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Book of Abstracts

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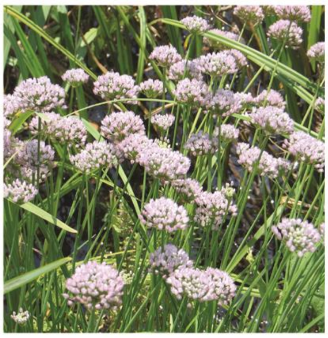

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Contents

Foreword

This conference presents the culmination of the PGR Secure project (www.pgrsecure.org) – a collaborative project involving eleven partners funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394. It is jointly organized with the section on genetic resources of the European Association for Research on Plant Breeding (EUCARPIA). This international conference showcases innovative and potential novel characterization techniques and conservation strategies to identify and safeguard crop wild relative (CWR) and landrace (LR) genetic diversity to increase potential options for crop improvement as a means of underpinning food security in the face of climate change. The conference brings together a wide range of biodiversity expertise from the international community to debate current and future enhanced conservation and utilization of CWR and LR diversity for improving agricultural production, increasing food security and sustaining the environment for better livelihoods. The conference represents a landmark in the plant genetic resources science arena, highlighting exotic plant germplasm as a potentially critical but neglected resource for crop improvement.

Part 1 of the book of abstracts contains the abstracts of the oral presentations and Part 2, those of the posters. They are organized under the four conference themes, viz. characterization techniques, conservation strategies, facilitating CWR and LR use and informatics development. The oral presentations will be the subject of a book entitled “Enhancing Crop Genepool Use: Capturing wild relative and landrace diversity for crop improvement” that will be published by CABI as the conference proceedings. All duly registered participants will be receiving a copy of the book when it is published.

We hope you will enjoy the conference.

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Guest lecturer

Making use of germplasm diversity for crop improvement in a range of tropical crops

Jean Christophe Glaszmann

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Abstract

Tropical crops offer a broad range of situations that allow illustration of diverse approaches for enhancing genepool utilization. The actors for genetic improvement can be very different among crops, e.g. between food crops, for which genetic improvement is largely a continuous and distributed process, and plantation crops where improvement is formally organized and targeted; annual grain crops and vegetatively propagated crops evolve at different paces, in time and in space; diploid crops allow recurrent processes while complex-genome crops go through critical steps in a discontinuous process. This presentation will use examples developed at AGAP (http://umr-agap.cirad.fr/en) on sorghum, rice, groundnut, banana and sugarcane to illustrate the pervasiveness of the various topics that this conference is considering. Current experience leads us to discuss a more inclusive vision of crop diversity, the frontier between breeding and prebreeding as well as the management of crop genetic resources.

Part 1
Oral presentations

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Part 1. Oral Presentations

Theme 1: Characterization techniques

Traditionally, phenotypic characterization and evaluation of conserved diversity involves field trials where breeders select accessions for inclusion in their breeding programmes. However, this method is resource intensive, with the result that the vast majority of conserved CWR / LR diversity accessions remain uncharacterized and largely unutilized. This theme examines novel characterization and evaluation techniques to enhance the exploitation of CWR and LR diversity in crop improvement activities.

Abstracts under Theme 1 fall into three sub-themes:
- 1.1 Pre-breeders’ use of exotic germplasm
- 1.2 Breeders’ use of exotic germplasm
- 1.3 Novel germplasm characterization techniques

1.1 Pre-breeders' use of exotic germplasm

Geno-Pheno in plant breeding

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Abstract

In crop genetics and breeding research, phenotypic data are collected for each plant genotype, often in multiple locations and field conditions, in search of the genomic regions that confer improved traits. Currently, virtually none of the data generated from the hundreds of phenotypic studies conducted each year are being made publically available as raw data; thus there is little we can learn from past experience when making decisions about how to breed better crops for the future. This ongoing loss of phenotypic information, particularly about crop productivity, must be stopped if we are to meet the considerable challenge of increasing food production sufficiently to meet the needs of a growing world population. I will present a number of plant-breeding case studies that demonstrate the value of introgressions from wild tomato species and of sharing information on crop plant genotypes and phenotypes.

