne. Two trials (in 2003 and 2004) with 4 Lithuanian, 3 Estonian varieties and 16 accessions of lucerne were established in the Lithuanian Institute of Agriculture. According of average data of 4 years trials majority of tested varieties and accessions produced lower dry matter and seed yield than standard variety ‘Žydrūnė‘.However some of accessions showed rather high yielding capasity, had good leafiness, resistance to leaf and steam diseases and other useful morfobiological characters. They are promising material for breeding new varieties of lucerne, especially for pasture type varieties.

THE EXPLOITATION OF EXOTIC RESOURCES IN POTATO PRE-BREEDING: VIRUS AND LATE BLIGHT RESISTANT PROGENIES OF SOMATIC HYBRIDS WITH THE WILD SPECIES *SOLANUM TARNII*

Ramona Thieme[1], Marion Nachtigall[2], Jörg Schubert[2], Elena Rakosy-Tican[3], Olga Antonova[4], Tatjana Gavrilenko[4], Udo Heimbach[5] and Thomas Thieme[6]
[1]Federal Centre for Breeding Research on Cultivated Plants, Institute of Agricultural Crops, Rudolf-Schick-Platz 3a, 18190 Groß Lüsewitz, Germany; [2]Federal Centre for Breeding Research on Cultivated Plants, Institute of Resistance Research and Pathogen Diagnostics, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany; [3]Babeş-Bolyai University, Clinicilor str. 5-7, 3400 Cluj-Napoca, Romania; [4]N.I. Vavilov Institute of Plant Industry, B. Morskaya Str. 42, 190000 St. Petersburg, Russia; [5]Federal Biological Research Centre for Agriculture and Forestry, Institute for Plant Protection in Field Crops and Grassland, Messeweg 11/12, 38104 Braunschweig, Germany; [6]BTL Bio-Test Lab GmbH Sagerheide, Birkenallee 19, 18184 Sagerheide, Germany; (email: r.thieme@bafz.de)

The introduction of ‘exotic’ germplasm from wild species of *Solanum* provides a new source of durable resistance to pathogens and pests, and a chance of increasing the gene pool for potato breeding. World-wide the abundance, ubiquitous occurrence and adaptability of aphids, viruses and late blight threatens potato production.

The diploid tuber-bearing Mexican wild species *Solanum tarnii* Hawkes et Hjerting, which belongs to the Series *Pinnatisecta*, is an interesting exotic resource for potato pre-breeding but is difficult to cross with cultivated potato. The accession of *S. tarnii*, GLKS 96.203.1 from IPK Genebank External Branch ‘North’, Gross Lüsewitz, Germany, is resistant to late blight, Potato Virus Y

(PVY) and Colorado Potato Beetle, according to laboratory and field tests. Twenty four hexaploid somatic hybrids produced by protoplast electrofusion of *S. tarnii* and cv. Delikat were resistant to foliage blight caused by the oomycete *Phytophthora infestans* (Mont. De Bary) (detached leaf test). None of the plants of ten somatic hybrids became infected with PVY after mechanical inoculation with six isolates of all of the known strains of this virus or after grafting and growing in the field. Eight hexaploid hybrids, all extremely resistant to PVY and highly resistant to foliage blight were used in backcross experiments. A total of 227 BC_1 clones were obtained from three of these hybrids. Of 139 BC_1 clones three were highly and eight slightly resistant to foliage blight.

A two-year field study indicates that tuber number, weight, and the characteristics of tubers of the somatic hybrids and 22 BC_1 clones are similar to those of the parent cv. Delikat and the standard cv. Sonate. The extreme PVY resistance was confirmed by growing the plants in the field. Furthermore, backcrosses of eight selected BC_1 clones, originating from two different somatic hybrids, with cv. Sonate was successful. More than 50 berries are available for producing BC_2 clones.

EVALUATION OF WILD SPECIES OF COOL SEASON FOOD LEGUMES IN BREEDING PROGRAMS AS A GENE RESOURCES

Cengiz Toker, Huseyin Canci, Nisa Ertoy Inci, Fatma Oncu Ceylan and Serap Melike Icoz
Department of Field Crops, Faculty of Agriculture, Akdeniz University, TR-07058 Antalya, Turkey; (email: toker@akdeniz.edu.tr)

Cool season food legumes are taxonomically classified into three tribes: Cicereae Alef., Vicieae (Adans.) DC. and Genisteae (Adanson) Bentham and they consist of six genera namely chickpea (*Cicer* L.), pea (*Pisum* L.), faba bean (*Vicia* L.), lentil (*Lens* Mill.), grass pea (*Lathyrus* L) and lupin (*Lupinus* L.).

The genus *Cicer* L. encompasses 9 annuals species including the cultivated chickpea, *Cicer arietinum* L., 33 wild perennial and one unspecified wild. *C. reticulatum* Ladiz. is recognized as wild progenitor. The taxa *Pisum* L. comprises distinctly different two species, *P. sativum* L. and *P. fulvum* Subth & Smith; whereas *P. sativum* ssp. *sativum* var. *sativum*, *P. sativum* ssp. *sativum* var. *arvense*, *P. sativum* ssp. *elatius* var. *elatius*, *P. sativum* ssp. *elatius* var. *brevipedinculatum* and *P. sativum* ssp. *elatius* var. *pumilio* (*P. humile* is putative pregenitor) are considered as form a single species. *Vicia faba* L. is taxonomically classified in section *Faba* (Miller) Lebed. and consist of four taxa: *V. faba* ssp. *paucijuga* Murat., *V. faba* ssp. *faba* L. var. *minor*, *V. faba* ssp. *faba* L. var. *equina*, *V. faba* ssp. *faba* L. var. *faba*. Wild progenitor of *V. faba* has not been recognized so far. The genus *Lens* Miller consists of seven species i.e. *L. culinaris* ssp *orientalis* (Boiss.) Handel-Mazetti (wild progenitor), *L. culinaris* ssp. *odemensis* Ladiz., *L. culinaris* ssp. *tomentosus* Ladiz., *L. ervoides* (Brign.) Grande, *L. lamottei* Czefr. and *L. nigricans* (Bieb.) Godron and *L. culinaris* ssp. *culinaris* Medikus. The genus *Lathyrus* L. is large with 187 species and *L. cicera* L is considered as progenitor of grass pea, *L. sativus* L. The genus *Lupinus* L. consists of four cultivated types: *L. albus* L., *L. luteus* L., *L. angustifolius* L. and *L. mutabilis* Sweet. Only 11 or 12 species exist in the Old World.

Wild species are classified into gene pools according to crossability degrees between cultivated forms and the wild taxa. In this review, the wild forms and gene pools of cool season food legumes are given.

UKRAINIAN PROGRAM OF GRAPE BREEDING BASED ON THE GLOBAL DIVERSIFICATION OF GENETIC RESOURCES OF THE SPECIES

Vladimir Volynkin
National Institute for Vine and Wine “Magarach”, 31 Kirov St., Yalta, Crimea, 98600, Ukraine; (email: volynkin@ukr.net)

Grapevine as an agricultural crop is cultivated under different soil and climatic conditions. Combinations of such conditions underlie the principles of establishing individual zones of grape and wine growing where grapes are grown to be made into specific products.

On the other hand, individual forms of grapevine have emerged in the course of natural evolution in such eco-geographical regions and may be divided into variety groups, variety types, eco-geographical groups and individual species.

Such individual species isolated from a standpoint of origin are important for breeding purposes since forms within a species have acquired specific biological features typical of this very species. Thus, high frost resistance is typical of forms of the Amur grape; good resistance to fungal diseases and phylloxera is inherent in those of American species of grapevine, and the highest level of fruit quality has been achieved through natural selection in European and Asian grapevines. Thanks to the existence of individual species of grapevine with peculiar traits of interest and in pursuit of increased heterogeneity of grapes under commercial cultivation, the Ukrainian program of grape breeding "Analog" aims at the development of a new generation of varieties and is based on the use of initial forms from different centers of origin of grapevine: the European center (*Vitis vinifera L.*), the East Asian Center (*Vitis amurensis* Rupr.) and the North American center (*Vitis riparia* Michx., *Vitis cinerea* Engelm. etc.).

VANISHING VARIATION – THE DIVERSITY OF TIMOTHY (*PHLEUM PRATENSE* L.) IN HISTORICAL GRASSLANDS

Jens Weibull[1], Fredrik Ottosson[2], Agnese Kolodinska Brantestam[2], Lena Dafgård[2], Peder Weibull[3] and Arnulf Merker[3]
[1]Swedish Biodiversity Centre, P O Box 54, SE-230 53 Alnarp, Sweden; [2]Nordic Gene Bank, P O Box 41, SE-230 53 Alnarp, Sweden; [3]Swedish Univ. Agric. Sci./Plant breeding and biotechnology, P O Box 44, SE-230 53 Alnarp, Sweden

The distribution of ancient meadows and pastures – grasslands with a cultivation history of more than 200 years – is rapidly decreasing in Sweden. Today less than 1 300 ha remain. Nothing is known about the diversity of the wild crop relatives in these threatened habitats. A further reduction of historical grasslands may incur losses of genetic diversity and prove fatal for future crop breeding. We therefore try to answer the following questions:

- To what extent does modern Swedish timothy differ in diversity from the original material from which it was developed?
- Can ancient meadows and pastures still provide new unique variation for the good of Swedish timothy breeding?
- Is it worthwhile, from a genetic point of view, to return to these grasslands in search for new adaptive traits?
- Can any wild population of timothy equally well serve the purpose of gene pool for future breeding?

The project compares phenotypic and molecular diversity of the commercially important forage grass timothy in genotypes sampled from historical grasslands vs. modern varieties and natural populations. Sampling localities are distributed all over the southern half of the country. Analysis of phenotypic traits includes botanical and agronomic descriptors important for breeding work, e.g. winter survival, shoot re-growth and tolerance or resistance against biotic stress factors such as diseases. We will also look at the molecular diversity using microsatellites (SSRs), where we will study the variation within and between populations.

Firstly, we hope to make a valuable contribution to Swedish forage crop-breeding. Secondly, historical grasslands will be valued from the point of view of crop genetic diversity, and judged whether they justify the special conservation arrangements currently in practice.

This study constitutes one contribution to the recently established joint Nordic project on diversity of timothy genetic resources, that will be completed in 2010.

RELATIONSHIP BETWEEN PLOIDY LEVEL AND THE FORMATION OF PHENOLIC COMPOUNDS IN PLANT CELLS

Zagoskina V. Natalia
Timiriazev Institute of Plant Physiology, Russian Academy of Sciences, ul. Botanicheskaya 35, Moscow, 127176 Russia; (email: phenolic@ippras.ru)

The level of ploidy is one of the most important cytogenetic factors determining physiological and biochemical properties of plants. Phenolic compounds are among the the most abundant secondary plant products; they are essential and active participants of cell metabolism. Although considerable advances have been made in the study of phenolic metabolism, the interrelations between ploidy level and the capacity for phenolic synthesis in plant cells have not been elucidated.

The goal of this study was to gain a better understanding of the significance of plant cell ploidy for phenolic metabolism. Tea plant calluses, synthesizing substantial amounts of phenolics typical of intact plants, were chosen as experimental material. Callus were grown in darkness on a modified Heller nutrient medium. Some calluses were transferred to a medium with 0.03% or 01% colchicines added.

In our experiments, colchicines treatment increased ploidy in the tea callus cultures (TC-1) resulting in a new callus strain (TC-2). The TC-1 strain contained a diploid set of chromosomes, similar to the intact tea plants. The TC-2 strain contained relatively few diploid cells; the most abundant were triploid cells. In general, the increase in the ploidy level of tea callus tissues was accompanied by reduced callus capacity for the synthesis of phenolic compounds manifested in the reduced content of phenolics in tissues and the depressed activity of PAL, one of the key enzymes of phenolic biosynthesis.

A NEW SUPER-HIGH YIELD GERMPLASM HS Z6-06-56 FROM INTERSPECIFIC HYBRIDIZATION BETWEEN COMMON WHEAT AND DURUM WHEAT

Fengwu Zhao[1], Huimin Li[1], Jianzhong Yang[1], Shaohua Yuan[1], Zaisong Ding[2], Ming Zhao[2], Pavol Hauptvogel[3] and Daniela Benedikova[3]
[1]Dry Farming Institute, Hebei Academy of Agricultural and Forestry Sciences, Hengshui 053000; [2]Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 10081; [3]SARC-Research Institute of Plant Production Piešťany, Bratislavska 122, 921 68 Piestany, Slovak Republic

Successive 9 years research has been carried out on an interspecific hybridization between common wheat (T.aestivum) and durum wheat (T.durum). A new germplasm of HS Z6-06-56 with super-high yield (SHY) was developed from a cross of (Shi 4185/Neixiang 4184//Shi 4185) in which common wheat as both acceptor and recurrent parent (RP). Dates of flagging, heading and maturing were 1, 1, 2 and 2 days earlier compared with its RP of Shi 4185, a check cultivar in both national and provincial yield trial, respectively, there were no differences among traits of plant height, head length, spikelets/head by means of anova analysis. (2). Among the 3 yield components, heads/plant and seeds/head were same than RP, 1000-kernel weight (TKW) was the only factor caused its SHY and 26.96% advantage was found compared with RP. (3). It was an effective method to develop wheat SHY germplasm by ways of IH heterosis.

THE USE OF *IN VITRO* TISSUE CULTURE TECHNOLOGY IN GRAPE BREEDING

Valerii Zlenko and Vladimir Volynkin
National Institute for Vine and Wine "Magarach", 31 Kirov St., Yalta, Crimea, 98600, Ukraine; (email: select_magarach@ukr.net)

It is known that seedlings of grapevine come into bearing in the fourth to fifth year of cultivation when grown in the field. That is why the process of breeding a new variety in which up to five generations of seedlings should be obtained may last for up to thirty years. Besides, the polygenic inheritance of the majority of traits, high heterogeneity and domination of individual negative traits in the progeny, which is typical of grapevine, make it necessary to investigate the presence and the degree of expression of traits in large numbers of seedlings, leading to the need of large areas for doing this in the field. The procedure may be accelerated by diagnosis of traits and selection of positive genotypes at early developmental stages.

In our Institute, we started research into design and use of technology enabling acceleration of the breeding process of grapevine by using *in vitro* culture. The technology implies that seedlings should be selected at the stage of seed germination, desired and unwanted traits diagnosed in the first year of development, early bloom induced and crosses or inbreeding performed in the first to second year of cultivation in the greenhouse. Research is underway into *in vitro* diagnosis of such traits as sugar and acid accumulation in the berries of the future yield (which are genetically determined) in the first year of the development of seedlings and potential number of inflorescences. A method to obtain grape plants with mature wood by *in vitro* culture was developed. The chilling of these plants brought into dormancy under *in vitro* conditions makes it possible to select seedlings with frost resistance and winter hardiness. We also started to select genotypes resistant to phylloxera both in the process of growing the seedlings and during *in vitro* culture of explants from vegetative organs of grape plants.

Another direction of research is to involve the species *Vitis cinerea* Engelm. which is is highly resistant to frost and pathogens into hybridization with varieties of *Vitis vinifera* L. The goal of this is to achieve a new variety combining resistance to a number of biotic and abiotic factors with good quality of the fruit. Selection of seedlings in the first year of development by using methods to diagnose valuable traits during *in vitro* culture and by inducing an early bearing will enable five generations of seedlings to be obtained over a ten-year period.

ACCUMULATION AND TRANSLOCATION OF NITROGEN AT OLD AND MODERN SLOVAK WINTER WHEAT VARIETIES

Alžbeta Žofajová, Martin Užík, Pavol Hauptvogel and Magdaléna Bieliková
SARC – Research Institute of Plant Production Piešťany, Bratislavská 122, 92168 Piešťany, Slovak Republic; (email: zofajova@vurv.sk)

Knowledge of the changes in physiological traits associated with genetic gains in yield potential and quality are essential to improve factors limiting yield and quality and to formulate future breeding strategies. Ten winter wheat varieties realised in the years 1921 – 2003 in Slovakia were evaluated in pot experiment at 4 variants of N-fertilization and in 2 terms of harvest (heading, maturity). Modern varieties had more effective N-uptake, more accumulated N (mg.plant^{-1}) at heading and at maturity, had more effective N translocation, had higher N harvest index, but in spite of that had lower N content in grain (1.976 % - 2.224 %) than old varieties (2.268 % – 2.760 %), because had two times higher grain yield. Relative high N concentration in straw and root at maturity represents source for increasing N harvest index and N content in grain.

