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Section Genetic Resources

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Abstracts of oral presentations and posters



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Foreword

Welcome to Wageningen, City of Life Sciences!

This time the EUCARPIA conference on Plant Genetic Resources (PGR) will focus on two themes, namely 'how can genebanks improve service to their users' and 'how can genebanks better cooperate with each other in order to more efficiently manage their stored PGR'. We have chosen a conference format which differs from preceding conferences as we would like to stimulate discussion among the conference participants. Therefore the number of oral presentations was limited and considerable time has been allocated for discussion. We hope that this conference will give you a good overview of the state-of-the-art in the genebanking world, not only during the regular program, but also in interaction with the other participants in the margins of the program and during the social events.

The three day meeting is also organized to commemorate the 25th anniversary of the Centre for Genetic Resources, the Netherlands (CGN). Over the past 25 years CGN has gained a well-recognized role in the international genetic resources community. This role can be ascribed to various factors, including CGN's innovative genetic resources management approaches, its close cooperation with both public and private sector stakeholders, its focus on genetic resources policies, and its firm roots in the scientific community of Wageningen University and Research Centre. It is our ambition to maintain this role and to contribute to solutions which will safeguard the precious genetic resources worldwide.

We wish you an inspiring conference !

Bert Visser (director CGN)
Theo van Hintum
Chris Kik



Oral Presentations

(ordered alphabetically on the name of the first author)

Pre-competitive research on genebank material in the Netherlands

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Key words: collaboration, plant breeding industry, genebank

The Dutch plant breeding industry contributes to biodiversity by the release of new breeding products. Mostly these products are available for further breeding under the Breeders' Exemption of the Union for the Protection of New Varieties of Plants (UPOV). In addition, the Dutch plant breeding industry contributes to the conservation and sustainable use of plant genetic resources by cooperation with gene banks. They do this in several ways: they give financial support for collection missions and in-kind support by multiplying accessions on request of the gene banks.

When it comes to sustainable use, it is interesting to note that private companies find each other as allies when it comes to evaluating the collection of the Centre for Genetic Resources in the Netherlands. Several of such collaborations exist, in which Plantum NL coordinates, the Centre for Genetic Resources provides material and compiles the collected data, and the participating companies perform or finance the testing. These collaborations seem unnatural, because every breeding company would like to be the first to discover a new trait and introduce it into the market. Nevertheless, there are cases where companies change their strategy and step over the fact that they are competing in the market and join forces to discover new traits.

Despite the combat for market shares between the companies, there are many reasons to work together in pre-competitive research on plant genetic resources. These can be found in the complexity of the traits, difficulties in measuring the traits, the large numbers that need to be evaluated before the trait is found or the urgent need to find the new trait.

The role of the Germplasm Resources Information Network (GRIN) in unifying the U. S. National Plant Germplasm System (NPGS)

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Key words: Germplasm Resources Information Network; GRIN; U. S. National Plant Germplasm System; NPGS; plant genetic resource information systems; GRIN-Global

The United States Department of Agriculture's National Plant Germplasm System (NPGS) currently comprises more than 20 diverse individual genebanks and supporting laboratories. Some manage hundreds of thousands of seed-propagated accessions, others conserve several hundred clonally-propagated accessions, and some specialize in plant exploration or information management. Some NPGS elements are more than 100 years old, whereas others were founded less than a decade ago. Located from the sub-Arctic of Alaska to the tropics of the Pacific and Caribbean, these genebanks conserve and deliver highly varied germplasm and information to scientific, educational, and agricultural clientele globally.

The Germplasm Resources Information Network (GRIN) serves not only as the NPGS's common information management system, but it also constitutes the NPGS's most important unifying factor. Through GRIN, the NPGS genebanks manage the information associated with more than 539,000 germplasm accessions; Agriculture and Agri-Food Canada similarly manages information associated with more than 100,000 accessions via GRIN-Canada. GRIN arose from several precursors—including GRIP—Germplasm Resources Information Project—during the 1980s, and was first implemented throughout the NPGS in 1987. Since then, it has evolved through several different computer hardware platforms, software languages, and implementation modes, from an early “log-in” wide-area networked system connected by modems, to the current version which delivers millions of digital data points and images to clientele via the Internet, and is indexed by major search engines.

During the last 25 years, a national (and now with GRIN-Global, international) collaborative user community has also emerged concurrently with GRIN. This “community of practice” has served to unify the NPGS—not only around a common database and standards for information management—but also through common standards for plant genetic resource curation. It has fostered the evolution of Crop Germplasm Committees—a formal mechanism for clientele input into the NPGS's operations; GRIN Taxonomy for Plants—the online global standard for plant taxonomic information; pcGRIN—a version of GRIN implementable by stand-alone personnel computers; and GRIN-Global—powerful, flexible, and easy-to-use global plant genetic resource information system for worldwide users, which is currently under development. Not only must GRIN-Global meet the needs of plant genetic resource curators, it also must enable researchers to integrate passport, provenance, phenotypic, and genomic information to achieve high-priority agricultural research objectives.

Promoting conservation and use of Plant Genetic Resources for Food and Agriculture –Information services for users worldwide

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Genebanks, the main custodians of millions of accessions of plant genetic resources (PGR), today play a primary role in insuring food quality and security for future generations. To answer questions such as “which genebank holds what?” and “where can I find specific materials?” the European region developed a web-based window for access to European data about genebank accessions, in a user-friendly, online format. That well established window is called EURISCO, a one-stop shop that uses international standards for access to and exchange of information on *ex situ* plant collections. It enables users to search for and access information from 41 National Inventories (NIs), on crops, forages, wild and weedy species, farmers' varieties and breeding lines maintained in the European genebank collections, using a wide set of search criteria. This information allows users to better understand the distribution, conservation and status of PGR while helping policy makers to meet their countries' goals and commitments, to the conservation and utilization of these materials, namely those related to the FAO-Global Plan of Action (GPA), the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) and, the Convention on Biological Diversity (CBD).

EURISCO contains accession-level passport data on almost 1.1 million accessions of crop diversity representing around 1 300 genera and 35 000 species. These accessions of crop diversity represent almost half of the *ex situ* accessions maintained in Europe and roughly 15% of the total worldwide holdings.

The National Inventories are the backbone of EURISCO, providing the essential data to meet users' needs. Now that Europe has established a solid network of sustainable data providers, the next immediate goal is to develop the functionality to help the data providers to publish characterization and evaluation data to meet users' needs for trait information, thus promoting the sustainable use of the material conserved.

To answer research questions related to biodiversity and to reach out beyond the regional level covered by EURISCO, to encompass the global scenario, a complementary project that facilitates access to and use of information on a global scale has been underway. The main output of this project is a global portal – GENESYS - created to improve access by breeders and other plant scientists to the germplasm they need from genebanks around the world, in a format that is easy to understand. GENESYS specifically addresses the challenge of making available information about germplasm collections readily available, which has been repeatedly identified as a crucial key to increasing the use of PGRFA to address the challenges of climate change and to maintain the sustainable production of agricultural crops.

The foundation data for the GENESYS global portal is the information provided by three major international project partners: the European Cooperative Programme for Plant Genetic Resources (ECPGR - EURISCO), the System-wide Genetic Resources Programme (SGRP-SINGER) of the Consultative Group on International Agricultural Research (CGIAR) and the United States Department of Agriculture (USDA-GRIN) Agricultural Research Service National Genetic Resources Program. Together these systems account for some 2.4 million accessions held in *ex situ* collections worldwide, about a third of the total number of accessions estimated to be held in genebanks globally. GENESYS adds further dimensions to these information systems through the inclusion of some 11 million records of characterization and evaluation

data, as well as a similar number of records on climatic data for geo-referenced accessions. Users can build customized queries in GENESYS to search across all data categories and identify accessions meeting their particular needs.

About the PGR networks in France: the collaboration between users and the Genetic Resource Centre on small grains cereals

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Key words: cereals, genetic resources, data management, seeds distribution

Genetics resources (GR) are used by breeders since many decades in their plant breeding programs to produce modern varieties by introducing genes of interest (i.e. resistance genes). These resources appear nevertheless underestimated if we focus on abiotic stress tolerances or new agricultural techniques which combine productivity and respect of environment. More recently, new users, such as scientists and farmers, discovered diverse and new sources of interest in screening and exploiting natural diversity conserved in GR collections.

Presently, the major question is how better promoting genetic resource present in collection to answer both to socio-economic evolution of the agriculture and to the development of basic scientific knowledge in genetic and genomic?

In the case of the French cereals GR Network, a share of responsibility based on knowledge and ability of its members have been decided: phenotyping activities are carried out by private breeders who describe genetic resources for specific descriptors through multilocal evaluation network, while the Genetic Resources Centre (GRC) at INRA Clermont-Ferrand (<http://www.clermont.inra.fr/umr1095/>) produces molecular data in relationship with its high-throughput genotyping platform and manages collections of small grain cereals (multiplication, conservation and distribution) under quality process. Main species of *Triticum* (wheat), *Hordeum* (barley), *Secale* (rye), *Triticosecale* (triticale), *Avena* (oat) genus and their wild relatives are hold in the collection. The main part of the preserved accessions are patrimonial genetic resources (landraces, breeding lines, registered cultivars) which represent about 11 800 hexaploid wheats, 2 800 tetraploid wheats and wild relatives, 6 550 barleys, 1 200 triticales, 1 200 oats, 450 *Aegilops* sp. and 85 ryes accessions. All these genetic resources form a valuable toolbox as much for fundamental genomic approaches as for basic breeding processes.

Combining phenotyping and genotyping data, the whole genetic resource collection have been structured in smaller functional groups of accessions (i.e. soft wheat FAO collection, INRA core collection,...) in order to facilitate the reply to an increasing number of different requirements by the distribution of adapted samples of accessions.

New panels are under process to give to breeders and scientists new useful tools to study for instance stresses resistance or to develop association studies. All these evaluation data obtained from the French small grain cereal Network will be progressively available through INRA Genetic Resource Website (<http://urgi.versailles.inra.fr/siregal/siregal/welcome.do>).

Utilization of Czech collection of wheat genetic resources in breeding

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Key words: wheat, genetic resources, “core” collection, choice of donors, services to users

Almost 51.5 thousand accessions are maintained in crop collections covered by the Czech National Programme on Plant Genetic Resources. The largest one is wheat collection containing 10.7 thousand accessions plus additional about 1 thousand wild relatives. The accessions belong to 31 wheat species according to Dorofeev classification and among them *Triticum aestivum* L. is the prevailing one (9 241 accessions). As the winter wheat cultivars are sown on more than 95 % wheat growing area in the country, the winter forms dominate (60 %) also in the wheat collection. Owing to a long tradition of care on PGR in Czechia, we have managed to preserve most of indigenous Czech landraces which originated at the beginning of the last century.

Wheat collection is well documented (evaluation data are in a different extent available in 72.2 % accessions, pedigree data in 80% bred cultivars). The collection is almost completely stored in the Gene Bank in CRI Prague (97.7 % accessions).

With the aim to rationalise wheat genetic resources collection parallel “core” collections of winter and spring wheat have been established. The separate approach to winter and spring wheat was used to meet the specific demands of both forms on growing practices. The main objective of a “core” is to gather maximum of existing genetic diversity of entire collection in much smaller extent of accessions. The general method to reach “core” is a “clustering” of related accessions in such a way as to maximize the variation between clusters and minimize the variation within clusters. Precondition for rationalization of collection management is a reliable and sufficient characterization and evaluation information which allows perform analyses of genetic diversity in the collection. Beside morphological and agronomical data, protein and DNA markers also pedigree analyses have been employed during wheat “core” collection preparation in the Czech gene bank.

Entire winter wheat collection consisted of 5.857 accessions, among them evaluation data (in a different extent) were available in 69% accessions and pedigree was known in 55.5 % accessions. Because we did not have a capacity to characterize the entire collection by means of DNA markers, we had to apply a gradual approach based on the following steps:

1. Application of pedigree analyses (Martynov et al., 2003) to identify clusters and genetically distant accessions.
2. Collection curator, in consultations with other specialists and users, selected a broader set of “candidate” accessions for the “core” collection, using available passport and evaluation data, results of the pedigree analyses, characteristics of HMW-Glu subunits and personal experience. The selected set of 426 accessions was evaluated in the field trials (4 years, 2 sites). All accessions were characterized by DNA markers (SSR).
3. Using data on genetic distances among the accessions (based on the SSR markers and experimental data) we were able to reduce the set by 74 accessions. In the last step we completed the “core” by missing accessions carrying rare HMW-Glu alleles. The final “core” is composed of 380 accessions (6.5% of the entire collection)

Spring wheat collection comprised originally 4.252 accessions; 90% of them were described by characterization and evaluation data and the pedigree was available in 51%. We used the same

method to develop a “core” collection. Thanks to the almost complete evaluation data we were able to select a smaller set of 212 “candidate” accessions which could be further reduced by 28 accessions. The final “core” includes 184 accessions, that is 4.5% of the entire collection.

Limited extent of the “core” and complex data on all accessions have increased the value of wheat collection for users (breeders, researchers) and allowed to identify and describe the donors for breeding. E.g. valuable donors of grain quality, earliness and winter hardiness were identified among wheat landraces. High crude protein content (14 - 18%) was found in many landraces and obsolete cultivars. The acquired information also allowed to extend the knowledge on genetic diversity within collections.

Access to PGR in the wheat collection is specified in the documentation system on PGR (EVIGEZ) and guaranteed in harmony with ITPGRFA. Access can be restricted due to technical circumstances as limited stock or the need for regeneration of PGR. Currently 96.5% of gathered accessions are freely available to users. We gradually decrease these limits by regeneration and replenishment of seed samples in the gene bank, as well as by conservation of a satisfactory quantity of quality seeds. In the last 6 years 0.7 – 1.7 thousand of wheat samples were annually provided to local and foreign users, under terms of national legislation and International Treaty on PGRFA.

Recently, the seed samples of wheat genetic resources are provided for research (73%), breeding (7%), education (13%), at about 7% are used for regeneration and only very low share is used by farmers or in expositions.

Provided wheat genetic resources are used in practice in two main areas –

1. to increase diversity within species, mainly in bread wheat. For this purpose advanced cultivars are requested very frequently. Nevertheless, for this aim there are used also wild relatives as e.g. *Triticum monococcum* in breeding of Czech bread wheat cultivar ‘Vlasta’. High resistance to powdery mildew of this cultivar was transferred just from the wild relative. There is also possibility to select within multiline landraces specific lines having high quality parameters as crude protein content etc.
2. to extend spectra of cultivated wheat species. Small farmers are usually users of such wheat species as *T. spelta*, *T. dicoccon* or *T. monococcum*. Spelt wheat is greatly popular in the Czech Republic because of ‘spelt programme’ developed in cooperation with spelt processing company. Registered winter spelt cultivar Rubiota was bred using source from wheat collection. Also emmer wheat cultivar Rudico which is legally protected was developed on base wheat genetic resources.

With the aim to increase utility of plant genetic resources including wheat collection, the Czech genebank lay stress on availability of information

(database of genetic resources in Czech collections <http://genbank.vurv.cz/genetic/resources/>, European wheat database <http://genbank.vurv.cz/ewdb/>, wheat pedigree and identified alleles database <http://genbank.vurv.cz/wheat/pedigree/>) and high quality of provided seed samples.

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Standards and best practices for genebank management

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Key words: genebanks, standards, best practices, *ex situ* collections, seeds

Standards and best practices are both needed for germplasm conservation in genebanks. While standards are needed to ensure that the genetic integrity of conserved materials is maintained, best practices provide the means in achieving those standards and are often crop specific. The two are thus complementary. This paper describes the revisions being made to the current Genebank Standards (FAO/IPGRI 1994) and advancements in the development of best practices.

The first standards for genebanks were drawn in 1975 by the Panel of Experts on Plant Exploration and Introduction who made the first recommendations on preferred and acceptable standards. Ten years later, the IBPGR Advisory Committee on Seed Storage established standards not only for ensuring the integrity of plant genetic resources collections but also the safety of staff working in genebanks. In 1992 the FAO/IPGRI Experts Consultation Group on Genebank Standards refined the standards established in 1985, adapting them to the advances made in seed storage technology (FAO/IPGRI, 1994). Since then, those international standards are being followed in national, regional and international genebanks. Recently on request of the Twelfth Regular Session of the Commission on Genetic Resources for Food and Agriculture and the Governing Body of the International Treaty for Plant Genetic Resources for Food and Agriculture, FAO together with the International Treaty, Bioversity International, other CGIAR centres, the Global Crop Diversity Trust and other relevant national and international institutions started the process of revising the 1994 standards in the light of the changes in the global policy landscape and advances in the field of science and technology.

The draft revised Genebank Standards, like the previous edition, is composed of separate sections. However their structure and presentation have been improved to provide more specificity. The revised standards contain four main sections: Introduction, Underlying Principles, Standards and Appendices. The ‘Introduction’ covers the context of the revision and scope of the Standards. It is followed by the ‘Underlying Principles’, which provide a framework for setting the Standards and serve as the overarching principles of genebank management. The section on ‘Standards’ provides the specificity to adhere to the underlying principles. These Standards are presented upfront in a straightforward manner, followed by a narrative on technical aspects, contingencies and selected references.

The draft revised Genebank Standards do not distinguish between ‘preferred’ and ‘acceptable’ standards, used in the previous edition, mainly to avoid ambiguity or unnecessary duplications and to optimize the use of limited resources. The revised standards take into account the changes in *ex situ* conservation conditions, diversity in storage requirements, purpose and period of germplasm conservation. The revised standards are provided for nine areas related to germplasm stored as seed, that cover acquisition, seed drying and storage, viability monitoring, regeneration, characterization, documentation, distribution, safety duplication and security/personnel.

While the revised standards only cover orthodox species, the need for developing standards for the conservation of non-orthodox seeds and vegetatively propagating plants in field collections and/or *in vitro* and cryopreservation is recognized.

Best practices are methods by which standards are achieved in the most effective and efficient manner and ensure that results are achieved in a consistent manner across genebanks and at adequate quality level. In order to ensure that crop germplasm is being conserved in a consistent way, crop specific best practices for nine crops have been developed by experts of CGIAR centers and national genebanks under a World Bank funded project and coordinated by the System-wide Genetic Resources Programme. These best practices are available online through the Crop Genebank Knowledge Base (<http://cropgenebank.sgrp.cgiar.org>), a knowledge sharing web site developed within that same project. In addition to crop best practices the knowledge base provides a wealth of knowledge and resources for *ex situ* conservation of germplasm. The web site is being updated and expanded, is open to contributions from the whole *ex situ* conservation community and can serve as one of the major resources to assist genebanks in the implementation of the standards.

A European Genebank Integrated System (AEGIS): concept and reality

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Key words: plant genetic resources for food and agriculture; genebanks; germplasm collections; Europe Collaborative Programme for Plant Genetic Resources (ECPGR); AEGIS; European Collection; quality management system; International Treaty.

Germplasm collections began to be established in Europe at the time Vavilov conducted his research on centres of diversity in the 1920s and 1930s. Collections aimed to provide a wider genetic base to the breeding programmes. Following the recognition that traditional crop varieties and adapted landraces were being replaced by new improved varieties, systematic germplasm conservation activities were initiated in the 1940s and new genebanks established in the 1960s and 1970s. Collecting missions of predominantly landrace material and crop wild relatives (CWRs) for many of the major European food crops were also being organized by the respective centres of diversity. National sovereign rights and responsibilities over genetic resources, as defined by the Convention on Biodiversity, promoted the establishment of more national genebanks in the 1990s. Collecting of national material, as well as acquisitions, from international genebanks raised the number of accessions in Europe to an estimated two million, conserved in 625 genebanks or germplasm collections, according to the FAO State of the World Report II in 2010. A little more than half (1,084,671) are reported today in EURISCO. On the basis of existing passport data, germplasm conserved in the country of origin represents 28% of the total (and can be seen as an indicator of minimum level of uniqueness), varying from 22% in northern countries to 54% in southern countries. An estimated 32.5% has been obtained through collecting (i.e. CWR and landrace material). These data are compatible with past estimates that only 30-40% of all European accessions are unique.

From a regional perspective, the level of unwanted duplication of germplasm accessions between collections is only one of the aspects of possible inefficiency in the management of collections. Other elements of inefficiency that have been frequently expressed by European PGR conservation systems are the difficulties to properly maintain genetic resources at a homogeneous and high quality level across Europe, as well as the insufficient level and quality of the existing information on the identity and breeding value of the material conserved. Availability of the material under clear and uniform terms and conditions has also been an uncertainty and a constraint for potential users.

With the establishment of the International Treaty in 2004, a common policy on access and benefit sharing became a reality. This result encouraged countries to operate collaboratively towards a public domain Multilateral System and further strengthened the recognized requirement to increase the sharing of responsibilities among European countries in the conservation and use of PGRFA. This resulted in a decision by the ECPGR Steering Committee (SC) to create a European Genebank Integrated System (AEGIS) in order to allow all designated germplasm accessions and their related information to be readily available and easily accessible to users; the *ex situ* conservation of germplasm to be carried out according to common, agreed quality standards, independently of where the germplasm is physically located; to provide close linkages with *in situ* conservation; and to facilitate the use of and research into the germplasm. It is intended to develop AEGIS, as far as possible, within the existing organizational structures of ECPGR and to use the legal framework of the International Treaty, extending its scope to non-Annex 1 crops, according to the spirit and intentions of the Treaty. To

this end, and to formally establish AEGIS, a Memorandum of Understanding, concluded with individual countries, provides a legal basis for collaboration and includes Associate Membership agreements with collaborating genebanks at the national level, aimed at conserving the identified unique accessions for the long-term and making them readily available. The totality of these unique accessions will form the European Collection that will be managed as a dispersed collection according to agreed technical standards and procedures that make up a quality management system. The SC will oversee AEGIS, whilst the Advisory Committee will provide day-to-day supervision and the existing ECPGR Networks and Working Groups (WGs) will play a key technical role in its operation.

At present, 26 countries have signed the MOU and a total of 19 Associate Membership agreements have been concluded in 10 countries. Selection requirements that have to be met for all the European Accessions have been endorsed by the SC. A simplified procedure to select European Accessions through an iterative process between countries and WGs has been agreed, as well as implementing a framework for the quality management system (i.e. AQUAS).. For the generic genebank standards it has been decided to join the ongoing FAO updating process of the existing Genebank Standards, whereas the WGs are requested to lead the process of preparing crop specific technical standards.

The SC has accorded high priority to the implementation of AEGIS and this has been fully endorsed by the recent ECPGR External Review. Consequently, the SC allocated funds to AEGIS, including for a competitive grant scheme. Nevertheless, a number of difficulties and constraints have been encountered in the development process. The current speed of developing the various components and processes for the establishment of AEGIS are slow and sometimes cumbersome. Possible reasons for this could be lack of sufficient funds to conduct the AEGIS related work and/or to fund required molecular analysis at the accession level, the importance accorded to identify unique accessions in the absence of adequate passport data, and the time limitations surrounding individual scientists. Furthermore, progress is also constrained by the fact that not all countries and genebanks are actively engaged, and in the identification process of European Accessions, it has become apparent that the data quality and coverage in EURISCO and the Central Crop Databases is, in many instances, inadequate. Therefore, it was proposed to start determining concrete portions of the European Collections for a given crop for which information suffices and to make efforts to define, agree and apply the crop specific quality standards.

In summary, AEGIS provides an important mechanism to assist in the implementation of the International Treaty in the European region. The Standard Material Transfer Agreement has been adopted for the exchange of germplasm, extending its applicability in principle also to non-Annex I material that will be registered as part of the European Collection. It is expected that the European conservation method will be able to demonstrate the feasibility of a regional approach to the rational management of a regional collection. Ease of access to high quality germplasm, together with related information, is expected to be the most visible output of AEGIS in the short-term. The establishment of the European Collection should also be an attractive argument for obtaining funding for projects such as evaluation of collections, including genotyping and phenotyping activities at the regional level, as well as working towards sustainable sources of funding for long-term conservation.

The Dutch German collaboration on Plant Genetic Resources

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Key words: genebank, collaboration, AEGIS

The Dutch German collaboration on Plant Genetic Resources (PGR) effectively started 1974. It was initiated by the two Ministries of Agriculture from the Federal Republic of Germany and the Netherlands, who had annual meetings in the German Dutch Commission for Agricultural Research (since 1968), which should promote the collaboration between the two countries in the field of Agriculture. The acquisition, maintenance and evaluation of PGR was considered to be a strategic task supporting food security, from which private breeding companies, consumers and the environment could also profit.

In the preceding years a Europe wide initiative on *Solanum* PGR had been discussed, following the idea of crop specific collaboration and concentrating the work in regional genebanks. For example at a meeting at the OECD in Paris in 1971 (with prof. Hawkes representing EUCARPIA) the establishment of a European *Solanum* Germplasm station was discussed. It included a common potato collection in Braunschweig (Germany) and targeted for tomato conservation at regional genebanks in Izmir (Turkey), responsible for the eastern Mediterranean, and Bari (Italy) responsible for the central and western Mediterranean. The European countries were interested but reluctant in making (financial) commitments, possibly also being afraid that their national institution working in this field would be marginalized. For potato, only the negotiations between Germany and the Netherlands continued, involving e.g. a documentation specialist as well as potato researchers discussing the traits to be evaluated and the screening methods.

February 1974 the bilateral agreement was signed by the Ministers of Agriculture and the German Dutch collaboration on potato genetic resources started. Any wild and primitive potato material from within the sphere of competence of the two ministers would be placed at the disposal of the collaboration in Braunschweig. A Programming Board to guide the work was established. Its members included a representative of both Ministries, the directors of the cooperating Institute of Crop Science and Plant Breeding (FAL, Braunschweig) and the Foundation of Plant breeding (SVP, Wageningen) as well as two potato researchers from each country. The Board had to report to the German Dutch Commission for Agricultural Research. The costs of the collaboration were to be split between the two countries. Besides the pure genebank tasks, also some research (on hard to cross species was) foreseen. In September 1974 a Dutch scientist moved to Braunschweig and the Dutch German potato collection started to operate with the scientist acting as curator. The working collections Erwin Bauer Sortiment (EBS) and Wageningse Aardappel Collectie (WAC) from the Max Planck Institute (MPI, Köln) and the Institute for Plant breeding (IvP, Wageningen) were merged in the national German genebank at Braunschweig-Völkenrode. Additional germplasm collected during expeditions (1974/75; 1980; 1993/94; 1995; 1996) was included. The collection was rationalized by identifying probable redundancy, based on passport data. Research and breeding institutes from both countries contributed to the collaboration by extensively evaluating the germplasm on

disease resistance and quality traits. In those days the research institutes were almost completely financed by national governments. 1984 the Programming Board was replaced by a Board of trustees.

In 1986 the collaboration was extended to *Beta* and *Cichorium* and a German scientist moved to Wageningen, to join CGN and become curator of the common beet collection. A series of *Beta* collecting expeditions were organized. Private breeding companies supported the screening of the germplasm. Besides the running program, the Board of trustees also discussed PGR developments and possible collaborations in other crops (*Brassica*'s, *Lolium*, oat, etc.). It clearly was in favor of concentrating the management of PGR per crop. Behind the scenes, it was a driving force in pushing the EU to start the GENRES program in 1995.

The PGR and crop research landscape changed in Germany after its reunification in 1989. In 1991 the *Beta* collection moved to Braunschweig and in 1995 the potato collection moved to Wageningen, following its repatriating curators. The common collections were integrated in the national genebanks. The last Board meeting took place in 1999.

The German Dutch cooperation was worldwide recognized as an excellent example of collaboration in the field of PGR, and it was mainly due to the changing political situation in Germany that it ended. However, many lessons regarding collaborations between genebanks can be learned; the lessons for AEGIS will be discussed.

EVA II: A German network for the use of PGR in resistance breeding

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Key words: evaluation, disease resistance, national network, plant genetic resources

To improve a crop or enhance its resistance to diseases, plant breeders frequently increase the genetic diversity in their breeding populations using plant genetic resources (PGR) either stored in gene banks or selected and maintained by farmers. In order to be able to select appropriate genotypes, breeders have to rely on information describing their traits (e.g. characterization and evaluation data).