Keywords: Genomics, phenotypic data, breeding

Using Phenomics and Genomics to unlock landrace and wild relative diversity for crop improvement

Koen Pelgrom[1], Garima Sharma[2], Roeland Voorrips[1], Colette Broekgaarden[1], Jeremy Pritchard[2], Sean May[3], Stanley Adobor[3], Bart Janssen[4], Wilbert van Workum[4], Brian Ford-Lloyd[2] and Ben Vosman[1*]

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Abstract

With the expected growth of the world population and the public demand for sustainability there is a strong need for more robust varieties. Current cultivation methods rely heavily on the use of insecticides to control insect pests, which is undesirable. Alternative control measures are needed, of which the use of resistant varieties is the most promising. Brassica crops, in particular Brussels sprouts, kale and Savoy cabbage suffer from the cabbage aphid (*Brevicoryne brassicae*) and whitefly (*Aleyrodes proletella*). In this project we focus on the identification of resistance factors to these specialist insects. Often such resistances are found in crop wild relatives (CWR) and landraces (LR). As a first step to identify resistant material we screened a collection of 432 accessions, including wild material and landraces of Brassica oleracea as well as crop wild relatives for whitefly resistance in no-choice field and greenhouse experiments. Resistant accessions were identified among B. oleracea var. capitata (heading cabbage) landraces and some of the wild relatives. Where in heading cabbage resistance is only expressed in plants of at least twelve weeks old, some wild relatives were already starting to express resistance at six weeks; since farmers plant these crops at an age of 5-6 weeks this earlier expression of resistance is of great practical importance. QTL mapping was used to identify chromosomal regions involved in whitefly resistance. Molecular markers were developed based on next-generation sequencing data. Transcriptomics was used to identify genes differently expressed in resistant and susceptible plants. Combining all these data will facilitate the identification of the gene(s) responsible for the resistance and promote their use in breeding.

Keywords: Brassica, whitefly, aphid, screening, characterization

Pre-domesticating wild relatives as new sources of novel genetic diversity

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Abstract

Wild relatives of many domesticated crop species have been used mainly as a source of specific genes for disease resistance. It is often difficult to efficiently exploit these gene pools because they lack a number of essential traits necessary for cultivation and management using modern agricultural technology. Many of these traits were developed in our modern crops as part of the process of domestication. These traits are usually associated with seed dispersal, seed size, seed coats, and seed dormancy that are essential to survival in the wild, but undesirable in domesticated crops. By incorporating these 'domestic' traits into the wild species, they may then be managed using standard farming methods. It would then be easier to select desirable gene combinations within these diverse and variable populations, and then more effectively introgress these selected traits into modern, elite germplasm and cultivars. Cultivated barley (*Hordeum vulgare*) and its wild progenitor, *H. spontaneum,* will be used as a model to employ the proposed methodology and illustrate the increased efficiency and effectiveness of this approach to taming wild relative germplasm. By 'pre-domesticating' a diverse population of *H. spontaneum* and conducting breeding and selection within this background, it is possible to exploit the vast reservoir of quantitative genetic variation that is not being utilized at this time. Applying recurrent selection, via an efficient genetic male sterile system within *H. spontaneum* itself, may lead to greater genetic diversity for nutritional quality, agronomic traits, processing quality, and even yield, than currently exists within cultivated barley. This approach is essentially re-domesticating barley on a much greater scale than the original domestication event(s); and it could address the current issue of lack of diversity. This concept is applicable to most other crop species.