POSTER PRESENTATIONS

Session 3

Molecular and information technologies for plant genetic resources – challenges and opportunities

GENETIC STRUCTURE AND DIVERSITY IN *PHASEOLUS COCCINEUS* L. BY USING SSR (SIMPLE SEQUENCE REPEAT) MOLECULAR MARKERS

Paola Arcaleni[1], Barbara Tiranti[1], Giorgia Spataro[1], Giovanna Attene[2], Roberto Papa[3], Pierluigi Spagnoletti Zeuli[4] and Valeria Negri[1]
[1]Dip. Biologia Vegetale Biotecnologie Agro-ambientali Zootecniche, Università di Perugia , Borgo XX Giugno 74, 06121 Perugia, Italy; [2]Dip. Scienze Agronomiche Genetica Vegetale Agraria, Università di Sassari, via E. De Nicola, 07100 Sassari Italy; [3]Dip. Scienze degli Alimenti, Università Politecnica Marche, via Brecce Bianche, 60131 Ancona, Italy; [4]Dip. Biologia, Difesa e Biotecnologie Agro-forestali, Università della Basilicata, Campus Macchia Romana, 85100 Potenza, Italy; (email: vnegri@unipg.it)

P. coccineus L. (2n = 2x = 22) is widely cultivated in the mountains and in Northern Europe because of its suitability to cool environments. At the present, little information about the level of genetic diversity of the *P. coccineus* germplasm is available.

Aim of this study was to:

a) obtain a core collection representative of the world wide variation held in germplasm banks,
b) investigate its genetic variation,
c) compare the level of genetic diversity in groups of accessions coming from European and Meso-America,
d) improve the knowledge of the evolutive process caused by introduction in Europe,
e) obtain an overall picture of diversity which can be useful for future plant breeding activities.

The 10 SSRs used were efficient in detecting *P. coccineus* diversity. The obtained core collection (297 accessions) appears to be representative of the species diversity and can be useful in future studies. In the area of original adaptation and domestication (Mesoamerica) landraces shows a wide diversity which appears to be continuously enriched by introgression from wild forms. Introduction in Europe, which was presumably realised with a few seeds and landraces, caused a consistent reduction of diversity (Shannon's diversity index equal to 1.260 and 0.833 for Mesoamerican and European landraces, respectively). Drift, selection and lack of relevant migration among European populations triggered a differentiation process from original gene pool which appears to be in progress.

CHARACTERISATION BY MORPHOLOGICAL AND MOLECULAR MARKERS OF POPULATIONS OF *RESEDA LUTEOLA* L. FROM PORTUGAL

Maria do Rosário Barroso[1], Carlos Ribeiro de Carvalho[2], Sandra Martins[2] and Valdemar Carnide[2]
[1]Direcção Regional de Agricultura de Trás-os-Montes, 5370-87 Carvalhais-MDL, Portugal; [2]Centro de Genética e Biotecnologia da UTAD, IBB, Universidade de Trás-os-Montes e Alto Douro, 5001-801, Vila Real, Portugal; (email: vcarnide@utad.pt)

Until the end of nineteenth century the textile were coloured with natural dyes. With the advent of synthetic dyes in the beginning of twentieth century the interest of textile industry for the natural dyes almost disappear. As the synthetic dyes are responsible for high pollution and as some of them show skin toxicity, the interest of textile industry in the natural dyes has increased not only in Europe but also in U.S.A. and in Japan. Weld, *Reseda luteola* L., is a dye plant that produces luteolin, a very stable yellow pigment used mainly for dyeing wool and silk. Once genetic resources can be better profited if they are well known, the characterisation by morphological characters, molecular markers and flavonoids content of Portuguese germplasm of weld was done. The aim of this study was to evaluate the genetic diversity within seven populations of weld from North inner of Portugal by morphological characters and two molecular markers (RAPD and ISSR). Morphological data showed significant differences ($P<0.05$) between populations for dry matter yield, height of the main stem, number of primary basal branches, number of no basal branches, height of last secondary branche, average height of secondary branches. ISSR markers showed a higher total heterozygocity and intra-populational heterozygocity then RAPD markers (0.1399 and 0.0197, 0.0863 and 0.0197 respectively). Cluster analysis was performed with the morphological characters and with the two molecular markers. The dendrogram for morphological characters shows a good relationship between the geographic origin and the clusters. Dendrograms derived with RAPD and ISSR showed some similarities. The clusters obtained with ISSR have a reasonable concordance with population's origin.

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GENETIC DIVERSITY IN CULTIVATED COMMON BEAN, BASED ON SEED COAT COLOUR

Jean-Pierre Baudoin[1], Nasya Tomlekova[2] and Svetla Sofkova-Bobcheva[2]
[1]Faculté Universitaire des Sciences Agronomiques de Gembloux, Gembloux, Belgique ; [2]Maritsa Vegetable Crops Research Institute, 4003 Plovdiv, Bulgaria; (email : tomlekovi@mail.bg)

Knowledge of genetic diversity patterns enhances the efficiency of germplasm conservation and improvement. Previous studies using phaseolin seed protein as a marker have revealed four groups (designated as T, Ca, C and S) among 189 Bulgarian cultivated common bean (*Phaseolus vulgaris* L.) accessions.

This study examined the organization of diversity for seed coat colour estimated according to the *Phaseolus* Descriptor List. In this study the relation between seed coat colour and the phaseolin types among the material is examined. The marker–based analysis using phaseolin as an initial classification criterion, followed by a corroborating analysis of morphological traits, suggested the existence of subgroups within each of the major Andean and Mesoamerican groups, with distinctive morphology. Morphological evaluation of gene bank accessions complemented with molecular data increased the resolving power of genetic diversity analyses. No strong correlation was established between seed colour and the two phaseolin types "T" and "S" of the breeding materials. Among the accessions with "C" phaseolin type those which possessed beige–brown colour predominated. White seed colour is characteristic for the "Ca" phaseolin type group.

GENETIC DIVERSITY OF WHEAT GERMPLASM USING ISSR MARKERS

Penelope J. Bebeli and Panayiotis J. Terzopoulos
Agricultural University of Athens, Department of Plant Breeding and Biometry, Iera Odos 75, Athens, Greece, 11855; (email: bebeli@aua.gr)

Using Inter-Simple Sequence Repeat (ISSR) method the genetic diversity of durum wheat landraces and cultivars was studied. Commercial bread wheat cultivars and wild wheat relatives were included. In a preliminary study, four ISSR primers were selected based on the quality and reliability of their amplification and the polymorphism they revealed. The ISSR primers yielded 131 amplified bands, 120 (91%) of which were polymorphic. The genetic similarity between all pairs of genotypes was calculated using Jaccard's coefficient. The genetic similarity values ranged from 0.03 to 0.8. Cluster analysis was carried out by UPGMA method. All the accessions were discriminated from each other. The present results show that ISSRs can be used efficiently for the differentiation of wheat genotypes.

UTILISATION OF PROTEIN GENETIC MARKERS FOR EVALUATION WHEAT AND BARLEY GENETIC RESOURCES

Jana Bradová and Světlana Sýkorová
Research Crop Institute, Drnovska 507, 161 06 Prague 6, Czech Republic; (email: bradova@vurv.cz)

Protein markers are an effective tool for characterization and identification genotypes. Their use is very important part of work with genetic resources. The data about these characters of genetic resources that are stored in collections manifold increase their worth. Wheat and barley varieties recommended by CISTA in the Czech Republic in 2005 were characterized by the electrophoretic methods of protein genetic markers for evaluation of their genetic structure. This information is important for breeding, seed production and trade. Identification of the evaluated varieties was verified according to specific electrophoretic composition of wheat gliadins, HMW glutenins and barley hordeins and barley esterases.

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VARIABILITY IN CUCURBITA POPULATIONS FROM NORTH PORTUGAL

Sandra Martins[1], Maria do Rosário Barroso[2], Valdemar Carnide[1]
[1]Centro de Genética e Biotecnologia da UTAD, IBB, Universidade de Trás-os-Montes e Alto Douro, 5001-801, Vila Real, Portugal; [2]Direcção Regional de Agricultura de Trás-os-Montes, 5370-87 Carvalhais-MDL, Portugal; (email: vcarnide@utad.pt)

Cucurbita genera includes 22 wild species and five cultivated (*C. pepo*, *C. maxima, C. moschata*, *C. ficifolia* and *C. argyrosperma*). The origin and early spread of *Cucurbita* species was the Americas. *C. pepo* is native in high elevations of Mexico and Northern Central America while *C. maxima* is native in the warm temperate areas of Uruguay and Argentina. *Cucurbita* species show a great morphological variability for several parameters. In North Portugal there are several *Cucurbita* species which are used both for human and animal consuming. Nevertheless, during the last decades the local varieties are being replaced by modern cultivars with the subsequent genetic erosion. The aim of the present study was to estimate genetic variability in Portuguese populations of *C. pepo* and *C. maxima* from North inner Portugal with RAPD markers. Fourteen populations from each species were evaluated by nine primers. The number of amplified fragments ranged from 200 to 462 with an average of 271. Number of polymorphic fragments ranged from 47 to 428 with an average of 169. Total heterozigocity was 0.1788 and intra-populational heterozigocity was 0.0594. The dendrogram obtained separate very well the two species of cucurbita.

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THE USE OF RAPD MARKERS FOR IDENTIFICATION OF CELERY CULTIVARS

Domblides Arthur, Domblides Elena and Kharchenko Victor
Russian Research Institute of Vegetable Breeding and Seed Production, Moscow district, Odintsovo region, p/o Lesnoy Gorodok 143080, Russia; (email: domblidesarthur@yahoo.com)

It has been well shown that RAPDs provide relatively quick and extremely useful information about genetic variation among large range of living organisms. Screening of celery cultivars with random primers is the way to avoid mistaking in distinguishing sometimes similar looking genotypes. Since rapidly increased demands require many quality cultivars, it is necessary to have definite information about genetic backgrounds.

For optimization of RAPD analysis 32 primers were tested. Five primers of them show distinct polymorphism between presented cultivars. The number of bands varies from 8 to 16. Suitable primers generated 47 markers and 18 of them were polymorphic. A similarity matrix was formed with use Jaccard’s coefficient. Group average method was employed to construct a dendrogram. With having used these set of primers the cultivars were grouped into three clusters according to three cultivated types, var. *dulce* (salad celery), var. *rapaceum* (turnip celery), var *secalinum* (cutting celery). The salad celery entries were close to plants of turnip celery with similarity 0.73 between them, where as the distance between genotypes of cutting celery, and turnip celery was 0.68. At the same time there was revealed the genetic variation within cultivars. Through only 12 cultivars have been analyzed the specific product amplified with OPX1 has been observed in the three presented cultivars of cutting celery. Doubtlessly RAPDs help to determine the genetic relationships between celery cultivars and give important information for celery breeding proposes.

MOLECULAR- PHYLOGENETIC STUDY OF THE GENUS *TRIFOLIUM*

Zofia Bulińska-Radomska[1], Jakub Dzienkiewicz[1] and Piotr Bednarek[2]
[1]National Centre for Plant Genetic Resources, [2]Department of Plant Biochemistry and Physiology, Plant Breeding and Acclimatization Institute, Radzików 05-870 Błonie, Poland; (e-mail: z.bulinska@ihar.edu.pl)

The phylogenetic study was focused on the putative ancestors of white clover (*Trifolium repens* L.). Phylogenetic relationships were inferred from genetic distance analyses based on amplified fragment length polymorphism (AFLP) markers. The AFLP method proved to be a powerful tool to resolve the complex genetic relationships among closely related species and to investigate genetic diversity at the intra-specific level.

A total of 59 wild Trifolium populations belonging to *T. argutum*, *T. fragiferum*, *T. glomeratum*, *T. hybridum*, *T. isthmocarpum*, *T. montanum*, *T. nigrescens*, *T. nigrescens petrisavii*, *T. repens* and *T. uniflorum* species were the materials of this study. Four AFLP primer combinations were applied. Unweighted pair group method based on arithmetic average (UPGMA) was performed using Nei's similarity matrices. According to the expectation, populations of the same species were grouped together in the same clusters. Additionally, *T. repens* and *T. uniflorum* showed more close affinity, in relation to the remained species. The most separated cluster is represented by populations of *T. fragiferum*. The result confirm that the AFLP method is a useful tool in phylogenetic studies of closely related taxa.

MICROSATELLITE (SSR) POLYMORPHISM IN TUNISIA PERENNIAL RYEGRASS

Salma Ghariani, Nidhal Chtourou-Ghorbel, Mohamed Chakroun[1], Hanen Elazreg, Mohamed Marrakchi and Neila Trifi-Farah
Laboratoire de Génétique Moléculaire, Immunologie et Biotechnologie. Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar Tunis, Tunisie; [1]Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Rue Hédi Karray, 2049 Ariana, Tunisie; (email: neila.trifii@fst.rnu.tn)

In Northern Tunisia, perennial ryegrass (*Lolium perenne* L.) is one of the important forage grass species widely used as a turf grass and for soil conservation. Samples of five spontaneous populations are collected in the North of Tunisia ranging from the humid to the semiarid bioclimatic areas. Microsatellite polymorphisms in Tunisian perennial ryegrass are identified by using 6 specific SSR primer pairs. Results showed an alleles number ranged from 2 to 7. The polymorphic microsatellite loci are used to evaluate the intra- and inter genetic diversity level in the spontaneous populations. This study indicates that SSRs are sufficiently abundant and sufficiently polymorphic to discriminate the studied spontaneous populations and to detect useful genetic markers correlated to agronomic traits. These molecular markers can be employed to improve Tunisian perennial ryegrass germplasm.

THE USE OF MOLECULAR MARKERS FOR SELECTION OF GENETIC RESOURCES AND BREEDING CLONES FOR RESISTANCE TO DISEASES

Ján Heldák[1], Milan Bežo[2], Veronika Štefúnová[2], Kvetoslava Forišeková[1] and Andrea Galliková[1]
[1]PRBI - Potato Research and Breeding Institute s.c., Popradská 518, 05952 Veľká Lomnica, Slovak Republic; [2]Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic; (email: heldak@sinet.sk)

The applications of markers for selection genetic resources, introgression breeding and marker assisted selection of potato play a dominant role in research activities of many institutes. It is expected that demands for the crops with better traits will be getting stronger with intensity of climate changes.

Within the last decade only a small progress has been registered in research of quantitative traits with strong associations to environment like yield, tuber size, tuber shape, cooking quality, glycoalcaloid content and tuber defects. Better results were achieved in the field of qualitative traits, mainly resistance to pathogens and pests but still did not reach the level of the other agricultural crops. Selection of resistant genetic resources and breeding materials is hampered by the fact that evaluation of resistance to pathogens is time consuming, costly and in some cases inconsistent. DNA-based markers diagnostic for resistance to pathogens would facilitate to effectively select genetic resources and breeding clones of potato.

Wild Solanum species have been widely used in breeding programs mainly in breeding for resistance to diseases and pests. Many of gene pools and varieties possess resistances derived from *Solanum tuberosum* subsp. *andigena*, *Solanum stoloniferum*, *Solanum demissum*, *Solanum sparsipilum* and others wild species. There were found several DNA markers that were validated and used for selection of experimental resistant materials and can be applied for marker assisted selection. The genes Ry_{adg} and $Ry\text{-}f_{sto}$ control extreme resistance to PVY and can be reliably detected by the markers RYSC3 and $GP122_{718}$ respectively. It was found that the marker $SC811_{260}$ is linked to *Ns* gene conferring resistance to potato virus S (PVS) and can be used for selection of resistant genotypes. Detection of resistance to potato cyst nematode *Glodobera pallida* by several molecular markers is used in many breeding programmes. The markers developed for detection of resistance to the other pathogens are validated at different genetic resources.

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PATHOGENES AS A SOURCE OF POSSIBLE NEW RESISTANCE GENES

Elena Hlinková[1], Milan Bobák[2], Vladena Hlinková[3] and Ján Rafay[4]
[1]Department of Genetics, Faculty of Natural Sciences, Comenius University, Mlynská dolina B-1, Sk-84215 Bratislava, Slovakia; [2]Department of Plant Physiology, Faculty of Natural Sciences, Mlynská dolina B-2, 84215 Bratislava; [3]Institute of Molecular Biology SAS, Dubravská cesta 21, 845 51 Bratislava; [4]Research Institute of Animal Production, Hlohovecká cesta 2, 949 92 Nitra

Powdery mildew (*Blumeria graminis* (DC) Speer f.sp. hordei) is an obligatory ectoparasite fungus from class *Ascomycetes* and family *Erysiphaleae* that exclusively attacks epidermal leaf tissue of its host –barley. This fungus with high plasticity of its genome is characteristic with presence a large amount of none and specific genes enabled interactions with the host plants. Obtained biochemical results (Hlinkova et al. 2005, Freiaidenhoven et al. 1994) indicated that a resistance response is an active complex of coordinate processes of the infected barley leaves. Different resistance genes of the host barley plants trigger specific as well non specific defense pathways. Plasticity of powdery mildew genome showed that conservative defense of barley plants with fungicide preparations are effective only limited period and have be used more complex compounds or higher concentrations. As a new model can be used selected genes of powdery mildew as a source of new resistance genes for the barley.