In the past, huge amounts of evaluation data for PGR have been generated for various species, but the use of these historic data for breeders is often very limited, mainly caused by a lack of comparability caused by varying and poorly documented test conditions. The EVA II network aims to provide plant breeders with accelerated access to reliable evaluation data and to resistant genotypes, thereby supporting the sustainability of agriculture by increasing the genetic diversity present in cultivars. The overall goal of EVA II is a better transfer and dissemination of new resistance genes into commercial breeding programs. For this purpose, a system for secondary evaluations of wheat and barley was established. A Network of fifteen private German cereal breeders mostly organized in the “German Federation of Private Plant Breeders (GFP)”, Bonn, and three research institutes conduct evaluation trials for scoring resistance and collect data. Resistance to most important fungal pathogens in wheat and barley are scored in multi-site field trials. Standard varieties (susceptible/resistant) for each pathogen are included in order to characterize the infestation conditions of all sites. Usually, micro-plots of 1m² in one or several replications. Each partner screens the whole set for all the relevant diseases according to a standardized systems for resistance evaluation. For wheat and barley (both spring and winter forms) sets of a maximum of 50 genotypes are tested each year. The genotypes are chosen by reference to earlier disease evaluations or known resistances. The sets consist of PGR as well as foreign varieties and pre-breeding material from research projects. The contributing partners also may supply the network with their own breeding material. Prepared Excel-files to assist data compilation, and relevant pedigree and resistance information are sent to all partners together with the seeds by the Institute for Resistance Research and Stress Tolerance of the Julius Kuehn-Institute (JKI) as the coordinator of the EVA II network. Evaluation scoring will be made by % infected leaf area or scores (1-9) with three replications over time to assess also quantitative resistance. The results are compiled by JKI and shared among the project partners for direct use in their own breeding programs. An state-of-the-art information system is under development and will allow the participants in the network to browse the results online and to up- and download data. After a defined period (3 years) the data will be made public. The conditions of the cooperation are regulated by a contract between all partners; the most important detail is the right of the breeders to use all of the screened material for their own breeding programs and the obligation to score a defined minimum of the cereal sets. Thus, the EVA II network acts for the mutual benefit of all participants.

Whither Genebanks?

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Key words: collections, conservation, crop, *ex situ*, genebank, genetic resources, germplasm, information system, *in vitro*, pre-breeding, seed, wild relative

FAO's 2nd Report on the State of the World's Plant Genetic Resources (SoW-2), 2010, states that some 7.4 million accessions are currently held in 1,750 genebanks worldwide, an increase of 23% since the first SoW report (1996). However, SoW-2 estimated that from 1996 to 2007 only about 240,000 new accessions were collected, implying that the majority of the additional 1.4 million accessions in genebanks resulted from the duplication of existing accessions rather than the conservation of new ones. Only about 25-30% of the total world holdings are thought to be distinct. Cereals, food legumes and forages still account for more than 75% of all material conserved with vegetatively propagated, recalcitrant seeded and minor crops, as well as wild relatives, remaining under-represented.

There is still a lack of reliable information on the nature, structure and status of many collections, and most of the SoW-2 information on trends had to rely on data from the international genebanks and a small sample of national genebanks. It would be extremely helpful for future planning to have more, and more accurate data.

SoW-2 identified the following priority needs for future *ex situ* conservation:

- Increased institutional and human capacity to conserve and use PGRFA;
- Additional, sustainable financial support;
- Major gaps in *ex situ* collections identified (especially of minor crops and wild relatives);
- Better feedback from recipients of materials on their needs;
- A more rational global system of *ex situ* collections developed and implemented;
- Unintended duplication reduced and increase levels of safety duplication attained;
- Characterization, evaluation and documentation all improved;
- Data standardized data management systems made more compatible;
- Regeneration backlogs reduced;
- Awareness raised of the importance of conserving and using PGRFA.

The CGIAR Collections and those maintained by AVRDC remain the world's largest and most widely used internationally held collections. Comprising some 3,200 species of more than 500 genera, they have grown from 627,000 accessions in 1995 to 743,000 in 2008 and are expected to exceed 800,000 by 2015. They currently distribute more than 100,000 samples per year, more than half to external recipients in developing countries. The recent CGIAR reforms have resulted in a new strategy (the 'Strategy and Results Framework') with the research being carried out through a small number of 'CGIAR Research Programmes' (CRPs). While much of the evaluation, pre-breeding and breeding work involving the Centres' collections will now be carried out within specific CRPs, basic curation will fall outside their scope. With the demise of the Systemwide Genetic Resources Programme, the CGIAR is currently exploring new funding, coordination and management mechanisms to ensure the Centres continue to meet their obligations under the International Treaty. A recent study concluded that approx. US\$15 million

are required annually for the CGIAR’s basic conservation activities, with a further US\$3 million for other critical activities such as collecting, training, and providing global leadership.

Several important institutional developments have taken place in recent years that have significant implications for the future of *ex situ* conservation. Among the most important are:

- The Global Crop Diversity Trust, an essential element of the Funding Strategy of the Treaty, was established in 2004 to support, in perpetuity, the conservation and distribution of the world’s most important collections of PGRFA. In addition to providing grants for long-term conservation, the Trust supports other activities such as regeneration, information systems and the conservation Crop Wild Relatives. To date almost \$220 million have been pledged with more than US\$155 million already received.
- The Svalbard Global Seed Vault is a unique international facility that serves as a safety net for collections worldwide. Built in 2008 by the Norwegian Government in the permafrost, 100 meters into the side of a mountain on the island of Spitsbergen, SGSV currently houses more than 600,000 duplicate seed samples.
- The Millennium Seed Bank, established by the Royal Botanical Gardens, Kew in 2,000 has to date conserved seed samples of more than 28,000 species. It aims, by 2020 to have conserved more than 60,000 species (25% of all flowering plants). This is particularly significant given the growing importance of wild relatives as a source of novel traits.

To develop a more rational global system for conserving PGRFA, as called for in the Global Plan of Action and the International Treaty, many issues still need to be addressed and an international consensus reached. Not all genebanks can, or should, carry out all functions equally. A rational system needs to build on institutional strengths and comparative advantages in a spirit of mutual cooperation and support. Agreement is needed on the future role of different types of genebank and the division of roles and responsibilities among them with respect to the conservation of different crops, for example:

- Should resource-poor national genebanks concentrate more on providing support to farmers and breeders nationally, through the maintenance and distribution of materials of immediate interest, in both minor and major crops, and largely leave to others the task of long-term conservation and international distribution? Should such genebanks strengthen their role as a conduit for materials to and from abroad and as conservers of indigenous knowledge?
- To what extent should the larger national and international genebanks become more involved in evaluation and pre-breeding and in the management of comprehensive, international information systems?
- To what extent should international collections be dispersed among different genebanks or consolidated? (e.g. in response to human and financial resource availability, management efficiency, or to meet quarantine concerns).
- Will it be necessary to handle crops that are included within the multilateral system of the international treaty differently from those that are outside the system?
- Can systems for safety duplication be made more efficient and effective?
- Various technical issues also require attention such as: how much and what type of material should be conserved, and how? When should conservation focus on alleles rather than genotypes? How much effort should be put into conserving wild compared to domestic germplasm? How much effort should go into increasing efficiency, e.g. through eliminating duplicates, increasing regeneration intervals, and/or cleaning samples from disease?

Many of these issues have been addressed for specific crops (and regions) in the conservation strategies supported and published by the Global Crop Diversity Trust. However, much more remains to be done to get a greater buy-in to the agreed strategic approaches, to extend them to many more crops and, above all, to ensure they are fully and effectively implemented.

Quality management at the Centre for Genetic Resources, The Netherlands

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Key words: QMS, quality management, genebank

Genebanks play an important role in safeguarding the world's food security and assuring economic interests of the agricultural sector. Therefore many countries have committed themselves to contribute to the conservation of those resources. In the Netherlands, the government sees this contribution as one of its 'legal tasks', a task that is delegated to the Centre for Genetic Resources, The Netherlands. Since it is a legal task CGN has to implement and use a Quality Management System (QMS) to assure that it is done at a sufficient quality level.

The implementation of the QMS at CGN in 2004/2005 was a difficult process that was only possible thanks to the support of a specialized company experienced in implementing QMS in organizations (van Ravensteijn & Partners). Given the nature of the genebank operation, it was decided to use the methodology of ISO9001:2000. Based on the requirements of ISO9001:2000 the implementation process involved proper and detailed description of the management (policy, funding, project management, etc.), organization and staff (structure, responsibilities, expertise and competences, training, etc.), administration (documents and data, resources, public relations, outsourcing, etc), improvement activities, and finally the genebank-specific parts, one for each of the three domains that CGN is involved in, i.e., crop plants, animals and forest genetic resources. The crop genebank specific part involved a large set of flow charts describing in increasing level of details how the genebank operates. At the lowest level of detail are textual descriptions of the activities such as the 'Protocol for wet-process cleaning of seed' or the 'Procedures for updating GENIS data on the Internet' (GENIS is the CGN documentation system). These detailed protocols and procedures allow the processes to be studied, monitored and improved in detail, are useful for instructing new staff, and form the basis of out-sourcing the activities if activities can not be done in-house or if out-sourcing is more efficient. Since the QMS is audited twice each year, in an internal and an external audit, it also creates a transparent basis for the funding body and potential collaborators to judge if the work is done at an appropriate quality level.

Initially, the staff of CGN had mixed feelings about the implementation of a QMS, some were eager to start whereas others were very reluctant. It became clear very quickly that during the implementation phase it would involve a lot of additional work to describe all activities, and a lot of administration during the operational phase. By some, the transparency was perceived as a threat. Some feared that the strict procedures would make work less interesting and very bureaucratic. Especially the introduction of performance indicators (PIs) received much opposition, some staff perceived these PIs as showing lack of confidence. However, discussing the flow-diagrams and describing and discussing the activities was also experienced as stimulating; domains that so far were never entered by colleagues were suddenly openly discussed, and it appeared that there was generally great appreciation, if not admiration for the way things were done. In some cases weak spots appeared, that were improved immediately. An example of a weak spot is the procedure involving the backup of the documentation system.

Every day a backup was made and properly stored, however, it appeared that no one ever checked if these backups could actually be restored!

Once the manual of the QMS was created and all new procedures were implemented, CGN was certified. In December 2005, the large German technical inspection organization RWTÜV audited and certified CGN. CGN was the first genebank with a certified QMS !

From that point on, CGN has been operating under a QMS. Staff is moderately positive. Especially the handling of feedback and complains is appreciated: every feedback and complaint is handled seriously, usually resulting in improvements in the procedures. The administrative burden varies from process to process.

The QMS continues to evolve. As the ISO norms slightly change over the years (CGN started with ISO9001:2000 and was recently re-certified under ISO9001:2008) the requirements also change. In case some processes have been described in too much detail, they are simplified, whereas at times protocols and procedures are added or modified. This can be based on feedback from the audits (‘Procedure for status change of CGN accessions’) but also on initiative of the staff who sees that recording procedures makes it easier to remember how it should be done (‘Protocol for approaching GENIS passport data via web-services’).

The rule of thumb that a QMS costs c. 10% of an annual budget to be implemented and 5% to be run has proven valid for CGN. The benefits are more difficult to calculate. It is undisputable that the quality of the CGN operations have improved since the implementation and operation of a QMS. Also undisputable, from the perspective of CGN, is the conviction that collaboration between genebanks is mainly hindered by the lack of transparency regarding the quality of the operations, an obstacle that can be resolved by the implementation of a QMS.

The political context of PGR conservation: CBD, ITPGRFA, ABS and other acronyms

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Key words: access and benefit sharing (ABS), Convention on Biological Diversity (CBD) International Treaty on Plant Genetic Resources for Food and Agriculture (IT PGRFA), Nagoya Protocol, Standard Material Transfer Agreement (SMTA), multilateral system, plant breeding

Participating as breeding sector in the negotiations on access and benefit sharing (ABS) has been interesting but also frustrating. In this presentation an overview will be given on the political negotiations with regard to ABS during the last 10 years through the authors eyes.

With the adoption of the Convention on Biological Diversity (CBD) in 1992, the discussions on ABS started. Access and fair and equitable benefit sharing arising out of the utilization of genetic resources is one of the objectives of the CBD next to the two objectives on the conservation and sustainable use of the components of biological diversity.

The text of the CBD was not sufficient for most member countries to appoint national focal points and competent authorities and/or establish national rules and legislation on ABS. Also the Bonn guidelines on tools for implementation of national ABS legislation did not really stimulate member countries to establish clear and practical national rules and regulations. Especially, the developing countries felt that benefits were not received and therefore were in favour of binding rules on benefit sharing. This resulted in the adoption of Nagoya Protocol on ABS in October 2010. It is now up to member countries to develop national rules and regulations on ABS to make ABS work in practice. It is the question if this will happen or that member countries will await new tools such as the proposed Global Multilateral Benefit Sharing Mechanism in the Nagoya Protocol.

With the coming into force of the CBD, the International Undertaking (IU) had to be revised. The IU, a voluntary agreement to ensure that plant genetic resources of economic and/or social interest, particularly for agriculture, would be explored, preserved, evaluated and made available for plant breeding and scientific purposes was used as a basis to negotiate the International Treaty on Plant genetic Resources for Food and Agriculture (IT PGRFA). The IT PGRFA maintained the spirit of the IU, but is now in line with the CBD. One of the core elements in the IT PGRFA is the Multilateral System (MS). The idea of the MS is to develop an efficient, effective and transparent system both to facilitate access to plant genetic resources for food and agriculture, and to share the benefits arising from the utilization of these resources. The ratification of the IT PGRFA in 2004 did not result in implementation of the MS. Only when the Standard Material Transfer Agreement (SMTA) was approved in 2006, a standard contract for ABS, the implementation of the MS started, in particular in developed countries. However, unfortunately, a lot of countries that ratified the IT PGRFA have not fulfilled their obligations of enclosing their genetic resources in the public domain in the multilateral system. Reasons could be for example the lack of capacity, lack of trust in benefit sharing, more expectations from the Nagoya Protocol, and national legal difficulties. Also the lack of further elaboration of certain elements of the IT PGRFA such as farmers' rights, sustainable use, compliance and financial rules and funding strategy may limit further implementation of the MS.

As the plant breeding sector is creating genetic resources from genetic resources, the sector has participated in the negotiations of the ABS tools to explain the functioning of the breeding sector, the responsibility of the breeding sector on conservation and sustainable use,

the complexity of the use of genetic resources in their work, existing practices on benefit sharing, and common business practices on contracts in order to defend their interests. The role of the seed sector was specifically important in the breakthrough on the text of the IT PGRFA on sharing of monetary and other benefits of commercialization. In addition, they contributed a lot in the development of the SMTA.

The outcomes of the negotiations and in particular the lack of implementation of ABS rules and regulations have or may have consequences for the daily activities of the breeders. Through the CBD access to new genetic resources has been limited if not impossible. Only in a few cases it has been possible to establish an agreement on ABS through the CBD. In many more cases negotiations have been stopped or could not even be started as competent authorities could not be found and/or the inability of the competent authority to take the responsibility to finalize an ABS contract.

The Nagoya protocol still results in a lot of uncertainty with regard to ABS, in particular related to implementation of national rules and regulations, checkpoints and certificates and compliance.

Through the implementation of the IT PGRFA more ABS agreements could be made with the help of the SMTA. Unfortunately, the use of the SMTA is limited to a small group of food crops represented in Annex 1 of the ITPGRFA. This list does not include soy beans, various important vegetable and fruit crops and the ornamentals. Fortunately, several European and North American countries use the conditions of the SMTA also for non-Annex 1 crops. Even though the implementation is limited the multilateral system of the IT PGRFA seems to be a workable ABS system for the breeding sector and therefore the breeding sector would like to extend it to all breeding activities for all crops.

Notwithstanding the obligations of the conventions, seed companies continue with several benefit sharing activities that take place for a long time. Breeders constantly develop new varieties that are adapted to farmers and consumers' need. Moreover, most modern varieties can be used freely for further research and breeding. Breeding companies also support several gene banks in the multiplication, characterization and collection of genetic resources, support development projects, and contributed to the Global Crop Diversity Trust. However, some other benefit sharing projects have come to a halt because of the lack of implementation of ABS rules.

So, two conventions on conservation and sustainable use of biodiversity and on facilitated access and fair and equitable benefit sharing exist. However, implementation of the conventions in particular related to ABS has been limited. There seems an unstoppable need for further tools, capacity building, benefit sharing and even maybe a need for compensation for inequity in the world, before ABS is made workable in practice.

The author is also concerned that the negotiations on ABS have a negative impact on the conservation of genetic resources. Signals are received, also from seed companies, that genetic resources are being lost or destroyed, while nothing could be done due to lack of ABS rules and regulations. The author wishes therefore that the ABS conventions do not further get politicized. A suggestion to prevent this could be the establishment of an agreement on the solution for inequity in the world, as this seems to be an issue for many participants in the negotiations.

Utilization of plant genetic resources at the Vegetable and Ornamental Plant Institute of the ARC

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Key words: certification scheme, potato, sweet potato, indigenous vegetables, flower bulbs, medicinal plants

The Roodeplaat Vegetable and Ornamental Plant Institute of the Agricultural Research Council (ARC-Roodeplaat), maintains more than 9000 different accessions of various plant species. These include accessions of potato, sweet potato, indigenous and traditional vegetables, indigenous flower bulbs and various medicinal plants. Most of these collections are linked to active research programs at the institute with direct utilization in either breeding programs, or cultivation research.

A number of these collections originated to supply material for breeding programs at the ARC. Material maintained are collected in nature, obtained from other genebanks or developed through breeding. Currently the potato, sweet potato and flower bulb genebanks are still actively utilized for breeding purposes. The utilization of material leads to the generation of new cultivars that address the needs of the various industries in terms of appearance, taste, cultivation requirements and disease tolerance.

Besides the supply of genetic material for breeding programs the genebanks also supply material for cultivation trials on water use, fertilization, spacing, drought tolerance and production methods. The genebanks are further more an important source of material for trials on the identification, control and development of different pest and disease complexes. Most of the material utilized for these trials is multiplied from the genebank and supplied on annual basis for trials.

The Plant Genetic Resources at ARC-Roodeplaat thus plays an important role in the availability of material for research purposes. Material is supplied to other institutes within the organization, but also to external research organizations including universities and other research councils. In some of these cases the supply of material is linked to co-operative research projects, but quite often the material is utilized for basic research purposes and post graduate studies.

Material from the genebanks is also utilized to assist in the sustainability of commercial and informal industries. ARC-Roodeplaat is the only source of disease free potato and sweet potato cultivar material in South Africa. The genebank thus serves as the starting point of the potato certification scheme and ensures that the potato industry receives quality material to sustain good harvests and meet the demand for production. Similarly the genebank also supply disease free sweet potato and flower bulb material to the different industries, again supporting profitable production of material.

The use of quality starting material is just as important for small-scale and upcoming farmers. Once again the genebank plays an integral role in the supply of disease free material to sweet potato nurseries in various rural areas. These sweet potato nurseries supply clean material to farmers to improve their sustainability. The genebank in this way thus plays an indirect role in improving the food security in rural areas. Besides sweet potato, seed of other indigenous vegetables are also supplied for the establishment of food gardens at schools and in various rural communities to address food security and nutritional issues.

In the indigenous vegetable, indigenous flower bulb and medicinal plant genebanks, characterization of accessions is an important aspect of sustainable maintenance. Very little information is available on many of these species and most of them do not even have descriptor lists for characterization. To optimize the utilization of these plants there is a need for research on their variation in terms of phenotype, genotype, multiplication, production and pest and disease occurrence. The availability of this basic information can assist in the planning of crossing strategies, the selection of superior lines, the establishment of basic cultivation requirements and the identification and control of pests and diseases.

The indigenous vegetable genebank is of specific importance as it is the only source of certain seed available in the country. This leads to requests for seed from a variety of role-players ranging from home-gardeners to community projects to universities. Evaluation of material in this genebank for post-harvest cooking and storage properties plays an important role in the improvement of the utilization of these crops. The preference for certain tastes/crops can vary from area to area and among different cultural groupings. The availability of information thus assists researchers in recommending certain crops for certain areas and indicates the more widely accepted crops for possible promotion as more commercial crops.

Medicinal plants are still utilized extensively in South Africa as a source of health care. Unfortunately some of these plants have been harvested to the brink of extinction. The maintenance of important medicinal plants in genebanks and the establishment of production procedures have thus become extremely important. Basic information on seed germination requirements and other multiplication methods has to be developed to improve the utilization of these plants. The establishment of characterization criteria is receiving attention and material is furthermore supplied for trials to determine what the effect of cultivation practices are on the medicinal activity of the plants.

In conclusion, the plant genetic resources maintained in genebanks at the ARC-Roodeplaat are utilized in various different ways and very little of the research conducted would have been possible without these resources. Utilization can still be increased with the establishment of specific characterization protocols (especially on the lesser researched indigenous crops), the development of multiplication protocols and the establishment of basic information on various aspects of cultivation, pest and disease occurrence and post-harvest requirements.

Quality standards in genebanks – improvement of sustainability of plant genetic resources

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Key words: documentation, genebank, ISO 9001, quality management system

Globally germplasm collections contain more than 7.4 million accessions of plant genetic resources. Wheat represents the biggest group with about 860,000 accessions followed by rice (775,000 accessions) and barley (470,000 accessions). The largest collections worldwide are in the USA (509,000 accessions), China (392,000 accessions) and India (366,000 accessions) (FAO 2009). The German *ex situ* genebank, located at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany, is one of the ten largest global collections. About 150,000 accessions are maintained including cereals (65,000), legumes (28,000), vegetables (18,000), forage crops (14,000), oil crops (8,000), potatoes (6,000) and medicinal and spice plants (6,000). This collection comprises wild and primitive forms, landraces as well as old and more recent cultivars of cultivated plants. Wheat is the major crop having almost 30,000 accessions. Beside the long term storage and frequent regeneration of the material phenotypic characterisation and evaluation data are collected (Börner 2006). Having such big collections worldwide it is necessary to define general, well documented standards in order to improve the quality of the assortments and to simplify the exchange between genebanks itself and between genebanks and users. Clear organizational strategies and goals, efficient and transparent processes, measurable results and continual improvement characterize an effective quality management system. The benefits are (1) to increase the customer satisfaction (2) to create clear responsibilities (3) to motivate the employees (4) to reduce costs by avoiding errors (5) to improve competitive ability (6) to reduce risks (7) to improve the image. These seven points are the advantages of an efficient quality management system. Today, the ISO 9000 series of standards has a high level for significance for international business. They are a universal means of communication as well as a contract tool that is widely understood in all languages and cultures. They are the gateway to new markets and customers and their use will continue to increase along with the need for worldwide trade. The establishment of a quality management system and a certification according to ISO 9001:2008 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 plant genetic resources.

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Temperate forage and pulse legume genetic gap analysis

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Keywords: legume, wild relatives, genetic resources, conservation, protected area.

Wild legume species and genetic diversity of the Mediterranean Basin provide an invaluable source of traits for the improvement of cultivated temperate forage and pulse legume crops. The research illustrates how the existing geo-referenced passport data associated for *Cicer*, *Lathyrus*, *Lens*, *Medicago*, *Pisum* and *Vicia* species can be used to identify gaps in current *ex situ* conservation and develop a more systematic *in situ* conservation strategy for both the genera individually and for all six genera combined.

Taxonomic, ecological, geographic and conservation information for the six genera were collated from ICARDA and GBIF datasets as well as datasets collected by the authors over the last 25 years. The combined database contained 200,281 unique geo-referenced records (*Cicer* - 452, *Lathyrus* - 61,081, *Lens* - 672, *Medicago* - 42,248, *Pisum* - 728 and *Vicia* - 95,100) collected between 1884 and 2008. Patterns of specific richness, based on the germplasm accession and herbarium specimen data, were analysed and *in situ* hotspots identified using complementarity analysis. The *ex situ* conservation status of each genus was assessed and used to provide a priority ranking for future collection priorities in the Mediterranean Basin. Specifically, target IUCN-recognised protected areas are identified as potential sites to establish genetic reserves. However, the premier temperate forage and pulse legume hotspot on the Syrian/Lebanese border is not coincident with any existing internationally recognised protected areas and here there is a need to establish a novel protected area.

The challenges of molecular genetics for genebanks

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Key words: SNP genotyping, next-generation sequencing (NGS), genotype-to-phenotype, rice

The recent advances in sequencing and genotyping technologies have accelerated the pace of molecular characterization of accessions and derivative genetic stocks leading to an imminent deluge of billions of datapoints and thousands of sequences. Curation and analysis of this data must be addressed for immediate value to germplasm conservation and utilization. A new mandate for germplasm conservation is to combine the data with accurate, replicated, and detailed phenotypes so that the genotype-to-phenotype divide is bridged through association genetics. These technologies also provide opportunities to quantify and reveal the basis of hidden variation in genebanks and to create novel allelic combinations that through genotyping and phenotyping will facilitate more effective use of their donors. All of these issues demand creation, adoption, and delivery of extensible databases and tools to facilitate accessing germplasm from the genotype/phenotype landscape.

The International Rice Genebank (IRG) collection located in IRRI's T.T. Chang Genetic Resource Center holds ~112,000 accessions. Under the Global Rice Science Partnership or GRiSP (a CG research program involving IRRI, AfricaRice, CIAT, CIRAD, IRD, JIRCAS, EMBRAPA and other partners), projects are underway to genotype, sequence, phenotype, and expand these germplasm resources: 1) We are genotyping 2,000 diverse genetic stocks with 1 million SNPs with partners from GRiSP, Cornell University, USDA, Syngenta, Bayer CropSciences among others (www.ricesnp.org). 2) Whole genome sequencing of 10,000 genomes is underway using NGS with BGI-Shenzhen and the CAAS, 3) A global network for phenotyping in multi-environment trials is being established so that genome-wide association studies may be achieved, and 4) Specialized populations are under development for enhancing gene discovery and breeding such as RIL and MAGIC populations from cultivated and wild founders.

Key to all of this is accurate tracking of samples from seed to plant to tissue to DNA so resulting information is linked to the correct entities without error. Sample tracking among collaborators is necessary at finer precision than accession-level tracking provided by Multi-Crop Passport Descriptors. Individual seed lots must be documented, and the derivation of pure lines selected from accessions must be described as well as how they are conserved separately from their parent accessions. The IRG database has been migrated to the International Rice Information System (IRIS) where a Genealogy Management System provides a generalized sample tracking system unifying acquisition, multiplication, pure line selection, hybridization, tissue archiving, and DNA extraction. IRIS is also being extended to support high-density SNP data. Assembled and annotated genomes must be linked to germplasm, pedigree, and passport information. A federated system with common identifiers among databases may be the pragmatic, short-term approach. Recognizing that accession identifiers are no longer sufficient, the first requirement will be to agree and establish a new ontology for sample types. However, the biggest challenge will be to instantiate an expert system to glean and deliver the information needed by the end-users of genetic resources. An out-of-the-box approach might be to create a 'kernel' of data and code that will allow integration, computation, modification, extension and access to germplasm information in a dynamic manner instead of 'yet another database'.

Lessons learned from the 2010 ECPGR review

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Key words: ECPGR review, lessons learned, genetic resources, crop wild relatives, institutionalization, policy making

As a member of the 2010 Independent External Review of the European Cooperative Program for Crop Genetic Resources (ECPGR) I took some time to update my understanding of the role and importance of crop genetic resources for food and agriculture.

There is no doubt that crop genetic resources, both *in situ* and *ex situ*, represent a valuable source and reservoir of genetic diversity, which have played and will continue to play an important role in current and future plant breeding. During the external review I made a number of observations, which might improve the conservation and utilization of these genetic resources in Europe. The most important are:

- The number of collections is very high and should be drastically reduced through consolidation and integration, resulting in a far higher efficiency of management and access regimes of these collections,
- Whereas *in situ* and *ex situ* genetic diversity represent a continuum, there is far more attention for *ex situ* than for *in situ* diversity. National Coordinators should take responsibility for both ,
- Whereas in plant breeding there is an increasing interest in crop wild relatives, these genetic resources are underrepresented in *ex situ* collections,
- Although there is quite some variation, the overall impression is that the focus is rather on conservation than on utilization, on characterization than on evaluation,
- Utilization by public and private scientists and plant breeders should be promoted by (1) furthering the establishment of core collections, (2) consolidation of the existing crop data bases through uploading from national to regional and global crop data bases using the same software and (3) by engaging users (scientist and plant breeders) in an advisory role, and may be even in a partnership role, in the management of the collections,
- ECPGR should be institutionalized in such a way, that it will become **the** European authority taking responsibility for all crop genetic resources within Europe. In order to be better facilitated for this important task, together with the European Association for Research on Plant Breeding (EUCARPIA) and the European Seed Association (ESA) it should lobby with the European Union for stable funding,
- ECPGR should get more engaged in European policy making related to the Convention on Biological Diversity (CBD) and the International Treaty on Plant Genetic Resources for Food and Agriculture (IT PGRFA).

Exploiting the wealth of gene bank collections in breeding

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Plant gene banks were established to collect and preserve varieties that were once grown and were replaced by more modern varieties. Such a collection was partly kept for cultural historic reasons, to be used in demonstrations, research and teaching to compare modern day varieties with varieties that were important in ancient days. However, the main argument to establish such gene bank collections was to preserve genetic variation that might otherwise be lost when older varieties and landraces were replaced by modern varieties and that might be needed again for future breeding. For the same reason, to provide breeders with genetic variation, wild relatives of the cultivated species were added to gene bank collections, also in cases such as lettuce, where there is no threat of an extinction or genetic erosion of the wild population.