Keywords: *Hordeum spontaneum*, pre-domestication, male sterility, novel genetic diversity

Buglossoides; its journey to becoming 'Ahi Flower'

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Abstract

Buglossoides arvensis also known as Corn Gromwell was identified as a new, potentially sustainable and improved source of stearidonic acid (SDA, C18:4n-3) from a novel crop plant. SDA is a key precursor in the biosynthesis of long chain (LC) omega-3 (or n-3) polyunsaturated fatty acids (PUFAs) such as eicosapentaenoic acid (EPA, C20:5n-3) and Docosahexaenoic acid (DHA, (22:6 n-3) that are commonly found in fish oils. The potential health benefits of increasing n-3 PUFA in an ageing population, with low levels of fish consumption and declining availability, was the key driver to development of alternative dietary sources of these fatty acids. Currently one of the best sources of SDA is *Echium plantagineum* seed oil. There are, however, significant issues with cultivation and production of good quality oil from this crop.

This paper will consider the issues that were tackled in seeking to convert *Buglossoides arvensis* to a crop that could be cultivated under UK conditions. Identification and utilisation of wild accessions in a breeding programme are considered.

Keywords: omega-3 Fatty acid, *Buglossoides arvensis*, polyunsaturated fatty acids, crop wild relative, stearidonic acid, Corn Gromwell

Unraveling quinoa domestication with wild ancestors

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Abstract

There is little knowledge about the genetic, geographic and climate adaptation mechanisms and patterns involved in quinoa domestication. Its high nutritive value associated with a combination of traits conferring tolerance to extreme temperatures, water deficits and salinity stress make this crop an interesting research subject. Recently, the interest in its consumption and cultivation grew dramatically beyond its traditional cultivation range raising new challenges. Smallholder farmers are losing their traditional landraces because commercial interest is focused in just one genetic group and to the lack of tolerance to high temperatures and waterlogging. Being unpredictable weather conditions a central aspect of climate change, looking for sources of tolerance to these stresses is almost mandatory. *Chenopodium hircinum* -quinoa's wild ancestor-, is found in most lowlands in the Pampas and Chaco biomes in Argentina, Uruguay, Brazil, Paraguay and Bolivia. It produces fertile offsprings with quinoa. Germplasm conservation and evaluation of this species excluding Bolivia but only partially is almost null. This paper aims at unraveling quinoa domestication process and showing that some useful traits to face environmental changes were perhaps lost during domestication or during recent times.

Keywords: quinoa, Chenopodium hircinum, Chenopodium quinoa, wild relatives, global change, high temperature stress, water stress, domestication syndrome

1.2 Breeders' use of exotic germplasm

Gene discovery and its applications in rice

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Abstract

We present several highlights of the gene discovery research that is currently done at the CIAT-IRD Rice Genetics and Genomics Laboratory using rice-relative species. We take the example of the exploitation of interspecific crosses (*Oryza sativa* x *O. glaberrima*; *Oryza sativa* x *O. rufipogon*) to tackle new alleles that can be used to improve cultivated rice. This work uses libraries of chromosome segment substitution lines (or CSSLs) developed at CIAT. We also present our approach of interspecific bridges (or iBridges) that will help to massively introgress alleles from the African rice species to the Asian species.

Keywords: Gene discover, Rice, iBridges

Widening the genetic base of rice varieties by introgressing novel genes/ traits from wild species: an Indian perspective.