We analyzed four pathotype of powdery mildew (RU-3; Sk-5/11; Sk-12/1; A-4/0 cached in various Middle European regions) with different virulence and avirulence genes on genetic and biochemical level. Protein analysis confirmed genetic differences between studied powdery mildew pathotypes. Abundant acid glucanases were found between 35-25kDa, 22-15kDa. Pathotypes RU-3 and A-4/0 contained low molecular glucanases between Mr≈12-9kDa. Probably low molecular glucanase act first hours by host plant occupation and by compatible interactions destroying micellar structure of cell walls. Pathogen chitinases as a next type of hydrolytic enzymes are more specific to the host. Slot-blot imunoblots with partially specific antibody prepared to the extracellular acid plant Chi14.4 were positive only for two powdery mildew races (Sk-5/11 and A-4/0) what indicated on the fact that chitinases are immunological more specific among race of fungi than to host plants of barley where are orthological genes presence. Both these pathotypes were more aggressive compared to Sk-12/1 and contained in their genome more virulence genes. Obtained results indicated that some powdery mildew pathotypes contained in their genome orthological genes to their host plants what make them suitable subjects to deepest molecular and genetic analysis as the source of new genes.

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SURVEY OF INTER SIMPLE SEQUENCE REPEAT POLYMORPHISM IN TUNISIAN TALL FESCUE (*FESTUCA ARUNDINACEA* SCHREB.)

Nidhal Chtourou-Ghorbel, Salma Ghariani, Mohamed Chakroun[1], Hanen Elazreg, Mohamed Marrakchi and Neila Trifi-Farah
Laboratoire de Génétique Moléculaire, Immunologie et Biotechnologie. Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar Tunis, Tunisie; [1]Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Rue Hédi Karray, 2049 Ariana, Tunisie; (email: neila.trifii@fst.rnu.tn)

In Tunisia, local phytogenetic resources have been currently damaged by severe genetic erosion. Among spontaneous crops that are reliable to promote pastoral lands, *Festuca arundinacea* is of a great agronomic interest. This species, growing from the humid to the semiarid bioclimatic areas, is an important high yielding cool-season forage grass.

In order to evaluate the genetic diversity in Tunisian tall fescue, the inter simple sequence repeats method (ISSR) was exploited in five spontaneous populations collected from different geographic areas of Northern Tunisia. Using appropriate primers complementary to simple sequence repeats (SSR), a large number of polymorphic DNA fragments was generated. These molecular markers were used to estimate genetic diversity among and within populations. Our data provide evidence of high molecular polymorphism at the intra- and inter-specific levels showing that the Tunisian tall fescue germplasm constitute an important pool of diversity.

DEVELOPMENT OF THE INFORMATION SYSTEM FOR LATVIAN TREE SPECIES GENETIC RESOURCES

Gunars Lacis and Edite Kaufmane
Latvia State Institute of Fruit-Growing, Graudu - 1, Dobele, LV 3701, Latvia; (email: gunars.lacis@lvai.lv)

Tree species form a very important part of plant genetic resources. Remarkable number of accessions, high interest for local breeding programs (1309 accessions of fruit crops) and high economical importance of forest trees species makes this group of plant genetic resources a substantial part of Latvia PGR program. Maintenance of tree species genetic resources related with high variety of methods: field collections, seed gene banks, in situ etc., wherewith many maintenance locations, institutes, diversity of owners and users. This cause problem of the coordination of genetic resources policy development, common maintenance and research management and information exchange.

Therefore it is useful to develop a virtual focal point to solve these difficulties. Such information system will ensure data accumulation among institutes in common format, information exchange with other national and international genetic resources systems. The development of information system for tree species genetic resources in Latvia was started in 2006, in the Latvia State Institute of Fruit-Growing in cooperation with Latvian Forestry Research Institute "Silava" and Riga Technical University.

Planned information system will ensure integrated, systematized maintenance of Latvia tree species genetic resource maintenance, environmental, characterisation and evaluation and research information for further web based viewing, searching and analysing. Information system will be based on SQL type data base and data warehouse and data marts technologies. Introduction of these approaches allow realising On-line Transaction Processing and On-line Analytical Processing systems, which help users to analyse data in different ways. Common data platform and analysis capability allow built up more close connections between institutions and give common view on tree species genetic resources in Latvia for sustainable maintenance and use.

EVALUATION OF MELON (*CUCUMIS MELO* L.) GENETIC RESOURCES IN LATVIA

Līga Lepse[1], Andris Bāliņš[2], Ilze Veinberga[3] and Dainis Ruņģis[3]
[1]Pūre Horticultural Research Centre, Abavas iela 2, Pūre, Tukuma raj., LV-3124, Latvia; [2]Latvia University of Agriculture, Lielā iela 2, Jelgava, LV -3001, Latvia; [3]Genetic Resource Centre, LVMI „Silava“, Rigas iela 111, Salaspils, LV-2169, Latvia; (email: liga.lepse@puresdis.lv)

Latvia is at the northern boundary of melon (*Cucumis melo* L.) growing in open-field conditions. The first local varieties were bred at the beginning of the 20th century using Russian and Western European varieties. These varieties vere well adopted for Latvian climatical conditions. High tolerance to low temperature and resistance to different pathogens were the main characteristics of Latvia melons. Taste of these varities was characterised as good. In the following years seed production was performed in insufficient quality and therefore genotypes were destroyed because of cross-pollinating of different varieties. Homogenisation and dividing of the local melon population into distinctive lines was started in 2003 at Pūre Horticultural Research Station with the aim to derive homogeneous lines of excellent taste and rich aroma, early ripening and high resistance to pathogens. In 2006, five of the most promising inbredlines and siblines of the 3rd generation were investigated according to phenology, morphological features and organoleptical evaluation.

Molecular markers (SSRs) were used to gentically fingerprint melon lines acquired from the local population and Europe varieties. Fifteen SSR markers were tested, of which ten detected polymorphism between lines. Using these ten polymorphic markers, all tested lines could be distinguished from each other. The polymorphism information content (PIC) values ranges from 0.13-0.83, (av. 0.59). Further work will involve extending the fingerprinting to further Latvian melon lines, and also assesing the extent of intra-varietal variation.

MOLECULAR AND PHENOTYPIC DIVERSITY OF COMMON BEAN LANDRACES FROM SOUTHERN ITALY, BASILICATA

Masi P.[1], Logozzo G.[1], Donini P.[2] and Spagnoletti Zeuli P.L.[1]
[1]Dipartimento di Biologia, Difesa e Biotecnologie Agro-Forestali, Università degli Studi della Basilicata, viale dell'Ateneo Lucano, 10 – 85100 Potenza, Italy; [2]National Institute of Agricultural Botany (NIAB), Huntingdon Road, Cambridge, CB3 0LE, UK; (email: giuseppina.logozzo@unibas.it)

The knowledge and understanding of the genetic structure of bean (Phaseolus vulgaris L.) landraces is important for the implementation of measure addressed to their management and conservation. In this study three landraces, ‘Marrozzo’, ‘Poverella’ and ‘Verdolino’, that are grown by farmer in Basilicata, locally and widely distributed in different agroecological areas and with diverse growth habit were genotyped. The amount and distribution of genetic variation within landraces was assessed at the DNA level with 29 gene-based microsatellite in 7 multiplex assay and 8 AFLP primer combinations markers. All together 73 individuals were genotyped. 16 phenotypic traits were also measured. Passport data and field data were included in this analysis. Data collected were analyzed by means of multivariate techniques.

A significant genetic differentiation among the three landraces was found both for molecular and phenotypic markers.

27 SSR loci were polymorphic with an average of 3.79 alleles per locus. 48 alleles were unique to individual landraces. The gene diversity within populations averaged over all loci was 0.45. ‘Marrozzo’ indeterminate growth habit and largely distributed did show the highest value of alleles and expected heterozygosity (n_o=2.79, He=0.36). AFLP analysis, revealed 393 bands with 99% polymorphic with rare allele frequencies higher than 5%. ‘Poverella’ was the landrace with the highest number of polymorphic bands (58%) and He (0.20). The total gene diversity (Ht) was 0.49 and genetic differentiation among populations 0.35. Fst=0.72 was significant too. Results showed that each population is easily distinguishable and heterogeneous as a result of farm fragmentation and adaptation to environmental conditions that may be adopted as criteria to select sites and populations for in situ/on farm conservation.

CYTOGENETIC AND MOLECULAR DIVERSITY OF POMEGRANATE (*PUNICA GRANATUM* L.) CULTIVARS

Masoud Sheidai
Biology Department, Shahid Beheshti University, Tehran, Iran

Cytogenetic and RAPD markers studies were performed on about 40 Iranian pomegranate (*Punica granatum* L.) cultivars considering the polyploidy level, chiasma frequency and distribution, chromosome association and segregation, occurrence and effects of B-chromosomes and cytogenetical mechanisms of unreduced (2n) gametes. All cultivars possessed n = 8 = 2x chromosome number mainly formed bivalents in metaphase but in a few of them quadrivalents were formed due to the occurrence of translocation mainly between the longest chromosome pair of the genome and one of the small chromosome pairs. The cultivars studied differed significantly in their cytogenetical characters indicating their genomic difference. B-chromosome (0-6) occurred in some of the cultivars. They were much smaller than the A-chromosome and did not pair with them. The effects of Bs on chiasma frequency and distribution varied in different cultivars and was related to the genotypic background of the cultivar. In some of the cultivars unreduced (potential 2n) meiocytes and pollen grains were formed due to cytogenetical abnormalities such as multipolar cell formation and cytomixis. Details of such cytogenetic phenomena will be discussed. RAPD analysis revealed the presence of diversity among the cultivars studied. Percentage of molecular variation was determined and the most variable RAPD markers were identified by principal components analysis. Clustering and PCO grouping of the cultivars were based on molecular diversity, compared with cytogenetical results. The results obtained may be used for planning the selection and hybridization of pomegranate cultivars.

POLYMORPHISM OF MICROSATELLITES IN GENETIC RESOURCES OF SPRING BARLEY WITH DIFFERENTIAL TOLERANCE TO *RHYNCHOSPORIUM SECALIS*

Hana Nevimová and Jan Bednář
Department of Plant Biology, Mendel University of Agriculture and Forestry in Brno, Zemědělská 1, CZ-613 00, Brno, Czech Republic, (email: xnevimov@node.mendelu.cz)

For the study of polymorphism of microsatellites in genetic resources of spring barley 15 genotypes was chosen with differential tolerance to *Rhynchosporium secalis* from collection of gene resources Agricultural Research Institute Kroměříž Ltd. – Abyssinian, Atlas, Atlas 46, Atlas 57, Bay, Cambrinus, Clipper, Jet, Kitchin, Kompakt, Korál, La Mesita, Nigrinudum Abyssinum, Psaknon a Rapid. We tested 70 microsatellite markers, which are localized mainly at 1H, 3H, 4H and 7H chromosomes in spring barley, where are numerous genes of resistance to leaf disease *Rhynchosporium secalis*. The products of PCR were separated on vertical electrophoresis at 300 V on polyacrylamide gel in TBE buffer and then they were coloured by silver ($AgNO_3$). These obtained gels were converted into the form of a binary matrix and they were statistically elaborated by the computer programme FreeTree with using the conformity coefficient Jaccard. From these results dendrogram was configured. The dendrogram characterizes genetic affinity of the tested spring barley genotypes. The low genetic variability was confirmed at genotypes Atlas, Atlas 46 and Atlas 57. The high relationship was detected at genotypes Jet and Nigrinudum Abyssinum.

PROLAMINS *VS* TECHNOLOGICAL PROPERTIES OF COMMON WHEAT INTROGRESSION LINES WITH LEAF RUST RESISTANCE FROM *TRITICUM TIMOPHEEVII ZHUK*

Ludmila V. Obukhova and Ekaterina B. Budashkina
Institute of Cytology and Genetics, Russian Academy of Sciences, Siberian Division, Novosibirsk; (email: entin@isp.nsc.ru)

Triticum timopheevii Z. (Tt) is the most immune wheat species, which is used in breeding programs of common wheat (*Triticum aestivum* L.). It has been involved in raising new wheat cultivars and so-called secondary donors of disease resistance. In particular, E.B. Budashkina and N.P. Kalinina (1998, 2001) developed a collection of introgression *T. aestivum* lines bearing the leaf rust resistance character from Tt. This collection is stored at the Institute of Cytology and Genetics (Russia) and partly in Gatersleben Gene Bank (Germany). It is under comprehensive study.

Here we investigate the major storage proteins (gliadins and glutenins) in these introgression lines (11 lines raised from 5 commercial cultivars), compare them with the parents, and describe Tt-related products. Study of storage proteins in individual grains from different plants revealed polymorphism in lines. One kind of polymorphism is inherited from polymorphic parental cultivars (Saratovskaya 29, Novosibirskaya 67, and Irtyshanka 10). Another kind of polymorphism in lines 67 and 175 appears to be related to the polymorphism for ω gliadins in Tt. The third kind of polymorphism, observed in lines 67 and 175, is related to different introgressions of gene material from Tt. All lines inherited the HMW glutenin pattern from their parental cultivars. It is likely that the low gene density in the long arms of chromosome group 1 prevents the Glu-1 locus from introgression [Y. Q. Gu *et al.* (2004)]. This factor is favorable for the BMQ of introgression lines. An impairment of BMQ in comparison with the parental cultivars is expected only in lines 67 and 175 because on the increasing amount of S-poor ω gliadins. Lines 676, 732, 821, 832, 837 and 140 show no introgression products.

Line 175 is the result of substitution of chromosome arms $1AS/1A^{t}S$ (supposedly) and two homological recombinations in chromosomes 1 and 6 involving two linked loci (Gli-B1/Gli-G1 and Glu-B3/Glu-G3) and individual genes rather than whole loci (Gli-B2 and Gli-G2). Line 67 is the result of homological recombination at the level of two linked loci Gli-B1/Gli-G1 and Glu-B3/Glu-G3 and at the level of individual genes of the Gli-G2 locus. Lines 191 and 206 show a homological recombination between individual genes within the Gli-2 locus. Neither of the studied lines shows products absent from the parental accessions, which is indicative of simple mechanisms of formation of new cytologically stable hexaploid wheat accessions characterized by these traits. According to our data on bread-making indices of grain and flour (Obukhova *et al*, in press), all lines studied meet the requirements no worse than "valuable", except for lines 191 and 206, whose grain texture is too soft. Lines 821, 676, 140, and 67 correspond to strong wheats according to all studied indices. The information on grain quality obtained in the study should be taken into account in planning breeding programs with the use of those lines as donors of leaf rust resistance.

EFFECT OF *IN SITU* CONSERVATION ON ALLELIC FREQUENCIES IN RYE

Olinda Pinto-Carnide[1], Manuela Matos[1], César Benito[2] and Valdemar Carnide[1]
[1]Genetics and Biotechnology Centre-IBB, University of Trás-os-Montes and Alto Douro, Ap. 1013, 5001-801 Vila Real, Portugal; [2]Department of Genetics, Biology Faculty, Complutense University, 28040-Madrid, Spain; [3]Plant Portuguese Gene Bank, S. Pedro de Merelim, 4700 Braga, Portugal; (email: olindac@utad.pt)

In the North Region of Portugal, there is a great variability of local rye populations. This variability is a very precious source of genes that doesn't exist in other places, where the varieties keep an outstanding position in the agricultural system, but induced a dramatic genetic loss of variability. The good characteristics of regional ryes, namely the good adaptation to a low fertility soils, tolerance to acid soils, etc., imply their maintenance for a long period in the regional agricultural system. The decreasing of cereal production and the introduction of new varieties give rise to regional varieties elimination. So, collecting and conservation of these populations in germplasm banks must be done in order to avoid the genetic erosion.

The Genetics and Biotechnology Department and the Plant Portuguese Gene Bank (BPGV) started a rye germplasm collection several years ago. Small farmers are yet grown some of these populations.

With the aim to analyse the evolution of regional rye populations during the last twenty five years, two molecular markers (SSR and ISSR) were used. The DNA fingerprints were compared in order to detect differences/similarities between germplasm from two different periods. This markers revealed a great number of alleles/*loci* and a high percentage of heterozigozity in all the populations. The selection effect and the importance of the maintenance of this germplasm will be analysed.