Genetic variation is the basic substrate of plant breeding. Breeders continuously create and work on genetic variation, to be able to select genotypes that are better than or could add traits to existing elite material. The type of genetic variation that breeders are searching for can vary very much depending on the breeding goals and the type of crop that is bred. In staple food crops generally yield and yield related traits such as resistance to biotic and abiotic stress dominate the breeding goals. In other crops, such as vegetables and ornamentals, variation for many other traits (size, taste, vitamin content, colour, shelf life etc.) can be of interest to the breeder.

Gene bank accessions as such only seldom are of interest to a breeder. They are either wild accessions or old cultivars that don't fit anymore in modern cropping systems. It is a specific trait or specific gene(s) that interest the breeder in a certain gene bank accession because it can add value to elite material. Therefore extensive morphological descriptions of gene bank accessions are usually of little value to a breeder, unless exactly the trait is described that he or she is looking for at that moment, which is seldom the case. General morphologic descriptions can be used to choose accessions that are closest to the material in the breeding program, when several accessions display a gene or trait of interest to the breeder. More important than a morphological description is a correct botanical classification of the species and information on the crossability of accessions of different species.

When introgressing a trait from a gene bank accession into elite material the breeder must try not to loose genes involved in the expression of the trait, and at the same time try to remove all linkage drag: genes that are on chromosome fragments adjacent to genes of interest and that affect the phenotype negatively. When introgressing traits from a very distant plant type or from wild material it is often difficult to recognize linkage drag, as most of the material displays an unwanted phenotype. Only when the material has advanced to the level of elite material, linkage drag can clearly be recognized. Introgression is most easy when it concerns monogenic traits with a clear expression, also in populations obtained after a wide or an interspecific cross. Many resistance genes fall into this category and gene bank material has been widely used as source of new resistance genes for breeding programs. Other traits, with a more complex inheritance and a more quantitative expression are much more difficult to introgress from gene bank accessions into elite material. The reason is that 1) the extreme variation obtained after wide or interspecific crosses may obscure the effect of the genes of interest; 2) it is more difficult to keep several genes together in such an introgression program and not lose some of them, and 3) the problem with linkage drag increases with the number of genes to be introgressed, as each gene can have its own linkage drag.

Modern genomic tools are revolutionizing the practice of plant breeding and also have an impact on the use of gene bank material in breeding programs. In most crop species a large number of molecular markers is now available and soon for most crop species we will have at least a draft genome sequence. These tools facilitate the use of gene bank material in breeding programs. With markers, the introgression of genes for the trait of interest can be followed precisely, which reduces the chance of losing genes during the process. Marker technology is also used to minimize the size of introgression fragments, thus reducing problems with linkage drag. Another application of marker technology is the creation of Backcross Introgression Library (BIL) lines, in which the genome of a donor accession is fragmented and individual genome fragments are all introgressed into the same genomic background. In this way the phenotype effect of each genome fragments can be measured in a constant background, thus avoiding confusing effects of the large variation normally found in wide crosses. When interesting effects are found linked to a specific introgression fragment, it is relatively easy to zoom in on the locus that causes the effect, developing closely linked molecular markers or isolating the causal gene. In this way genes have been identified that would have been very difficult to detect without marker technology, such as genes for large fruit size in wild accessions having itself very small fruits.

The availability of gene and genome sequences also stimulates the use of gene bank collections by applying knowledge developed in one species to other species. Knowledge developed from model species such as *Arabidopsis* or from other crops can be applied to other species now: if we know which type of gene causes a certain effect in one species, we can search for similar genes in our crop of interest. The possibilities to screen populations by sequencing or tilling for certain genes or allelic variants are almost unlimited. And it can be expected that in the near future large parts of (core) gene bank collections will be resequenced, allowing the breeder to pick her accession with the allele of interest “in silico” using bio-informatics tools. Core-collections will be redefined based on sequence information to have maximal allelic content.

The availability of genomic tools in breeding has caused a strong revival of mutation breeding. After the first phase of mutation breeding some 50-60 years ago, this technique became outmoded in almost all crops except ornamentals because of practical problems involved in screening very large populations for interesting mutations. Now, with the new sequencing techniques, screening large collections for a specific mutation is easy, whether the allelic variant is searched for in a gene bank collection or in a mutant population. A next step in mutation breeding will be targeted mutation breeding (allele surgery, DNA or genome editing), in which specific mutants are made. Although it seems that such a development could make gene bank collections superfluous as sources of genetic variation because the required genetic variation could be made by means of directed mutagenesis, I expect that also for such techniques the starting point would be taken in an allele found somewhere in a collection that is already closest to the sequence that one would like to realize by means of targeted mutations.

Thus, new tools have greatly increased the capacity of breeders to evaluate and absorb new genetic variation from gene bank collections. Therefore breeders would like to have access to collections that are as large as possible to search for alleles of interest. Gene banks can serve breeders by open access to well maintained collection, preferably sequenced (a new field of private public partner-shipping?), of which the information and accessions are accessible through the Internet. Collections can be further enlarged by collection expeditions. We very much appreciate the active role that CGN has played, supported by breeding companies, in collecting new germplasm during its 25 years of existence. Further, gene banks can play a broker function when access to germplasm is restricted for whatever reason, be it specific to the collection where the interesting accessions are held or to the country of origin.

South East European Development Network on Plant Genetic Resources - SEEDNet

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Key words: SEEDNet, South East Europe, conservation, utilization, genetic resources, network

The South East European Development Network (SEEDNet), established in 2004, is a collaborate programme for countries in Southeast Europe. The network has 13 partner institutions within the following countries; Albania, Bulgaria, the two entities of Bosnia and Herzegovina, Croatia, Hungary, Kosovo, Republic of Macedonia, Republic of Moldova, Montenegro, Romania, Serbia, and Slovenia.

The overall aim of the programme is long-term conservation and sustainable use of the diversity of PGR within the South East European region through a well co-ordinated network of operational national PGR programs.

Capacity building has been an important element of the network and an area where considerable efforts have been employed. During the existence of the network a total of 30 training courses have been organised covering a wide range of topics, running from: a 2 year international Master of Science programme in management of biological diversity; information and documentation technology; application of genetic and molecular markers in gene banks; conservation strategies; gene bank management and operations and; *in vitro*, *in situ*/on farm conservation; PGR policy; project administration, reporting, accounting and auditing.

During the course of the programme gene banks with facilities for long term conservation have been set into full operation in all partner institutions. Active and base collections are being established and internationally accepted gene bank standards are being implemented. Field gene banks for fruit and *Vitis* are as well established in most partner countries.

SEEDNet operates through six crop oriented (Cereals and Maize, Medicinal and Aromatic Plants, Vegetables, Fruit Crops and *Vitis*, Fodder Crops, Industrial Crops) and one thematic (Documentation and Information) regional working groups. Their activities are overseen by a Regional Steering Committee. The working groups have initiated a number of common projects. Most of the project activities have been directed towards inventorying and collecting of local material since many areas in the region are still unexplored for occurrence of valuable plant genetic resources. Landraces of most cultivated crops are to a certain extent still cultivated by farmers. However due to conversion of the agricultural systems in most countries most of this material is under direct threat and needs to be collected and conserved *ex situ* in the gene banks.

The most recently carried out projects includes:

- “*Exploring, collecting and characterizing the local forms of industrial crops from SEEDNet area*” by the working group for Industrial crops in which local cultivars of potatoes and industrial crops have been collected;
- “*Characterization of apple local varieties (Malus x domestica Borkh.) from South East European region*” and “*Collection and field evaluation of local plum (Prunus domestica) genetic resources from South East European network*” by the working group for Fruit and *Vitis* in which local cultivars have been collected and characterized. Collected data

and photos taken will be compiled into two separate pomologies of Balkan local cultivars of apple and plum.;

- The same working group has carried out the project “*Identification, characterization and conservation of old and autochthonous vine varieties in Eastern European countries*” in which local *Vitis* cultivars have been identified and described for both morphological and ampelografic characters and unique accessions have been identified with the help of DNA markers.;
- In the project “*South East European Solanaceae Germplasm Collection, Conservation and Sustainable Use*” the working group for Vegetables has collected accessions of pepper, tomato and eggplant. In the project “*Inventorying and collecting of indigenous onion (Allium cepa L.) and leek (Allium porrum L.) germplasm for further ex-situ conservation*” by the same working group quite a number of accessions of leek, garlic and onion have been collected and in a third project “*Collection, characterization, and regeneration of local kale (Brassica oleracea var. acephala) population germplasm from eastern Adriatic coast region for their conservation in gene banks*” the project partners have collected and described local cultivars of kale.;
- “*Collecting local landraces of maize and cereals (wheat, barley, rye, oat, millet and buckwheat) in South Eastern Europe*” was a project by the working group for Cereal and Maize in which a large number of maize, wheat, barley, rye, oat, millet, buckwheat and accessions of some other species of *Sorghum* and *Triticum* have been collected.;
- The working group for Fodder crops has carried out collecting of accessions of red clover, yellow alfalfa, cock’s foot and meadow fescue within the project “*Regional collecting expedition and ex situ conservation of Trifolium pratense L., Festuca pratensis Huds., Dactylis glomerata L. and Medicago falcata L.*”;
- In the project “*Genetic Structure of Dalmatian Sage (Salvia officinalis L.) Populations: A Model for a Collaborative Research on MAP Genetic Resources*” by the working group for Medicinal and Aromatic Plants the biodiversity of Dalmatian sage populations have been studied and the amount and structure of population genetic diversity, the geographic differentiation, the occurrence of demographic bottlenecks and the ecotypic divergence have been assessed.

Several partner gene banks are regularly uploading accession pass port data to the common European inventory data base EURISCO. Characterization of collected and conserved accessions is now a standard activity of most of the partner gene banks. Evaluation of accessions of selected species has also been initiated by several gene banks. In some cases this is done in collaboration with breeders.

The SEEDNet partners are in general very active with regards to raising awareness of the importance of conservation and use of plant genetic resources. Activities have been directed towards schools, farmers and the general public through various media. It seems as if the actions have resulted in a higher degree of awareness of the need for a sustainable conservation and utilisation of PGR and not the least involvement of new stakeholders from both general public and the farming community in this joint effort.

All partners have made important progress in the field of PGR within a rather short period of time and are now in a much stronger position having acquired knowledge that allow them to better manage, conserve and utilise their PGR. In addition the network participants have built up and strengthened a solid partnership and a platform for future project collaboration and sharing of conservation responsibilities.

State of the World's Plant Genetic Resources and the Global Plan of Action

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Key words: Plant Genetic Resources, Global Plan of Action, FAO, Commission on Genetic Resources for Food and Agriculture

In 1995 the Commission on Genetic Resources for Food and Agriculture (CGRFA) agreed to the preparation of a Report on the State of the World's Plant Genetic Resources and a subsequent Global Plan of Action as a framework and guide to the conservation and sustainable use of plant genetic resources at national, regional and international level. The **First Report of the State of the World's Plant Genetic Resources for Food and Agriculture**, based on 154 individual country reports, was presented to the Fourth International Technical Conference on Plant Genetic Resources in Leipzig, Germany, in June 1996, and published in 1998. It constitutes a comprehensive assessment of the status of plant genetic resources worldwide. The **Global Plan of Action**, which was adopted at the same conference, comprises of programmes and activities aimed at filling gaps, overcoming constraints and facing emergency situations identified in the report.

The main aims of the Global Plan of Action as stated in the introduction are:

- to ensure the conservation of plant genetic resources for food and agriculture (PGRFA) as a basis for food security;
- to promote sustainable utilization of PGRFA;
- to promote a fair and equitable sharing of the benefits arising from the use of PGRFA;
- to assist countries and institutions to identify priorities for action; and
- to strengthen national programmes, as well as regional and international programmes, and enhance institutional capacity.

The Global Plan of Action includes 20 priority activities organized into the following four main areas:

- *In Situ* Conservation and Development;
- *Ex Situ* Conservation;
- Utilization of Plant Genetic Resources; and
- Institutions and Capacity Building.

At its Eighth Regular Session the CGRFA, commissioned FAO anew to assess the state of the world's plant genetic resources and in particular analyse the changes since the publication of the first report and identify gaps and needs for conservation and sustainable use of PGRFA. The **Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture** was published in 2010.

The report reveals that although some progress has been made since the time of the first report the majority of countries shows either stable or decreasing capacity with regards to the management of their PGRFA. Issues of emergency identified in the report are related to sustainable agriculture, the need to breed underutilized as well as bio fuel and bio energy crops, health and dietary diversity and climate change.

The report shows that the state of diversity in the developed countries is designated by high input agricultural systems and strict market standards but low level of diversity. In most of the

developing countries farming systems still rely on diverse crops and varieties with high level of diversity. The understanding of on farm management has in general increased since the first report and there is more interest in neglected and under-utilized species as well as awareness of the importance of conserving crop wild relatives (CWR). Nevertheless to a large extent countries still lack PGRFA national strategies and policies.

The assessment of the state of *ex situ* conservation shows that the collections in countries have been increased with many new accessions of especially obsolete cultivars, landraces and CWR. It is however, evident that a high level of duplications, mainly for the major crops, exists and documentation, characterization and evaluation need to be strengthened and data needs to be more accessible.

An apparent need is to increase the plant breeding capacity. Investments in public plant breeding have drastically decreased while private plant breeding has increased. New plant breeding tools including base broadening and pre-breeding are being requested in order to meet the impending challenges of climate change.

Based on the findings in the second report the rolling GPA is currently being updated. Regional consultations have been organized in order to receive inputs from countries during the process. The updated GPA will be considered by the CGRFA at it's next Regular Session during 2011.

Genebanks work together

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Key words: gene banks, collaboration, networks

Gene banks have a long tradition of co-operation. This international collaboration has been one component of the operations that have ensured the development of various gene bank functions and the diversity of collections. All primary gene bank tasks such as conservation, documentation, characterization and evaluation and promotion for gene bank utilization have also been carried out in various types of consortia. In addition, social and global responsibility is common in efforts where new gene bank have been established or collections in danger have been rescued. An important contribution in a global scale is the establishment of Svalbard Global Seed Vault to safeguard the world's most important plant genetic resources for food and agriculture. An overview of the gene bank collaborations will be given in my presentation through personal reflection from the Nordic and European angle over the past 20 years.

The collaborative operations between and within gene banks have been coordinated and guided in different levels: bi/multi-laterally, sub-regionally, regionally and globally. From this perspective it is not easy to achieve a holistic picture of the extent and effectiveness of the entire field of co-operation. Globally, former IPGRI (International Plant Genetic Resources Institute) and present Bioversity International together with FAO, have had an important role in increasing cohesion among the gene banks. However, clear operational modes for co-operation needs to be developed. Among others there is an urgent need to push forward crop conservation strategies, information systems and common research agendas. Also gap analyses on the state of the diversity of the plant genetic resources both in *ex situ* and *in situ* in the world scale is required urgently in order to link the different conservation forms into a rational system. In Europe the co-operation challenge has resulted in AEGIS (A European Genebank Integrated System) within the frame of European Cooperative Programme for Plant Genetic Resources (ECPGR). This virtual European Genebank, when fully operational, can improve the security, quality, access and economic efficiency of European PGR collections. The expectations for more coordinated European and global gene bank co-operation need continuous analysis and further discussion.

The gene bank world is facing many new challenges that should shape the forms and nature of co-operation. Self-evident driving forces present already are the global climate change, need for better food and nutrition security, as well as on-going biodiversity loss. These forces call for proactive collaboration that enables all gene banks to streamline their functions to better respond to the challenges of the changing environment. Gene banks should also be prepared to secure their own existence in changing economic and political environment. Sustainable and continuous maintenance and development of gene banks is possible only when there is a wide understanding and appreciation in all levels of the society about the fundamental importance of genetic diversity for products and services that people need. To raise the awareness is a demanding task not even mentioning integrating diversity issues in societal decision-making. The gene banks have from their professional role a responsibility to make sure that the existing genetic resources are available in the future and to achieve this goal they should therefore be in front of developing structures for co-operation.

From QMS Ideal to Performance Reality - a hybrid performance management approach for genebanks

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Key words: quality management system, genebank, *ex situ*, crop conservation, performance indicators, Global Crop Diversity Trust, long-term grant, monitoring

The Global Crop Diversity Trust (the Trust) is working to ensure the long-term conservation and availability of crop diversity for food security worldwide. The Trust is a direct and unique response to the chronic underfunding of *ex situ* collections – the genebanks that store the genetic diversity of crops of importance to humanity.

It is a great irony that while the value of crop diversity remains undisputed, the unreliability of funding is probably the single largest risk to effective long-term conservation. The endowment fund of the Trust seeks to resolve this, by providing annual guaranteed funding to ensure that crop diversity is safe and available forever. To date, the Trust is providing in perpetuity grants to 400,000 accessions of 15 major crops in 18 international collections. These collections serve a public-good role as the backbone of the global system for conserving PGRFA. Collectively they provide greater access to more plant breeders, researchers and farmers than any other institutions in the world. Trust long-term grants currently total USD 2.05 million per year, every year, and will increase as more donors commit funds to the endowment.

When the Trust initiated its long-term grant programme in 2007, it also developed a methodology to assess the effectiveness of its long-term grants. Trust grants are not 'normal' grants in that they don't have outputs and milestones as most "fixed-term" grants do. The long-term grants provide annual funds for the genebanks to use according to their own priorities to conserve key priority crops - essentially for "business as usual". The Trust needed to develop an approach that provided the ability to measure annual progress and performance across a range of genebank-specific goals in an absence of genebank quality management systems.

In an ideal world, genebanks would all employ quality management. The concept used here is broad and not restricted to a quality management system (QMS) such as those certified by ISO (9000 generic management standard) or accredited by ISO (17025 management and technical standard). It does, however, align with the traditional approach of:

1. Plan – say what you do
2. Do – do what you say
3. Check – check that you do what you say
4. Act – correct and improve what you say you do

Thus, quality management term encompasses three key components:

- Assessment – define the goals, assess the operating environment, identify the risks, plan the approach
- Management – standard operating procedures (by crop), agreed minimum genebank standards, policies, best practices,
- Monitoring – quality control, monitoring of performance against targets, indicators, reporting, audits, accreditation

Incorporating a feedback loop highlighting whether a risk is still of concern or whether it is under control or whether a standard is resulting in the right outcome at the acceptable quality.

A number of realities needed to be added to this model. Given the absence of QMS systems across the genebanks, the Trust sought, drawing on the theory of QMS, to develop performance reporting with the genebanks to address the immediate goal of assessing performance but to also provide a framework by which a quality management approach was actively encouraged. Indeed, to provide a platform to initiate such an approach. This hybrid approach uses elements of the formal approach such as certification where possible or critical, but also includes internal documentation for lower risk processes. The following challenges also needed consideration:

1. The in-perpetuity nature of Trust grants and so the system needs to have longevity;
2. The lack of uniformity in genebank operating environments (for example geographic location, security, political stability, funding, capacity and skills);
3. The variance in the biology, and hence management, of crops;
4. The difficulty in defining and adhering to certified procedures for activities, such as fieldwork, in uncontrolled environments;
5. The need for standardized data management systems;
6. The internally imposed system requirements on many genebanks that reside within larger institutions;
7. The requirements by the Trust, Board and donors to see well-defined impacts from the significant investment in these genebanks.

The Trust genebank performance indicator development work took place over a 3-year period, building initially on the work coming out of the 2007 CGIAR Global Public Goods 2 workshop in Lunteren, Netherlands. It should be noted that these genebank performance indicators are also being used by a non-CGIAR genebank that is also a recipient of a long-term grant from the Trust with success.

The Trust recognizes the value of working towards a longer-term goal to develop an approach of worth to all grantee genebanks and achieve something monumental by doing so. Moving towards a quality management approach should result in greater transparency, cost efficiencies, improved quality standards, greater knowledge sharing, and collaboration among genebanks. In addition, the Trust recognizes the great value and synergies in working on this together as a group of genebanks over each genebank having to do it alone.

A rational global system for conserving PGRFA can only be built upon collaboration and trust between genebanks. The adoption of a quality management approach, that is pragmatic in design but delivers against these goals, is a key requirement for ensuring this outcome.

Poster Presentations

(ordered alphabetically on the name of the first author)

(Poster 1)

AFLP characterization of field pea accessions collected from different regions in Oman

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Key words: Oman, field pea accessions, AFLP

Local landraces are an important source of genetic diversity for use in genetic improvement programs. Due to the introduction of new and improved commercial crop varieties, the local landraces are being neglected gradually by the farmers resulting in genetic erosion of the local varieties. Conservation and characterization for more efficient use of these valuable resources is important. Little is known of the genetic diversity of legume landraces in Oman. In this study, 25 accessions of field pea (*Pisum sativum* L.) landraces from different geographic sites scattered throughout northern part of Oman were studied for their genetic diversity and relationships using Amplified Fragment Length Polymorphism (AFLP) technique. DNA fragments obtained from eleven different AFLP primer combinations were sequenced using ABI3130 genetic analyzer (Applied Biosystems, CA) and data analysed by GeneMapper V4.0 program. A total of 1077 alleles were scored, of which 98% were polymorphic. The genetic distances between all field pea accessions ranged from 35 to 76% based on Jaccard's similarity index coefficients. Cluster analysis revealed a clear separation of all 25 field pea accessions into three distinct clusters among which Al- Rustaq accessions appeared in all three clusters. The highest diversity was found in accessions collected from Al-Rustaq region and this could be due to its geographical location in relation to the other sampling regions. The results from this study can be used in future breeding studies and germplasm conservation of these field pea genotypes.

(Poster 2)

Finnish PGR utilization: cases of breeding and branding

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Key words: utilization, timothy, apple, potato, ornamental plants

Utilization of Finnish PGR landraces has been realized by means of two different approaches: plant breeding programs based on hardy landrace material, and selecting tested old cultivars as such to be branded quality products. We present here examples of successful practical cases from both of these two approaches.

Iki-timothy cultivar was developed combining 850 elite individuals selected from four landraces ‘Tervola’, ‘Sodankylä’, ‘Posio’ and ‘Pelso’. Many of the original populations were growing on peat lands, and therefore they had special adaptive characters for this type of growing conditions. The material was selected in extremely northern conditions in the Finnish Lapland. Institute of Plant Breeding Jokioinen (now represented by Boreal Plant Breeding Ltd.) released the cultivar in 1986, and it is still recommended as the best choice for central and northern Finland, where special wither hardiness is required.

‘Huvtus’ apple landrace cultivar was originally raised from a chance seedling on a small farm in Yläne Finland. The promising new seedling was spotted by a local fruit enthusiast and sent to a horticultural research station for testing. The seedling was named as ‘Huvtus’ according to a local manor house, and it became widely popular in early 20th century fruit growing. Furthermore, it became the most important founder cultivar in national apple breeding programs, and was used as one of the parents in most of the present Finnish apple cultivars. The original seedling tree was recently re-discovered on the now abandoned farm land, and its identity was verified by DNA fingerprinting.

‘Puikula’ potato landrace is an old local potato strain from the northern part of the Nordic countries. Before 1840s potato blight epidemics arrival this long, almost banana shaped cultivar was popular in many parts of Europe. Because of blight sensitivity, growing withdrew into more northern locations, where it became locally popular. Puikula’s yield potential is high, but due to the short growing season in north the tubers are always harvested immature. Although the yield is low, immature harvesting gives the tubers their special taste. In 1997 ‘Puikula’ potato grown in Lapland was registered as Lapland’s Puikula in the European Union under the terms of Protected Designation of Origin (PDO). This designation has drawn a lot of attention to this local potato strain, and promoted it into becoming a popular landrace product.

FinE (Finnish Elite)-plant label was created to highlight tested good quality nursery plant material, with shown hardiness properties in Finnish climate conditions. During 1989-2000 over 700 interesting individual findings were recorded in a Helsinki University inventory of winter-hardy woody ornamentals in our country. Plants from eight most interesting genera were selected for field, and in some cases also urban parks, testing in different climate zones, starting from Piikkiö research station in southern Finland all the way up to Rovaniemi, Lapland. Hardiness, plant health as well as ornamental and utility values were evaluated during five years. In the end of the project, the best cultivars were named, and a special label was created for marketing them. At present the FinE status has been granted for 19 ornamental shrubs and 20 fruit and berry cultivars.

(Poster 3)

Landscape approach in developing a red list for crop landraces In Romania

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Key words: farming, red list, crop landraces, landscape approach

Over 69 percent of Romania’s agriculture is subsistence-based – which is not ideal in today’s economic terms, but is however highly valuable for the preservation of wildlife biodiversity and for the development of innovative economic strategies in this field. Over 32 percent of Romania’s land is covered by mountains and that combined hilly-mountain landscape favours the above-mentioned type of agriculture. The latest inventory of farms in the country’s mountain areas has indicated that today there are over 815 813 land-owners, most of whom practice subsistence agriculture. Moreover, a large part of the hilly - mountain areas have been declared protected areas and are rich in traditions and traditional knowledge, due to the small farmers that have been saving seeds for generations and have been growing old landraces such as maize, cabbage or beans. Unfortunately, in Romania there is no complete inventory of these genetic resources represented by these crops, which are essential to further support food and feed security, given the future climate change impact and the growing economic pressure of conventional agriculture on crop landraces. Through a landscape approach, we expect to develop new policies and apply dynamic action plans in agriculture, based on the degree of tolerance of crop landraces and the vulnerability of their ecosystems to climate change. Based on the above-mentioned rationale, discussions are underway for a case-specific methodology, in order to develop a red list of crop landraces in Sibiu county and thus help farmers to practice on-farm conservation.

(Poster 4)

The role of CGN in a national network conserving Dutch biocultural heritage

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Keywords: old varieties, network, NGO's, biocultural heritage

In the Netherlands there are many initiatives which are concerned with the conservation and use of the Dutch biocultural heritage. These initiatives are often not well organized, have different goals and are largely based on volunteering. This results in a poor knowledge diffusion affecting all sorts of issues, from maintenance of crops to acquisition of budget. In 2006 the establishment of the network Eternal Kale was initiated to enhance the cooperation of these initiatives. The role of the Dutch national genebank CGN in this network of 50 NGO's is to facilitate the internal and external communication (website maintenance, co-organizing meetings), to carry out research to develop a list of old Dutch varieties which can be considered as the Dutch national biocultural heritage (so-called Orange List; www.deoerakker.nl), to function as a safety back-up for collections, to help with regenerating material and to act as a helpdesk for specific questions. So far the efforts of the network have resulted in, amongst other things, the safeguarding of a collection of around 180 old Dutch horticultural and agricultural varieties and an evolving Orange List of more than 3000 vegetable varieties grown between 1850 and 1940 in the Netherlands with information on their availability. Furthermore forgotten knowledge has been retrieved by exchanging experiences and making variety descriptions from catalogues and other sources digitally available. Foreseen future activities encompass the refining of the Orange List and to extend the shared information on old Dutch varieties and their availability. In general CGN will keep on playing an active role in the promotion of crop agrobiodiversity in the Netherlands.

(Poster 5)

Inheritance of spontaneous panicle inflorescence mutation in lucerne (*Medicago sativa* L.)

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Key words: inflorescence, inheritance, lucerne, mutation, panicle, raceme, seed productivity, seed yield.

Lucerne is one of the main forage legumes cultivated around the world and increasing interest of the seed production is observed. However, most research has concentrated on maximizing forage production, and little information has been developed on the crop's specific fertility requirements for seed production.

The aim of research was to explain mode of inheritance of the lucerne mutation that causes the formation of panicles instead of racemes on stems. Panicles on mutant plants were consisted of a lot of branches that caused several fold increase of flower numbers in inflorescences. Usage of this character in lucerne breeding creates new opportunities to increase its seed yield potential.

The inheritance of this character was studied in S_1 and S_2 progenies obtained by selfing a mutant plant, as well as in F_1 , F_2 and F_3 generations of hybrids obtained by crossing plants that produce racemes with S_2 mutant progenies. The analysis of segregation in the selfed progenies of the mutant plants and in $F_1 - F_3$ progenies of the hybrids showed that the character of panicle inflorescence is controlled by single gene in the configuration four recessive alleles $pi\ pi\ pi\ pi$ (pi – panicle inflorescence).

(Poster 6)

Utilization of HMW and LMW- glutenin subunits in evaluation of wheat genetic resources

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Key words: wheat, glutenin subunits, genetic diversity

The basis of sustainable genetic improvement and successfulness of breeding programs is an extension of knowledge about genetic diversity in the wheat germplasm. An important task in wheat research is an examination of the genetic diversity in a wheat collection using protein markers. High and low molecular weight glutenin subunits (HMW-GS and LMW-GS), owing to their relatively high level of polymorphism, are apparently suitable for such use. Glutenin subunit composition is of particular interest to wheat breeders since these subunits are the major factors responsible for the unique viscoelastic dough characteristics of wheat flour determining mixing and bread making. This study was aimed at genetic diversity evaluation in the set of 74 Czech wheat cultivars and 174 foreign wheat cultivars originated from twenty countries of Europe and Asia. Sodium dodecyl sulphate polyacrylamide-gel electrophoresis (SDS PAGE) was used in order to detect the different alleles encoded at 6 glutenin loci in total of 248 cultivars. At *Glu-A1*, *Glu-B1* and *Glu-D1*, encoding HMW-GS, 3, 8 and 3 were found respectively. LMW-GS showed a slightly higher polymorphism as 6, 10 and 6 alleles were identified at *Glu-A3*, *Glu-B3* and *Glu-D3* respectively. A total of 158 glutenin profiles at the *Glu-1* and *Glu-3* loci were detected. The allele combination *A1c/B1b/D1d*; *A3d/B3g/D3c* was determined in 9 genotypes as the most frequent glutenin profile.