HORIZONTAL TRANSFER OF TRANSGENIC DNA

Pietro Perrino[1] and Ho Mae-Wan[2]
[1]CNR, Plant Genetic Institute - ex Germplasm Institute, via G. Amendola 165/A, 70126 Bari, Italy; [2]Institute of Science in Society, PO Box 32097, London NWI OXR, UK

It is often argued that transgenic DNA, once incorporated into the transgenic organism, will be just as stable as the organism's own DNA. But direct and indirect evidence contradict this supposition. Transgenic lines are notoriously unstable and often do not breed true. There are no molecular data documenting the structural stability of the transgenic DNA in either GM crops or GM animals in successive generations, both in terms of its site of insertion in the host genome and its arrangement of genes (genetic map). Instead, secondary mobility and rearrangements often occur, along with silencing of the transgenes, so that they are no longer expressed. There are several evidences showing that transgenic DNA is different from natural DNA and that it may be more likely to undergo horizontal gene transfer, a process that's responsible for potentially the greatest hazards from genetic engineering. Most of the findings are based on experiments not designed to address questions directly, so most of the evidences are more indirect, though there are also more direct evidences. Evidences of why transgenic DNA may be more prone to horizontal gene transfer and that it is different from natural DNA with examples that horizontal transfer can occur will be provided.

DEVELOPMENT OF THE MULTIMEDIA WEB-BACKED GENETIC DATABASE FOR UKRAINIAN, RUSSIAN AND MOLDAVIAN GERMPLASM VITIS VINIFERA USING MICROSATELLITE MARKERS

Valentina Risovanna[1], Francois Lefort[2], Svitlana Gorislavets[1] and Leonid Troshin[3]
[1]National Institute of Vine and Wine Magarach, 31 Kirov St. 98600 Yalta, Crimea, Ukraine; [2]Laboratory of Biotechnology and Applied Genetics, Ecole d'Ingénieurs de Lullier, Haute Ecole Spécialisée de Suisse Occidentale, 150, route de Presinge, 1254 Jussy, Switzerland; [3]Viticulture Department, Kuban State University of Agriculture, 350044 Krasnodar, Kuban, Russia; (email: vrisovan@rambler.ru)

For identification of cultivars and ordering of the information about them at the international level modern information technologies in a combination with the molecular-genetic characteristics of cultivars as databases, accessible by Internet recently are used. To such bases concerns Europe Vitis database (http://www.genres.de/eccdb/vitis/) and Greek Vitis database (http://www.biology.uch.gr/gvd).

Genetic resources of a grapevine in the area of the ISC countries may account for more than 6000 accessions. The information on them is scaterred between different sources and different ampelographic collections or is accessible only in Russian, Ukrainian and other languages through electronic diskettes or compact discs. The 52 Crimean and 27 Moldavian cultivars, included in this study, are conserved in the ampelographic collection of the National Institute of Wine and Vines Magarach in Yalta, Crimea, Ukraine and represent a major part of the grapevine genetic resources from these provenances. Crimean cultivars are cultivars from the region of Crimea and not from other regions of Ukraine. The 24 Russian cultivars, are conserved in the ampelographic collection of Russia, located at the University of Agriculture of the Kuban state in Krasnodar. Cultivars were selected as being potentially the most ancient cultivars cultivated in these regions, without prejudice of their native or foreign origin, since it could be likely for historical reasons that some Greek, Turkish or Caucasian cultivars would have been transmitted to these regions.

The basic components of a database - an information database (names, synonyms, history, known pedigrees, cultivar characteristics etc.); an ampelographic database (image database of a young shoot, a mature leaf and a cluster); a nuclear microsatellite profiles database (genetic identity database). Genetic profiling of these cultivars was carried out with 9 nuclear microsatellite loci previously characterized: VVS2, ssrVrZAG21, ssrVrZAG47, ssrVrZAG62, ssrVrZAG 64, ssrVrZAG79, ssrVrZAG83, ssrVvUCH11 and ssrVvUCH29. Microsatellites are used as marker because they display a high polymorphism, are ubiquitous throughout the genome and find out high stability at comparison of the data of different European laboratories.

COMPARATIVE ANALYSIS OF TUNISIAN FIG CULTIVARS AS INFERRED BY MOLECULAR MARKERS

Salhi-Hannachi Amel[1], Olfa Saddoud [1], Baraket Ghada [1], Khaled Chatti [1], Messaoud Mars [2], Mohamed Marrakchi [1] and Mokhtar Trifi [1]

[1]Laboratoire de Génétique Moléculaire, Immunologie & biotechnologie, Faculté des Sciences de Tunis, Campus Universitaire, 2092 El Manar Tunis, Tunisie; [2]Institut Supérieur Agronomique de Chott Mariem, 4042 Chott Mariem, Tunisie; (email: hsalhi@eudoramail.com; Amel.SalhiHannachi@fsb.rnu.tn)

Tunisian fig resources are threatened by severe genetic erosion due to biotic and abiotic stresses. Therefore, the establishment of a strategy aimed at the evaluation and the preservation of these important phytogenetic resources, has become imperative. For this purpose, molecular markers (RAPDs, ISSRs, SSRs…) have been evidenced to assess genetic diversity and its distribution. The objective of this analysis was also to examine the ability of these markers to discriminate among genotypes for certification of plant material identities and to resolve consequently problems of synonymy and homonymy. Data exhibited a relatively high level of polymorphisms among the considered varieties. However, this diversity was lower at the inter-collection level. This could be attributed to the dioecious nature of this crop and its reproduction system. The absence of significantly divergent genotypes' clusters suggests a narrow genetic base among cultivated figs despite their pomological and morphological distinctiveness. As a result the genetic diversity is typically continuous and the cultivars tested are clustered independently from the geographic origin and from the sex of trees. In addition, taking advantages of the identified microsatellites alleles, it was made possible to establish ecotypes' identification key. Our data provided molecular markers useful as descriptors and in the true to typeness fig material. Results are discussed in relation with a sustainable management of the local germplasm and to promote its valorisation and conservation for a durable use.

DEVELOPMENT OF RETROTRANSPOSON-BASED MARKER SYSTEM FOR GENETIC DIVERSITY CHARACTERIZATION OF FLAX (*LINUM USSITATISSIMUM* L.) AGRITEC LTD. GERMPLASM

Petr Smýkal[1], Ruslan Kalendar[2] and Martin Pavelek[3]

[1]Agritec Plant Research Ltd., Plant Biotechnology Department, Zemědělská 2520/16, CZ-787 01 Šumperk, Czech Republic; [2]MTT/BI Plant Genomics Laboratory, Institute of Biotechnology, University of Helsinki, FIN-00014 Helsinki, Finland; [3]Agritec Plant Research Ltd., Department of Technical Crops, Zemědělská 2520/16, CZ-787 01 Šumperk, Czech Republic

Although flax is traditionally grown for high quality fibre and oil, it has a high potential for cultivation under less favourable conditions in low input ecological farming systems. Flax breeding so that the crop can reach its potential as a health- and environmentally friendly crop requires an effective marker system to tag disease resistance and analyse germplasm genetic diversity for efficient marker-assisted selection. There is no currently available DNA-based marker system for achieving these ends. The goal of the fellowship is to develop retrotransposon-based molecular markers from flax retrotransposons. The flax genome is currently very little investigated, and consequently no good DNA marker system exists which would allow efficient germplasm characterization and disease resistence marker breeding.

The goal of this study was to develop a molecular marker system for *Linum* based on retrotransposons and used it to germplasm diversity evaluation and flax core collection development. The first step was to exploit conserved domains such as RNase H and especially PBS sites, within the retrotransposon, to PCR amplify and isolate retrotransposon ends. In this step we have sequenced 85 clones in total length of over 100.000 bp. Subsequent cluster analysis has identified 27 different retrotransposon fragments corresponding to LTR ends.

Based on this analysis, 75 PCR primers were designed and tested in IRAP (Inter Retrotransposon Amplified Polymorphism) protocol.In this second step, 75 outward-facing primers designed to match the LTRs of the various elements identified in the first step were screened against a small set of germplasm accessions (10) representing the diversity of the germplasm as a whole. We have identified 27 primers that displayed clear banding patterns and useful levels of polymorphism, yielding multiloci fingerprint. 23 primers have produced low multiloci pattern, but can be further combined. Next, REMAP (Retrotransposone – Microsatellite Amplified Polymorphism) protocol was applied, based on combination of one retrotransposon and second microsatellite repeat primers. In this scheme combinations of 50 retrotransposon versus 8 microsatellite primers were tested. All, but 10 combinations produced scorable multiloci pattern, different from simple IRAP. The data will be presented for selected set of 50 geographically diverse common flax varieties as well as 10 wild *Linum* species.

In summary, use of 3 to 4 single primer IRAP protocol have potential fully discriminate and identify tested set of 50 flax varieties. Based on primer used, 15 to 30 (100 to 3500 bp) PCR amplified fragments can be visualized, of which 5 to 25% was polymorphic eg. informative. All these results are used in further work aiming at core collection development from current over 2.000 accessions of flax collection hold at Agritec Ltd.

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MICROSATELLITE MARKERS VARIATION IN ARTICHOKE AND RELATED TAXA

Gabriella Sonnante, Anna Vittoria Carluccio and Domenico Pignone
Institute of Plant Genetics (IGV), CNR, Via Amendola, 165/A, 70126 Bari

Artichoke, *Cynara cardunculus* L. var. *scolymus* (L.) Fiori is a diploid outcrossing species, originated in the Mediterranean basin, which has been much appreciated both for its tasty heads and pharmaceutical properties since ancient times. The cultivated and wild cardoon, and artichoke belong to the same species and are freely interfertile.

In Italy, some artichoke varieties are cultivated on a large scale, while a high number of landraces is grown on a small scale. Cultivated cardoon is mainly diffused in northern Italy, southern France and Spain. The wild cardoon grows in the Mediterranean Basin, and in Italy is present in central and southern regions.

Microsatellite (SSR) markers consist of tandem repeats of di-, tri- or tetra-nucleotide patterns, are frequent and usually well distributed in plant genomes, and can be exploited to develop locus-specific codominant markers, useful for assessing genetic diversity and mapping. Only a few of these markers have been developed to date in artichoke. We could identify 24 new SSRs present in the artichoke genome, using different approaches. Primers were designed on the flanking regions of these sequences, and fragments comprised between 150 and 400 bp were amplified. The presence of allele variants was ascertained in a set of artichoke accessions representative of genetic variation and geographical origin, in some samples of cultivated cardoons from Italy and Spain, of wild cardoons from Italy, Spain, and Greece, and in four wild *Cynara* allies.

Out of the 24 SSRs identified, 22 were polymorphic, while the remaining two were monomorphic. For some of them, a high number of alleles was observed, and in some cases the frequency of the different alleles was related to artichoke morpho-agronomic traits. Private alleles were found for cultivated and wild cardoons, respectively and a relationship with geographical origin was observed.

UTILIZATION OF PROTEIN AND ENZYME GENETIC MARKERS FOR THE CHARACTERIZATION OF GENETIC RESOURCES OF POTATOES

Světlana Sýkorová, Eva Matějová and Jana Bradová
Reserach Crop Institute, Drnovska 507, 161 06 Prague 6, Czech Republic, (email: sykorova@vurv.cz)

The examination of electrophoretic profiles of soluble tuber proteins, which are highly polymorphic and stable, can be considered as valuable for variety characterization and identification. The modified PAGE methods (TRIS – Glycine buffer pH 8.9 for patatins and peroxidases; TRIS – Boric Acid pH 7.9 for esterases) were used for the characterization of registered potato varieties. These methods enabled to identify each variety from the examined variety set. The varieties – calibrators recommended by UPOV were used as a tool of genetic interpretation of the electrophoretic patterns. The calculation of identity indexes (proportion of common bands) helped to evaluate the similarity of varieties.

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MATING PATTERNS IN PERENNIAL RYEGRASS: CONSEQUENCES FOR SEED REGENERATION

Robbert van Treuren[1] and Magdalena Ševčíková[2]
[1]Centre for Genetic Resources, the Netherlands, Wageningen University and Research Centre, P.O. Box 16, 6700 AA Wageningen, the Netherlands; [2]OSEVA PRO Ltd., Grassland Research Station, 75654 Zubří, Czech Republic; (email: sevcikova@oseva.cz)

Genebank accessions stored *ex situ* as seed populations require periodic rejuvenation in order to maintain sufficient numbers of viable seeds. During regeneration the genetic integrity of an accession may be compromised by various factors, including variation in pollination rates between plants. For a rejuvenated accession of *Lolium perenne* (L.), consisting of 49 parental plants, a paternity exclusion analysis was performed by means of molecular analysis. Investigation of a total of 551 offspring showed that mating within the study population was clearly non-random, as 61.9% of the identified pollen donors were located within 1m distance from the mother plant. Observed pollination rates were very well described by an inverse quadratic function of inter-plant distance between potential mating pairs. However, contamination was considered more threatening to the genetic integrity of the accession than variation in pollination rates between plants. Within the total sample 5 cases of pollen contamination and 4 cases of seed contamination were observed. This indicated the need for improved measures during the rejuvenation of perennial ryegrass germplasm in order to avoid gene flow between accessions.

DIVERSITY OF SEED STORAGE PROTEIN PATTERNS IN JOINTED GOATGRASS (*AEGILOPS CYLINDRICA* HOST) POPULATIONS FROM SLOVAKIA

Gábor Vörösváry[1], Edita Gregová[2], Pavol Hauptvogel[2], László Holly[1], Gábor Málnási Csizmadia[1], Tibor Baranec[3] and René Hauptvogel[2]
[1]Central Agricultural Office, Directorate of Plant Production and Horticulture, Research Centre for Agrobotany Tápiószele, Hungary; [2]SARC-Research Institute of Plant Production Piešťany, Piešťany, Slovak Republic; [3]Slovak University of Agriculture in Nitra, Nitra, Slovak Republic; (email: gaborv@agrobot.rcat.hu)

Variations in seed storage protein patterns for twelve *Aegilops cylindrica* populations collected in Slovakia within the framework of Hungarian-Slovakian Intergovernmental S and T Cooperation Programme in 2006 was investigated. The present study covered the populations of jointed goatgrass collected from the southwestern (Sereď, Dunajská Streda), southern (Chľaba, Kamenica nad Hronom) and southeastern (Čierna nad Tisou, Dobrá) parts of Slovakia. Seed storage protein patterns were analyzed using acid polyacrylamide gel electrophoresis (A-PAGE) method. Electrophoreogram peaks for each population were scored. Electrophoretic analysis has revealed appreciable polymorphism in the number of gliadin bands. The most variation in gliadin bands among the populations were observed from Dunajská Streda. Small differences were detected among the populations from Čierna nad Tisou, Dobra, Kamenica nad Hronom and Sereď. The lowest variations were detected in populations from Chlaba. The result from comparison with protein types of Hungarian populations reveal that protein type from Kamenica nad Hronom population contain similarity bands with Bokros 4 populations from Hungary. The present investigation showed that the jointed goatgrass populations collected from Slovakia exhibit valuable genetic resources for wheat crop improvement programs.

USING OF MOLECULAR MARKERS IN TRITICALE

Tomáš Vyhnánek and Jan Bednář
Department of Plant Biology, Mendel University of Agriculture and Forestry in Brno, Zemědělská 1, CZ-613 00, Brno, Czech Republic; (email: vyhnanek@mendelu.cz)

Genetic variability was detected in 15 varieties of triticale (X*Triticosecale* Wittmack., 2n = 6x = 42, BBAARR) registered in the Czech Republic from 1994 to 2004 by means of polymorphism of DNA using the RAPD method and the SSR method. For detection we used 80 RAPD primers. The lower reproducibility of the RAPD markers was resolved by means of repeated analyses (3–4 times). On the basis of statistical evaluation a dendrogram was set up, which allows high significant differentiation the varieties Kolor, Modus and Tornado. The remaining 12 analysed varieties formed 4 clusters. In addition to the RAPD markers a protocol of detection of DNA polymorphism was elaborated and optimised with microsatellite (SSR) markers. For the analyses we used 2 SSR markers (1A chromosome [*Xpsp2999*] and 1B chromosome [*Xpsp3000*]), which have been discovered in wheat (*T. aestivum* L.). Basing on these two SSR markers the only variety Triamant was distinguished from the clusters of the other analysed varieties. In our experiments better resolution of the varieties by the RAPD method was obtained than using SSR markers. The 72 polymorphic RAPD primers highly significantly differentiated 3 varieties while only one was differentiated by 2 SSR markers. The use of a higher number of SSR markers would probably increase the resolution and the results would be in favour of SSR markers similarly as reported by other authors.