The genetic diversity index based on glutenin patterns was high in both Czech ($H=0,974$) and foreign ($H=0,911$) cultivars. The lowest genetic diversity index was observed in cultivars originated from countries of Western Europe ($H=0,788$). The high glutenin variability guarantees great efficiency in all breeding programs concerning the development of new wheat varieties. The analysis of glutenins enables the choice of parents – donors of characteristics in breeding program or the selection of accessions representing genetic diversity of wheat to set up a core collection in Gene Bank.

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(Poster 7)

Homegardens of Eastern Algarve

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Key words: homegarden, germplasm, conservation, on-farm conservation, genetic resources

Homegardens are recognized for being a redoubt of traditional varieties, and in some cases linked with pollicropping and traditional agriculture techniques.

The present study intended to be a first approach to the recognition of the community and their roles and motivations in landraces conservation (e.g. local traditions, flavors, food quality) at the municipalities of Castro Marim and Alcoutim, Algarve, Portugal. For this purpose two main approaches were used: 1) Survey to 32 homegardens; 2) Qualitative and quantitative analyses from five homegardens on a daily base (e.g. harvest products weight) from October 2008 to 2009.

The results indicate that the average size of the homegardens is 1190 m². The farmers make their selection and keep landraces for generations based on some traits that they consider important (e.g. flavor, adaptation to local conditions, production). These farmers produce for their own consumption, and they are able to produce a significant part of their food.

(Poster 8)

Germination and early seedling growth of winter camellias in peat alternative substrates: advancing *ex situ* conservation

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Key words: *Camellia* spp., coconut fiber, green compost, genebank, genetic resources

Germination requirements in *Camellia* spp. are largely unknown. Seeds from 16 open-pollinated cultivars belonging to *C. sasanqua* (10), *C. x vernalis* (4), and *C. x hiemalis* (2) were gathered in November 2009, cold treated 1 month at 4-6°C, soaked for 3 days in GA3 at 1000 ppm and placed on different substrates (100% peat, 50% peat + 50% coconut fiber, 50% peat + 50% green compost, 50% peat + 25% fiber coconut + 25% green compost, 100% fiber coconut and 100% green compost). Germination tests were carried out in a climatic chamber, where a constant temperature of 23°C and a long-day photoperiod (16h light at 267 lux) were provided, while the moisture level of the substrates was regularly checked. In terms of germination rate, a wide level of variability among cultivars was observed. In many cultivars, the standard peat-based substrate and the substrate bearing 50% of coconut fiber succeeded in inducing to germinate up to 100% of the seeds. Conversely, coconut fiber alone resulted the worst substrate tested. On average, 42% of seeds *per* cultivars germinated, within which 31% rooted and properly developed shoots. At now, 85% of the seedlings are collected in the greenhouse of the University of Turin (Italy) and their ornamental characteristics are in course of evaluation. The obtained data will implement a previous morphological and genetic study. The final purpose is a long-term preservation of these ornamental camellias which flowers in autumn-winter time.

(Poster 9)

Cutting propagation in evergreen azaleas. A way to conserve an Italian local germplasm.

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Key words: biodiversity, *Rhododendron* spp., catalogue-field, vegetative multiplication, genebank

In Italy, during the 19th century, the hybridization activity on *Rhododendron* genus produced a significant gene pool of evergreen azaleas, locally sorted into three groups according to the phenotype: (1) Indica, including plants characterized by large flowers, (2) Amoena, formed by azaleas with very small, purple flowers, and (3) Japonica, a morphologically intermediate group. Today, these historical genotypes are present in few or unique specimens, mainly in parks and gardens of Northern Italy. In order to safeguard and use this germplasm, its propagation and conservation in catalogue-fields are needed. Rhododendrons can be reproduced from seeds, cuttings, layering, by grafting and tissue culture but there is extreme variability among species and cultivars. In a previous study, an evaluation of the rooting aptitude of cuttings of ancient Italian cultivars was performed. Here, in order to better evaluate the responses of 104 azalea genotypes (50 Japonica, 50 Indica and 4 Amoena) to the vegetative multiplication by cuttings, their growth aptitude, height/diameter ratio (H/D), roundness index, number of branches *per* plant, and branch length were investigated after two years of cultivation. For all parameters, the variability present within and among each group was described by means of the univariate ANOVA, and the distribution of variability was shown using a Principal Component Analyses (PCA).

Overall, results showed a high level of differences between genotypes within group, even if differences between systematic groups were found, confirming their horticultural classification. Amoena genotypes showed the highest number of branches (10.9), and the lowest roundness index (0.96), opposite to the Indica genotypes (number of branches = 6.29; roundness index = 1.03). Both groups resulted higher (33.7 and 34.4 cm for Indica and Amoena) than Japonica (32.2 cm), revealing a more compact growing form. The PCA distributed specimens without a precise clustering. In general, genotypes were mainly separated by the HD ratio (eigen vectors= -0.220) and the branch length factors (eigen vectors= 0.198). Vegetative propagation allowed to obtain numerous plants of uniform characteristics (mean = 54 plants/genotype). One year later, with the aim to conserve this germplasm, a total of 3400 plants were planted in six catalogue-fields located in the Lake Maggiore area (North-West Italy). In conclusion, morphological differences found within and among groups revealed a wide phenotypic variability. A molecular fingerprinting approach, previously applied, showed the genetic diversity and relationships among genotypes. All these data together could be useful for both breeding programs and germplasm safeguard.

(Poster 10)

Contribution of the French network on chicory genetic resources to a European *ex situ* management of leafy vegetables genetic resources

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Key words : chicory, network, disease resistance evaluation

For 25 years, management of genetic resources in France has been different to that applied in other countries : managed through specialized networks by species or group of species (carrots, cereals, ...), they bring together all actors involved in this topic around a pilot structure. Besides the preservation of patrimonial material, this organization has identified and characterized accessions through work carried out by the different partners of each network. Comprising 14 private and public partners (breeding companies, local organizations, technical institute) around GEVES (Group for Testing and control of Varieties and Seeds), the *Cichorium* network has carried out general operations (regenerations, morphological characterizations, evaluations and distribution) on 1800 chicory accessions of which 650 belong to the national collection.

Nevertheless, at European level, before 2007, the European gene bank community did not have a good overview of their stored leafy vegetable germplasm due to the absence of a global crop databases available for spinach, chicory and minor leafy vegetables and the existing international lettuce database already existing needed significant updating. There was also limited access to trait data in databases which made it difficult for the user to select appropriate accessions. In 2007, a consortium of twelve partners from ten European countries, including three universities, six public research institutes and three non-governmental organizations began a four year project entitled 'Leafy Vegetables, stimulating use' in the framework of the European GENRES programme. Finished in 2010, this project was coordinated by the Centre for Genetic Resources, the Netherlands (CGN) and resulted in an unique leafy vegetable crops portal on the web (<http://documents.plant.wur.nl/cgn/pgr/LVintro/>). Most of the time spent on this project was devoted to regeneration, characterization and evaluation for the genetic resources management and workshops to general public for the use stimulation.

Among evaluation activities done within this program, work on pest and disease resistance was undertaken by a number of specialists. Especially on witloof cultivated mainly in France, Belgium and the Netherlands (total area of 15 000 ha), evaluation against root and foliage disease was conducted : *Alternaria cichorii*, *Sclerotinia sclerotiorum* and *Thielaviopsis basicola*. For *S. sclerotiorum* and *T. basicola*, recent years have shown great impacts on the root and witloof production for both conventional and organic producers. A specific method has been developed for an early resistance test against *T. basicola* and accessions have been identified for new breeding programs. Even if *A. cichorii* is more of a problem for the Italian leaf chicory, interesting accessions have been identified within the framework of the legislation on MRL (Maximum Residus Level) on vegetables. For *S. sclerotiorum*, other screenings need be done on other accessions. Nevertheless, the developed method is currently used for commercial varieties providing useful information for the producers. On endives (cut and plain chicory), sclerotinia has been largely developed and its impact is growing. Besides that,

development of organic productions and reduction of MRL will give new opportunities to screen our gene bank for genetic resistance.

Action 001 AGRI GEN RES 870/2004 (Leafy Vegetables, stimulating use) received financial support from the European Commission, Directorate-General for Agriculture and Rural Development, under Council Regulation (EC) No 870/2004. More information on the project can be found at: <http://documents.plant.wur.nl/cgn/pgr/leafyveg>.

(Poster 11)

Characterization and preliminary evaluation of Polish *Lolium perenne* L. ecotypes

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Key words: : ecotypes, perennial ryegrass, seed production, agronomic value, stresses,

Permanent grassland are a source of healthy feed for a large group of ruminant animals. They also serve to conserve biodiversity, reduce environmental pollution, including nitrogen oxide and sulfur in the air and prevent soil erosion. Perennial ryegrass, due to favorable properties, morphological, biological and chemical, has become economically most important species among the forage grasses.

There are two different opinions regarding the impact of agricultural intensification on biodiversity. Some authors suggest that is that caused the extinction of many ecotypes and replacing them with new forms of crops. According to other authors the negative impact on the biodiversity is not observed, because the genetic resources *in situ* and *ex situ* form are included into the breeding programs and the wide variation within the newly created varieties could be maintained.

Because of this, the aim of this study was preliminary evaluation of Polish ecotypes, which may be the source of the important agronomic characters. The base collection gathered in the Grasses and Legumes Laboratory of Plant Breeding and Acclimatization Institute consist of 10 ecotypes selected in the preliminary experiments from group of 50 genotypes, 22 clones obtained after crossing *Lolium perenne* ecotypes, cultivars or breeding materials, 13 clones obtained after intergeneric crosses *Lolium perenne* with *Festuca pratensis* and 59 commonly used Polish and European cultivars. Ecotypes and clones, propagated previously in spatial isolation, were characterized using the method of sowing row (distance between rows 50 cm), which is more adequate for natural conditions. Ecotypes were collected in the Mazury area- 50 forms, and after a preliminary description, 10 were selected for further study of the population. Mazury are areas dominated by permanent pasture and natural preserves for many years. The pre-breeding materials were characterized in respect to the most economically important biological characters, based on which it was possible to conclude about their yield potential under forage and seed management. Due to the fact that perennial ryegrass is a species highly responsive to biotic and abiotic stresses special attention was given for the description of the interaction genotype - environment. Factor analysis method was used to analyze the results.

Ecotypes, diploid clones obtained after within specific crosses and intergeneric *Lolium perenne* x *Festuca pratensis* hybrids formed a homogeneous group, together with selected Polish or European cultivars. These materials were medium early or early, with a shorter flag leaf than the first tetraploid cultivars group and were characterized by a short and light ear, low number of spikelets in the ear and low TSW.

(Poster 12)

Barley landraces as sources of resistance to *Blumeria graminis* f.sp. *hordei*

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Barley (*Hordeum vulgare* L.) is an economically important crop. In many regions barley is grown in marginal agricultural areas. Landraces of barley are important in many mountain regions, because they are often the only crop possible to be cultivated on slopes at high elevations (Czembor 1996, 2005).

Powdery mildew, caused by the pathogen *Blumeria graminis* f. sp. *hordei*, is one of the most destructive foliar diseases of barley in Central and Western Europe. In countries where mildew is a problem, yield losses in experimental tests often exceed 25%, although average losses in barley production are smaller and about 10%.

Barley landraces constitutes a rich genetic resource, and many examples of their successful use have been reported. However only for less than 2 percent of barley landraces the attempts were made to identify powdery mildew resistance genes using differential lines and isolates. These types of studies were mostly conducted in Germany, Denmark and Sweden and on smaller scale in other countries such as Czech Republic, The Netherlands, USA and Poland (Czembor 1976, 1996, 2005).

Seed samples of 122 barley landraces were used for screening for resistance to powdery mildew. In preliminary study, about 30 plants per landrace were evaluated in greenhouse with isolate 33. Isolate 33 represented the most avirulent isolate available allowing the expression of maximum number of resistance genes.

From 14 resistant landraces single plant lines were selected. These lines were tested in seedling stage with 20 differential isolates of powdery mildew. The isolates were chosen according to their virulence spectra on the Pallas isolines differential set and 7 additional differential cultivars. These isolates had virulences corresponding to all major resistance genes used in Europe. Twelve tested lines were resistant to all isolates used.

This investigation identified new sources of resistance to barley powdery mildew in lines selected from barley landraces. These new sources may contribute significantly to the diversity of the powdery mildew resistance gene pool available for barley breeders.

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(Poster 13)

Conservation of herbaceous ornamental plant genetic resources in botanical garden of Vilnius University

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Key words: genetic resources, ornamental plants.

Collection and investigation as well as conservation of plant genetic resources have become a important task for the countries in the world. By signing the Rio Convention on Biological Diversity in 1992, Lithuania has committed to conserve its plant genetic resources. The Botanical Garden of Vilnius University is taking part in the National programme on Plant Genetic Resources since 1994. Botanical Garden performs activities as a Coordination Centre for Ornamental Plants Genetic Resources, and manages the Central European data base for *Ribes* L. and *Rubus* L. genera. There are about 10000 plant accessions from 190 families and 866 genera in the collections Botanical Garden. The collection of woody plants includes more than 2500 specimens. Field collections are established for the conservation of the genetic resources of ornamental plants.

Researches of Floriculture Department of Botanical Garden of Vilnius University joined the program for investigation and conservation of genetic resources in 1994. At present, there are about 600 flower taxa developed by Lithuanian plant breeders in collections of Floriculture Department. Authors of Lithuanian flower cultivars (both amateurs and professionals) have bred a beautiful flower cultivars and hybrids. Therefore, collection, preservation, investigation and evaluation of Lithuanian flower genetic resources are a new trend for researches, not only in the botanical gardens, but for researches of other scientific institutions in the country as well. Lithuanian flower breeders released a lot of new cultivars of *Crocus* L., *Dahlia* Cav., *Gladiolus* L., *Hemerocallis* L., *Iris* L., *Lilium* L., *Paeonia* L., *Primula* L., *Tulipa* L. and some others. One of the aims is to collect, investigate, evaluate and describe according to the appropriate descriptors flower cultivars created by Lithuanian breeders. Obtained data enable to select the most valuable ornamental plant cultivars and to develop suitable growing system for effective preservation and rational use of plant genetic resources. Lithuanian flower cultivars are good adapted to local climate conditions, tolerant or resistant to fungal diseases and it make a possibility to foster usage of flower cultivars for parterre, landscape gardening and other purposes.

A group of ornamental plant cultivars were put on the national list of plant genetic resources: 44 cultivars of *Paeonia lactiflora* Pall, 4 cultivars of *Paeonia suffruticosa* Andrews, 4 cultivars of *Primula malacoides* Franch, 41 cultivars of *Iris* L., 15 cultivars of *Gladiolus* L., 8 cultivars of *Dahlia* L. and 5 accessions of wild flora (*Helianthemum nummularium* (L.) Mill., *Tulipa bifloriformis* Ved., *Trollius europaeus* L., *Salvia officinalis* f. *rubicunda* and *Lathyrus maritimus* (L.).

(Poster 14)

The European Cooperative Programme for Plant Genetic Resources (ECPGR) Cucurbits Working Group

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Key words: database, passport data, characterization, safety duplication, Most Appropriate Accessions, guidelines

The establishment of the Cucurbits Working Group (CWG) was approved by the Steering Committee in October 2003. The general objective of the Group is the organization of the genetic resources of cucurbits in Europe. The main achievements of the Cucurbits WG has been the creation of the European Central Cucurbits Database (ECCUDB), the development of lists of minimum descriptors for primary characterization of melon, cucumber, *Cucurbita* and *Lagenaria* and watermelon, the increase of safety duplicates among European collections of cucurbits and the inventory of European institutions involved in on farm conservation activities on cucurbits. The database at present includes passport data of 27.489 accessions of 21 genera and 72 species. 42% of the accessions belong to the genus *Cucumis*, followed by the genus *Cucurbita* with 30% of the accessions and the genus *Citrullus* with 25%. Characterization data of 775 accessions of *Cucumis sativus*, 107 of *Citrullus lanatus* and 53 of *Cucurbita pepo* are also available as well as 223 images of *Citrullus lanatus*, *C. sativus* and *C. pepo*. Information about a core collection of *Cucurbita pepo*, including characterization data and images, is included. The data come from 39 institutions from 23 countries. An increase of the level of safety duplication has been achieved by arranging a “black box” containing 1064 accessions of cucurbits transferred from Bulgaria to CGN, The Netherlands. Arrangements for safety duplicating Georgian cucurbits at CGN are in progress.

At present the Group concentrates its activity on the four Network goals for Phase VIII, largely related to AEGIS: (1) Develop mechanisms for determining Most Appropriate Accessions (MAA) (2) Agree on quality standards for maintaining MAAs (3) Adapt the Central Crop Database for the identification of MAAs and (4) Improve the level of safety-duplication. Regarding these four areas, in its last meeting held in Tbilisi (Georgia), the Group developed the criteria to be followed for the selection of MAAs for cucurbits, including both general and crop-specific criteria (Díez et al., 2011). General guidelines for regeneration, processing and storing of cucurbit species have been developed and agreement of the document by all members of the WG is currently in progress. Improvements of the ECCUDB are being carried out in order to facilitate the selection of the MAA.

The CWG has met four times. The Reports of these meetings are available on the webpage of the Group <http://www.ecpgr.cgiar.org/Workgroups/Cucurbits/Cucurbits.htm>.

Díez, M.J.; van Dooijeweert, W.; Maggioni, L.; Lipman, E. 2011. Report of a Working Group on Cucurbits. Second Meeting, 8-10 November 2010, Tbilisi, Georgia. Bioversity International, Rome, Italy.

(Poster 15)

On-farm seed production practices of organic and low-input farmers in Portugal

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Key words: homegarden, germplasm, on-farm conservation, genetic resources

The recent development of organic and low input farming systems across the world highlighted the importance of local varieties and on farm seed production, since the seeds and varieties currently grown in high input agriculture are not adapted either to different locations or to the annual variation observed in organic and low input systems.

The results presented in this poster are the first output of an investigation, under the frame of the SOLIBAM project. This research was carried out in order to understand the current on-farm seed production practices of organic and low input Portuguese farmers and to prioritize research and policy needs in this field.

Twenty-eight farmers were interviewed and the results show that most farmers save seeds from season to season and from year to year. In general they declare to be satisfied with the traits of the varieties they chose, although some paths of improving, related to attributes such as size, productivity and the duration of the harvest season, were identified.

(Poster 16)

The Role of the Gene bank in conservation of plant genetic resources in Republika Srpska

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Key words: Gene bank, Republika Srpska, plant genetic resources, *ex situ* conservation

A gene bank is a collection of seeds and other plant reproductive material, mostly of cultivated plants and their wild relatives. It is the most popular, the best researched, most widely used and most convenient method of *ex situ* conservation. Today there are over 1300 gene banks and germplasm collections around the world, maintaining an estimated 6,100,000 accessions.

Gene bank of Republika Srpska has been established in 2005. within the SEEDNet (South East European Network for Plant Genetic Resources) project. Officially establishment and management of Republika Srpska Gene Bank are defined in Programme for protection of plant genetic resources in Republika Srpska adopted by the Government of Republika Srpska in May of 2008.

Up till now Gene bank of Republika Srpska counts 712 accessions with 150 accessions stored long term, around 100 accessions in clonal archives and the rest are stored medium term or on farm. For medium term storage, the germplasm is stored at + 4°C temperature and 15% to 20% humidity, and for long term storage at -18°C and 3 to 7% humidity. Base, active and safety base collections are formed for long term stored accessions. Work on *in vitro* conservation methods is in initially phase and for now only autochthonous garlic, onion and potato accessions are stored *in vitro*.

It is necessary to continue with germplasm collection and preservation of autochthonous material and cultural heritage of Republika Srpska. By promoting utilisation of plant genetic resources, and making both information and plant material available to researchers and other interested users, gene banks are fulfilling their role in improving human well being.

(Poster 17)

Bioinformatics approach to the strawberry transcriptome analysis in the context of the response to fungal pathogen

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Key words: strawberry, Verticillium wilt, differential expressions analysis, PCA,

Statistical and bioinformatics interpretation of the results of transcriptome analysis conducted using automated high throughput system like Illumina-Solexa is not a trivial issue. One experiment can provide the investigator of the huge amount of raw data which needs elaboration. Obtained results depend highly on the statistical methods implemented to analyze the data - a set of numerous tags differentially expressed in the given tissue. The main aim of the experiment is to select differentially expressed fragments and to draw conclusion about these differences. In our study we based on the result of an experiment conducted in the Institute of Horticulture, Skierniewice and aimed to investigate changes in transcriptome of tolerant and susceptible strawberry cultivars after plant infection with *V. dahliae*. Generated database contained 1,9 milion of unique sequences of 21-22 base length. Selected RNA sequences were divided into several groups (clusters) according to the relation between the expression levels in tolerant and susceptible tissues and respective controls using Principal Component Analysis (PCA). To obtain additional information the BLAST search on the *F. ananasa* nucleotide sequences deposited in GenBank was performed (with E value threshold = 1) to obtain preliminary information on distribution of scores and hits. As the last step of analysis, the database for *F vesca* complete genome was searched using selected tags as a query to identify possible similarities. Clustering according expression levels were used for looking for consensus sequences and tags elongation. The first selected sequences were identified as the fragments of putative genes active in strawberry- *V. dahliae* interactions.

(Poster 18)

Variability of field and technological parameters of traditional Czech and Slovak common wheats

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Key words: common wheat, wheat landraces, modern wheat cultivars, morphological, phenological and technological parameters

The intensive breeding programs, supported by effective international cooperation, enabled high efficient wheat production over the last 30 years. On the other hand, it led to the complete replacement of original wheat landraces by modern semi-dwarf and high-yielding cultivars, correlating with a decrease in wheat genetic diversity. That's way, wheat landraces have received priority for collection, conservation and documentation in recent years, because of the increasing threat to their continued existence by the spread of improved modern cultivars. Additional demands of wheat producers on production stability and a specific quality of grain force the breeders to find new potential genetic resources including a mapping of original old wheat materials. With regard to mentioned above, this study was aimed at a complex of important morphological, phenological and technological parameters (in sum 18 parameters) in a wide number of 271 winter and 62 spring wheat collection (*Triticum aestivum* L.) of the purely Czech and Slovak origin. The pivotal ratio of wheat materials was consisted of older wheat materials and landraces which were gathered by mutual Czech and Slovak cooperation within the frame of the common project. The obtained annual results generally indicated similar variability of tested parameters in winter and spring cultivars. The highest variability was found out in lodging resistance from 50% for winter- to 68% for the spring wheats. For powdery mildew, there were also detected extreme differences (highly susceptible or highly resistant) among wheat materials and final variability among classification scores achieved 38% (winter wheat) and 44% (spring wheat) respectively. The found high differences in both parameters (plant height and powdery mildew resistance) mostly related to the significantly higher plant height and powdery mildew susceptibility of older wheat materials compared to modern wheat cultivars. In contrast to these negative parameters detected predominantly in older wheat materials, older landraces generally showed significantly higher protein content (e.g. Trebišovská 76: 18.2% and Bučianská V.T.16: 18.3%) and their range in other parameters (e.g. earliness and technological characteristics) was comparable or even higher than in modern wheat cultivars. Only multi-annual results can bring significant information about properties and their stability in particular wheat cultivars and especially in some older wheat materials suitable for specific breeding programs. In spite of this fact, the annual results have already indicated series of wheat landraces (Košutská, Bučianská 16/438 and Slovenská 777) with very high protein content (17.1% – 17.7%), technological (baking) quality of grain (e.g. Zelený sedimentation index: 61 – 62ml) and quite acceptable spike productivity (2.11 – 2.30g per ear) compared to modern wheat cultivars (e.g. the best modern registered wheat cultivar Bohemia: protein content – 15.52%, Zelený sedimentation index – 65ml and ear productivity 2.28g).

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(Poster 19)

***Ex situ* conservation of Plant Genetic Resources in Albania**

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Keywords: *ex situ* conservation, plant genetic resources, documentation

The *ex situ* conservation of plant genetic resources in Albania is reorganized. The Genebank of Albania is transferred to the Agricultural University of Albania. Activities on PGRFA conservation and use are renewed in Albania, when SEEDNet project has started the support for Albanian Gene Bank (AGB).

Ministry of Agriculture and Agricultural University of Tirana carries inventory of genetic resources in *ex situ* conservation in Albania during 2008. The aim was to genetic resources inventory in storage, storage conditions, method of recording, data collection, processing and preparation of database to be used for setting up a national network of documentation and its integration into international network of genetic resources documentation. The inventory was conducted in all research institutions for agriculture then conserve and use genetic resources. After being identified gaps were identified and measures have achieved some concrete results. In addition, the development of Filed Gen Bank for fruits and vittis of AGB, has been initiated. In the course of the SEEDNet support the Albanian genebank was equipped with a new, efficient and comprehensive genebank management system (Genebank Information System). Collection stored according to the standards and data documentation are completed and transferred to the European Search Catalogue for Plant Genetic Resources (EURISCO) for 2100 accessions and SESTO for 1058 accessions. Department of documentation of AGB, has coordinated the process of recording resources research centers and their inclusion in the international system of information. Already the national inventory is easily accessible by users.

(Poster 20)

Developing a global strategy for the conservation and utilization of cacao genetic resources

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Key words: global network; cacao; genetic resources conservation and use; characterization and evaluation; crop strategy; information system

The future of the world cocoa economy depends significantly on the conservation and sustainable use of a broad genetic base to adapt to biotic and abiotic stresses and changing environments. With this in mind, CacaoNet was launched in 2006 under the leadership of Bioversity International as a global network to optimize and coordinate the conservation and use of cacao genetic resources. One of the first internationally agreed priorities for CacaoNet was the development of a Global Strategy for the conservation and utilization of cacao germplasm. An Expert Working Group has been created for the drafting of the Strategy based on broad consultations. The expert group has allocated responsibilities for different components, i.e. *in situ* conservation, *ex situ* conservation (including “virtual” strategic global base and active collections), germplasm characterization (morphological and molecular), collecting and germplasm acquisition, germplasm exchange (legal aspects and safe movement), information management at different levels, and facilitating the utilization of cacao germplasm.

A central component of this Strategy is the proposed creation of a Global Strategic Base Collection (GSBC), providing a rational and cost-effective basis for the long-term conservation of cacao genetic resources. Composition of the GSBC will be based on an innovative selection process using molecular genetics data. Selected accessions will be conserved as a virtual collection in their countries of origin and duplicated for safety purposes in one of the international collections, including the use of cryopreservation. Furthermore, a Global Strategic Active Collection (GSAC) will be created as a dynamic and dispersed collection composed of accessions that are in the public domain and with combinations of characteristics of immediate value to breeders. A specific component of the Strategy will cover the organizational, managerial and policy considerations relevant to germplasm dissemination. The Strategy will also consider ways to improve communicating the importance of safe germplasm movement to the cacao community to minimize the risk of spreading pests and diseases.

The development of CacaoNet’s Information Management System (IMS) is another key component of the Strategy. Central to the development of the IMS is CANGIS (CacaoNet Germplasm Information System), a web-based inventory of passport, morphological characterization and evaluation data for CacaoNet accessions. Additional data is accessible through links to existing databases. A germplasm ordering system will also be established for easy access and monitoring of exchanges. The widely dispersed nature of accessions also means that a particularly important aspect of the Strategy will be the successful integration of local and diverse genebank information management systems.

The development of the CacaoNet Strategy is a highly participative process, taking account of the views of as many cacao genetic resources specialists and other stakeholders as possible [www.cacaonet.org].

(Poster 21)

Conservation and management of plant genetic resources in the Latvian Gene Bank

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Key words: PGR, conservation, evaluation, descriptors

Conservation of plant genetic resources (PGR) in Latvia is performed through the Action Plan for 2011 accepted by the Ministry of Agriculture, which is responsible for PGR activities. The Latvian Gene Bank (LGB) preserves seed samples of generatively propagated species mainly of Latvian origin. The main groups of species conserved are cereals (54%) and forage grasses (26%). 47% of the forages collection are accessions which have been collected from wild populations within Latvia. In recent years, the main priorities have been the regeneration of repatriated accessions (which comprise about 16% of all accessions in the LGB) and the characterization and evaluation of gene bank material. Evaluation and characterization of PGR according to previously developed crop descriptors was done in partnership with co-operating institutions within Latvia. At present 57% of repatriated material has been regenerated and prepared for long-term storage, and 19% of LGB material has been evaluated and characterized. To ensure efficient handling of PGR material, and to ensure access to germplasm and data: 1) protocols for all major GB activities have been established; 2) the main passport data, germination and storage information are available through the SESTO database; 3) software for entering and maintaining the plant descriptor data has been established and data for 383 accessions have been entered into the PGR descriptor database.