POSTER PRESENTATIONS

Session 4

Plant genetic resources in context of climatic changes

WINTER WHEAT GENOTYPES SCREENING FOR CLIMATE CHANGE CONDITIONS BASED ON THE PHOTOSYNTHESIS PARAMETERS MEASUREMENT

Marián Brestič[1], Marek Živčák[1], Katarína Olšovská[1], Peter Ferus[1] and Pavol Hauptvogel[2]
[1]Slovak University of Agriculture in Nitra, Dept. of plant physiology, A. Hlinku 2, 949 76 Nitra, Slovak Republic; [2]SARC-Research Institute of Plant Production Piešťany, Bratislavská 122, 921 68 Piešťany, Slovak Republic; (email: Marian.Brestic@uniag.sk)

At the Dept. of plant physiology of the SAU Nitra which is an interdisciplinary workplace of photosynthesis and environmental stresses research a multifactorial phenomenon of climate change has been studied as well as plant adaptability to it. As plants within a canopy express a great variability of physiological processes in respect to their environmental conditions, the photosynthesis measurements may bring a promising and valuable contribution to the plant tolerance evaluation. We have specifically evaluated in our work the increased sensitiveness of wheat genotypes to environmental stresses by help of polyphasic kinetic curves of chlorophyll *a* fluorescence, parameters characterizing the plant photochemistry, energy dissipation into non-photochemical processes, spatial imaging chlorophyll fluorescence and simultaneous measurements of photosystem II and photosystem I activities. The winter wheat landraces were tested and the respresentative genotypes of world winter wheat sortiment from different proveniences as well. The results show the differences between the drought and high temperature effects on the photosynthesis mechanism. While the drought inhibits mainly the stomata-related photosynthetic processes, high temperature (around 38ºC and more) affects the primary processes of photosynthesis, such as inactive PSII reaction centers increase and thermal energy dissipation. We stress that the photosynthesis parameters are suitable for winter wheat parametrization under climate change conditions.

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XEROPHITIC PLANTS IN SLOVAK FLORA AS POTENTIAL GENETIC RESOURCES IN CONTEXT OF CLIMATIC CHANGES

Pavol Eliáš jun., Tibor Baranec and Ivan Ikrényi
Slovak University of Agriculture in Nitra, Department of Botany, Tr. A. Hlinku 2, SK-94976 Nitra, Slovak Republic

Global climatic changes, especially global warming presents real threat for cultivation of traditional crops in Central Europe. Native flora of this region offers many xerophilous taxa usable as genetic resources. These taxa can be exploited to breeding processes for improving recent races. A preliminary list of Slovak xero- and thermophites was made; it contains 696 plant taxa including native species, archaeophytes and some neophytes respectively. From the point of view of life plant forms 249 annual and biennal species, 368 hemikryptofytes, 42 fanerophytes and 37 geophytes are presented.

DETECTION OF GENETIC RESOURCES OF *TRIFOLIUM PRATENSE* WITH EFFECTIVE NODULATION ABILITY AT LOW PH AND HIGH N LEVEL IN THE SOIL

Natália Faragová and Juraj Faragó
[1]SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: faragova@vurv.sk)

Pot experiments were conducted to assess the N_2-fixation effectivity and nodulation ability of diploid and tetraploid cultivars of red clover (*Trifolium pratense* L.) in conditions of low pH and increased content of mineral N in the soil. Four types of soils were used as substrates for culturing plants, namely 1. neutral soil (pH=7) from the garden of RIPP Piešťany, 2. acidic soil supplemented with P, K, Mg, 3. acidic soil supplemented with P, K, Mg and 3.4 mol.m^{-3} N and

4. natural acidic soil (pH=3,8, from around Pribylina, SR).

In both sets of cultivars (20 diploid and 20 tetraploid cultivars, Gene Bank Piešťany, Slovak Republic) we observed a positive influence of inoculation of plants with a suspension of mixture of commercially available strains D659, D598 and D603 of *Rhizobium leguminosarum* bv. *trifolii*. The effect was most prominent in the diploid cultivar Vltavín, where the increase of dry weight (DW) of green matter in inoculated plants reached 80 % comparing with the non-inoculated control. Roots of inoculated plants had 10.5 % (in diploid cultivars) and 15.0 % (in tetraploid cultivars) higher DW than non-inoculated roots.

Addition of mineral N into acidic soil supplemented with P, K and Mg had significantly inhibitory effect on the average number of nodules on roots. The diploid cultivars formed 33 % and the tetraploid ones 25 % less nodules in comparison with numbers of nodules on roots of plants grown in acidic soil supplemented with P, K and Mg only. Contrary, in diploid cultivars Vignola, Pirat, Manuela and Rode Maasklaver, more nodules and green matter formed in conditions of higher N in acidic soil, than in the same soil without added N. This allows to detect genotypes of red clover with higher nodulation and production ability in conditions of high N and low soil pH.

The highest content of total N in stems and leaves was detected in diploid cultivars Bjursele, Rajah and Nike, and in tetraploid cultivars Grasslands G27 and Kolpo, respectively. The highest agronomic effectivity, measured as ratio of difference between DW of inoculated and non-inoculated variants to non-inoculated control, was found in the diploid cultivar Vltavín (80.4 %) and the tetraploid cultivar Grasslands G27 (71.8 %). Physiologigal effectivity increased in inoculated plats of cultivars Matrai and Grasslands G27 up to 13 632, resp. 10 662 mg of DW of green matter cumulated per unit of fixed N. Maximum N_2-fixation effectivity, calculated as a ratio of the increase of total N content in aboveground biomass of inoculated variant to total N content in non-inoculated variant, was observed in cultivar Vignola (36,8 %), in which we also detected a positive effect of inoculation on aboveground and root biomass as well.

A NEW METHOD FOR RAPID STRESS TOLERANCE EVALUATION OF CROP GENOTYPES

Peter Ferus, Marek Živčák, Jana Repková, Katarína Olšovská and Marián Brestič
Slovak University of Agriculture in Nitra, Department of Plant Physiology, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic; (email: marian.brestic@uniag.sk)

Developing climate change, intensive cultivation technologies and secondary effects of anthropogenic activities are the most important stress sources for crop plants. In spite of this, limited capacity of arable land makes us to utilize stress-laden areas, as well. Therefore we need to grow cultivars able to overcome or at least alleviate stress constraints to their growth and production. In this respect, photosyntesis is one of the most sensitive physiological processes in plants (limited at stomatal, enzymatic and electron transport level). Fortunatelly, leaves dispose of more protection mechanisms (accumulation of compatible solutes, thermal dissipation of excitation energy, photorespiration and antioxidative system), which help them to save the stability of photosynthetic processes.

Antioxidative system (AS) of plants represents a number of enzymatic end non-enzymatic elements participating in scavenging the reactive oxygen species. It is hardly to say which is the most important component of AS. Moreover, concentration or activity determination of some antioxidants do not provide a complex view of antioxidative defense. So, the most proper way how to match this goal is the total antioxidant activity (TAA) determination. More methods are available, but no one is so rapid, simple and infrastructurally little demanding as utilization of TAA determination kits. We tested the leaf TAA in winter wheat (*Triticum aestivum* L.) cultivars of different proveniences after experiencing environmental stress by use of Bioxytech AOP-490 (OxisResearch, USA) kit. The results were analysed in relation to photosyntem II stability.

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CAN CONTINUOUS NO TILLAGE APPLICATION POSITIVELY INFLUENCED SOIL COMMUNITIES?

Zuzana Lehocká and Marta Klimeková
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: lehocka@vurv.sk)

The soil microorganisms which determine the soil structure and its fertility, is an important factor for crop growth and productivity, therefore the soil has to be managed as such in agriculture to improve sustainability.

All management practices affect soil microbial communities. Proper management of numbers, diversity, and activity, both spatially and temporally, of various components of the soil biota will have a positive influence on soil ecosystem processes. Conservation farming is an alternative agricultural system, which could help avoid soil erosion and improve soil properties.

The aim of our research project was to detect whether perennial, continuous use of no tillage farming system will improve selected soil biological properties and will lead to the microbial population increase. This seven year study was carried out on degraded Chernozem on loess in a maize and barley growing region in south western Slovakia (near Piešťany) in Borovce. The no tillage and conventional farming systems were compared. The soil microbial biomass was determined in year 2003 and 2004 by the alcohol-free chloroform fumigation-K2SO4 extraction method (Vance et al., 1987). The number of cellulolytic bacteria was specified in mineral agar with filter paper. The earthworms were hand – sorted from soil pit (0.25 x 0.25 x 0.3 m) and earthworms' biomass was measured on the scale in the laboratory. The results were evaluated by a Distribution-Free Rank Sum Test. Higher values of all monitored biological soil indicators were in no tillage farming system. The difference in number of cellulolytic bacteria represented 15.6 % in favour of no tillage farming system. Statistically higher soil microbial biomass values were in no tillage farming system (789.5 g Cmic / g dry matter) than in conventional farming system (671.6 g Cmic / g dry matter). Our study has shown also the positive effect of no tillage farming system on the number of earthworms (76 % difference between the system), their biomass (82.4 % difference between the systems) and the average mass weight of single earthworm (54.0 % difference between the systems).

In conclusion the total microorganisms and earthworms population development was more intensive in no tillage farming system especially because of organic matter accumulation in surface soil layer.

SOIL MICROBIAL BIOMASS AND EARTHWORMS' POPULATION INFLUENCED BY THE DIFFERENT FARMING SYSTEMS

Zuzana Lehocká, Marta Klimeková and Štefan Žák
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic; (email: lehocka@vurv.sk)

The intensification and expansion of modern agriculture is ranked amongst the greatest current threats to worldwide biodiversity. Over the last quarter of the 20th century, dramatic declines in both range and abundance of many species associated with farmland have been reported in Europe. One explicit goal of sustainable farming systems such as organic farming is to preserve and develop biodiversity.

The microorganisms play a leading role in soil development and preservation. Since microorganisms respond rapidly to changing environmental conditions, they are considered as sensible indicators of soil health and this is why they can be usually used for soil status monitoring. On the basis of facts mentioned above the aim of our research project was to compare the effect of organic and conventional farming systems on soil microbial biomass (C_{mic}) and earthworms population.

This study was carried out on degraded Chernozem on loess in a maize and barley growing region in south western Slovakia (near Piešťany) in Borovce. The field experiment has been running since 1996. The organic system was incorporated a year later. Soil microbial biomass was determined in the years 2003 – 2004 by the alcohol-free chloroform fumigation-K_2SO_4 extraction method (Vance et al., 1987). The earthworms were hand – sorted from soil pit (0.25 x 0.25 x 0.3 m) and earthworms' biomass was measured on the scale in the laboratory. The results were evaluated by a Distribution-Free Rank Sum Test. Soil microbial biomass and earthworms' population were significantly affected by the climate conditions of each year. Higher soil microbial biomass values and number of earthworms were in year 2004, with more suitable precipitation conditions. During the spring samples there were higher values of soil microbial biomass and higher earthworms' population in comparison with autumn samples in both farming systems. The highest values of soil microbial biomass were in alfalfa (696.7 g C_{mic} / g dry matter), followed by pea (686.6 g C_{mic} / g dry matter) and winter wheat (684.3 g C_{mic} / g dry matter). In 2003, in 2004 and also on average higher values of soil microbial biomass were in the organic farming system and lower values were in the conventional farming system with the difference of 47.9 g C_{mic} / g dry matter. This study has shown that the number of earthworms, their biomass and the average mass weight of single earthworm were higher in the organic farming system than in the conventional farming system.

The conclusion so far is that organic farming has a positive effect on soil microbial biomass and earthworms' population. Our results support the hypothesis that diverse microorganisms' populations make better use of the available resources (the manured organic farming systems vs. the unmanured conventional farming system).

RESISTANCE – TOLERANCE TO AIRBORNE AND SOILBORNE PATHOGENS IN EUROPEAN DURUM WHEAT (*TRITICUM DURUM* DESF.)

Masár Štefan, Bojnanská Katarína, Gubiš Jozef and Pastirčák Martin
SARC-Research Institute of Plant Production Piešťany, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic

Resistance-tolerance to airborne and soilborne pathogens in thirty European durum wheat (*Triticum durum* Desf.) varieties was analyzed. Very resistant reaction to prevalent pathotypes of *Blumeria graminis* (DC) Speer f. sp. *tritici* Marchal was observed in the durum wheat varieties from Central European countries.

Mostly Mediterranean *Triticum durum* varieties showed satisfactory field resistance and low infection type reactions to large majority of *Puccinia recondita* Rob. ex Desm. f. sp. *Tritici* isolates.

Stagonospora nodorum resistance-tolerance in European durum wheat varieties was detected in field trials and in laboratory conditions by infecting the leaf segments with pathogen and using the molecular markers respectively. Durum wheat varieties above from South-European countries were very susceptible in field conditions and when artificially infected the heads by *Fusarium culmorum.* Some durum wheat varieties from Mediterranean area are suitable as possible donors of resistance to major part of commercially important fungi diseases.

CHARACTERISTICS OF TRITORDEUM (X *TRITORDEUM* ASCHERSON ET GRAEBNER) UNDER CENTRAL-EUROPEAN CLIMATIC CONDITIONS

Petr Martinek[1], Jarmila Mikulcová[1] and Ludmila Ohnoutková[2]
[1]Agrotest fyto, Ltd., Havlíčkova 2787, 767 01 Kroměříž, Czech Republic; 2)Institute of Experimental Botany v.v.i., Academy of Sciences of the Czech Republic, Sokolovská 6, 772 00 Olomouc, Czech Republic; (email: martinek@vukrom.cz)

The chromosome duplication of *Hordeum chilense* Roemer et Schultese (2n = 2x = 14; $H^{ch}H^{ch}$) and *Triticum durum* Desf. (2n = 4x = 28; AABB) crosses have led to the development of tritordeum (x *Tritordeum* Ascherson et Graebner), a novel hexaploid amphiploid (2n = 6x = 42; $H^{ch}H^{ch}$AABB) cereal crop. Tritordeum was first mentioned in 1977. It was developed in Spain using local spring wheats. Only spring forms have been developed until now. Based on published data, the highest-yielding lines produce 80% of spring wheat in Mediterranean Spain. Tritordeum sown in spring in the Czech Republic (CR) with the typical Central-European (CE) climatic conditions matured very late and non-uniformly because of a semiperennial character of original *H. chilense*. Yields of hexaploid tritordeum reached on average 28% of spring wheat check cultivars in the CR in 1999-2006. A mild course of the winter did not damage tritordeum sown in autumn and the vernalisation effect limited problems with late and non-uniform maturing of the heads. In case no visible injury was observed during the winter period, it yielded on average 40% in comparison with winter wheat check cultivars. If tritordeum were a winter crop exhibiting sufficient frost resistance, it would give much better results under CE conditions. The development of winter forms of tritordeum by means of (a) chromosome duplication of hybrids of *H. chilense* and winter *T. durum* (or *T. aestivum*) forms with high level of frost resistance, (b) backcrosses of selected winter frost resistant wheat cultivars (*T. aestivum*) with perspective hexaploid tritordeum lines is proposed. It is also evident that the development of double-haploid lines can partly limit problems with late and non-uniform maturing. In the exceptionally favourable year 2006, the best tritordeum double-haploid line yielded 51% of spring wheat. High protein content (16-22%) indicates potential perspective of this crop. Development of winter forms of tritordeum will provide preconditions for wider use of this crop. The study was supported by the project MSM 2532885901.

MONITORING AND ESTIMATION OF PLANT GENETIC RESOURCES IN ECOLOGICALLY DANGEROUS ZONES

Natiga A.Nabiyeva
Genetic Resources Institute of Azerbaijan National Academy of Sciences, Baku, Azerbaijan; (email: gen_eht@yahoo.com)

Lately increasing degree of antropogenic effects to the biosphere makes PGR be lost. So, situations like these should cause threat of increasing mutation process rate, gathering genetic loads at the plant populations and at the result losing PGR. All these required constant control on the plant viability process. To make early prognostications on threat PGR for Food and Agriculture and to take into account the importance of the control, monitoring on genetic durability condition of *T. aestivum L.* was carried in the regions (Gabala-Oghuz r.), where Radar Station is situated, that is considered very dangerous in our republic.

As known, the character and level of mutational activity of genetic system is a major adaptive indication of the system information on plant tolerance. Therefore, the monitoring of frequency and range of chromosomal aberrations in the root meristem is taken as the basis for the study. Conditions of metabolic protection in plant cells influence on the mutability of genome. As the key parameter, we use the criterially significant parameter of intensity of free radical processes in cells - the quantitative amount of products of malonic dialdehyde lipid peroxide oxidation (LPO) in leaves.

At the result of investigation it became clear the collected *T. aestivum L* accessions from the places which are rounded with high-frequency radar electromagnetic waves intensity of LPO and the level of spontaneous mutation is higher than the regions that are less radiation. It warns the negative influence of Radar Station to the plant genetic apparatus and cell membrane and these results with the genetic erosion in plant populations.