(Poster 22)

Towards sustainable utilization of apple germplasm collections in Sweden: marker-based genotyping and screening for useful diversity

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Key words: apple, germplasm collections, molecular markers, genotyping, useful diversity

In Sweden, preservation of genetic resources in fruit crops is the responsibility of the ‘Programme for Diversity of Cultivated Plants’ which has defined a set of mandate cultivars for publicly funded conservation. About 220 apple cultivars, either indigenous or with a long history of cultivation in the country, are maintained in numerous clone archives as part of the Swedish cultural history. The clone archives serve mainly home gardeners and presently have limited or no interactions with scientists and plant breeders. About 100 apple mandate cultivars are also included in the research and breeding oriented germplasm collection at Balsgård, Swedish University of Agricultural Sciences. However, all these collections contain mainly older plant material, often of uncertain origin, which creates problems with correct cultivar identification.

To improve the quality of the Swedish apple germplasm collections, we used SSR (Simple Sequence Repeats) to provide mandate cultivars with ‘molecular profiles’. SSR markers were also used to detect duplicates and mis-labellings in germplasm collections (Balsgård and clone archives around Sweden), to verify pedigrees of some cultivars and to evaluate the extent of diversity within mandate cultivars.

To make the apple collection at Balsgård more valuable for the on-going plant breeding program, screenings of self-sterility genes (S-genes), fruit texture genes (*Md-ACS1*, *Md-ACO1* and *PG1*) and scab-resistance genes have been performed with molecular markers (mainly SCAR and CAPS). Screenings for S-genes and fruit texture genes will be extended to the entire set of mandate cultivars within the newly initiated project ‘Evaluation of useful diversity in Swedish mandate cultivars of apple’. A large part of the collection has also been screened for fruit firmness with penetrometer measurements at harvest and after 6 (early ripening) or 12 (late ripening) weeks of cold storage.

A number of mandate cultivars are now also being phenotyped with inoculation tests for resistance to storage diseases (*Penicillium expansum*, *Pezizula malicorticis* and *Glomerella cingulata*) and resistance to European canker (*Nectria galligena*).

Proper characterisation of germplasm collections is a first step towards sustainable utilization of apple genetic resources in Sweden.

(Poster 23)

Plant genetic resources conservation activities and network in Lithuania

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Key words: genetic resources, ornamental plants

The collection and evaluation of plant genetic resources of agricultural crops in Lithuania was started when Dotnuva plant breeding station was founded in 1922 (Lazauskas, 1998). In nowadays 8 institutions are involved in activities of collection, investigation and conservation of plant genetic resources. A National Plant Genetic Resources Coordinating Centre was founded at the Lithuanian Institute of Agriculture in 1993. The Baltic-Nordic project for plant genetic resources (PGR) was initiated by Nordic Gene Bank (NGB) in 1994. The main objective of the project was to develop the national PGR conservation network in Lithuania. This project activated the cooperation and coordination work among the education and research institutions involved in PGR investigation and conservation. In 1994-1997 was pursued the first research programme “Genetic resources of cultivated plants”, which was funded by the State science and studies foundation. The next research programme “Investigation and conservation of genetic resources of cultivated plants and home animals” was approved and implemented in 1998-2002. The activities of 10 institutions (universities, research institutes, botanical gardens and breeding centres) were concentrated on plant, livestock, poultry and honey-bee genetic resources. From 2003 ongoing research programme “Investigation of plant genetic resources” and it was ended in 2008. This programme was funded by the Ministry of Education and Science as previous one as well.

In 2001 the law on National plant genetic resources was enacted by the Seimas (Parliament) of the Republic of Lithuania. Government of Lithuania adopted a resolution about the foundation of Plant Gene Bank from the 1st of January 2004. The main goals of Plant Gene Bank are to coordinate activities for collection, investigation and conservation of plants genetic resources, secure long-term preservation and sustainable use of plant genetic resources, to secure accessibility, safety and particularity of information about plant genetic resources. Five institutions were identified as a main institutions responsible for activities on plant genetic resources collection, investigation and conservation according to plant groups: agricultural crops, horticultural plants, forest trees and shrubs, medicinal and aromatic plants, ornamental plants.

One of the ways to preserve plant genetic resources is to maintain seed at long- or medium-term storage conditions. Today about 75 countries have facilities for long- and medium-term storage (FAO, 1998). A long-term seeds store was established at a former National Plant Genetic Resources Coordinating Centre in 1997. It is equipped with all necessary facilities for seeds drying, packing and storage. Vegetatively propagated plants, as a rule, are maintained in field collections.

(Poster 24)

The damaging effects of oxygen on seed viability are underestimated

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Key words: seed longevity, storage conditions, oxygen

Maintenance of seed longevity is an important issue in the conservation of plant genetic resources by genebanks. A decrease in seed viability may result in loss of genetic variation and requires a new cycle of propagation, which may weigh heavy upon the limited budgets of gene banks. Gene banks generally store seeds at low moisture levels and temperatures, but the role of the storage atmosphere, in particular oxygen, is usually not considered. Positive results of storage under anoxia have been reported, whereas others show no or even negative effects. Investigation of the role of oxygen on seed longevity is hampered by time constraints, and accelerating the ageing process by increasing the temperature or moisture levels is not representative for conditions during genebank storage.

Here we report on a method that tackles these problems by storing seeds in steel tanks under an elevated partial pressure of oxygen (EPPO). By increasing the air or oxygen pressure till 18 MPa (180 bar), the oxygen concentration in the seeds can be increased by a factor of about 900. Storage under high pressure nitrogen is performed as control. Lettuce seeds stored at 20 °C and 30% relative humidity under high pressure air or oxygen deteriorated within four weeks of storage. The morphological effects were comparable to those of naturally aged lettuce seeds, i.e. reduced germination rate and total germination, reduction in seedling growth and occurrence of midvein necrosis at the cotyledons. Storage under high pressure nitrogen resulted in longitudinal cracks in the testa of some seeds, but germination rate and seedling morphology were similar to seeds stored under air at ambient pressure. The EPPO method was also successfully applied to seeds of cabbage, soybean and barley. We are aware that also this EPPO method is artificial and may not mimic natural ageing completely but it offers new opportunities to study seed aging. Moreover, it demonstrates the deleterious effect of oxygen on seed viability. The main advantage of the EPPO method is that seed aging can be studied within a relatively short period and at seed moisture levels and temperatures that are common in seed conservation facilities.

Based on the results obtained so far, we expect that a reduction in oxygen levels during seed storage will result in a decline in the rate of seed aging. Most of the damage occurring in seeds during natural ageing is related to oxidation of lipids, membranes, DNA, RNA and proteins. Reduction of the oxygen concentration can be achieved by storing under nitrogen, vacuum packaging, inclusion of oxygen absorbers in the seed containers, or a combination of these methods. Obviously, the containers used for packaging should be impermeable for moisture as well as for oxygen. Most likely, seeds need to be stored dry under anoxia soon after harvest in order to prevent the initiation of autocatalytic lipid oxidation.

(Poster 25)

Conservation of PGR at the Research Centre for Agrobiodiversity, Hungary

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Key words: *ex situ*, on-farm conservation, Pannon Seed Bank, germplasm transfer

Established in 1959, the former Institute for Agrobotany, now Research Centre for Agrobiodiversity (RCA, Hungary) holds the largest germplasm collection in Hungary and acts as a coordinating centre for national PGR activities as well as for the national participation in international PGR programmes. The germplasm collections include 91 768 samples of field and annual horticultural crops suitable for cultivation in Hungary (belonging to over 900 taxa of 300 genera). The main activities of RCA include exploring and collecting of PGRFA, characterisation and evaluation, documentation, multiplication and regeneration of accessions, *ex situ* and *in situ*/on-farm conservation.

Expanding its current functions RCA is the coordinating beneficiary of the “Establishment of the Pannon Seed Bank for the long-term *ex situ* conservation of Hungarian vascular wild plants” LIFE+ project that aims at the long-term *ex situ* seed preservation of the wild vascular flora of the Pannonian biogeographical region in order to assist and complement *in situ* conservation activities. By the end of this project period (2010-2014), seed samples of approximately 50 percent –at least 800 species- of the native flora will be collected and preserved. The establishment of a joint seed bank for the agricultural and wild flora would be a unique and demonstrative example worldwide in line with the objectives of the Convention on Biological Diversity, as the genetic diversity of the Pannonian biogeographical region's entire flora, including the wild flora as well as crop and vegetable plants serving human nutrition are aimed to be conserved at one place.

Complementing traditional *ex situ* genebank conservation activities with additional conservation methodologies may result in slowing the tendency of disappearing traditional varieties from cultivation. There is a significant increase in seed requests received due to the growing interest of farmers/breeders in genetic resources as sources of genes for important characters including resistance and tolerance to biotic and abiotic stresses and as a basis for high quality niche productions. The motivation for this changing attitude is due to awareness raising (media, expositions, etc.), unique traits (quality, tolerance, shape/colour) of land races and traditional varieties, historical considerations, organic farming practices and subsidies available for the maintenance of rare, endangered varieties. This tendency clearly shows that strengthening *in situ*, on-farm conservation activities of farmers, home gardeners and NGO's is crucial for sustainable use and conservation of native PGR.

From 1973 to 2009 85.433 samples have been distributed by the genebank for collaborators and upon request of potential users. The distribution of PGR samples is facilitated by the Catalog of Seeds issued by RCA and EURISCO can also be used as a source of information on RCA's collections. There are several well-documented cases of successful use of accessions but in fact the feedback on the utilization of germplasm supplied is limited. The future aims of RCA include the development of a web-based information system that provides access to reliable information on the evaluated characteristics and maintenance of traditional varieties and also serve as a platform for germplasm users to inform the genebank staff on their experiences concerning the utilization of accessions supplied.

(Poster 26)

Genetic resources of medicinal and aromatic plants in Albania

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Keywords: Genetic resources; Medicinal and Aromatic plants; Albania, SEEDNet project

Albania is distinguished by its rich biological and landscape diversity, with favourable climatic conditions varying from subtropical to continental, has a very rich flora. The mountainous terrain combined with steep cliffs creates ideal conditions for maintaining and protecting a large number of ancient species, some of which are endemic or sub-endemic. The Albanian flora comprises 3250 vascular plant species or approximately 30 % of all European Flora occur in Albania, with about 30 endemic and 180 sub-endemic species. More than 300 species are aromatic or medicinal plants, which are very important economic natural resources. Further, they play an important role in everyday life; from all these species, 68 species are endangered (EN).

The rate of loss of the Albanian's biodiversity of MAPs during the past 20-30 years is believed to be high and increasing. Moreover, insufficient knowledge and studies on a wide range of flora, especially for MAPs limit an accurate historical evaluation of the biodiversity status of the country. The number of endangered wild species of MAPs of high and expected to increase if appropriate evaluation and conservation measures are not taken. This paper presents in brief, activities in plant genetic resources (PGR) relevant to medicinal and aromatic plants in Albania initiated and increased by support of SEEDNet Project.

(Poster 27)

Genetic diversity and breeding value of forty common bean (*Phaseolus vulgaris* L.) landraces from Nicaragua

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Key words: *Phaseolus vulgaris*, genetic diversity, landraces, breeding value, microsatellite markers

The common bean (*Phaseolus vulgaris* L.) is one of the most important crops around the world. Nicaragua is located in the Mesoamerican region where a high level of genetic richness is expected. Most bean production rests on the exploitation of local landraces, which are adapted to different environments but have yields lower than those of bred cultivars. The current Nicaraguan bred cultivars were produced by regional breeding programs using mostly foreign germplasm, but they are not fully preferred by consumers. The objectives of this study are to investigate the genetic diversity of forty common bean landraces using twenty microsatellite markers (SSRs) and to identify promising populations for further selection. These SSRs markers are presumably linked to important traits (yield, number of pods per plant, seed size, tolerance to drought, resistance to bruchids, and days to flowering and maturity). Additionally, the bred cultivar 'INTA ROJO' will be used as a target genotype when yield and yield components are analyzed. We hypothesize that many Nicaraguan landraces are very promising for the improvement of agronomic and physiological traits. The resulting information will enhance the common bean improvement using modern molecular tools and local bean variation as the main input for plant breeding programs.

(Poster 28)

SEED Net regional collecting expedition and *ex situ* conservation of *Trifolium pratense* L., *Festuca pratensis* Huds., *Dactylis glomerata* L. and *Medicago falcata* L.

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Key words: collecting expedition, *ex situ* conservation, fodder crops, grasses, legumes.

South East Europe is a region rich in biodiversity and significant parts of the region are covered by grassland, constituting a great potential for utilizing such biodiversity in forage plants breeding programs. Due to changes in climate conditions and agricultural practices there is an impending risk of losing valuable genetic diversity. In order to ensure a long-term conservation of its valuable plant genetic resources and promote for a sustainable utilisation a number of national institutions in the region established SEEDNet (South East European Development Network on Plant Genetic Resources) in 2004 in order to strengthen the national efforts. The main objective of SEEDNet is long-term conservation and sustainable utilisation of the diversity of PGR within the region through a well co-ordinated network of functional national programmes and working groups.

The strategy of the SEEDNet Forage crops WG reflects the needs and interest for conservation and exchange of the most important and priority forage species of the whole region. Over the period of three years (2007-2010), collecting expeditions of ten project partners were focused on four fodder crops species and were carried out in different floristic, environmental or pedological regions belonging mainly to permanent grassland habitats. The main objective was to enlarge the genetic basis of regional forage genetic resources collections with new germplasm of two grass (*Festuca pratensis* Huds., *Dactylis glomerata* L.) and two legume species (*Trifolium pratense* L., *Medicago sativa* ssp. *falcata* (L.) Arcang.) defined as priority species for the region.

Collecting was focused on different bio-geographic regions, altitudes, grassland types and land use. Each project partner visited characteristic locations that were chosen based on prior knowledge and inventorisation of target species. In total 896 accessions were collected, from those 272 of cock's foot, 226 of meadow fescue, 313 samples of red clover and 85 yellow alfalfa samples. Collected seeds were included in national gene bank collections in the form of active and base collections as a source of forage germplasm for breeding. Seeds were regenerated, processed and accessions have been deposited in the storage vaults at -20°C. All collected and multiplied seed accessions are supplied with multi crop passport descriptors (EURISCO) and with information on collection sites and grassland habitats. As a final benefit of this project not only material collected, but as well a better knowledge of ecotype populations deriving from well-defined habitats could help in planning of future collection missions, selecting adapted genotypes for direct further use and/or for breeding purposes and finally in defining valuable sites for *ex situ* and *in situ* conservation.

(Poster 29)

Cryopreservation of young inflorescences bases in bolting garlic for germplasm storage

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Key words: droplet vitrification, PVS, *Allium sativum*, European project, cold pretreatment

Cryopreservation is the safest and most cost-effective method to maintain vegetatively propagated germplasm. Garlic falls into this category. So far cryopreservation is relying on bulbils, basal plates of in vivo and in vitro material. Additionally to this, a novel source can be used from the bases of unripe inflorescences. Within the AEGIS system, a small project was completed which aimed at adopting this new method to genebank material under European conditions and to increase the effectiveness of cryopreservation in bolting garlic. Using unripe inflorescence bases, the usability of the mother plants is expanded, the preculture time is reduced and the risk to lose mother plants during preparation is diminished. Three European genebanks (IPK Gatersleben, Germany; RIVC Skierniewice, Poland; BPGV Braga, Portugal) compared the various steps of the vitrification and droplet-vitrification protocols and optimised the procedure. Three clones fulfilling the requirements of a Most Appropriate Accession were selected as standard material and were investigated by all partners according to the method described by Kim et al. (2007). In the accession from the German collection, the best regeneration after rewarming from cryopreservation, which was obtained in all three laboratories, amounted to rates between 94 % and 75 %. Comparing the two cryopreservation methods, the droplet-vitrification was more effective than the vitrification method. Using inflorescences of different developmental stages higher regrowth rates were obtained for the older ones. Furthermore, three different durations (2 days, 4 weeks and 6 weeks) were tested in order to explore the best-suited time for cold storage of young inflorescences. Finally different durations of the pretreatments with PVS3 solutions and the use of other PVS were tested.

Kim, H.-H., Lee, J.-K., Hwang, H.-S. and Engelmann, F. 2007. Cryopreservation of garlic germplasm collections using the droplet-vitrification technique. *CryoLetters* 28:471-482.

(Poster 30)

Actions for a better use of PGRFA in Switzerland

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Key words: National Action Plan, concepts, database, landraces, fruit trees, spelt wheat

After the adoption of the FAO Global Plan of Action in Leipzig 1996, the Federal Office for Agriculture (FOA) prepared the Swiss National Action Plan (NAP). Since 1999, a yearly budget line of about 3 million Swiss francs is at the disposal for projects that fill gaps and needs identified in the NAP. Projects may be proposed by public as well as private organizations and both are often collaborating very closely. The first 4 years had as main priority the inventory of landraces of fruit trees. Up to now 1200 landraces of apple, 1000 of pear and 500 of cherry have been found. The main priorities during the second 4 years phase were the elaboration of conservation concepts and the characterization and evaluation of accessions whereas the third phase mainly dealt with the continuation of the characterization and evaluation as well as the *in situ* conservation of forage crops.

The Swiss Commission for the Conservation of Cultivated Plants (CPC) coordinated the elaboration of the conservation concepts. These concepts allow the different organisations involved to share the conservation approach and the quality standards. These concepts include also the criteria for accessions to be admitted on the ‘positive list’ which should be conserved, characterized and evaluated through NAP projects. The CPC, in mandate of the FOA, developed and runs the national database (www.bdn.ch) regrouping all the information on passport, characterization and evaluation data of the accessions conserved in Switzerland.

Agroscope ACW holds the national genebank since 1900. Seeds of generative propagated crops are stored at Agroscope, including accessions from private organisations, which are integrated in NAP projects. Accessions from vegetative propagated crops integrated in NAP collections, such as fruit trees, berries, grapevine, etc. are mainly conserved by private organisations and are also part of the national genebank. The national genebank makes accessions available under the conditions of the International Treaty for Plant Genetic Resources for Food and Agriculture with the Standard Material Transfer Agreement.

During the last eight years, characterization and evaluation of vegetables and grain legumes have been realised for 450 accessions of 12 different species. More than 500 landraces of spelt wheat have been analysed for agronomical traits and disease resistances. The same for 200 landraces of wheat, where also baking quality was analysed. Fruit trees have also been characterized and evaluated over the last 4 years, including with molecular markers.

The outcomes of the NAP are a strengthening of the collaboration between private and public organisations, an increase of public awareness by the creation of demonstration gardens and the commercialisation of products from landraces on local markets and even in supermarkets. Three seed producers promote the distribution and use of landraces and old varieties of vegetables and grain legumes in Switzerland. Landraces of cardoon from Geneva, pears from Fribourg and maize from the Rhine valley have obtained an international valid legal protection (AOC). Finally, Swiss legislation has been adapted to permit cultivation of landraces and old varieties for niche production without inscription in the national variety catalogue.

(Poster 31)

Analysis of historical observation data of IPK genebank accessions of barley and wheat

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Key words: barley, wheat, *Hordeum vulgare*, *Triticum aestivum*, characterization and evaluation data, statistical analysis, genebanks

During seed multiplication of genebank accessions at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, a number of characters related to characterization and primary evaluation is being recorded in the field. This started in Gatersleben in 1946 and continued to the present day. Before the establishment of the seed store in 1976, cereal accessions were multiplied every 2-3 years, so that a large part of the material that entered the collection between its establishment in 1943 and ca. 1970 has been in the field for regeneration/rejuvenation in several different years.

Thus, a large amount of quite uniform and homogeneous records of such observation data has accumulated especially for the large genebank collections such as those of barley and wheat, comprising ca. 22,000 and 27,000 accessions, respectively. For cultivated barley (*Hordeum vulgare*) and bread wheat (*Triticum aestivum*), the traits Days to Flowering, Plant Height, and Thousand Grain Weight have been chosen for a feasibility study aimed at showing the value of such long-term characterization and evaluation data.

Standard statistical analysis methods usually applied in plant breeding cannot be applied here, due to a number of reasons. Due to capacity reasons, not all accessions can be cultivated in each year. The accessions grown in a particular year do not necessarily represent a statistical sample of the complete collection, and seed multiplication cultivation is carried out without repetitions. Moreover, agricultural techniques changed considerably since 1946.

Therefore, suitable analysis and aggregation methods have to be developed. In addition, it is expected that, when including weather data of the respective years of cultivation, the conclusions about the genebank accessions can be improved.

An overview of these data for the above crops will be presented, and conclusions made about the value of such long-term observation data for the selection of suitable genebank accessions by users.

(Poster 32)

***In vitro* preservation of PGR in Estonia**

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Key words: slow growth, preservation, meristem plant, *in vitro*

The PGR of vegetative propagated plant species are commonly stored in field collection. There is a risk of germplasm loss *via* infection from pests and pathogens or natural disasters in these collections. Those risks can be avoided by applying *in vitro* techniques and by introducing germplasm into tissue culture. Moreover, *in vitro* techniques enable to eradicate the material from pathogens before preservation in controlled conditions.

In Department of Plant Biotechnology EVIKA at ERIA the potato cultivars are preserved as meristem plants *in vitro*. All accessions are disease-free and tested for virus infection for several times. For the disease eradication, the technology created in EVIKA is used. The potato plants regenerated from meristem are initially transferred on a propagation medium containing no growth regulators. In every 3.5-4.5 months the collection is renewed by micro-cuttings and the whole collection is duplicated in two storage rooms with different temperature and light regime.

The cultivars and breeding lines of horticultures are preserved as micro-plants. First three weeks, plants are regenerated at the temperature 18-23°C and within a photoperiod of 16 h. After regeneration, plants are transferred into slow growth conditions (temperature 4-5°C, photoperiod 16 h). Under these conditions, plants are stored depending on the genotype for 4-9 months.

The priority of our activities is to preserve advanced cultivars, initial material for breeding, breeding lines and land races of Estonian origin as well as the most valuable accessions of foreign origin, to provide easy access to the gene pool for plant breeders. At present there are 431 potato cultivars, breeding lines and land-races, as well as 898 potato meristem clones in the *in vitro* gene-bank. The gene-bank also includes 34 plum, 21 sour cherry, 6 sweet cherry, 7 apples, 5 pears, 10 dwarf apple root-stock, 9 raspberry, 25 strawberry, 49 chrysanthemum, 52 carnation, etc., genotypes. There are more than 1500 accessions from 16 species all together in the gene-bank.

Our common activities include collecting the material, eradicating it from different plant diseases, propagating and preserving *in vitro*, but also evaluating and to distributing the most valuable accessions. The most important research areas are the study of different *in vitro* preservation methods, including cryo-preservation, and the influence of long-term preservation *in vitro* on the morphological characteristics and agronomical traits of varieties.

The PGR preserved *in vitro* is used as initial material for breeding, research, for the propagation of disease free material for seed production and for the establishment of field collections. There are a number of varieties in the gene-bank not widely used at present but possibly including valuable genetic material for future use.

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(Poster 33)

The collection of genetic resources of garlic

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Key words: germplasm, landraces, variability, cryopreservation

The germplasm collection of garlic (*Allium sativum* L.) maintained at the Institute of Horticulture in Skierniewice was established in 1986. The collection includes 373 accessions of garlic: 176 non-bolting garlic accessions suitable for spring growing season and 194 accessions of bolting garlic for autumn growing season. The garlic accessions originated from 23 countries. The accessions of garlic, after initial multiplication, are included in 3-year trials (3 – 4 replications) to characterize and evaluate their economic value. After a 3-year research cycle, the accessions are maintained in the field collection in one replication (50 -100 plants of each accession). Characterization is conducted according to the descriptors for *Allium* developed by IPGRI (IPGRI et al. 2001).

Bolting garlic accessions revealed great variability of the weight and number of bulbils and also flower number in the inflorescence. On the base of measurements of these parameters in 97 bolting garlic accessions, five classes for weight and number were distinguished. Because these traits are stable over years, they can be used as criteria for grouping accessions in collections. Twenty-one types of cloves arrangement on transversal cut of the head were observed in 185 garlic accessions of both forms.

The maintenance of vegetatively propagated garlic collection in each year in the field cause phytosanitary troubles and high costs. Therefore it is necessary to search for alternative methods of long term storage of the most valuable garlic germplasm. In this aim the cryopreservation using vitrification method is applied in garlic research program. Up to now were placed in liquid nitrogen 44 bolting garlic and 20 non-bolting garlic accessions from Polish collection in the frame of EURALLIVEG project.

(Poster 34)

Characterization of tomato landraces

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Key words: collection, genetic resources, variability, morphological traits

The collection of tomato germplasm maintained at the Institute of Horticulture in Skierniewice contains 1114 accessions. The collection includes different types of accessions. The most valuable are the old national cultivars and landraces of tomato collected in Poland and other countries. The new collected tomato accessions and those kept in the genebank store are multiplied and characterized in the field working collection. The observations have been made according to the IBPGR descriptors. For tomato each year 42 traits (10 traits for the plant and 32 for the fruit) are evaluated in field trials in 3 replicates, each of 20 to 25 plants. The results of investigations obtained on 15 tomato landraces (type of buffalo heart) originated from Poland are presented. The selected traits of fruit as: size, shape, firmness and colour of fruit, intensity of greenback, ribbing, easiness of detaching fruit from the pedicel, fruit cross-sectional shape, thickness of the pericarp, the number of locules and also the growth type were described. The tomato collection is designated to preserve the germplasm against disappearance, and as a source of genetic variability.

(Poster 35)

Breeding value of old lettuce cultivars and landraces in germplasm collections

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Key words: *Lactuca sativa*, landraces, morphology, *Bremia lactucae*

National plant germplasm collection of the Czech Republic consists of about 900 accessions of lettuce (*Lactuca sativa* L., family Asteraceae), the most important leafy vegetable species. During regeneration of accessions, international standards are followed, however, repeated multiplications could lead to a genotypic shift of accessions with potential expression in phenotypes. Old cultivars and landraces can be important donors of resistance factors to actual spectra of pathogens and their races. The set of 30 lettuce accessions (landraces and cultivars bred and/or traditionally grown on the territory of the Czech Lands) provided from the Czech national germplasm collection was assessed for 22 traits (19 morphologic traits and 3 traits for developmental stages) in field trials. Actual description of 23 accessions was similar to data from literature sources. Five accessions showed significant differences when compared actual data to literature information. These differences are fixed genetically. Original description of one accession was not found. One accession was completely heterogeneous in phenotypic expression of traits. This heterogeneity is probably caused by crossing with another accession(s) during regeneration. Identical set of 30 lettuce accessions was evaluated for response to 20 isolates (races) of lettuce downy mildew (*Bremia lactucae*) by *in vitro* tests in growth chamber. These isolates (races) are actually highly virulent and largely distributed throughout Europe. Only 4 accessions were either susceptible to isolates, either incompletely resistant, either developed heterogeneous reaction to some isolates. Remaining 26 accessions were resistant at least to one of isolates tested. Race-specific resistance genes to *B. lactucae* were detected also in old cultivars of lettuce, same-named accessions expressed different race-specific reaction to *B. lactucae* isolate(s).

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(Poster 36)

Exploring genetic diversity of core-set rice germplasms using their physiological responses against salinity

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Key words: core-set germplasm, physiological trait, rice, salt tolerance

A core-set of rice germplasm collections was developed based on their identical genetic backgrounds. Those core-set germplasms were tested for the genetic diversity of salt tolerance using key physiological parameters, especially, related to osmotic and ionic relations. Long-term moderate salinity imposed to young seedlings in the water culture within a growth chamber, providing an optimal plant growth environment except salt stress. In order to understand the physiological responses of rice seedlings in the presence of long-term moderate salinity, this study set precise physiological assessment protocol for the rice genotypes using the relative water content of shoots, osmotic potentials and ion concentration of the expressed cell sap and the simultaneous water uptake and transpiration of intact plants. This study revealed that the core-set germplasm showed a great diversity in each physiological parameter in response to salinity, as compared with cv. ‘Pokkali’, which is a well-known salt-tolerant genotype, and cv. ‘IR29’, which is a reference genotype for salt-sensitive. The genetic diversity could enhance the utilization of the genetic resources for further studies on functional genomics, metabolomics as well as conventional breeding. This presentation also includes the potential of their utilizations.