WATER RELATIONS AS A CRITERION TO SELECT WINTER WHEAT GENOTYPES FOR THEIR IMPROVED DROUGHT TOLERANCE

Katarína Olšovská, Marián Brestič, Marek Živčák, Jana Repková, Jana Ferencová and Elena Hunková
Slovak University of Agriculture in Nitra, Dept. of plant physiology, A. Hlinku 2, 949 76 Nitra, Slovak Republic; (email: Katarina.Olsovska@uniag.sk)

The ability of wheat genotypes to use water is crutial for maintaining the growth-production process under stress conditions. Among all the Central European countries including Slovakia, there is a need to pay attention to improved wheat drought tolerance. We discuss in our work reliability of water potential, osmotic adjustment, leaf diffusion resistance, cuticular transpiration and metabolic changes parameters measurements which may reflect different genotype provenances and different drought tolerance levels as related to their productivity. Special attention has been paid to expeditious measuring protocols of drought tolerance evaluation. The results show the higher osmotic adjustment, heterogenous stomata closure as well as leaf properties to regulate cuticular transpiration as very valuable wheat traits to look for more drought tolerant genotypes.

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ASSESSEMENT OF GENETIC VARIATION IN ETHIOPIAN DURUM WHEAT GERMPLASM BY SSR MARKERS

Enrico Porceddu, Anna Farina, Linda Mondini and Mario A. Pagnotta
Department of Agrobiology and Agrochemistry, University of Tuscia, via S. De Lellis 01100 Viterbo, Italy; (email: porceddu@unitus)

A collection of 234 genotypes belonging to nine populations of durum wheat from three Ethiopian regions (Tigray, Gonder and Shewa) was analysed by SSRs markers in order to detect: i) the genetic variation among and within regions, and among and within populations in a region, ii) the population structure, iii) the presence and frequency of rare or unique alleles was assessed in. The markers were randomly chosen on the graingenes databese to have 28 chromosome specific loci one for chromosome arm.

Results indicated a great variation among regions and both among and within populations, the presence of specific haplotypes and rare alleles. The number of alleles per locus ranged from 1 to 10. Genetic distance between populations indicated that the material from Tigray is far apart, whereas populations from Gonder and Shewa were rather mixed up. The expected heterozigosity over populations was, for most of the loci, around 0.5 indicating an equivalent distribution of the alleles in the populations; whereas the observed heterozygosity was on average 10%, indicating a significant level of outcrossing.

CLIMATIC DISTRIBUTION OF GENETIC TUNISIAN LOCAL BARLEY RESOURCES

Abdellaoui Raoudha[1,2], Rouaissi Mustapha[1], Ben Naceur M'barek[1] and Ben Hmida Jeannette[2]
[1]Institut National de la Recherche Agronomique de Tunisie. Rue Hédi Karray, 2049 Ariana, Laboratoire de Biotechnologie et Physiologie Végétale; [2]Faculté des Sciences de Tunis, Université EL Manar. Département de Biologie; (email: raoudhamabdellaoui@yahoo.com)

Fourteen Tunisian barley (*Hordeum vulgare* L.) ecotypes were collected from different bioclimatic stages. Morphological traits were studied and analyzed using principal components analysis (PCA) and clusters were constrained based on median joining distance. Genetic diversity was also studied using RAPD markers. Results of the morphological and molecular analysis showed a high degree of variation among analyzed ecotypes, indicating an important source of genetic diversity that can be used in future breeding programs. The morphological method grouped barley ecotypes according to climate conditions. However RAPD markers showed different groups that are more linked to genetic criteria such as ear attitude, length of glum and its awn relative to grain. They were not sufficient to detect traits highly affected by environmental conditions. Five groups were found; using morphological analysis; showing that 'Tozeur 2' and 'Kébilli 1', which are collected from south of Tunisia belong to the same group. The same remark is given for 'Kébilli 2' and 'Kébilli 3'. Also, we remark that 'Kalaâ', 'kélibia 1 and 2' which belong to the sub-humid climatic stage are included in the same group. Further more, 'Jendouba 1 and 2'; commenly cutivated in the humid inferior climate; are associated in a same group.

INVESTIGATION AND UTILISATION OF WINTER WHEAT GERMPLASM FROM DRY CLIMATE COUNTRIES

Vytautas Ruzgas and Zilvinas Liatukas
Lithuanian Institute of Agriculture, LT-58344, Akademija, Kedainiai distr., Lithuania; (email: ruzgas@lzi.lt)

More than 1000 varieties and breeding lines from the FAWWON programme developed in dry climate countries have been tested under Lithuanian conditions over the period 1995 – 2006. Analysis of the data showed that the most part of the tested varieties were of good or acceptable winter hardiness for Lithuanian climate condition. The stem height of all the tested varieties was lower than the standard variety Sirvinta1. Varieties were notable for early ripening. 12% of the tested varieties were very early, 50% early, 38% of moderate ripening. Grain yield analysis showed that 6% of Southern varieties were higher, 70 % lower yielding than the local variety Sirvinta. According to the results of field trials the most part of the tested varieties were more susceptible to leaf diseases than the local check. The Southern winter wheat varieties were of higher grain quality as compare to the West- type varieties. The greatest advantage to include the germplasm from dry climate countries in to the winter wheat breeding programme is high grain quality. Winter hardiness is usually not a limiting factor however in our tests a positive correlation between plant height and winter resistance was found. The greatest constraint is the grain yield and susceptibility to the most wide-spread disease in wet climate, especially powdery mildew.

GENETIC RESOURCES FROM THE NORTH AND ENVIRONMENTAL CHANGES

Merja Veteläinen[1], Sergei Alexanian[2], Even Bratberg[3], Lene K. Christensen[4], Áslaug Helgadóttir[5], Lorenzo Maggioni[6], Marianne Philipp[7], Ken Richards[8], Outi Savolainen[9], Jens Weibull[10], Frans-Emil Wielgolaski[11] and Stoney Wright[12]

[1]MTT AgriFood Research Finland, Tutkimusasemantie 15, FI-92 400 Ruukki, Finland; [2]N.I. Vavilov Research Institute of Plant Industry, Bolshaya Morskaya Street 42-44, 190000 St. Petersburg, Russian Federation; [3]Department Horticulture & Crop Sciences, Norwegian University of Life Sciences, P.O. Box 5003, N-1432 Ås, Norway; [4]Nordic Gene Bank, P.O.Box 41, 23053 Alnarp, Sweden; [5]Agricultural University of Iceland, Keldnaholti, IS-112 Reykjavik, Iceland; [6]Bioversity International, Regional Office for Europe, Via dei Tre Denari 472/a, 00057 Maccarese (Fiumicino), Roma, Italy; [7]Institute of Biology, University of Copenhagen, Universitetsparken 15, 2100 Copenhagen Ø, Denmark; [8]Canadian Genetic Resources Program Agriculture and Agro-Food Canada, Saskatoon Research Centre, 107 Science Place, S7N 0X2 Saskatoon, Saskatchewan, Canada; [9]Department of Biology, University of Oulu, 90014 Oulu, Finland; [10]Swedish Biodiversity Centre, Swedish Uni. of Agricultural Sciences, P.O. Box 54, 230 53 Alnarp, Sweden; [11]Department of Biology, University of Oslo, Oslo, P.O.Box 1066 Blindern, N-0316 Oslo, Norway; [12]Alaska Plant Materials Center, 5310 S. Bodenburg Loop Spur, Palmer, Alaska 99645, USA; (email: merja.vetelainen@mtt.fi)

The anticipated climate change means new challenges for conservation and use of genetic diversity in the North. It has probably the most significant effect on the diversity of wild relatives of crops and wild species utilised. However, for plant breeding in the North it has to be considered that even with warmer climates the use of cultivars bred in the more southern latitudes will not be an option. The unsuitability of more southern varieties to the northern conditions is due to the need for adaptation to the extreme long-day conditions and special growth rhythm, as well as diverging edaphic conditions prevailing in the North.

Today, the genetic resources of the North do not receive any special attention by the genetic resources community. The established gene banks possess germplasm from the area, but since they are usually located in the south they may not always be aware of the vulnerable nature of the genetic resources of the North.

With these aspects in mind, a workshop was organized as an ECPGR cross-cutting activity. Eleven participants representing eight countries north of the 64ºN were brought together to discuss the consequences of the global climate change on plant genetic resources. The aim of the two-day workshop was to review the present state of the most northern germplasm collections, as well as climate change scenarios for the area and knowledge on genetic diversity and adaptive capacity of the most northern plant populations. Our poster shall high-light the scientific background, discussions and outcomes of the workshop.

List of participants

ARMENIA
Alvina Avagyan
EC Food Security programme in Armenia
Ministry of Agriculture, Government Building 3, Republic Square
375010 Yerevan
E-mail: alvinaav@mail.ru

Margarita Harutyunyan
Armenian State Agrarian University
Teryan Str. 74
375009 Yerevan
E-mail: pgr_lab@mail.ru

Marina Hovhanisyan
Armenian State Agrarian University
Teryan Str. 74
375009 Yerevan
E-mail: pgr_lab@mail.ru

AUSTRIA
Markus Schmidt
Organisation for International Dialogue and Conflict Management
Abt-Karl-Gasse 19/21
A-1180 VIenna
E-mail: markus.schmidt@idialog.eu

Peter Ruckenbauer
Institut für Pflanzenbau und Pflanzenzüchtung
Gregor Mendel-Straße 33
A-1180 Vienna
E-mail: peter.ruckenbauer@boku.ac.at

AZERBAIJAN
Natiga Nabiyeva
Genetic Resources Institute of Azerbaijan
National Academy of Sciences
Azadlig Ave 155
AZ1106 Baku
E-mail: gen_eht@yahoo.com

BELARUS
Alexander Kilchevsky
Institute of Genetics and Cytology
27 Academicheskaya str.
22007 Minsk
E-mail: A.Kilchevsky@igc.bas-net.by

Bosnia and Herzegovina
Semina Hadziabulic
Agromeditterenean faculty
USRC
88000 Mostar
E-mail: semina_mo@yahoo.com

Lidija Tomić
Faculty of Agriculture
Bulevar Vojvode Petra Bojovića 1A
78000 Banjaluka
E-mail: lidijatomic@hotmail.com

Gordana Djuric
Faculty of Agriculture
Bulevar Vojvode Petra Bojovica 1A
78000 Banjaluka
E-mail: gordanadjuric@blic.net

BULGARIA
Nasya Tomlekova
Institute of Vegetable Crops Research Institute
32, Brezovsko shosse Str.
4003 Plovdiv
E-mail: tomlekovi@mail.bg

Liliya Krasteva
Institute of Plant Genetic Resources
2 Drujba Str.
4122 Sadovo
E-mail: krasteva_ipgr@abv.bg

CROATIA
Darko Preiner
Faculty of Agriculture
Svetosimunska 25
385 Zagreb
E-mail: dpreiner@agr.hr

Silvio Šimon
Faculty of Agriculture, Department of Plant Breeding
Svetošimunska 25
10 000 Zagreb
E-mail: ssimon@agr.hr

CZECH REPUBLIC
Stanislav Boček
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: bocek@mendelu.cz

Natálie Březinová Belcredi
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: belcr@centrum.cz

Jaroslava Ehrenbergerová
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: ehren@mendelu.cz

Pavlína Hrstková
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: hrstkova@mendelu.cz

Jiří Kopáček
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: kope8@email.cz

Jaroslava Marková
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: markova.jaroslava@seznam.cz

Hana Nevimova
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: xnevimov@node.mendelu.cz

Vojtěch Řezníček
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: reznicek@mendelu.cz

Tomáš Vyhnánek
Mendel University of Agriculture and Forestry in Brno
Zemědělská 1
613 00 Brno
E-mail: vyhnanek@mendelu.cz

Jiri Sedlak
Research and Breeding Institute of Pomology Holovousy LTD
Holovousy 1
508 01 Horice
E-mail: sedlak@vsuo.cz

Jarmila Milotova
Agricultural Research Institute Kromeriz, Ltd.
Havlickova 2787
767 01 Kromeriz
E-mail: milotova@vukrom.cz

Katerina Vaculova
Agricultural Research Institute Kromeriz, Ltd.
Havlickova 2787
767 01 Kromeriz
E-mail: vaculova.katerina@vukrom.cz

Petr Martinek
Agrotest fyto. Ltd.
Havlíčkova 2787
767 01 Kroměříž
E-mail: martinek@vukrom.cz

Lenka Nedomová
Agricultural Research Institute Kromeriz, Ltd.
Havlíčkova 2787
767 01 Kroměříž
E-mail: nedomova@vukrom.cz

Ivo Ondrasek
Mendel University of Agriculture & Forestry, Faculty of Horticulture
Valtická 337
691 44 Lednice
E-mail: ondrasek@zf.mendelu.cz

Jiří Uher
Mendel University of Agriculture & Forestry, Faculty of Horticulture
Ústav zelinářství a květinářství
691 44 Lednice
E-mail: uher@zf.mendelu.cz

Boris Krška
Mendel University of Agriculture & Forestry, Faculty of Horticulture
Valtická 337
691 44 Lednice
E-mail: krska@zf.mendelu.cz

Karel Dušek
Crop Research Institute
Šlechtitelů 11
783 71 Olomouc
E-mail: Dusek@genobanka.cz

Elena Dušková
Crop Research Institute
Šlechtitelů 11
783 71 Olomouc
E-mail: Duskova@genobanka.cz

Kateřina Karlová
Crop Research Institute
Šlechtitelů 11
783 71 Olomouc
E-mail: Karlova@genobanka.cz

Eva Křístková
Palacký University in Olomouc, Faculty of Science
Šlechtitelů 11
783 71 Olomouc
E-mail: eva.kristkova@upol.cz

Aleš Lebeda
Palacký University in Olomouc, Faculty of Science
Šlechtitelů 11
783 71 Olomouc
E-mail: ales.lebeda@upol.cz

Ludmila Ohnoutkova
Institute of Experimental Botany, v.v.i.
Sokolovska 6
772 00 Olomouc
E-mail: ohnoutkova@ueb.cas.cz

Helena Stavělíková
Crop Research Institute
Šlechtitelů 11
783 71 Olomouc
E-mail: Stavelikova@genobanka.cz

Jana Chrpova
Crop Research Institute
Drnovská 507
161 06 Praha 6 - Ruzyne
E-mail: chrpova@vurv.cz

Zdeněk Stehno
Crop Research Institute
Drnovská 507
161 06 Praha 6 - Ruzyne
E-mail: stehno@vurv.cz

Jana Bradova
Crop Research Institute
Drnovska 507
161 06 Praha 6 - Ruzyne
E-mail: bradova@vurv.cz

Ladislav Dotlačil
Crop Research Institute
Drnovská 507
161 06 Praha 6 - Ruzyne
E-mail: dotlacil@vurv.cz

Olga Jandurová
Crop Research Institute
Drnovská 507
161 06 Praha 6 - Ruzyne
E-mail: jandurova@vurv.cz

Světlana Sýkorová
Crop Research Institute
Drnovska 507
161 06 Praha 6 - Ruzyne
E-mail: sykorova@vurv.cz

Iva Faberova
Crop Research Institute
Drnovska 507
161 06 Praha 6 - Ruzyne
E-mail: faberova@vurv.cz

Vojtech Holubec
Crop Research Institute
Drnovská 507
161 06 Praha 6 - Ruzyne
E-mail: holubec@vurv.cz

Leona Leišová
Crop Research Institute
Drnovská 507
161 06 Praha 6 - Ruzyně
E-mail: leisova@vurv.cz

Miroslav Hybl
Agritec Plant Research Ltd.
Zemedelska 16
787 01 Sumperk
E-mail: hybl@agritec.cz

Martin Pavelek
Agritec Plant Research Ltd.
Zemedelska 16
787 01 Sumperk
E-mail: pavelek@agritec.cz

Petr Smýkal
Agritec Plant Research Ltd.
Zemedelska 16
787 01 Šumperk
E-mail: smykal@agritec.cz

Pavlína Gottwaldová
Agricultural Research, Ltd.
Zahradní 1
664 41 Troubsko
E-mail: gottwaldova@vupt.cz

Hana Moravcová
Agricultural Research, Ltd.
Zahradní 1
664 41 Troubsko
E-mail: moravcova@vupt.cz

Jan Nedelnik
Agricultural Research, Ltd.
Zahradní 1
664 41 Troubsko
E-mail: nedelnik@vupt.cz

Jan Pelikán
Agricultural Research, Ltd.
Zahradní 1
664 41 Troubsko
E-mail: pelikan@vupt.cz

Tomáš Vymyslický
Agricultural Research, Ltd.
Zahradní 1
664 41 Troubsko
E-mail: vymyslicky@vupt.cz

Bohumír Cagaš
OSEVA PRO Ltd., Grassland Research Station Rožnov-Zubří
Hamerská 698
756 54 Zubří
E-mail: cagas@oseva.cz

Helena Marková
OSEVA PRO Ltd., Grassland Research Station Rožnov-Zubří
Hamerská 698
756 54 Zubří
E-mail: markova@oseva.cz

Magdalena Ševčíková
OSEVA PRO Ltd., Grassland Research Station Rožnov-Zubří
Hamerská 698
756 54 Zubří
E-mail: sevcikova@oseva.cz