(Poster 37)

Molecular markers based analysis for the preservation and valorization of vegetable landraces in Piedmont (North-west Italy)

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Key words: Conservation, Landrace, Molecular markers, Valorization

Crop landraces are locally adapted dynamic populations with a distinct identity and evolved under local climatic, pedological, biotic conditions as well as anthropic pressure. They lack formal crop improvement and are still maintained by farmers due to the added value consumers attributes to the taste, appearance, nutritive value of their production and their link with the culture and tradition in certain areas.

In Piedmont (North-west Italy) a wide number of vegetable landraces are still grown but most of them progressively have given the way to commercial varieties and hybrids which guarantee higher yield and higher incomes to farmers. Thus conservation strategies, both *ex situ* and *in situ* (including on farm), need to be applied in order to increase insurance against their loss and to optimize conservation efforts.

DNA-based assays represent key tools for identifying the most suitable strategies for germplasm characterization and preservation. Recently the Piedmont Region, section Agricultural Development, has done extensive work in cataloging autochthonous local vegetable landraces (www.regione.piemonte.it/agri/biodiversita/orticolo/schede.htm) and has funded research projects for the molecular characterization of seven horticultural landraces grown in Piedmont Region and belonging to as many species: *Allium sativum* (garlic, landrace 'Molino dei Torti'), *Beta vulgaris* (red beet, landrace 'Rossa di Castellazzo Bormida'), *Cynara cardunculus* var. *altilis* (cultivated cardoon, landrace 'Gobbo di Nizza Monferrato'), *Phaseolus vulgaris* (common bean, landrace 'Bianco di Bagnasco'), *Allium porrum* (leek, landrace 'Lungo di Cervere'), *Apium graveolens* (celery, landrace 'Dorato d'Asti') and *Capsicum annuum* (sweet pepper, landrace 'Tomaticot'). For each landrace from 3 to 5 populations were chosen as representative of the area of cultivation and molecular analyses were carried out by applying both the multi-locus AFLP (amplified fragment length polymorphism) and the single-locus microsatellite (SSR- simple sequence repeats) markers.

Molecular markers analyses provided information on how genetic diversity is distributed within and among landrace populations as well as on the frequency of private and/or locally common alleles. Molecular data have resulted in (i) identifying the most suitable strategies for the sampling and *ex situ* management of each landrace, (i) recognizing the populations to which priority should be given for landrace dynamic conservation *in situ* (on farm)

At present activities involving farmer organizations are funded by the Piedmont Region with the goal to obtain, for at least some of the landraces in study, the registration as variety. Molecular data provided also key information for the identification of the most efficient selection programs aimed at reducing the within landrace genetic variation, so that to meet distinctiveness, uniformity and stability (D.U.S.) parameters required for registered varieties.

(Poster 38)

Complex view on biodiversity of *Lactuca saligna* L. germplasm

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Key words: Willow-leaf lettuce, geographic distribution, morphology, genetic variation, disease resistance, *Bremia lactucae*, powdery mildew, lettuce breeding

Modern breeding programmes of lettuce (*Lactuca sativa*) are built on wild related *Lactuca* species. Willow-leaf lettuce (*Lactuca saligna* L.) is used as an important donor of valuable traits (e.g. resistance) (Lebeda et al., 2007). In spite of its large distribution over the world only a limited area is represented by accessions in world germplasm collections (Lebeda et al., 2004). Data on *L. saligna* natural distribution and biodiversity are missing (Lebeda et al., 2009). Research activities developed in cooperation of three countries (Czech Republic, Israel and Slovenia) include eco-geographical studies and collecting, regeneration protocols, morphological characterization, evaluation of response to downy- and powdery- mildews and study of AFLP polymorphism, and to select progenies for further lettuce breeding. Original data on ecology and distribution of *L. saligna* in Europe, North America and Israel were obtained, new seed samples were acquired for further studies (Lebeda et al., 2001; Beharav et al., 2008). Large variation of morphological traits among samples related to their geographic origin was recognized (Lebeda et al., 2007). New sources of resistance to economically important races of lettuce downy and powdery mildew were identified (Beharav et al. 2006; Lebeda et al., 2009). Samples originating from various eco-geographical conditions (Near East vs. Mediterranean Basin) differ significantly in their polymorphism (AFLP) and they are genetically different (Kitner et al., 2008). *L. saligna* was crossed with *L. sativa*, F1 hybrids were identified by morphological traits and proved by AFLP(s) (Lebeda et al. unpublished).

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(Poster 39)

EVA II a national network for the use of PGR in the resistance breeding process

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Key words: evaluation, disease resistance, national network

Uniformity in the genetic base of resistance enhance the potential for plant disease epidemics. Many virulence genes in pathogens correlate to the corresponding resistance genes in the host populations, the pathogen is able to mutate rapidly and form new virulences. To improve a crop or enhance its resistance to diseases, plant breeders have relied on the genetic diversity on collections of genetic resources stored in genebanks, and on those varieties maintained and selected by farmers. Biotechnology, genetic engineering and marker assisted breeding allow incorporating desirable genes and gene complexes from wild relatives across species. In the past, huge amounts of evaluation data have been collected for various species, but often data from varying sources or test conditions cannot be compared.

EVA II aims to provide plant breeders with accelerated access to resistant genotypes, thereby supporting the sustainability of agriculture by increasing the genetic diversity present in cultivars. The overall goal is a better transfer and dissemination of new resistance genes into commercial breeding programs. For this purpose, a system for secondary evaluations of wheat and barley are being carried out and a network information system for data acquisition, overview, and provision has been developed. EVA II also pursues the refinement of standardized systems for resistance evaluation. For wheat and barley (both spring and winter forms) sets of a maximum of 50 genotypes are chosen for testing. The material is chosen by reference to earlier disease evaluations or known resistances. The sets consist PGR as well as foreign varieties and pre-breeding material from research projects. The contributing partners also may supply the network with their own breeding material. At least standards (susceptible/resistant) for each pathogen are included in order to characterize the infestation conditions of all sites. Twenty-two private German cereal breeders mostly organized in the “German Federation of Private Plant Breeders (GFP)”, Bonn, and 3 research institutes conduct the evaluation trials, score the material, and collect data. Field resistance to most important fungal pathogens in wheat and barley are evaluated in multi-site field trials. Usually, micro-plots of 1m² are used; the trials may use one or several replications. Each partner screens the whole set for all the relevant diseases. Artificial infestation with a pathogen race mixture is recommended according to local infestation conditions and the capabilities of the partners. Replicated scoring over more than one year is planned only for the most promising candidates, and in the case of missing information, e.g. due to insufficient infestation conditions in certain seasons. Prepared Excel-files to assist with filling in the scores, and relevant pedigree and resistance information are sent to all partners together with the seed.

Evaluation scoring should be made by % infected leaf area or scores (1-9). For a rating of quantitative resistance, the extent and the development of the infection need to be quantified. For these purposes, the area under the disease progress curve and the mean disease severity

is determined. Therefore, the partners are asked to conduct three scorings for every disease which occurs, starting when the infestation becomes apparent and then scoring every 7 to 14 days.

The results are summarized and soon after harvest shared among the project partners for direct use in their own breeding programs. An information system for data acquisition, overview, and provision was developed by the formerly German Centre for Documentation and Information in Agriculture (ZADI/IBV, Bonn). Actually a new information system is in development that the participants will allow additionally to browse the results the online up- and download of the data. After a defined period (3 years) the data access will be made public.

Contracts officially regulate the rights and duties of all partners; the most important detail is the right of the breeders to use all of the screened material for their own breeding programmes and the obligation to score a defined minimum of the cereal sets. Thus, the network information system acts for the mutual benefit of all participants.

(Poster 40)

Utilisation of DNA markers for the characterisation of Latvian flax germplasm

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There is a long history of flax (*Linum usitatissimum* L.) cultivation in Latvia, and breeding programs were active until 1970, when flax breeding in Latvia was halted. Currently, the flax varieties grown in Latvia are foreign varieties, which are not suited to Latvian soil and climatic conditions, and do not ensure stable flax fibre and seed yield. Successful development of the Latvian flax industry requires the creation of new, locally adapted varieties of flax. The Agriculture Science Centre of Latgale (LLZC) holds a collection of 497 flax accessions, as well as 9865 accessions of various lines and hybrids developed at the LLZC since 1993. This collection includes repatriated Latvian flax germplasm from various genebanks, as well as germplasm obtained from renewed, limited breeding activities in flax. Much of this material has not been characterised, and so in order to facilitate this process, we have utilised DNA markers to assess genetic diversity and relatedness, as well as surveying functional polymorphism. Simple sequence repeat (SSR) markers developed from both genomic libraries as well as expressed sequences were utilised to assess genetic diversity and relatedness. Candidate genes for fibre qualities were identified from published microarray and proteomic studies of fibre development in flax. The results of the DNA marker survey were utilised to determine the genetic polymorphism and relatedness within Latvian flax germplasm, and these results were compared with the analysis of agronomic traits carried out in field trials at the LLZC. The development of DNA markers linked to traits of agronomic importance will assist in the development of a Latvian flax breeding program. The use of DNA marker technology will allow more efficient assessment and rational utilization of Latvian flax germplasm.

(Poster 41)

Access to Barley Genetic Stocks – a key stone for research in plant biology

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Key words: mutant, BGS, diversity, genome.

'Genetic stocks' represent well described research material possessing characterised allele of a specific gene (induced mutation or natural variant), combinations of mutations that give a unique phenotype, series of mutant alleles of genetically linked genes, variant of cytoplasmic trait, various chromosomal aberration, monosomic or trisomic aneuploids, alternative ploidy (e.g.tetraploid) and other material that can be used as "tools" to determine the function of a gene discovered by sequence analysis.

The production of genetic stocks required many decades of extensive work and substantial **investments** giving us a possibility both to lay out a solid fundament and building up further knowledge in plant genetics. Since the beginning of barley mutation research in 1920s large collections of morphological, physiological mutations and different chromosomal aberrations have been assembled in gene banks world wide. More than 50 % of world's barley genetic stocks (BGS) are accessible to international barley community from Nordic Genetic Resource Center (NordGen). Collection comprises an enormous diversity, includes ten main categories with 116 different mutation subtypes and very important and useful near isogenic lines that serve for gene mapping.

These mutant lines are used in various studies increasing knowledge of the mutation process and genetic architecture of the different characters. In recent years mutant lines are extensively used for gene cloning projects as well as for locating gene analogues, e.g. genes determining spike type and architecture, day length sensitivity, seed morphology and culm composition. Along with the rapid development of sequencing technologies, BGS presents a valuable tool for research giving insight to the biology of crop plants. Thereby BGS offers a base for new efficient ways for targeted manipulation of plants for human benefit.

It is clear that creation of genetic stocks *de novo* is a very costly and challenging procedure and utilisation of existing collections in many cases is more feasible. However, the maintenance and quality assurance for the large number of BGS accessions world wide is a challenging task. Management of BGS requires access to highly specialised competence, and equipment not frequently available in research or genetic resources conservation community. There is an urgent need to develop a global and efficient conservation strategy in order to safeguard the BGS for their continuous access in the future.

(Poster 42)

Comparing efficiency of sampling strategies to establish a core collection of orchard grass (*Dactylis glomerata* L.) based on agronomic data

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Key words: core collection, genetic diversity representativeness, genetic resources, orchard grass, phenotypic variation, sampling strategies

Many germplasm collections currently are often so large that this interferes with achieving the main goals for which the collections have been established, namely, maintenance, evaluation and utilization of genetic diversity of crop species and its relatives.). To solve these problems, Frankel (1984), Frankel and Brown (1984) proposed the “core collection” concept. A core collection is a sample of an entire crop germplasm collection of a species (a large finite population of accessions), selected to adequately represent, with a minimum of redundancies, the maximum possible genetic diversity (to contain most genetic diversity) in the entire collection. In this study, relative efficiency of simple random and stratified random and re-sampling strategies, formed as combinations of statistical methods and techniques used to develop stratified sampling, was validated for 10% sample size core collection representativeness of genetic diversity for phenotypic characters (predicted genotypic values) of an orchard grass (*Dactylis glomerata* L.) germplasm collection as the entire collection. The spring triticale germplasm collection of 1971 accessions with 8 quantitative morpho-agronomic traits was used to construct core collections. Genotypic values of all quantitative traits of the collection were unbiasedly predicted based on mixed linear model approach. Based on the standardized predicted genotypic values of the traits, squared Euclidean distances were employed to measure the genetic similarities among the accessions. Simulations were conducted in order to draw consistent, stable and reproducible results. The proposed sampling strategies was evaluated by 10 000 independent random samples. The representativeness of core collections established using the studied sampling strategies was validated by the difference of means and three parameters of genetic variation for all traits in core subsets and the entire collection. The representativeness of core collections established using the studied sampling strategies was validated by the difference of means and three parameters of genetic variation for all traits in core subsets and the entire collection.

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(Poster 43)

Genetic resources of gooseberry in Czech Republic

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Key words: *Ribes uva-crispa*, cultivars, collection, fruit, germplasm

From the botanical point of view, cultivars of gooseberry grown in the Czech Republic belong to European species *Ribes uva-crispa* L. The germplasm of gooseberry is maintained in the Research and Breeding Institute of Pomology Holovousy Ltd. The germplasm collection, which includes three plants representing each cultivar, is planted at an altitude of 321 m at a spacing of 3 x 1.5 m. The mean annual temperature in Holovousy is 8.4 °C with a precipitation of 663.5 mm. There are 52 cultivars of gooseberry in the collection. Vegetative and fruit characters are evaluated. Fruit characters evaluated include: size, shape, colour, thickness of skin, veining and overall taste, presence of bristles, wax bloom, hairiness and weight of 100 fruits. Vegetative characters that were also evaluated include: beginning of flowering, end of flowering, flower set, fruit set, beginning of ripening and incidence of American gooseberry mildew. Older cultivars grown or bred on the territory of the Czech Republic are the basis of the collection. Most of these cultivars are seedlings of unknown origin from open pollination.

Important cultivars

- 'Triumphant' - Seedling of unknown origin, released in the 80ies of 19th century. Growth is medium to vigorous, semiupright, medium dense, with large thorns. Fruits are medium large (7.4 g), yellow green, soft hairy, taste sweet acidic, aromatic. Harvest is high and regular.
- 'Ceska koruna' - Seedling of unknown origin, originated in the year 1903. Growth is weak, crown medium dense, branches medium thorny. Fruits are very large (13.5 g), ovate, green-yellow, some time with brown red overcolour, sparsely hairy. Taste is sweet acidic, aromatic. Harvest is medium or lower, regular.
- 'Zlaty fik' - Seedling of unknown origin, grown since 1902. Growth is vigorous, semierect, thin, less thorny. Fruits are large (8.6 g), ovate, golden yellow, softly hairy. Taste is sweet acidic to sweeter, aromatic. Harvest is high, regular.
- 'Produkta' - Seedling of unknown origin, spread since 1975. The growth is more vigorous, upright, medium dense. Fruits are of medium size (5.3 g), nearly without hairs, rounded, yellow-green, sweet-acidic and aromatic. Harvest is high and regular.
- 'Solcova naděje' - Registered in 1984. Growth is medium, semiwide, medium dense, thorniness is medium. Fruits are large to very large (10.1 g), ovate, sparsely hairy. Taste is sweet acidic, aromatic. Harvest is high, regular.
- 'Skvost' - 'Dan's Mistake' x 'Zlaty fik', registration 1995. Growth is vigorous, with less thorns, usually dwarf. Fruits are large (8.9 g), cask-like to oval, light green to yellow, pubescent. Taste is sweet acidic, aromatic. Harvest is higher and regular.
- 'Astrid' - Hybrid of 'Dan's Mistake' x 'Zeleny hruskovity'. Growth medium vigorous, medium dense crowns, thorniness medium. Fruits are large to very large (11.2), shortly elliptic, wine red, with sparse hairs. Taste is sweeter, aromatic. Harvest is higher and regular.

Acknowledgement

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(Poster 44)

Utilization of einkorn (*Triticum monococcum* L. ssp. *monococcum*) to widen the genetic diversity of cereals

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Key words: einkorn, crossability, *Triticum monococcum*

An important part of the Martonvásár Cereal Gene Bank is the einkorn collection which consist about 350 accessions (landraces, breeding lines).

The cultivated einkorn is one of the most important resistance sources of cereals against biotic and abiotic stresses. It is widely known that einkorn has excellent fungal disease resistance (leaf rust, yellow rust, powdery mildew) and its drought tolerance and tillering is also very good. Einkorn has high content of fat soluble antioxidants (lutein, carotenoid, tocol) and it makes einkorn a potential raw material for functional food production. Unfortunately, most of the einkorn genotypes are hardly crossable with wheat and their uses in wheat breeding and pre-breeding programs are highly limited.

We have two concepts to transfer useful properties from einkorn to hexaploid wheat:

1. Developing *Triticum turgidum* x *Triticum monococcum* synthetic hexaploids and these lines will be used for crossing with bread wheat.
2. Direct crossing between the hexaploid wheat and einkorn.

Good crossable einkorn genotypes are needed to produce synthetic hexaploids and wheat-einkorn hybrids, respectively.

We have examined the crossability of several einkorn gene bank accessions and breeding lines with durum (*Triticum turgidum* ssp. *durum*) and emmer wheat (*Triticum turgidum* ssp. *dicoccon*). According to the recent results, the original einkorn accessions are completely incompatible with the tetraploid genotypes tested; meanwhile some newly developed semidwarf einkorn lines are showing a relatively high crossability with all of the other parental lines. After the genome duplication of the cytologically identified triploid seeds, highly fertile synthetic hexaploids were developed.

We also tested the crossability of two different einkorn genotypes (a traditional type: Mv Alkor, and a semi dwarf einkorn line: 1T-1) with a good crossable wheat line, Mv9kr1. The results confirmed the seed set and germination of F1 seeds of Mv9kr1 x 1T-1 was significantly higher.

(Poster 45)

No more paper ! The click-wrap procedure for handling SMTA's as implemented at CGN

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Key words: SMTA, genebank documentation, click-wrap

The Standard Material Transfer Agreement (SMTA) of the International Treaty on Plant Genetic Resources for Food and Agriculture (IT PGRFA) has to be used for all transfers under the Multilateral System of the IT PGRFA. It is obligatory, and its provisions and conditions cannot be changed.

Using the SMTA generally causes much paper moving around. After receiving a seed request from a user, a contract has to be prepared, the list of accessions added, and copies need to be signed, send to the requestor who has to send it back, before seeds can be shipped. Apart from the labor required this is also a very time consuming process, and hinders swift service to the users of genebanks. Therefor CGN developed in 2007, as part of its documentation system GENIS, a procedure for handling these transactions fully automatically.

CGN applies the SMTA to all its material, also the so-called non-annex 1 crops for which the SMTA is not obliged. The only exceptions are the requests that indicate that the material will not be used for ‘research, breeding and training for food and agriculture’, in these rare cases the curators will contact the requestors to draft a bi-lateral agreement.

After selecting material on-line (www.cgn.wur.nl/uk) using the GENIS query facilities on the basis of passport data, characterization and evaluation data, or on-line core selections, the user is shown a list of the selected material. If this selection is correct, the user can decide to order the material in which case (s)he has to fill in a form asking name and contact details, and the reason for ordering the material. Also the name and email address of the ‘authorized official’ has to be given. This is the person authorized to sign the SMTA.

After completing the form, automatically two emails are send: one to the requestor confirming the order, and one to the authorized official asking to ‘sign’ the electronic SMTA. This mail comes with a hyperlink that connects to a page where the SMTA is shown, including the ordered material. As soon as the authorized official clicks on the ‘sign’ button, mails are send informing the authorized official and the requestor that the order has been confirmed, and a mail is send to the CGN seed storage manager with the order that can then be processed.

No paper involved!

(Poster 46)

Increasing the genetic variability of *Triticum zhukovskyi* genetic resources via its reconstruction from the original genome donor species

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Key words: *Triticum zhukovskyi*, reconstruction, genetic variability, synthetic hexaploid

Triticum zhukovskyi Men. et Ericz. ($A^tA^tGGA^mA^m$) is one of the most interesting *Triticum* species carrying important resistance genes and organoleptic characters. Their use in breeding is highly limited, because the available genetic diversity of the existing *ex situ* collection is very narrow. Most of the gene bank accessions available in the different gene banks worldwide are duplicates or highly related to each other. To be able to increase its genetic variability one of the most promising way is its reconstruction from the original genome donor species. The repetition of such evolutionary steps should be based on crossing high number of different (genetically non related) *Triticum timopheevii* Zhuk. (A^tA^tGG) accessions with already prebred einkorn (*Triticum monococcum* L. ssp. *monococcum* (A^mA^m)) lines. The Cereal Gene Bank of the Agricultural Research Institute of the Hungarian Academy of Sciences (Martonvásár, Hungary) preserves more than 50 unrelated *timopheevii* accessions – 2 subspecies (ssp. *timopheevii*; ssp. *armeniicum*) and 8 varieties forms –, which were characterized during the last years. The accessions were examined for morphological traits and for the main biotic and abiotic stresses. The morphological parameters of the accessions can determine the tolerance of abiotic stresses (e.g. thick pubescence), and the possibilities of the agronomic utilization (e.g. plant-height, ear-type). There are several resistance genes on the chromosomes of G genome providing an outstanding resistance for fungal diseases (e.g. powdery mildew, leaf rust and stem rust). The accessions were examined under organic conditions – where the rates of stress-factors are higher than under conventional agricultural conditions –, in order to get better expressions of the differences between the accessions. On the basis of our recent results we had selected one (*Triticum timopheevii* (Zhuk.) Zhuk. var. *rubiginosum* – accession no.: MVGB845) out of the *timopheevii* accessions. Our main strategy is to create a synthetic hexaploid wheat via crossing the selected line with a semi-dwarf, prebred einkorn line (*Triticum monococcum* L. ssp. *monococcum* – line code: 1T-1), which was selected for its high crossability with different *Triticum* species. While the hybrids of this crosses are triploids, colchicine based genome doubling were carried out in order to get fertile hexaploid progenies. The new synthetic hexaploid has similar genome construction as the natural species *Triticum zhukovskyi* giving the chance not only to increase the genetic variability of the highly limited variation of this species, but also to improve the bread wheat breeding materials.

(Poster 47)

Drying and storage bacteria: study of viability of *Pseudomonas fluorescens* BTP1 freeze-dried during storage at 4 and 20°C.

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Key words: viability, freeze-drying, flow cytometric, cryoprotectants, cellular fatty acids

The drying of bacteria remains a major alternative in order to keep them long term. After centrifugation, the bacterial pellet of *Pseudomonas fluorescens* BTP1 was divided in two fractions one with and one without cryoprotectants (2% glycerol and 5% maltodextrine) and freeze-dried. After freeze drying, powders were sealed in aluminium bag under vacuum and storage at 4 or 20°C. The storage stability of freeze-dried powders was studied by parameters such as loss of viability on the Plate Count Agar (PCA) (e.g. Concentration of Cells with glycerol (PG) at Cfug before storage 10^9 and after 7 month, 10^8 at 4°C and 10^7 at 20°C), conductivity and evolution in membrane composition by measuring the ratio of unsaturated/saturated fatty acid. These ratios decrease in function of time (e.g. at 4°C the ratios of C18:3 and C18:2 by C16:0 decreases respectively of 0,013 to 0,001 and 0,05 to 0,03 after 60 days of storage). Viability (%) and concentration (cfu/g) of bacterial during storage at 4 or 20°C with $a_w = 0,32$ was determined using a procedure published by (Kurtmann et al., 2009). In the present study, flow cytometric analysis was applied to evaluate the state in which are the cells at the end of storage time. Furthermore, we compared result the survival of bacteria as obtained by plate count with the flow cytometric analysis results.

(Poster 48)

Fostering a global, public genetic diversity platform through the Global Rice Science Partnership (GRiSP)

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Key words: rice, partnerships, GRiSP, SNP, NGS, RIL, MAGIC, GBS

Crop improvement programs rely on the vast gene pools conserved in genebanks for the source of genes and novel alleles that can be used to mitigate problems in crop production. The International Rice Genebank of the T. T. Chang Genetic Resources Center (TTC-GRC) at IRRI maintains a collection of over 112,000 accessions, most of which are held in trust. However, only a small percentage of accessions have been used in rice improvement programs. The Global Rice Science Partnership or GRiSP, a CGIAR Research Program, addresses this issue as one of its objectives by implementing a global, public rice genetic diversity platform to characterize and harness rice genetic resources. Ultimately, this will facilitate the use rice germplasm by research and breeding communities worldwide. The GRiSP includes IRRI, AfricaRice, CIAT, CIRAD, IRD, JIRCAS, EMBRAPA among other partners. Under GRiSP, the TTC-GRC plays a pivotal role in research to characterize rice genomic diversity and create novel gene pools of recombinant populations.

One undertaking is the Rice SNP consortium that includes public (USDA, IRRI, Cornell University, Cirad, AfricaRice, CIAT among others) and private (Syngenta, and Bayer CropSciences) stakeholders. This activity involves high resolution genotyping of 2000 diverse accessions with 1 million SNPs on an Affymetrix genotyping chip (<http://www.ricesnp.org>) developed at Cornell University by McCouch et al. This association mapping panel will be phenotyped by a global network for traits of importance to rice improvement such as drought, heat tolerance, diseases, grain quality and yield. Analysis of the high-density genotypes in combination with trait data through genome-wide association studies (GWAS) will allow key SNPs and haplotypes to be associated with phenotypes and bridge the genotype-to-phenotype divide. These alleles and their donor accessions can then be targeted to marker assisted breeding programs.

A longer term goal of GRiSP is the whole genome sequencing by next-generation sequencing (NGS) of all unique accessions held in the GRiSP genebanks to reveal rare alleles. Ultimately, it will provide an *in silico* resource to identify useful genes for breeding. Our initial foray into NGS has been initiated in collaboration with BGI-Shenzhen and the Chinese Academy of Agricultural Sciences. This year, we are sequencing 10,000 cultivated (*Oryza sativa* and *O. glaberrima*) and wild AA genomes (*O. rufipogon*, *nivara*, *barthii*, *glumaepatula*, and *meridionalis*) at an initial depth of 5X coverage.

To achieve these goals, our group is spearheading the single seed descent purification of >12,000 entries for genotyping, NGS sequencing, phenotyping, and association studies. Furthermore, we are developing 20 RIL populations from pairwise crosses among the lines in the OryzaSNP panel (<http://www.oryzasnp.org>). Currently, we have over 15,000 lines at F3 to F5 generations that will be advanced to at least F6 for use in mapping, nested association mapping, and QTL studies. We are initiating multiple advanced generation intercross (MAGIC) populations from 8 wild AA genome founder accessions to enhance use of the 2° rice gene pool. These specialized populations will be genotyped by the new high-throughput genotyping by sequencing (GBS) methods developed by Buckler et al. (<http://www.maizediversity.net>).

(Poster 49)

Scientific curation of the UK National Fruit Collection

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Key words: Fruit, Genebank, UK, Apple, Pear, Plum, Cherry, Cryopreservation

The UK National Fruit Collection at Brogdale contains over 2,200 accessions of apples, 500 accessions of pears, as well as over 1,100 accessions altogether of plums, cherries, currants, gooseberries, hazlenuts, vines and other fruit. The collection is owned by Defra and forms part of the UK's overall collection of plant genetic resources. The collection is maintained as a field collection and the University of Reading and project partners the Farm Advisory Services Team are responsible for the scientific curation and maintenance of the collection.

The collection is included within the UK National Plant Inventory and listed within Eurisco. The collection is also linked within the ECPGR fruit networks. In line with the UK's commitments to the International Treaty on Plant Genetic Resources for Food and Agriculture, material from the collection is made available via the sMTA system.

The program of curational work includes the use of genetic marker studies within the apple and pear collections, both for the purposes of assessing the genetic variation within the collection and for the purposes of identifying mislabeled and duplicated accessions. Cryopreservation is used as a technique to provide a safety back-up to the trees in the field collection and this work is focused on the apple collection using dormant bud techniques. A public access database is available at www.nationalfruitcollection.org.uk where further details on each accession can be found.

(Poster 50)

Rheological characteristics of selected wheat genetic resources

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Key words: wheat landraces, rheological characteristics, Mixolab, farinograph

A heterogenic set of selected winter wheat samples from wheat genetics resources which are on deposit in Gene Bank in Prague was evaluated and two methods for evaluation of rheological characteristics were compared: standard determination by farinograph and determination using modern device Mixolab. The tested set was composed of 28 materials including 20 genetic lines derived from European landraces and obsolete cultivars, and 8 modern bread cultivars with high bread-making quality. Field trials carried out according to the internal protocol of Gene Bank (experimental plot size 4.5 m², regenerative fertilising, without fungicide and morphoregulators) in Prague-Ruzyně in 2009.

Lines derived from landraces in comparison with modern cultivars showed higher average values of Zeleny sedimentation index (50; 42 ml), falling numbers (435; 377 s) as well as higher water binding capacity (58; 55 %). Although these materials displayed slower dough development, the dough stability was much longer and the decrease of the consistence was lower during both farinograph and Mixolab determinations. The best results in these characteristics were found for lines derived from Hungarian landraces.

Mixolab characteristics displayed statistically significant correlations with several farinograph parameters such as water binding capacity ($r=0.96$), dough stability ($r=0.78$) or decrease of the consistence ($r=0.71$). Mixolab characteristics also correlated with standard technological parameters like Zeleny sedimentation index and falling number. Regarding to ability of apparatus Mixolab to evaluate parameters of protein and starch part simultaneously through controlled heating (to 90°C) and subsequent cooling (to 50°C), the rheological analysis conducted by Mixolab indicated broader application range than standard methods. This equipment seems to be owing to low flour demands (about 45 g per essay) and a short evaluation time very useful for the evaluation of genetics resources and of the breeding materials in the early generations.

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(Poster 51)

On farm conservation of fruit in the Czech Republic

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Key words: cultivars, maintenance, fruit species, germplasm, genebank

In previous centuries, growing of many different apple, pear and sweet cherry cultivars was very popular among the inhabitants on the territory of the Czech Republic. Since the half of the last century, there has been a serious threat of extinction of landraces in the Czech Republic due to the continuing destruction of old plantations and alleys. Because of the possible extinction of these indigenous landraces, the program for collecting and long term conservation of fruit landraces was started. On farm conservation is an alternative method for preservation of fruit genetic resources in indigenous areas. This method is currently investigated and employed in Research and Breeding Institute of Pomology (RBIP) Holovousy Ltd. Collecting expeditions have been conducted since 1994. Found important landraces were registered and *in situ* localized. On the basis of this activity, cultivars important for establishment of on farm plantations were selected. Planting material was prepared in the nursery of RBIP Holovousy Ltd. using the following method. Interstem cultivars were inoculated on seedling rootstocks. Selected cultivars were grafted in the height of 1.8 m. Trees with formed crown were transplanted to on farm plantation.

The first on farm plantation of fruit in the Czech Republic was established in the Krkonoše Mts. National Park (KRNAP) in Vrchlabí in 2002. There are 51 accessions of fruit resources conserved by this method. Apple collection with 27 accessions is the largest, sweet cherry with 12 accessions follows. Further, cultivars of pear, sweet cherry and plum are maintained (4 accessions of each fruit species).

The second on farm plantation was established in Orlické Mts. near the Polish border in the village Neratov. The original population of the village was displaced shortly after the Second World War. Therefore a plantation established in 2004 was named “Orchard of Reconciliation”. In the following years, the plantation was supplemented by other fruit trees. At present, there are 55 accessions of fruit genotypes in this plantation. These are 32 apple landraces, 21 pear landraces and 2 plum landraces.

On farm plantation in National Park (NP) Podyjí – Znojmo was established as the third in 2005. It is the smallest plantation formed by only 13 accessions of apple and pear.

The last on farm plantation was established in National Park Šumava in autumn 2008. Currently there are twenty one accessions (18 apple and 3 pear cultivars) included in this collection.

All collections will be continuously supplemented in the following years.

Acknowledgement

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(Poster 52)

Forgotten bean (*Phaseolus vulgaris* L.) landraces make a comeback in Piedmont (North-west Italy)

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Key words: common bean, germplasm bank, landrace, molecular markers

In several regions of Italy, as well as in other parts of Southern Europe, the heterogeneity of the land, the unique and variable climatic conditions as well as different types of soil have favored the survival in cultivation of a large number of specifically adapted landraces, which are rich in genetic variation. Some of them have prospective of survival because people require high quality products (i.e. good taste, but also productions linked to history and tradition of a territory, obtained with low inputs and certified by quality marks), nevertheless for others the area used for their cultivation is decreasing year after year, leading to the risk of extinction.

In the Seventies a Germplasm bank was established at the DIVAPRA, Plant Genetics and Breeding (University of Torino), with the goal to preserve local vegetable landraces grown in Piedmont (North –West Italy), which represent not only a valuable source of useful genes for plant breeding, but also an important cultural heritage.

Thanks to funding from the Agricultural Development Department of the Piedmont Region the germplasm collection has been recently characterized by applying both AFLP (amplified fragment length polymorphism) and SSR (simple sequence repeats – microsatellites) markers; this made possible the identification of duplications as well as the quantification of the genetic differentiation existing among accession of the same landrace from different provenances. Following a survey on the cultivation of the landraces in the Cuneo Province of the Piedmont Region, it has been realized that some bean (*Phaseolus vulgaris* L.) landraces, recognized of particular value for the quality of their production, have been completely or almost completely abandoned from cultivation; thus, a program for their re-introduction has been undertaken. In particular six bean landraces of the typology 'Regina' and three of the typology 'Borlotto' were grown for two years (2009 and 2010) in the experimental fields of CReSO, and compared with commercial varieties at present spread in cultivation. Extension days were organized in order to explore, in collaboration with local farmers, the potentiality for their reintroduction in cultivation. Most of the landraces have generated interest among farmers but particular attention has been focused on two of them: 'Regina di Boves' and 'Borlotto sanguigno' due to both the high productivity and qualitative characteristics of the legumes. Seeds of the 'forgotten' landraces will be made available to farmers in order to promote their reintroduction in cultivation.

(Poster 53)

The status and organization of fruit crops gene bank in the Institute of Horticulture in Skierniewice (Poland)

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Since 1951 the polish gene bank of fruit and ornamental plants was maintained by Research Institute of Pomology and Floriculture in Skierniewice., which now became converted into Institute of Horticulture in Skierniewice.

At the end of 2010 there were 6000 taxons in the *ex situ* collections, including 4600 genotypes of fruit and over 1500 ornamental plants.

The field collection of fruit plants covers the area of 14 ha and comprised separate collections of following crops: apple (over 1300 taxons), pear, plum, sweet cherry, sour cherry, peach, apricot, walnut, hazelnut as well as rootstocks for mentioned crops, wild species of *Malus*, *Pyrus*, *Prunus* and small fruit collections of: strawberry, raspberry, blueberry, black and color currants, gooseberry, grape and some others). The new genotypes are acquired from the other polish collections and from abroad. Old varieties are collected during scientific expeditions organized to different part of Poland and Europe. Other genotypes are obtained from gardeners, breeding programs realized by different institutions and amateur breeders.

Passport data are obligatory prepared for collected genotypes. Additionally, each genotype is evaluated in accordance with UPOV and IPGRI descriptors. The growth vigor, winter hardiness, crown habit, intensity and time of flowering, ripening period, yield, fruit description and other data are collected in each collection. Some of the data have been entered in the European Database.

The main goal of the collection is to protect and preserve the genetic resources of pomological plants for the next generations. Some of them are useful in breeding programs.

Collections serve a purpose professional courses for students and farmers

(Poster 54)

Stability of new wheat– *Ae. biuncialis* addition lines and the selection of *Ae. biuncialis* length polymorphic wheat SSR markers

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Key words: wheat, *Aegilops biuncialis*, addition lines, SSR markers, polymorphism

Aegilops (goatgrass) species, which are closely related to cultivated wheat, represent a large reservoir of agronomically useful traits (salt and drought tolerance, disease resistance) and also have great adaptability to different climate conditions, being widespread from Mediterranean climates, to the western part of Asia, and West China. One aim of hybridisation with alien species is the incorporation of resistance genes into the gene pool of cultivated wheat. A number of useful genes from various *Aegilops* species have already been introduced into the common wheat background. However, the successful production of genetic material requires a comprehensive understanding of the genetic structure of the species being used. High genetic variability within the *Aegilops* species causes substantial polymorphism in the fluorescence *in situ* hybridisation (FISH) patterns of the individual chromosomes.

Ae. biuncialis ($2n=4x=28$, $U^bU^bM^bM^b$) shows great genetic diversity, which complicates the exact detection of individual *Ae. biuncialis* chromosomes in the wheat background using FISH. Due to the high level of FISH polymorphism, it is advisable to confirm the identification of the *Ae. biuncialis* chromosomes with the help of SSR markers. The development of a whole set of wheat–*Ae. biuncialis* addition lines would be useful for the selection of U and M genome-specific wheat SSR markers. The $2M^b$, $3M^b$, $7M^b$, $3U^b$, $5U^b$ wheat (cv. Mv9kr1)–*Ae. biuncialis* addition lines have been produced yet in Martonvásár. In the course of the experiments 72 wheat SSR markers were tested on wheat line Mv9kr1 and on *Ae. biuncialis* MvGB642. Forty-eight markers were polymorphic and 24 non-polymorphic between wheat and *Ae. biuncialis*. In order to determine the chromosomal location of these polymorphic markers, a further aim is to test them on wheat–*Ae. biuncialis* addition lines. Development of new wheat–*Ae. biuncialis* addition lines is now in progress. The $2U^b$ disomic addition line is mostly stable, as 70% of the progenies contain this chromosome pair. Unfortunately the $6M^b$ disomic addition line proved to be dwarf and sterile. Progenies analysed from the $6U^b$ monosomic addition line did not carry the $6U^b$ chromosome. One plant containing the $5M^b$, $6M^b$ and $7M^b$ chromosomes, and one plant carrying $5U^b$, $3U^b$ and $7U^b$ chromosomes showed very low fertility, both plants produced only 1 seed. Progenies of a plant carrying the $7U^b$ chromosome pair have not yet been analysed. The present results demonstrate that the selection and stabilisation of new wheat–*Ae. biuncialis* addition lines is a time-consuming procedure.

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(Poster 55)

Genetic diversity of Scottish landraces: Shetland cabbage (*Brassica oleracea* L.)

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In recent years Scottish field crop landraces have been surveyed and collected for *ex situ* storage and a start has been made with their characterization (Scholten *et al.*, 2009). In addition, a scheme has been set up to provide maintainers of landraces with *ex situ* conservation support (Green *et al.* 2009).

Cultivation of field crop landraces survives in Scotland on three island groups: cereal landraces such as bere, small oat on Shetland and Orkney in the North, and the Hebrides in the West; Shetland kale or cabbage landrace (*Brassica oleracea* L.) in Shetland (Scholten *et al.* 2009). Shetland cabbage has been grown on Shetland for centuries, used both as an early vegetable and as winter feed. Although grown on commercial scale in the nineteenth century, especially on the island of Bressay, nowadays it has become rather rare and few growers keep plants for seed. It has been collected for its clubroot resistance, but has not been characterised. Broad descriptions existed however, suggesting a blue-purple coloured primitive *Brassica* with weak heading habit. Mixing plants of Shetland cabbage with other cabbages may have occurred as was mentioned by some growers on Shetland. During fieldwork, part of an MSc project of the University of Birmingham, there was no general agreement on what type the original Shetland cabbage looked like (Lever 2006).

Morphological and molecular characterization of Shetland cabbage was undertaken as part of a PhD project on the diversity and conservation of Scottish landraces at SAC in collaboration with SASA. Shetland cabbage germplasm collected in 2006, was characterised, using conventional IGPRI and CPVO descriptors and SSRs. Ten Shetland Cabbage populations, 24 plants each, representing several islands in the Shetland archipelago were compared with 16 traditional cabbage and kale varieties. 19 SSR primers detected 58 polymorphisms, six of these being unique to Shetland cabbage. Principal Component Analysis and cluster analysis were used to explore population genetic structure and differentiation between Shetland cabbage and the references cabbages and kales. To complement the frequency based clustering, two Bayesian based population structure analysis algorithms, STRUCTURE and BAPS, were applied to further study partitioning and admixture.

The aims of the SSR analysis were to study population structure and to check for possible introgression from other cabbage cultivars into Shetland Cabbage. Results will be summarised and implications for conservation will be discussed.

Green, N., Campbell, G., Tulloch, R., Scholten, M. (2009) Scottish Landrace Protection Scheme. In: Veteläinen, M., Negri, V., Maxted, N. (Eds.) 2009 *European Landraces: On-farm Conservation, Management and Use* Bioversity Technical Bulletin No. 15. Bioversity International, Rome. Chapter 24, pp 233 – 243.

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Scholten, M., Green, N., Campbell, G., Maxted, N., Ford-Lloyd, B., Ambrose, M. and Spoor, W. (2009) Landrace Inventory of the UK. In: Veteläinen M, Negri V, Maxted N, (Eds.) *European Landraces: On-farm Conservation, Management and Use*. Bioversity Technical Bulletin No. 15. Bioversity International, Rome, Italy. Chapter 15, pp 161-170.

(Poster 56)

Interactive characterization of Scottish *Avena strigosa* Schreb. – an evaluation

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In recent years Scottish field crop landraces have been surveyed and collected and a start has been made on their characterisation (Scholten *et al.*, 2009). In addition, a scheme has been set up to provide maintainers of landraces with *ex situ* conservation support (Green *et al.*, 2009). Cultivation of small oat (*A. strigosa*) in Scotland has become restricted to contracted to three island groups: Shetland and Orkney in the North, and the Hebrides in the West (Scholten *et al.* 2009). It is only on the southern Outer Hebrides - the Uists – that the scale of small oat cultivation is still substantial; it is often mixed with a rye landrace and/or with *bere*, an ancient barley landrace. All cereal landraces are used for winter feed for cattle and sheep, which are the most important crofting products of the Uists.

Characterization carried out so far was conducted ‘on station’ (*ex situ*) rather than ‘on location’ (*in situ*). A lack of awareness about landraces among growers had been observed, there was a need to take this into account and to try to combine research with outreach. An opportunity to conduct the characterization on location arose at the end of 2008 with the start of a new school module about crofting at the Community Secondary School in Lionacleit on the isle of Benbecula. Teacher and crofter-instructor agreed to include the characterization field trial into their lessons and to have students involved in practical activities. This was the starting point for an ‘interactive’ characterisation experiment, run over two seasons, aiming at raising awareness about landraces by seeking interaction with local stakeholder groups. Ideas were taken from Almekinders’ (2001) suggestions for management of plant genetic resources at community level and Rölings’ (1996) proposals for a more interactive agricultural science (1996).

Methods used for the outreach included publicity, Open Days, participating in local events, a workshop and liaising with stakeholder groups.

By conducting the characterisation on location, local stress factors such as high Ph, soil nutrient deficiencies, early summer drought, wind and salt spray stress formed an integral part of the comparison between Scottish and foreign *A. strigosa*. The characterisation aimed at positioning the regional Scottish genepools within Scotland and vis-à-vis foreign accessions; conventional oat descriptors were used, complemented by soil and tissue analysis.

The poster will present outcomes and evaluate this combined, interactive approach. Results of the agromorphological characterization will be summarised. Drawbacks and impact will be discussed.

Almekinders, C.J.M. (2001) *Management of Crop Genetic Diversity at Community Level*. Deutsche Gesellschaft für Technische Zusammenarbeit (GTZ) GmbH.

Green, N., Campbell, G., Tulloch, R., Scholten, M. (2009) Scottish Landrace Protection Scheme. In: Veteläinen, M., Negri, V., Maxted, N. (Eds.) 2009 *European Landraces: On-farm Conservation, Management and Use*. Bioversity Technical Bulletin No. 15. Bioversity International, Rome. Chapter 24, pp 233 – 243.

Röling, N. (1996) Towards an interactive agricultural science. In: *European Journal of agricultural education and extension*. Vol. 3 (4) pp. 35 – 48.

Scholten, M., Green, N., Campbell, G., Maxted, N., Ford-Lloyd, B., Ambrose, M. and Spoor, W. (2009) Landrace Inventory of the UK. In: Veteläinen M, Negri V, Maxted N, (Eds.) *European Landraces: On-farm Conservation, Management and Use*. Bioversity Technical Bulletin No. 15. Bioversity International, Rome, Italy. Chapter 15, pp 161-170.

(Poster 57)

Conservation of fruit genetic resources in actively growing *in vitro* cultures

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Key words: micropropagation, cultivars, long-term storage, medium, shoot tip, fruit species

The security of genetic resource collections requires their conservation by several techniques. Duplicate collections of selected cultivars and genotypes of fruit species are maintained in the form of actively growing shoot tip *in vitro* cultures in Research and Breeding Institute of Pomology (RBIP) Holovousy Ltd. since 1999. At present, totally 94 accessions of fruit crops are maintained on a long-term basis in RBIP Holovousy Ltd. The following numbers of cultivars and genotypes belong to particular fruit species: apple (22), pear (22), sweet cherry (5), highbush blueberry (7), lingonberry (3), common cranberry (1), American cranberry (1), apple rose (2), rugosa rose (1), cornelian cherry (10), currant (2), sea buckthorn (3), honeysuckle (2), guelder rose (3), rowan (6), chokeberry (2), *Amelanchier* (1), mulberry (1). MS medium according to Murashige and Skoog (1962) was used for apple, pear, sweet cherry, apple rose, rugosa rose, currant, sea buckthorn, honeysuckle, guelder rose, rowan, chokeberry, *Amelanchier* and mulberry. WPM (woody plant medium) according to Lloyd and McCown (1981) was used for highbush blueberry, lingonberry, common cranberry, American cranberry and cornelian cherry. Shoot cultures are subcultured on fresh media in monthly intervals. *In vitro* techniques use the micropropagation in the form of differentiated plant structures (*in vitro* shoots, rosettes) to maintain genetic stability. In differentiated cultures, new plants are derived either from existing meristems (axillary buds) or from adventitious meristems arising in culture (adventitious buds). Used *in vitro* methods complement other conservation strategies (field genebanks, *in situ* and on farm conservation). In the case of apple, pear, sweet cherry and currant, virus elimination *in vitro* techniques (chemotherapy, thermotherapy) are investigated and used for production of virus free plants.

Acknowledgement

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(Poster 58)

Preservation of Polish varieties of narcissi (*Narcissus* L.) in field collections and *in vitro* cultures

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Key words: breeding clones, ELISA, insect-proof tunnel, potyviruses, virus testing, ArMV, NLV, NMV, CMV

Six local cultivars of narcissi (*Narcissus* L.) were bred and commercialized in Poland in the 1990s – 'Posejdon' (large-cupped), 'Mistral', 'Cytrynek' (trumpet), 'Bursztynek', 'Heweliusz' and 'Passat' (large-cupped). A few other cultivars and breeding clones are also already cultivated or still being developed. All the cultivars were bred at the Institute of Horticulture (former Research Institute of Pomology and Floriculture) in Skierniewice using the traditional crossing method. However, later some research on shortening the juvenile phase of seedlings was conducted. The Polish varieties and breeding clones have been included in the collection of the genus *Narcissus* consisting of over 140 genotypes. The Polish cultivars are grown under field conditions as well as being duplicated *in vitro* on the standard MS medium to improve the quality and health status of the plants. The shoots and then the bulbs and plantlets obtained *in vitro* are tested by means of ELISA (Enzyme Linked ImmunoSorbent Assays) for the presence of a group of potyviruses and four other important viruses which could infect the crop: *Narcissus mosaic* - NMV, *Narcissus latent* - NLV, *Arabis mosaic* ArMV and *Cucumber mosaic* - CMV. It was proven in earlier experiments (Sochacki and Orlikowska 2005) that even plants infected with potyviruses can be used to obtain plants giving negative results in ELISA tests by regenerating adventitious shoots *in vitro*, without the need for chemo- and/or thermotherapy. After acclimatization, negatively-tested plants are grown in an insect-proof tunnel to protect the plants against re-infection. The other part of the plants obtained *in vitro* is grown under field conditions.

Sochacki D., Orlikowska T. 2005. The obtaining of narcissus plants free from potyviruses via adventitious shoot regeneration *in vitro* from infected bulbs. *Sci. Hort.* 103: 219-225.

(Poster 59)

Conservation and utilization of Slovene common bean (*Phaseolus vulgaris* L.) germplasm

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Key words: common bean, *ex situ* collection, characterization, evaluation, breeding, drought resistance

Common bean cultivation has a long tradition in Slovenia, which has resulted in the development of numerous landraces that are still grown today in addition to newly established cultivars. There have been several collecting missions organized in the last two decades aimed to collect the diversity of bean germplasm available on the Slovene territory. Nowadays, the Genebank of the Agricultural Institute of Slovenia (AIS) holds an *ex situ* collection of 1116 *Phaseolus* accessions (1058 *P. vulgaris* L., 58 *P. coccineus* L.); the majority (1055 accessions) are of Slovene origin. EURISCO passport descriptors are available for all the accessions stored. In a comprehensive study using molecular (AFLP, SSR, RAPD), biochemical (seed proteins) and morphological markers the genetic variation and relationships among and within autochthonous accessions were evaluated, and the origin was related to the Mesoamerican and Andean gene pools (Šuštar-Vozlič et al., 2006, Maras et al. 2006). Along with that the old common bean varieties and populations are being introduced to the farm production in line with the National Rural Development Programme. In the frame of a recently started EU project the collection will be further assessed including the accessions from the South Eastern European common bean gene pool, and a number of accessions will be evaluated for their nutritional value.

In addition to the *ex situ* conservation, characterization and evaluation of the collection, the material is used in the common bean breeding programme to biotic (resistance to *Colletotrichum lindemuthianum*) and abiotic (drought tolerance) stress. With this respect the response to drought stress is being studied using different approaches. Genes whose expression is altered under conditions of drought in leaves of different *P. vulgaris* accessions have been identified using relative gene expression analysis (Kavar et al., 2008). The influence of drought on the activity of different classes of proteases was studied; it was concluded that different proteases have complex and probably specific roles in the plant response to drought (Budič et al., 2009). Recently proteomic analysis has been used to identify differences on protein level between a drought tolerant and a drought sensitive common bean cultivar.

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Budič M, Kidrič M, Meglič V, Cigić B. 2009. Anal. Biochem., 1, 388: 56-62

(Poster 60)

Characterisation of sugar beet (*Beta vulgaris* L.) breeding lines using genomic microsatellite markers

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Key words: sugar beet, microsatellite markers, allelic diversity, heterozygosity, population analysis, breeding and gynogenetic lines differentiation

Sugar beet (*Beta vulgaris* L ssp *vulgaris*) is an obligate cross-pollinated species. Its breeding is based on crosses between diploid male sterile (CMS) lines and diploid or tetraploid pollinator lines. Sugar beet varieties consist of mixture of similar in appearance plants from different parental lines combinations. For their registration, description of more than 30 morphological traits of one- and two-year vegetation beet plants is in need and up to now there are no UPOV guidelines for this crop. DNA markers as novel descriptors can help in characterization of sugar beet lines and varieties at early stages of beet plant development.

Eleven co-dominant genomic microsatellites were used to study genetic diversity in 30 diploid cultivated sugar beet fertile and CMS lines which construct the core of Belarusian breeding germplasm collection. Key sequences of 6 SSRs were based on dinucleotide repeats and the rest – on trinucleotide repeats localized on four chromosomes - III, IV, V and VI. This set of microsatellite markers was applied to determine the genetic variation within and between lines which were either traditionally selected (15 lines provided by breeders from the Belarusian Sugar Beet Breeding Station) or of gynogenetic origin (15 lines provided by researchers from the Institute of Genetics and Cytology). SSR loci allele size and allele number, observed heterozygosity (H_o) and polymorphic information content (PIC) were analyzed. In total 42 alleles were revealed with the range of allele size in all loci from 98 bp to 273 bp and with highest number of alleles per locus equal to 6. The mean PIC value was in compliance with the data revealed by other researchers. For all 30 lines, the observed heterozygosity varied from 0.127 to 0.600. The average inbreeding coefficient F_{is} was -0.251 ± 0.050 with variation among microsatellite loci from $F_{is} = -0.448$ to 0.163. The genetic differentiation among diploid sugar beet lines was $F_{st} = 0.370 \pm 0.014$. According to statistical population analysis data (GenAlEx, MStools), there was no significant difference between groups of traditionally selected and gynogenetic sugar beet lines. Both were characterized by high heterogeneity and had approximately the same figures of SSR loci polymorphism and observed heterozygosity mean values (0.423 and 0.404) after few seed reproduction circles. Eight alleles out of 42 were rare ones showing frequency less than 2% in a whole sample set. The majority of rare alleles (6 out of 8) was revealed in lines of gynogenetic origin. The possibility of genetic identification for all sugar beet lines under investigation has been proved based on genomic 11 microsatellite set allele composition. Under breeders' request this sugar beet lines collection characterized by SSR data was enriched by mitochondrial genes *atpA* and *atp6* screening results, indicating each plant cytoplasm type (S, N or intermediate) and allowing removal of impurities – N type plants from CMS lines and S type plants from fertile pollinator lines.

(Poster 61)

Agronomical diversity of wild genetic resources of lucerne collected in Estonia

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Key words: lucerne, natural populations, dry matter yield, leaf-stem ratio, crude protein content

Estonia is situated on the northern border of area, where it is economically profitable to grow *Medicago media* Pers. and *Medicago falcata* L. These species were introduced and started to be used as cultivated crops approximately 150 years ago. Over the years more resistant imported lucerne forms have acclimatized and naturalized in Estonia and formed seminatural grasslands of lucerne – red fescue (*Medicagini – Festucetum rubrae*) association.

Thirteen natural populations of *Medicago media* P. and *Medicago falcata* L. were collected in Estonia, mainly from old deserted hayfields, grazed lands or roadsides. The collection was deposited in the Gene bank of the Jõgeva Plant Breeding Institute (Estonia). This germplasm was evaluated at the Jõgeva Plant Breeding Institute (Estonia) in 2004–2006. The experiment was carried out using completely random block design with four replications. The check cultivars were Jõgeva 118, Karlu and Juurlu. The yield was determined in the harvest years in three cuts. To estimate the quality of yield, the protein content in dry matter, the ratio of leaves and stems and the protein content of fractions were determined.

The objective of this study was to characterise agronomic variation of 13 natural populations of lucerne to try to surround the interest of wild germplasm in breeding of lucerne.

Statistics indicated that significant variation existed among natural populations. Natural populations produced less dry matter. Some populations produced relatively high yields. Average dry matter yield was in the first cut 3208 kg ha⁻¹ (min 337 – max 5954; SE ±0,12), in the 1st aftermath 2998 kg ha⁻¹ (min 1108 – max 4923; SE ±0,06) in the 2nd aftermath 1186 kg ha⁻¹ (min 116 – max 3164; SE ±0,047). The total DMY of trial years was 7391 kg ha⁻¹ (min 2479 – max 12194; SE ±0,18).

Average leaf-stem ratio was in the first cut 52,7% (min 47,5 – max 59,8; SE ±0,49), in the 1st aftermath 52,5% (min 41,9 – max 69,7; SE ±0,85) and in the 2nd aftermath 63,4% (min 33,3 – max 78,1; SE ±1,431).

Average crude protein content in the leaves was 24,37% (min 18,7 – max 27,4; SE ±0,260) in the 1st cut; 28,76% (min 23,47 – max 32,24; SE ±0,347) in the 1st aftermath; 26,89% (min 24,0 – max 29,53; SE ±0,23) in the 2nd aftermath.

Average crude protein content in the stems was 13,77% (min 8,67 – max 18,39; SE ±0,0,348) in the 1st cut; 12,91% (min 8,67 – max 18,89; SE ±0,0,299) in the 1st aftermath; 16,37% (min 12,15 – max 21,03; SE ±0,0,319) in the 2nd aftermath.

(Poster 62)

The Crop Genebank Knowledge Base

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Key words: *ex situ* conservation, genebank management, germplasm management, crops

The Crop Genebank Knowledge Base (CGKB), available at <http://cropgenebank.sgrp.cgiar.org>, is the first online resource for genebank managers and conservationists that provides easy access to a wealth of knowledge and resources that span from crop specific best practices for *ex situ* conservation of germplasm over management strategies for genebanks to a vast collection of publications and training manuals in one place. Nine crops – banana, barley, cassava, chickpea, forage grasses and legumes, maize, rice, wheat – are featured in detail, guiding through all steps of their conservation in a genebank. In addition specific regeneration guidelines are provided for further 16 crops. These crop-specific best practices and relevant information have been compiled by genebank experts of the CGIAR centres and national genebanks world-wide and were peer-reviewed by crop experts.

In addition to best practices on crops, the CGKB features general conservation procedures for genebanks as well as information on germplasm management strategies including decision support tools, maintenance of genetic integrity, performance indicators, policies and legal instruments, quality control and risk management, and safe transfer of germplasm and other specialized materials. The learning resources section provides access to a one-stop library with an extensive selection of publications, guidebooks, training manuals, photos, videos, a glossary, and other learning resources. It also has a Flickr photostream and a You Tube channel. The whole web site can be used as self-learning tool as well as a training tool. For example, the international genebank management course held once a year in Korea successfully used the CGKB twice already to organize training sessions.

The CGKB was developed within the framework of the second phase of the Collective Action for the Rehabilitation of Global Public Goods in the CGIAR Genetic Resources System (GPG2) project, which was funded by the World Bank and coordinated by the System-wide Genetic Resources Programme (SGRP) of the Consultative Group on International Agricultural Research (CGIAR). It is one of the outstanding products of this project and is an excellent example of collaboration between many experts to pull together their knowledge and share it in a consistent and easily accessible way for the benefit of their peers and the wider community, in order to improve the management, conservation and use of the invaluable treasure represented by the many *ex situ* collections existing world-wide.