Josef Hakl
Česká zemědělská univerzita
Kamýcká 957
165 21 Praha 6 - Suchdol
E-mail: hakl@af.czu.cz

ESTONIA
Külli Annamaa
Jõgeva Plant Breeding Institute
Aamisepa 1
48309 Jõgeva
E-mail: kylli.annamaa@jpbi.ee

Ants Bender
Jõgeva Plant Breeding Institute
Aamisepa 1
48309 Jõgeva
E-mail: ants.bender@jpbi.ee

Merlin Haljak
Jõgeva Plant Breeding Institute
Aamisepa 1
48309 Jõgeva
E-mail: merlin.haljak@jpbi.ee

Finland
Merja Veteläinen
MTT AgriFood Research Finland/genetic diversity
Tutkimusasemantie 15
92400 Ruukki
E-mail: merja.vetelainen@mtt.fi

FRANCE
Emmanuel Geoffriau
Institut National d'Horticulture UMR GenHort
2 rue Le Nôtre
49045 Angers
E-mail: Emmanuel.Geoffriau@inh.fr

Aurelia Luciani
ALTADIS - Bergerac Tobacco Institute
769, Rte Ste Alvere
24100 Bergerac
E-mail: aurelia.luciani@altadis.com

Audrey Didier
INRA
UMR 1095 Amélioration et santé des plantes 234 avenue du Brezet
63100 Clermont-Ferrand
E-mail: adidier@clermont.inra.fr

Jean Koenig
INRA
UMR1095 Amélioration et Santé des Plantes
63100 Clermont-Ferrand
E-mail: koenig@clermont.inra.fr

Koos De Bruijn
Barenbrug Tourneur Recherches
Route de Bourret
82600 Mas Grenier
E-mail: kdbr@barenbrug-recherches.fr

Anne Zanetto
INRA - DiA-PC
domaine de Melgueil
34160 Mauguio
E-mail: zanetto@supagro.inra.fr

GERMANY
Burkhard Schinkel
Lochow-Petkus GmbH
Bollersener Weg 5
29303 Bergen
E-mail: schinkel@lochow-petkus.de

Reinhard von Broock
Lochow-Petkus GmbH
Bollersener Weg 5
29303 Bergen
E-mail: v.broock@lochow-petkus.de

Andreas Boerner
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: boerner@ipk-gatersleben.de

E. R. Joachim Keller
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: keller@ipk-gatersleben.de

Helmut Knüpffer
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: knupffer@ipk-gatersleben.de

Ulrike Lohwasser
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: lohwasse@ipk-gatersleben.de

Sheeba Navakode
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: navakode@ipk-gatersleben.de

Kerstin Neumann
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: neumannk@ipk-gatersleben.de

Annette Weidner
Leibniz Institute of Plant Genetics and Crop Plant Research
Corensstrasse 3
D-06466 Gatersleben
E-mail: weidner@ipk-gatersleben.de

Heiko Becker
Georg-August-University Göttingen
DNPW Von Siebold Str. 8
37075 Göttingen
E-mail: hbecker1@gwdg.de

Atta Ofori
Georg August University Göttingen
DNPW Von Siebold Str. 8
37075 Göttingen
E-mail: ofori77@yahoo.com

Ramona Thieme
BAZ, Institute of Agricultural Crops
Rudolf-Schick-Platz
D-18190 Groß Lüsewitz
E-mail: r.thieme@bafz.de

Karl Hammer
Institute of Crop Science, University of Kassel
Steinstrasse 11
D-37213 Witzenhausen
E-mail: khammer@uni-kassel.de

GREECE
Penelope Bebeli
Agricultural University of Athens
Iera Odos 75
11855 Athens
E-mail: bebeli@aua.gr

HUNGARY
Marta Molnar-Lang
Agricultural Research Institute of the Hungarian Academy of Sciences
Brunszvik str. 2
H-2462 Martonvasar
E-mail: molnarm@mail.mgki.hu

Annamaria Schneider
Agricultural Research Institute of the Hungarian Academy of Sciences
Brunszvik str. 2
H-2462 Martonvasar
E-mail: scha@mail.mgki.hu

Gábor Vörösváry
CAO - Research Centre for Agrobotany
Külsőmező 15
2766Tápiószele
Hungary
E-mail: gabor@agrobot.rcat.hu

ITALY
Gaetano Laghetti
NRC - Institute of Plant Genetics
Via Amendola 165/A
70126 Bari
E-mail: gaetano.laghetti@igv.cnr.it

Pietro Perrino
NRC - Institute of Plant Genetics
Via Amendola 165/A
70126 Bari
E-mail: Pietro.perrino@igv.cnr.it

Domenico Pignone
NRCI - Institute of Plant Genetics
Via Amendola 165/A
70126 Bari
E-mail: domenico.pignone@igv.cnr.it

Gabriella Sonnante
NRC - Institute of Plant Genetics
Via Amendola 165/A
70126 Bari
E-mail: gabriella.sonnante@igv.cnr.it

Jozef Turok
Bioversity International
Via dei Tre Denari 472/a
I-00057 Maccarese
E-mail: j.turok@cgiar.org

Lorenzo Maggioni
Bioversity International
Via dei Tre Denari 472/a
I-00057 Maccarese (Fiumicino)
E-mail: l.koop@cgiar.org

Valeria Negri
DBVBAZ, University of Perugia
borgo XX giugno 74
6121 Perugia
E-mail: vnegri@unipg.it

Petra Engel
Istituto Sperimentale per la Frutticoltura
VIA Fioranello N. 52
134 Roma
E-mail: isfrmfid@mclink.it

Simonetta Bullitta
ISPAAM-CNR
Via Enrico de Nicola 1
7100 Sassari
E-mail: bullitta@cspm.ss.cnr.it

Enrico Porceddu
DABAC / University of Tuscia
Via S. C. de Lellis
I 01100 Viterbo
E-mail: porceddu@unitus.it

KOSOVA
Sali Aliu
The University o Prishtina
Str,Boulevard “Bill Clinton “10000 P.N
Prishtina
Kosova 10000
E-mail: s_aliu@hotmail.com

Shukri Fetahu
The University o Prishtina
Str,Boulevard “Bill Clinton “10000 P.N
Prishtina
Kosova 10000
E-mail: shfetahu@hotmail.com

LATVIA
Gunars Lacis
Latvia State Institute of Fruit-Growing
Graudu Str. 1
LV-3701 Dobele
E-mail: gunars.lacis@lvai.lv

Agnese Gailite
Latvian Gene Bank
111 Rigas st
LV-2169 Salaspils
E-mail: agnese@silava.lv

Dace Grauda
Institute of Biology University of Latvia
Miera Str.3
LV-2169 Salaspils
E-mail: dace@email.lubi.edu.lv

Isaak Rashal
Institute of Biology University of Latvia
Miera Str.3
LV-2169 Salaspils
E-mail: izaks@email.lubi.edu.lv

Dainis Rungis
Latvian Gene Bank
111 Rigas st
LV-2169 Salaspils
E-mail: dainis.rungis@silava.lv

Biruta Jansone
Research Institute of Agriculture
Zemkopibas instituts 7
LV 5126 Skriveri 1
E-mail: szc@inbox.lv

Aldis Jansons
Research Institute of Agriculture
Zemkopibas instituts 7
LV 5126 Skriveri 1
E-mail: szc@inbox.lv

Mara Bleidere
State Stende Cereals breeding institute
p.Dizstende
LV 3258 Talsi
E-mail: maara.bleidere@gmail.com

Līga Lepse
Pūre Horticultural Research Centre
Abavas iela 2, Pūre
LV 3124 Tukuma raj.
E-mail: liga.lepse@puresdis.lv

LITHUANIA
Bronislovas Gelvonauskis
Plant Gene Bank
Stoties 2, Akademija
LT-58343 Kėdainiai district
E-mail: b.gelvonauskis@agb.lt

Alge Leistrumaite
Lithuanian Institute of Agriculture
Instituto aleja 1, Akademija
LT-58344 Kedainiai district
E-mail: alge@lzi.lt
Vytautas Ruzgas
Lithuanian Institute of Agriculture
Instituto aleja 1, Akademija
LT58344 Kedainiai district
E-mail: ruzgas@lzi.lt

Antanas Svirskis
Lithuanian Institute of Agriculture
Instituto aleja 1, Akademija
LT-58344 Kedainiai district
E-mail: antanas@lzi.lt

MEXICO
Maria Zaharieva
CIMMYT
A.P. 6-641
6600 Mexico D.F.
E-mail: m.zaharieva@cgiar.org

NETHERLANDS
Marco Binnendijk
Enza Zaden
Postbox 7
1600AA Enkhuizen
E-mail: m.binnendijk@enzazaden.nl

Chris Kik
Centre for Genetic Resources, the Netherlands (CGN)
Bornsesteeg 65
6703 CG Wageningen
E-mail: chris.kik@wur.nl

Robbert van Treuren
Centre for Genetic Resources, the Netherlands
P.O.Box 16
6700 AA Wageningen
E-mail: robbert.vantreuren@wur.nl

NORWAY
Åsmund Asdal
Norwegian Genetic Resources Centre
pb 115
1431 Ås
E-mail: aasmund.asdal@bioforsk.no

POLAND
Jerzy Czembor
Plant Breeding and Acclimatization Institute
Radzikow
05-870 Blonie
E-mail: j.h.czembor@ihar.edu.pl

Marcin Zaczynski
Plant Breeding and Acclimatization Institute
Radzikow
05-870 Blonie
E-mail: m.zaczynski@ihar.edu.pl

Jakub Dzienkiewicz
Plant Breeding and Acclimatization Institute
Radzików
05-870 Błonie
E-mail: J.Dzienkiewicz@ihar.edu.pl

Denise Fu Dostatny
Plant Breeding and Acclimatization Institute
Radzików
05-870 Błonie
E-mail: d.dostatny@ihar.edu.pl

Mariusz Chojnowski
Plant Breeding and Acclimatization Institute
Radzików
05-870 Błonie
E-mail: m.chojnowski@ihar.edu.pl

Bogusław Łapiński
Plant Breeding and Acclimatization Institute
Radzików
05-870 Błonie
E-mail: b.lapinski@ihar.edu.pl

Bartosz Mysłowski
Plant Breeding and Acclimatization Institute
Blonie
05-870 Radzikow
E-mail:

Kamilla Kużdowicz
Plant Breeding and Acclimatization Institute
Al. Powstańców Wlkp. 10
85-090 Bydgoszcz
E-mail: k.kuzdowicz@ihar.bydgoszcz.pl

Pawel Nowaczyk
University of Technology and Life Sciences
Bernardynska 6
85-029 Bydgoszcz
E-mail: warz@utp.edu.pl

Wanda Kociuba
Institute of Genetics, Breeding and Plant
Biotechnology Agricultural University
ul.Akademicka 15
20-934 Lublin
E-mail: wanda.kociuba@ar.lublin.pl

Wojciech Swiecicki
Institute of Plant Genetics Polish Academy of
Sciences
Strzeszyńska 34
60-479 Poznań
E-mail: wswi@igr.poznan.pl

Wojciech Rybiński
Institute of Plant Genetics Polish Academy of
Sciences
Strzeszyńska 34
60-479 Poznań
E-mail: wryb@igr.poznan.pl

Apoloniusz Berbec
Institute of Soil Science and Plant Cultivation
Czartoryskich 7
24-100 Pulawy
E-mail: berbec@iung.pulawy.pl

Urszula Skomra
Institute of Soil Science and Plant Cultivation
Czartoryskich 9
24-100 Pulawy
E-mail: Urszula.skomra@iung.pulawy.pl

Mieczyslaw Stasiak
Institute of Soil Science and Plant Cultivation
Czartoryskich 8
24-100 Pulawy
E-mail: stamie@poczta.fm

Robert Borek
Institute of Soil Science and Plant Cultivation
Czartoryskich 10
24-100 Puławy
E-mail: rborek@iung.pulawy.pl

Dorota Laskowska
Institute of Soil Science and Plant Cultivation
Czartoryskich 11
24-100 Puławy
E-mail: Dorota.Laskowska@iung.pulawy.pl

Teresa Kotlińska
Rlant Genetic Resources Lab., Research Institute
of Vegetable Crops
Konstytucji 3 Maja 1/3
96-100 Skierniewice
E-mail: tkotlin@inwarz.skierniewice.pl

Katarzyna Machnicka
Rlant Genetic Resources Lab., Research Institute
of Vegetable Crops
Konstytucji 3 Maja 1/3
96-100 Skierniewice
E-mail: tkotlin@inwarz.skierniewice.pl

Anna Geszprych
Warsaw Agricultural University, Department of
Vegetable and Medicinal Plants
Nowoursynowska 166
02-787 Warsaw
E-mail: andage@gmail.com

Wieslaw Madry
Warsaw Agricultural University
Nowoursynowska 166
02-787 Warsaw
E-mail: wieslaw.madry@omega.sggw.waw.pl

Krzysztof Ukalski
Warsaw Agricultural University
Nowoursynowska 166
02-787 Warsaw
E-mail: krzysztof.ukalski@agrobiol.sggw.waw.pl

Marta Dziubiak
Botanical Garden - Center for Biological Diversity
Conservation of the Polish Academy of Sciences
Prawdziwka St. No. 2
PL-02-973 Warsaw 76
E-mail: obpan@obpan.neostrada.pl

Wiesław Łuczak
Botanical Garden - Center for Biological Diversity
Conservation of the Polish Academy of Sciences
Prawdziwka St. No. 2
PL-02-973 Warsaw 76
E-mail: wluczak@obpan.neostrada.pl

Maciej Niedzielski
Botanical Garden - Center for Biological Diversity
Conservation of the Polish Academy of Sciences
Prawdziwka St. No. 2
PL-02-973 Warsaw 76
E-mail: obpan@obpan.neostrada.pl

Jerzy Puchalski
Botanical Garden - Center for Biological Diversity
Conservation of the Polish Academy of Sciences
Prawdziwka St. No. 2
PL-02-973 Warsaw 76
E-mail: obpan@obpan.neostrada.pl

Stanisław Jeżowski
Institute of Plant Genetics Polish Academy of
Sciences
Strzeszyńska 34
60-479 Poznań
E-mail: ajez@igr.poznan.pl

PORTUGAL
Pedro Mendes Moreira
Escola Superior Agrária de Coimbra
Bencanta
3040-316 Coimbra
E-mail: pmoreira@esac.pt

João Santos
Escola Superior Agrária de Coimbra
Bencanta
3040-316 Coimbra
E-mail: jpsantos14@gmail.com

Pinto Carnide Olinda da Conceiçäo
University of Trás-os-Montes and Alto Douro
Genetics and Biotechnology Dep., UTAD, AP. 1013
5001-801 Vila Real
E-mail: olindac@utad.pt

Carlos Ribeiro Carvalho
University of Trás-os-Montes and Alto Douro
Genetics and Biotechnology Dep., UTAD, AP. 1013
5001-801 Vila Real
E-mail: ccarvalh@utad.pt

Carnide Valdemar Pedrosa
University of Trás-os-Montes and Alto Douro
Genetics and Biotechnology Dep., UTAD, AP. 1013
5001-801 Vila Real
E-mail: olindac@utad.pt

ROMANIA
Elena Rakosy-Tican
Babes-Bolyai University Plant Genetic Engineering Group
Clinicilor str. 5-7
RO-400006 Cluj-Napoca
E-mail: arina5744@yahoo.com

Adriana Sestras
Fruit Research Station
5 Horticultorilor St.
400457 Cluj-Napoca
E-mail: asestras@yahoo.com

Radu Sestras
University of Agricultural Sciences and Veterinary Medicine
3-5 Manastur St.
400372 Cluj-Napoca
E-mail: rsestras@yahoo.co.uk

RUSSIA
Kishtili Kurkiev
Dagestan Experimental Station of Vavilov All-Russian Institute of Plant Industry
City Derbent, vill. Vavilovo
368612 Derbent
E-mail: kkish@mail.ru

Anna Shirokova
Main Botanical Garden Russian Academy of Sciences
Botanicheskaya, 4
127276 Moscow
E-mail: glandularia@yahoo.com

Natalia Zagoskina
Timiriazev Institute of Plant Physiology, Russian Academy of Sciences
ul. Botanicheskaya 35
127176 Moscow
E-mail: phenolic@ippras.ru

Domblides Arthur
All-Russian Research Institute of Vegetable Breeding and Seed Production
VNIISSOK p/o Lesnoy Gorodok
143080 Odintsovo region, Moscow district
E-mail: domblidesarthur@yahoo.com

SERBIA
Zoran Lugic
Institute for forage crops
Trg Kosturnice 50
37 Krusevac
E-mail: zoran.lugic@ikbks.com

Jasmina Radovic
Institute for forage crops
Trg Kosturnice 50
37 Krusevac
E-mail: jasmina.radovic@ikbks.com