Collaboration tools such as a Wiki, comment boxes on nearly all pages, and a blog encourage participation and communication among users. The web site has in fact been developed in a way that it is easily expandable to include additional crop specific best practices, new pages and sections. Experts have volunteered to be contact persons for specific crops and sections in the web site and committed to keep the content in these pages up to date. The site is regularly updated with relevant learning resources, through user feedback and content updates provided by its contact persons. Additional sections currently being prepared for inclusion in the web site are best practices for the conservation of radish, guidelines for germplasm collecting and procedures for the development of core collections.

(Poster 63)

Building an indicator for *ex situ* conservation of crop genetic resources

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Key words: Indicator, *ex situ* collections, conservation, crop genetic resources

Plant Genetic Resources are essential in supporting the sustainability of farming systems. The usefulness of these resources and the priorities in conservation strategies depend on the knowledge that we have of the conserved material. While many *ex situ* collections of plant seeds exist worldwide, it is still difficult to get an integrative picture of what is conserved and how well this material has been conserved across years. The Biodiversity Indicators Partnership, formed in 2002, and bringing together several international organizations, is in charge of building indicators on biodiversity trends to assess progress towards the Convention of Biological Diversity 2010 target of biodiversity loss reduction. Among the partners, the FAO, together with Bioversity International and with scientific support from IRD were in charge of the development of an indicator to report on the changes over time in the conservation status of plant genetic resources maintained in *ex situ* collections. Based on basic descriptors (i.e. the number of species conserved, the number of accessions of each species and the location where accessions have been sampled) obtained from major international databases, an indicator has been developed that integrates at a given time the available information to provide a value reflecting the conservation level of biodiversity. Here, we report the building of this indicator, and its use on a few main collections.

(Poster 64)

Induced variation in *Cicer reticulatum* Ladiz., progenitor of cultivated chickpea

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Key words: chickpea, *Cicer reticulatum*, mutation, variation

Cicer reticulatum Ladiz. was collected from southeast Anatolia, Turkey by Ladizinsky and Adler (1976) and it is one of the endemic species in Anatolia (Robertson et al., 1995). According to morphological, cytological, biochemical and molecular studies, it is considered to be progenitor of the cultivated chickpea (*C. arietinum* L.) (Toker, 2009). Also, it can easily be crossed with cultivated chickpea (van der Maesen, 1987). Unlike the cultivated chickpea, some accessions of *C. reticulatum* have been found as resistant for biotic and abiotic stresses (Singh et al., 1998). National and international genebanks consist of only 18 original accessions of *C. reticulatum* (Berger et al., 2003). The morphological variation in those 18 original accessions is narrower than those of the cultivated chickpeas (Robertson et al., 1997). To exploit variation, induced mutation is one of the certain approaches. The aim of the study is to increase variation in *C. reticulatum* using mutation techniques.

About 1500 seeds of AWC 611 and AWC 612 were irradiated to gamma radiation at levels of 200, 300, and 400 Gy using ⁶⁰Co source at Turkish Atomic Energy Agency, Ankara, Turkey. M₁ plants were grown and harvested individually at Antalya location in 2004-05 growing season. M₂ generation was grown in separate rows and single seed decent as two sets was harvested each plant prior to harvest in 2005-06. M₃ generation was grown in 2006-07. After germination, observation was extensively made to determine all viable mutants throughout their life period in M₂ and M₃ generations. The following mutants e.g. large seeds, green seed, early flowering, white color flowers, small leaves, multipinnate leaf, erect growth habit and double-podded were isolated in M₂ and M₃ generations. One of these mutants was found as resistant imidazolinone herbicide.

In conclusion, morphological variations were increased as much as the cultivated chickpeas. Induced mutations could be strongly suggested to increase variations under bottleneck conditions.

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(Poster 65)

CGN: vegetable genebank!

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Key words: Collection composition, web portal, vegetable crops

Worldwide approximately 7.4 million accessions are maintained *ex situ* by approximately 1750 collection holders. Only twelve percent of these accessions involves vegetables. In the Netherlands, breeding of vegetable crops is of significant importance, and as a result the total CGN collection of more than 24,000 accessions exists for 47% of vegetable accessions. CGN has the ambition to focus more on vegetable genetic resources as a specific contribution to international efforts in the area of conservation of plant genetic resources. More precisely, the focus will be on vegetables that are cultivated and consumed in Europe. The new strategy of CGN is based on the observation that many institutes maintain large collections of staple crops, whereas vegetable crops are relatively poorly represented in collections. As one of the largest international players, the Dutch vegetable breeding industry depends for its genetic resources to a large extent on the CGN collections. The technical implementation of the new strategy involves:

- Disinvestment in the existing staple crop collections by reduction of the overlap with other collections and transfer of accessions to colleague genebanks.
- Strengthening of the existing vegetable collections of CGN via gap analyses and selective acquisition of new germplasm.
- Development of new collections of neglected and underutilized vegetables.

In parallel to these three activities, CGN is developing a web portal that will provide an up-to-date worldwide overview of vegetable collections and associated information.

(Poster 66)

Mini Core Collections as a means to access genetic resources for farmers' preferred and nutritional traits for informed use by the researchers

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Plant genetic diversity provides the source of variability to underpin adaptation of crops to varied environments and climatic conditions. Since the dawn of agriculture plant genetic resources (PGR) are maintained and used by the farmers and local communities for food and agriculture production to the changing requirements. Worldwide ~7.4 million germplasm accessions are preserved in ~1750 genebanks. More than 119,700 accessions of chickpea, pigeonpea, groundnut, sorghum, pearl millet, and six small millets originating from 144 countries are conserved in ICRISAT genebank and have supplied over 1.37 million samples to scientists in 144 countries in last 37 years. However, there has been exiguous use of these resources in crop breeding resulting narrow genetic base of improved cultivars making them vulnerable to pest and/or disease epidemics. Core (10% of the entire collection) and mini core (10% of core or 1% of entire collection and representing entire diversity) collections have been suggested as gateways to enhanced utilization of germplasm. At ICRISAT, core and mini core collections of chickpea, pigeonpea, groundnut, sorghum, pearl millet, finger millet and foxtail millet have been developed. The mini core collections are not only ideal to identify new sources of variation to combat the climate changes but also to study population structure and diversity, and for marker trait associations. These germplasm sets have been shared with the scientists in NARS, ARIs, and other institutions in 20 countries. Several new sources of variation: drought and salinity tolerance in chickpea, groundnut, sorghum, pearl millet, finger millet and foxtail millet; water logging and salinity tolerance in pigeonpea; low temperature tolerance in groundnut, high temperature tolerance in chickpea and pearl millet; and multiple resistances to pests/diseases, for nutritional traits in finger and foxtail millets (Fe, Zn, Ca, protein), pigeonpea, groundnut and pearl millet (Fe, Zn, protein) and for agronomic traits. Similarly, our partners have identified resistance to bacterial wilt, early leaf spot and rosette, *A. flavus* and high oil and O/L ratio in groundnut; early maturity, large-seed size and high yield in chickpea, groundnut, pigeonpea, pearl millet; early maturity, high yield and resistances to diseases in sorghum, finger millet and foxtail millet. Use of these sources in breeding programs would provide impetus to breeding programs in developing high yielding nutrient dense cultivars with a broad genetic base that can overcome the adverse effects of climate change.

(Poster 67)

Screening for flowering time in groundnut (*Arachis hypogaea* L.) germplasm reproduced in true Mediterranean type environment

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Key words: groundnut, *Arachis hypogaea* L., characterization, maturity, agro-morphological traits

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop cultivated over 100 countries in tropical, sub-tropical, and warm temperate regions of the world. It is an annual legume, grown primarily for high quality edible oil and easily digestible protein in its seeds. Over two-thirds of global groundnut production happens in seasonally dry regions and drought is an important inhibitor for production. For decreasing drought negative effect, early maturing cultivar with enhanced per-day productivity seems that one of the ideal and recommended approaches. Early maturing groundnut has also advantages like that short growing season farming, less watering and enabling high intensity multiple cropping systems. Time to flowering is one of the important parts in maturity and flowering and maturity of groundnuts are affected by certain climatic conditions. They should therefore be re-defined for each germplasm and different regions. We screened 267 groundnut germplasm in terms of time to flowering for identification of early maturity types in Antalya representing true Mediterranean type environment. Days to 50% flowering was used as indicator for time to flowering and obtained measurements indicated that it ranged from 35 to 50 days. The earliest flowering was observed in ACG 60 and ACG 80, the latest flowering was observed in ACG 1, ACG 14, ACG 15, ACG 81, ACG 108, and ACG 128 accessions. Wild types were also used in this study and *Arachis monticola*, *Arachis diogeni* and *Arachis duranensis* indicated 38, 39 and 40 days for the 50% flowering, respectively. ACG 60 and ACG 80 could be evaluated as early maturity types and these accessions are suitable for shorter season production in the true Mediterranean type environment. They are also important as a genetic resource and they will be useful in breeding programs which allow to obtaining adapted lines, high biomass, big pods and high shelling percentage thanks to crosses. Because early-maturity coupled with large-seed size and high yield potential is a desirable combination in groundnut. Early flowering which has important role in short growing season farming and high intensity multiple cropping systems was used in our study and pre-selection was carried on behalf of identification of early maturity types in groundnut mini core collection.

(Poster 68)

Exploring and gathering the Czech and Hungarian crop wild relative and landraces for increasing crop diversity in agriculture

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Key words: genetic resources, collecting missions, Czech Republic, Hungary, landraces, crop wild relatives, gene banks, conservation, evaluation.

Conservation of plant genetic resources for food and agriculture is a very important task from the strategic and economic points of view almost in the whole world. Collecting expeditions and gathering of landraces and crop wild relatives, such as meadow, aromatic, medicinal plants and some threatened species, are important parts of plant genetic resources activities and they enrich gene bank storage composition. In the years 2009 and 2010 eight collecting missions were organized within the framework of the Czech-Hungarian bilateral project MEB 04-09-11: „Exploring and gathering the Czech and Hungarian crop wild relative and landraces for increasing crop diversity in agriculture”. Four of them took place in Hungary and four in the Czech Republic. In total, 119 localities had been visited and 757 seed samples of landraces and crop wild relatives were collected. In the Czech Republic it was 55 localities and 496 seed samples, while in Hungary it was 52 localities and 261 seed samples. It presents large source of biodiversity, which can be utilized in breeding and in on farm and *in situ* conservation activities. Significantly more landraces were collected in Hungary; on the other hand in the Czech Republic more crop wild relatives were gathered. These collecting missions provided new information concerning to the distribution of crop wild relatives and traditional farming practices still present in some regions, especially in Hungary. Our preliminary results indicated that the wild and cultivated seed lots are a potential source of valuable genetic variability for utilization in breeding works. In the paper detailed survey of collected material and its utilization is presented.

(Poster 69)

Genetic Diversity in Lilacs (*Syringa vulgaris* L.)

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Key words: AFLP-analyses, conservation, cultivars, gene bank, morphology

The aim of the work was to study the genetic diversity of *Syringa vulgaris* plants which had been grown for more than 50 years. The collects were compared with old cultivars in order to find unique material and to select plants for further conservation in a national gene bank.

In total, 64 specimens of *Syringa vulgaris* were studied. These consisted of 45 collects of unknown plants from different parts of Sweden and 19 known cultivars from the collection at Bergius Garden in Stockholm. Leaf samples were taken in 2010 and analyzed by AFLP using 4 primer combinations. The collects were divided into four morphological groups based upon floret form and colour (single white florets; single coloured florets; double white florets; double coloured florets) and a fifth group with unknown shape and colour from plants not flowering at the time of sampling. Most collects from the old gardens had white or coloured single florets. Based upon the AFLP-analyses, the lilacs could be divided into 15 cluster groups. In 10 of the clusters flower colour was similar within the group. Some collects had, however, unknown floret colour and need to be studied further. The known cultivars were distributed into 5 of the groups. Cultivars with coloured single or double flowers were closer related to each other than to cultivars with white flowers. Many cultivars have closely related parents, which can explain why they ended up in the same group. Five clusters contained old lilacs which differed from each other and from the studied cultivars. Duplicates were identified in clusters I and III. These were old specimens with origin in the middle of the 19th century.

The results show large diversity in the collected material and many of the old lilacs need to be conserved for the future. Further work with morphological and genetic analyses is needed before decision for conservation in the national gene bank will be taken.

(Poster 70)

**Genebanks working together:
A European Forage Collection (EFC) as basis for AEGIS and the
planned Euro Genebank – Which final requirements are needed?**

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Key words: primary collection/holder, originality, forage standard terms, descriptor list, European *Poa* database

In the context of ECPGR's working group on forages, representatives from most European countries cooperate since 1997 in order to establish a European Forage Collection (EFC). The main objectives are the sharing of responsibilities for the conservation of European forage genetic resources, the secure conservation of these accessions and their continued access for all ECPGR countries. Several steps and priorities were compiled in a work plan for the primary collection holder, the EFC database manager and the genebank hosting safety duplicates.

For a European Forage Collection it was necessary to define unique guidelines and standards, respectively, for a descriptor list (EURISCO format as basis augmented by forage specific traits), regeneration and storage, safety storage (via MOUs). These standards facilitate the cooperation between the genebank curators and finally provide more information via the internet for the users (scientists, breeders, growers). The EFC accessions can thus serve as first choice candidates for a European Genebank.

In this presentation we show via results from the exemplary European *Poa* database, which status we have achieved concerning the definition of sample status (**M**ost **O**riginal **S**ample) and primary holder, which steps we have carried out in order to determine EFC accessions and which problems we still have to solve in this context (providing of data to close gaps in the database, genebank work according to quality management standards and on time, etc.). Finally we discuss which additional requirements are needed from the database manager's, curator's or genebank's point of view in order to enact a working EFC beneficiary to all stakeholders.

(Poster 71)

Mining for Useful Variation in the AE Watkins Wheat Collection

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Key words: wheat landraces, phenotypic diversity, genetic diversity, core collection

In the 1930s AE Watkins (University of Cambridge) collected wheat landraces from local markets in 32 countries across the world. The geographic distributions of the collection covers many European and Asian countries and some from Africa. Today the AE Watkins collection is held in the John Innes Centre germplasm collection. In work funded by the UK defra Wheat Genetic Improvement Network (WGIN) 814 of these lines have been recently studied for their phenotypic diversity. 28% of the AE Watkins Collection tested in the field showed heterogeneity for at least one of the three phenotypes heading date, height and vernalisation requirement. Apart from these scores a great many more diverse traits were noted e.g. awns, waxiness, ear colour. Ancient wheat landraces are believed to be a rich source of useful traits for modern breeding as the genetic diversity of modern wheat varieties is quite small due to bottlenecks during the breeding process. For a more effective exploitation of the diversity of the current AE Watkins collection the lines were genotyped with 45 SSR markers. We characterise the collection using commonly used statistics of genotypic diversity. The diversity measures clearly show that the collection is more genotypically diverse than modern bread wheat lines. We further investigate the population structure of the collection which will enable us to define a core collection which captures the majority of the diversity. This core collection will be a useful tool for wheat researchers and breeders to mine the AE Watkins collection for interesting traits. The knowledge on the population structure may also be used to find candidate genes for interesting traits in association genetics approaches. We also describe the construction of new germplasm resources derived from the collection including eight segregating populations made from crosses with the elite UK spring wheat variety, Paragon.

(Poster 72)

Genetic erosion of crop diversity

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Key words: genetic erosion, crop diversity, modernization bottleneck

The threat of genetic erosion has been the driving force in the creation of crop genebanks worldwide. As the concept of genetic erosion is so central to the work of genebanks, it forms an important theme in the research carried out at CGN.

Genetic erosion of cultivated diversity is reflected in a modernization bottleneck in the diversity levels that occurred during the history of the crop. Two stages in this bottleneck can be recognized: the initial replacement of landraces by modern cultivars and further changes in diversity as a consequence of modern breeding practices.

Literature showed that it is very likely that at the first stage of the modernization bottleneck a reduction in diversity occurred. The first introductions of modern cultivar might lead to an initial regional increase in diversity (if these cultivars have a least partly a foreign origin), but a loss of diversity occurred when landraces were increasingly abandoned.

A meta-analysis of 44 published papers on genetic diversity trends in released crop varieties, focused on the second stage of the modernization bottleneck. In this analysis no evidence was found of a gradual narrowing of the genetic base of the varieties released by breeders. A significant reduction of 6% in diversity in the 1960s as compared with the diversity in the 1950s was observed but indications were that after the 1960s and 1970s breeders have been able to again increase the diversity in the released varieties. This is probably due to the increased use of exotic germplasm, possibly indicating a better access to germplasm in genebanks.

Most published studies on genetic erosion, involved field crops, with very little information on vegetables. Current research at CGN focuses on genetic erosion in vegetable crops, using trends in diversity in European lettuce cultivars as a case study.

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List of Authors

(ordered alphabetically)

- Aavola, Rene, 107
 Abbasi Surki, Ali, 69
 Alcaraz, M., 94
 Al-Farsi, S., 45
 Al-Habsi, K.A., 45
 Al-Hanai, S., 45
 Alibegovic-Grbic, Senija, 73
 Al-Lwatyia, A.H., 45
 Al-Saady N.A., 45
 Al-Subhi, A.M., 45
 Al-Suqri, A., 45
 Amri, A., 30
 Annamaa, Külli, 107
 Antofie, Maria-Mihaela, 47
 Antonius, K., 46
 Assaf, Jenin, 40
 Baksh, Fazil, 95
 Balfourier, François, 11
 Barata, Ana M., 74
 Bardy, Lionel, 11
 Barrion, A., 94
 Bas, Noor, 48, 111
 Battey, Nicholas, 95
 Baudino, M., 82, 98
 Beharav, Alex, 83
 Ben David, Roi, 83
 Bender, Ants, 107
 Benigni, M., 54
 Berruti, A., 52
 Bilham, Lorelei, 117
 Bodzon, Zbigniew, 49
 Bolaric, Snjezana, 73
 Boom, A.H.M. van den, 7
 Bordes, Jacques, 11
 Börner, Andreas, 29, 76
 Boulineau, F., 54
 Bradová, Jana, 50
 Bretting, P.K., 8
 Brites, Claudia, 51, 60
 Cadot, V., 54
 Campbell, George, 101
 Carter, Stephen, 102
 Caser, M., 52, 53
 Caspillo, B.R., 94
 Ceylan, F.O., 110
 Cirotea, Gligor, 47
 Collette, L., 109
 Coquin, P., 54
 Cryer, N., 65, 95
 Csizmadia, G.M., 70
 Cyr, P.D., 8
 Czembor, Elżbieta, 49, 56
 Czembor, Henryk J., 57
 Czembor, Jerzy H., 57
 Dapkuniene, S., 58
 Daymond, A.J., 65
 de Groot, Liesbeth, 23, 69, 111
 de Ponti, Orlando, 32
 Dehmer, Klaus J., 116
 Destain, Jacqueline, 93
 Dias, S., 9
 Dicks, Jo, 117
 Didier, Audrey, 11
 Díez, M.J., 59
 Dinis, Isabel, 60
 Diulgheroff, S., 109
 Djuric, Branko, 73
 Djuric, Gordana, 61
 Doležalová, Ivana, 80, 83
 Dooijeweert, W. van, 59, 111
 Dotlačil, L., 12, 50, 96
 Dudkiewicz, M., 62
 Dulloo, E., 14, 108, 109
 Dunwell, Jim, 95
 Dvořáček, V., 50, 63, 96
 Eigenmann, Christian, 75
 Elezi, Fetah, 64, 71
 End, M.J., 65
 Engels, Jan, 14, 16, 65
 Exbrayat, Florence, 11
 Faberová, Iva, 12
 Faměra, O., 96
 Faslia, Ndoc, 64, 71
 Frese, Lothar, 18, 20, 84
 Friedel, Svetlana, 76
 Furat, Seymus, 113
 Gailite, Agnese, 66
 Gardner, C.A., 8
 Garkava-Gustavsson, Larisa, 67
 Gelvonauskis, B., 58, 68
 Ghoerghe, Laurian, 47
 Ghosh, Kakoli, 14
 Goldberg, Elizabeth, 108
 Goram, Richard, 117
 Gowda, C.L.L., 112
 Graner, Andreas, 76
 Green, Niall, 101, 102
 Griffiths, Simon, 117
 Grimault, V., 54
 Groot, Liesbeth de, 23, 69, 111

- Groot, Steven P.C., 69
 Guteva, Janka, 73
 Gyovai Ponicsán, Á, 70
 Hadley, Paul, 95
 Hargreaves, S., 30
 Harrer, S., 20, 84
 Hawtin, Geoffrey, 21
 Hermuth, J., 12, 50, 63
 Hintum, Theo van, 23, 91, 111, 118
 Hock, Zs., 70
 Hodgkin, T., 109
 Hoebe, Peter, 101
 Hoekstra, Roel, 18, 111
 Holly, L., 70
 Holubec, V., 114
 Horodecka, Elżbieta, 79
 Horváth, L., 70
 Hurk, A.M. van den, 25
 Ibraliu, Alban, 64, 71
 Inci, N.E., 110
 Jęcz, T., 62
 Jiménez, Oswalt, 72
 Juhanoja, S., 46
 Keilwagen, Jens, 76
 Kell, S.P., 30
 Keller, E. R. Joachim, 74
 Khan, A.J., 45
 Kidrič, Marjetka, 105
 Kik, Chris, 48, 111, 118
 Kilchevsky, A., 106
 Kilian, Benjamin, 76
 Kinard, G.R., 8
 Kitner, Miloslav, 83
 Kleijer, Gert, 75
 Kleynhans, R., 27
 Knotova, D., 114
 Knüpfner, Helmut, 76
 Koehler, Christoph, 75
 Koenig, Jean, 11
 Kollár, Zs., 70
 Kolodinska Brantestam, Agnese, 87
 Konopka, J., 30
 Korbelová, Pavla, 83
 Korbin, M., 62
 Korpelainen, Helena, 72
 Kotkas, Katrin, 77
 Kotlińska, Teresa, 74, 78, 79
 Kovács, Géza, 90, 92
 Kratovalieva, Suzana, 73
 Křístková, Eva, 80, 83
 Kuzminova, E., 106
 Kwon, T.R., 81
 Lanteri, S., 82, 98
 Lapierre, Annie, 11
 Latino, G., 82
 Lebeda, Aleš, 80, 83
 Lee, S.K., 81
 Lee, S.Y., 81
 Leistner, H.-U., 20, 84
 Leverington-Waite, Michelle, 117
 Lohwasser, Ulrike, 29
 Lubinskis, L., 86
 Ludvikova, Jarmila, 89
 Lundqvist, Udda, 87
 Mackay, M., 9
 MacPherson, Neil, 102
 Mądry, Wiesław, 88
 Maggioni, Lorenzo, 16, 59
 Málnási-Csizmadia, G., 114
 Malysheva, O., 106
 Maras, Marko, 83, 105
 Matejcek, Ales, 89
 Maxted, Nigel, 30
 McNally, Ken, 31, 94
 Meglič, Vladimir, 35, 73, 83, 105
 Megyeri, Mária, 90, 92
 Melichaříková, Zuzana, 80
 Mendes-Moreira, Pedro, 51, 60
 Menting, Frank, 91, 111
 Merlo, Francesco, 53
 Mieslerová, Barbora, 83
 Mikó, Péter, 90, 92
 Millard, M.J., 8
 Mojica, C.A.R., 94
 Molnár-Láng, Márta, 90, 100
 Mputu., Jean-Noël, 93
 Munda, Alenka, 105
 Nadaf, S., 45
 Nam, M.H., 81
 Naredo, M.E.B., 94
 Nehrlich, Stephanie, 116
 Nevo, Eviatar, 83
 Nybom, Hilde, 67
 Olas-Sochacka, Marta, 74, 78, 79
 Oppermann, Markus, 76
 Ordidge, Matthew, 95
 Ordon, F., 20, 84
 Orford, Simon, 117
 Ozugur, Z., 110
 Papoušková, L., 96
 Paprstein, Frantisek, 89, 97, 103
 Park, Y.J., 81

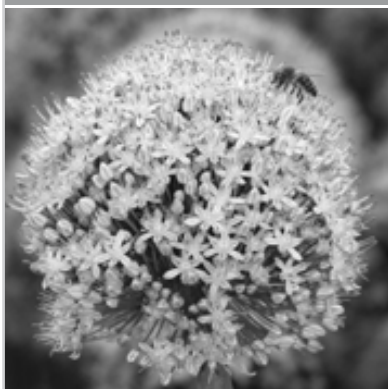
- Perrot, S., 54
 Peti, E., 70
 Petrovic, Danko, 73
 Petrželová, Irena, 80, 83
 Pham, J.L., 109
 Pierart, Céline, 93
 Piggitt, J., 30
 Ponti, Orlando de, 32
 Portis, E., 82, 98
 Prohasková, Anna, 63
 Quilloy-Mercado, S.M., 94
 Radun, Marina, 61
 Ramos, J., 94
 Rasmussen, Morten, 87
 Rayco, J.A., 94
 Reid, Alex, 101
 Reinink, Kees, 33
 Reis, Aida, 74
 Rellosa, M.C.C., 94
 Ricci, L., 82
 Roço, Evan, 73
 Rodriguez, M.A., 94
 Rosenberg, Viive, 77
 Rouard, M., 65
 Rozpara, Elżbieta, 99
 Ruas, M., 65
 Rungis, Dainis, 66, 86
 Sackville Hamilton, R., 31, 94
 Sand, Camelia, 47
 Sandru, Dan M., 73
 Santos, Daniela, 60
 Sari, D., 110
 Scariot, V., 52, 53
 Schliephake, E., 20, 84
 Schmidt, Jan, 88
 Schneider, A., 100
 Scholten, Maria, 101, 102
 Sedlak, Jiri, 97, 103
 Shehadeh, A., 30
 Shehu, Julian, 71
 Siddiqui, Z.S., 81
 Simon, A., 70, 114
 Simonse, Lau, 48
 Sochacki, Dariusz, 104
 Spoor, Bill, 101, 102
 Stehno, Zdeněk, 12, 50, 63
 Stramkale, V., 86
 Street, K., 30
 Studnicki, Marcin, 88
 Stukeniene, G., 58
 Šuštar-Vozlič, Jelka, 35, 73, 105
 Šveistytė, L., 68
 Svirshchevskaya, A., 106
 Tamm, Sirje, 107
 Thonart, Philippe, 93
 Thormann, Imke, 14, 108
 Thörn, Eva, 35, 37
 Thuillet, A.C., 109
 Toker, C., 110
 Tomic, Lidija, 61
 Tomic, Zorica, 73
 Torres, J.B., 94
 Treuren, Rob van, 69, 111, 118
 Turletti, A., 98
 Turnbull, C.J., 65, 95
 Ugrinović, Kristina, 105
 Uosukainen, M., 46
 Upadhyaya, Hari D., 112
 Uzun, Bulent, 113
 van de Wouw, Mark, 118
 van den Boom, A.H.M., 7
 van den Hurk, A.M., 25
 van Dooijeweert, Willem, 59, 111
 van Hintum, Theo, 23, 91, 111, 118
 van Treuren, Rob, 69, 111, 118
 Veteläinen, Merja, 39, 46
 Visser, Bert, 111, 118
 Vörösváry, G., 114
 Vymyslický, T., 114
 Wedelsbäck Bladh, Katarina, 115
 Weise, S.F., 65
 Wetten, Andrew, 95
 Williams, David, 108
 Willner, Evelin, 116
 Wingen, Luzie U., 117
 Wood, Melissa, 40
 Wouw, Mark van de, 118
 Yol, Engin, 113
 Yoon, I.S., 81
 Zadražnik, Tanja, 105
 Zanke, Christine D., 74
 Zijlstra, Sierd, 48



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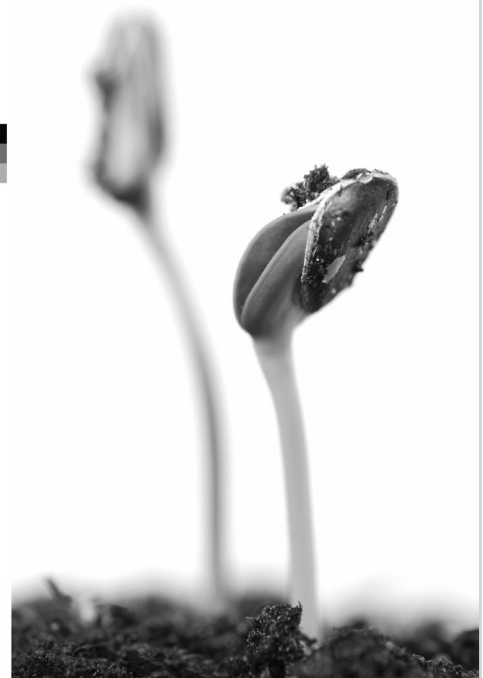
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