Dejan Sokolovic
Institute for forage crops
Trg Kosturnice 50
37000 Krusevac
E-mail: dejan.sokolovic@ikbks.com

Janko Červenski
Scientific Institute of field and vegetable crops Novi Sad
Maksima Gorkog 30
21000 Novi Sad
E-mail: jankic@ifvcns.ns.ac.yu

Aleksandar Mikic
Institute of Field and Vegetable Crops
Maksima Gorkog 30
21000 Novi Sad
E-mail: mikic@ifvcns.ns.ac.yu

Sanja Vasiljevic
Institute of Field and Vegetable Crops
Maksima Gorkog 30
21000 Novi Sad
E-mail: sanjava@ifvcns.ns.ac.yu

SLOVAK REPUBLIC
Jana Martincová
SARC-GMARI
Mládežnícka 36
974 21 Banská Bystrica
E-mail: jmartin@vutphp.sk

Elena Hlinková
Comenius University in Bratislava
Mlynská dolina B-1
842 15 Bratislava
E-mail: hlinkova@fns.uniba.sk

Peter Paľove-Balang
Botanický ústav SAV
Dúbravská cesta 14
845 23 Bratislava
E-mail: botubala@savba.sk

Daniela Dvoncova
SCPV - Research Institute of Plant Production
Research and Breeding Station at Vígľaš – Pstruša
962 12 Detva
E-mail: dvoncova@vurv.sk

Peter Hozlar
SCPV - Research Institute of Plant Production
Research and Breeding Station at Vígľaš – Pstruša
962 12 Detva
E-mail: hozlar@vurv.sk

Zdenka Balatova
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: zdenka.balatova@uniag.sk

Tibor Baranec
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: baranec@afnet.uniag.sk

Pavol Eliáš
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: pelias@afnet.uniag.sk

Diana Gregusová
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: diana.gregusova@uniag.sk

Olga Grygorieva
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: ogrygorieva@mail.ru

Jana Holecyova
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: jana.holecyova@uniag.sk

Svetlana Klymenko
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: ogrygorieva@mail.ru

Martin Kolník
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: martin.kolnik@savba.sk

Katarína Mitická Popiková
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: katarina.miticka@uniag.sk

Valéria Müllerová
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: valeria.mullerova@uniag.sk

Janka Nôžková
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: janka.nozkova@uniag.sk

Radovan Ostrovský
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: radovan.ostrovsky@uniag.sk

Olga Urbanovičová
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: olga.kunova@uniag.sk

Gabriela Antalíková
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: antalikova@vurv.sk

Daniela Benediková
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: benedikova@vurv.sk

Michaela Benkova
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: benkova@vurv.sk

Katarína Bojnanská
SARC - Research Institute of Plant Production
Bratislavská cesta 122
621 68 Piešťany
E-mail: bojnanska@vurv.sk

Rastislav Buso
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: buso@vurv.sk

Iveta Čičová
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: cicova@vurv.sk

Viera Červená
SARC - Research Institute of Plant Production
Bratislavská cesta 122
921 68 Piešťany
E-mail: cervena@vurv.sk

Jarmila Drobná
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 01 Piešťany
E-mail: drobna@vurv.sk

Juraj Farago
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: farago@vurv.sk

Natalia Faragova
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: faragova@vurv.sk

Edita Gregova
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: gregova@vurv.sk

Pavol Hauptvogel
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: hauptvogel@vurv.sk

René Hauptvogel
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: r.hauptvogel@vurv.sk

Michaela Havrlentova
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: havrlentova@vurv.sk

Dalibor Ješko
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: jeskod@vurv.sk

Ján Kraic
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: kraic@vur.sk

Marta Klimekova
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: klimekova@vurv.sk

Zuzana Lehocka
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: lehocka@vurv.sk

Stefan Masar
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: masar@vurv.sk

Ľubomír Mendel
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: mendel@vurv.sk

Daniela Mikulíková
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: mikulikova@vurv.sk

Maria Zakova
SARC - Research Institute of Plant Production
Bratislavska cesta 122
921 68 Piešťany
E-mail: zakova@vurv.sk

Andrea Plackova
Presov University
01,17th November St.
081 16 Prešov
E-mail: salamon@fhpv.unipo.sk

Tibor Maliar
UCM Trnava
Nám. J.Herdu 2
917 01 Trnava
E-mail: tibor.maliar@ucm.sk

Ján Heldák
VŠÚZ - Výskumný a šľachtiteľský ústav zemiakársky
Popradská 518
059 52 Veľká Lomnica
E-mail: heldak@sinet.sk

Miroslav Švec
Comenius University in Bratislava
Mlynská dolina B1
842 15 Bratislava
E-mail: msvec@fns.uniba.sk

Zuzana Amreinová
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: zuzana.amreinova@uniag.sk

Marián Brestič
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: marian.brestic@uniag.sk

Peter Ferus
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: peter.ferus@uniag.sk

Katarina Olšovská
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: katarina.olsovska@uniag.sk

Jana Pivková
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: jana.pivkova@uniag.sk

Jana Repková
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: jana.repkova@uniag.sk

Marek Živčák
Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2
949 76 Nitra
E-mail: marek.zivcak@uniag.sk

SLOVENIA
Vladimir Meglic
Agricultural Institute of Slovenia
Hacquetova 17
SI-1000 Ljubljana
E-mail: vladimir.meglic@kis.si

SPAIN
Maria Jose Diez Niclos
Universidad Politecnica de Valencia
Camino de Vera S/N
46022 Valencia
E-mail: mdiezni@btc.upv.es

Jaime Prohens Tomás
Universidad Politecnica de Valencia
Camino de Vera 14
46022 Valencia
E-mail: jprohens@btc.upv.es

MariaJose Suso
Instituto de Agricultura Sostenible
Alameda del Obispo s/n
14080 Cordoba
E-mail: ge1susom@uco.es

SWEDEN
Eva Thörn
Swedish Biodiversity Centre
P O Box 54
23053 Alnarp
E-mail: eva.thorn@cbm.slu.se

Jens Weibull
Swedish Biodiversity Centre
P O Box 54
230 53 Alnarp
E-mail: jens.weibull@cbm.slu.se

SYRIA
Ashutosh Sarker
International Center for Agricultural Research in the Dry Areas (ICARDA)
ICARDA, P. O. Box 5466
5466 Aleppo
E-mail: A.Sarker@cgiar.org

TUNISIA
Mohamed Marrakchi
Faculty of Sciences of Tunis
Campus universitaire ELMANAR
2092 Tunis
E-mail: neila.trif@fst.rnu.tn

Neila Trifi-Farah
Faculty of Sciences of Tunis
Campus universitaire ELMANAR
2092 Tunis
E-mail: neila.trif@fst.rnu.tn

Salhi-Hannachi AMEL
Faculty of Sciences of Tunis
Campus universitaire ELMANAR
2092 Tunis
E-mail: Amel.SalhiHannachi@fsb.rnu.tn

Zoghlami Khélil Aziza
INRAT (Institut National de la Recherche Agronomique) Rue Hédi Karray
Ariana
Tunisia 2080
E-mail: zoghlami.aziza@iresa.agrinet.tn

TURKEY
Mehmet Bilgen
Akdeniz University, Faculty of Agriculture
7059 Antalya
E-mail: bilgen@akdeniz.edu.tr

Cengiz Toker
Akdeniz University, Faculty of Agriculture
TR-07058 Antalya
E-mail: toker@akdeniz.edu.tr

Bulent Uzun
Akdeniz University, Faculty of Agriculture
TR-07058 Antalya
E-mail: bulentuzun@akdeniz.edu.tr

UNITED KINGDOM
Michael Jeger
Imperial College London
Wye Campus
TN25 5AH Ashford
E-mail: m.jeger@imperial.ac.uk

Maria Scholten
University of Birmingham
52 Oakfield Rd Selly Park
B29 7EQ Birmingham
E-mail: maria_scholten@hotmail.com

Gavin Ramsay
SCRI
Invergowrie
DD2 5DA Dundee
E-mail: gavin.ramsay@scri.ac.uk

Jonathan Latham
Bioscience Resource Project
PO Box 66
HR8 9AE Ledbury
E-mail: jrlatham@bioscienceresource.org

UKRAINE
Valentyna Gorina
Nikita botanikal Garden
Nikita
98648 Yalta
E-mail: gorina@yalta.crimea.ua

Index of authors

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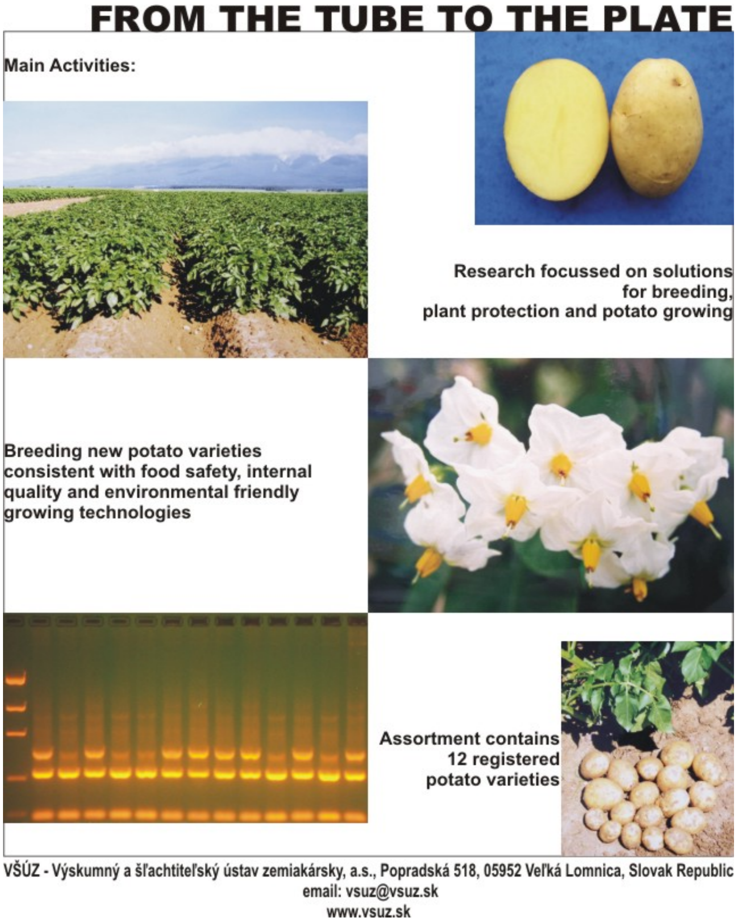

EUCARPIA
EUROPEAN ASSOCIATION FOR RESEARCH ON PLANT BREEDING
EUROPÄISCHE GESELLSCHAFT FÜR ZÜCHTUNGSFORSCHUNG
ASSOCIATION EUROPÉENNE POUR L'AMÉLIORATION DES PLANTES

General Information

EUCARPIA aims to promote scientific and technical co-operation in the field of plant breeding in order to foster its further development.

To achieve this purpose, the Association arranges and sponsors meetings of members, to discuss general or specific problems.

EUCARPIA organizes open conferences and colloquia throughout Europe each year.

Founded in 1956, EUCARPIA, a non profit organization, can look back on considerable contributions to improving international contacts in plant breeding research for almost fifty years. Nowadays EUCARPIA is more active than ever before with more than a thousand members of various nationalities and interests.

For everyone involved in plant breeding research or practical breeding, EUCARPIA has a lot to offer:

International Co-operation. The Association consists of members from all over Europe and over 30 other countries worldwide. EUCARPIA initiates relationships and co-operates with other national and international organizations in fields relevant to plant breeding.

Exchange of Methods. EUCARPIA is organized in 10 sections together with several subsections and working groups. Each section is engaged in a certain field of research, or in certain groups of crops. EUCARPIA encourages its members to take part in several sections. New methods and techniques can therefore be rapidly integrated into the wider field of plant breeding.

Exchange of Specialized Knowledge. The interaction between people working in the same field of interest, or with the same crop, can contribute effectively to plant breeding. The exchange of specialized knowledge has proven to be of the greatest importance to all researchers and breeders involved.

Exchange of Plant Material. Plant breeders from all over the world, who meet in EUCARPIA working groups, help each other through the exchange of genetic material. Furthermore the Genetic Resources section has played an important role in the establishment of regional gene banks.

Journal Suscriptions at Reduced Rates. Individual members are entitled to subscribe at very reduced rates to some scientific journals: *Plant Breeding*, *Euphytica*, *Molecular Breeding*, *Theoretical and Applied Genetics* and *Genetic Resources and Crop Evolution*. Ask the EUCARPIA Secretariate or visit the EUCARPIA web page for current rates.

Specialized Sections. Each member is welcomed to participate in one or more (or all) sections. EUCARPIA's 10 sections are:

- Potatoes
- Cereals
- Fodder Crops and Amenity Grasses
- Biometrics in Plant Breeding
- Genetic Resources
- Maize and Sorghum
- Vegetables
- Fruit
- Ornamentals
- Oil and Protein Crops

General Congress. Every four years a congress is held, together with the general assembly. These congresses are an open forum and have always been the main platform for presentation of the problems and challenges facing plant breeding both for today and in the future.

Membership.
Membership fees for 2007 are only € 40.- (individual members), € 30.- (members younger than 30 years or retired) and € 300.- (corporate members, including a maximum of 10 persons). Special rates apply for members from new EU countries and from non-EU Eastern Europe countries. An application form can be downloaded from the EUCARPIA web site. Every year, the Secretariat sends to EUCARPIA members the Membership certification together with the EUCARPIA Bulletin, which contains information on EUCARPIA activities, publications, dates and information of symposia, meetings and events, etc.

For more information:
EUCARPIA Secretariat / María L. Badenes, Instituto Valenciano de Investigaciones Agrarias
Apartado Oficial, E-46113 Moncada (Valencia), Spain
Fax: +34 963424106 E-mail: eucarpia.secretariat@ivia.es Web-page: http://www.eucarpia.org

EUCARPIA
EUROPEAN ASSOCIATION FOR RESEARCH ON PLANT BREEDING
EUROPÄISCHE GESELLSCHAFT FÜR ZÜCHTUNGSFORSCHUNG
ASSOCIATION EUROPÉENNE POUR L'AMÉLIORATION DES PLANTES

Valencia, May 2007

Recent activities

Latest publications ...

A. Mercuri & T. Schiva (eds.), 2006: Breeding for Beauty. Proceedings of the 22nd International EUCARPIA Symposium Section Ornamentals, 11-15 September 2006, Sanremo, Italy. Acta Horticulturae 714. Contents: 24 congress papers (selected contributed presentations) on 228 pages.

J. Vollmann, H. Grausgruber & P. Ruckenbauer (eds.), 2004: Genetic Variation for Plant Breeding. Proceedings of the 17th EUCARPIA General Congress, 8-11 September 2004, Tulln, Austria. BOKU – University of Natural Resources and Applied Life Sciences, Vienna, Austria. Contents: 216 contributions (congress papers or abstracts) on 514 pages.

A. Lebeda & H.S. Paris (eds.), 2004: Progress in Cucurbit Genetics and Breeding Research, Proceedings of Cucurbitaceae 2004, the 8th EUCARPIA Meeting on Cucurbit Genetics and Breeding, July 12-17, 2004, Olomouc, Czech Republic. Palacký University in Olomouc, Czech Republic. Contents: 76 congress papers on 559 pages.

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Forthcoming EUCARPIA events ...

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XIIIth Meeting of the EUCARPIA Capsicum and Eggplant Working Group, 5 – 7 September 2007, Warsaw, Poland

XII Meeting of the EUCARPIA Fruit Section, 16 – 20 September 2007, Zaragoza, Spain

Meeting of the EUCARPIA Oil and Protein Crops Section, 7 – 10 October 2007, Budapest, Hungary

1st Meeting of the Organic Breeding Working Group: “Plant breeding for sustainable, low imput agriculture: dealing with genotype-environment interactions, 7 – 9 November 2007, Wageningen, The Netherlands

2008: **IXth EUCARPIA Meeting on Genetics and Breeding of Cucurbitaceae”**, 21 – 24 May 2008, Avignon, France

XVIII EUCARPIA General Congress: “Modern Variety Breeding for Present and Future Needs”, 11 – 14 September 2008, Valencia, Spain

2009: **XXIII EUCARPIA Symposium – Section Ornamentals**, 31 August – 4 September 2009, Wageningen, The Netherlands

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http://www.eucarpia.org

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Chairman of the Organising Committee 18th Eucarpia Genetic Resources Section
Pavol Hauptvogel
SARC - Research Institute of Plant Production Piešťany
Bratislavská 122
921 68 Piešťany
Slovak Republic
Tel.: +421 33 7722311
Fax: +421 33 7726 306
E-mail: eucarpia.pgr@vurv.sk; hauptvogel@vurv.sk
www.eucarpia.vurv.sk
www.eucarpia.org