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Abstract

After the spectacular progress in enhancing the productivity of rice with the development of semi dwarf, fertilizer responsive and non-lodging varieties like IR8 and Jaya in the 60's, the breeding efforts in recent years have not met with greater success to break the yield ceiling, which may be due to narrow genetic base. The evolution of new and virulent races/biotypes of disease and insect pests in the changing climatic scenario are the other major factors for reducing the rice productivity. Wild species of *O. sativa* are the potential source of novel genes for biotic and abiotic stress tolerance and yield enhancement. The genes/QTLs for yield enhancement, salinity and phosphorus deficiency tolerance were introgressed from *O. rufipogon* and varieties Jarava and Dhanrasi were released for cultivation having yield advantage of 20% in normal and 46% in saline conditions with resistance to blast, BPH, rice tungro disease, tolerance to stem borer. Yellow stem borer tolerant lines developed from *O. longistaminata* and *O. glaberrima* are under field evaluation. Yield QTL's from *O. rufipogon* and *O. nivara* successfully introgressed into the restorer KMR-3 and high yielding variety at this Directorate. Several donors for resistance to blast and bacterial blight, BPH, WBPH and rice tungro disease and tolerance to yellow stem borer, and salinity were identified from *O. nivara, O.glaberrima, O. longistaminata and O. rufipogon,*. We successfully introgressed the genes/QTLs for broad-spectrum blast resistance, BPH and rice tungro disease resistance from *O. nivara* and *O. rufipogon,* yellow stem borer tolerance, blast, bacterial blight, and BPH resistance from *O. longistaminata* and *O. glaberrima* in to rice varieties. The bacterial blight resistance genes *Xa33* and *Xa34* were introgressed from *O.nivara* and *O.brachyantha*, respectively. The BPH resistance genes *Bph22*, *Bph23* and *bph24* have been introgressed from *O.glaberrima*, *O.minuta* and *O. rufipogon*, respectively. These genes are being used in developing multiple resistant varieties for different disease and insect pests. We are also mapping the novel genes for blast and BPH resistance introgressed from *O. rufipogon*, *O.nivara* and *O. longistaminata*. The genes such as *BPh18*, *Bph20* and *Bph21*, for BPH, *Xa21* and *Xa33* for bacterial blight and *Pi40* and *Pi9* for blast resistance from wild rices are presently used in developing multiple resistant varieties through MAB.

Keywords: wild rice, gene, introgression

The IBERS Diploid Avena Genomics Resource (DAGR) and its application to hexaploid oat breeding

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Abstract

An *Avena* A-genome zipper has been constructed based on sequencing of parents and inbred progeny from an interspecific cross between wild and domesticated diploid species (*Avena atlantica* x *A. strigosa*). Further sequencing of a C-genome diploid (*A. ventricosa*) and additional A-genome species (*A. damascena*, *A. longiglumis*, *A. canariensis*) is being carried out to provide references to aid assembly of the hexaploid oat genome, and to shed light on the evolution of lineage specific pathways which underlie agronomically important traits such as the production of beta-glucan or avenanthramides. Sequence information is being used to design screens to test for possible roles of these pathways in domestication or adaptation to specific environmental conditions. Pre-breeding screens are being applied to a panel of 1000 land race and wild hexaploid accessions to suggest the best candidates for inclusion in an exotic nested association mapping (NAM) population, to complement the existing 600 F7 NAM lines which include populations derived from landraces, and which are being phenotyped in the field in 2014.

Keywords: Oats, Cereals, Genome zipper, Land race

Screening wild Vigna species and cowpea (*Vigna unguiculata*) landraces for sources of resistance to *Striga gesnerioides*

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Abstract

Cowpea (*Vigna unguiculata*) is mainly grown with cereals such as sorghum and millet in the dry savanna regions of sub-Saharan Africa and it serves as a major source of protein in the diet. In this region cowpea production and productivity are adversely affected by *S. gesnerioides* (cowpea parasitic weed) which causes yield reduction running into millions of tons annually. The development of resistant varieties remains the most effective means to combat this parasitic weed. Screening of the crop's wild relatives and land races for the identification of additional sources of resistance genes is very important. Wild *Vigna* species and their geographically co-located cultivated cowpea (*V. unguiculata*) landraces were screened in the field by artificial inoculation with seeds of *S. gesnerioides* at the IITA experimental field in Minjibir Kano State, Nigeria during the planting seasons of 2012 and 2013. The 350 accessions of wild Vigna belonging to 45 species obtained from the Genetic Resources Center of the International Institute of Tropical Agriculture were planted in a replicated trial between August and December 2012. We used a *Striga gesnerioides* sick plot for planting the trial. Among the lines planted, 21 genotypes from 11 species (*V. ambacensis, V. davyi, V. glabrescens, V. marina, V. mungo, V. oblongifolia, V. parkeri, V. racemosa, V. reticulata, V. vexillata, V.unguiculata* sub-species *dekindtiana*) showed resistance to *S. gesnerioides* while others were susceptible to varying degrees. Of the 11 species only *V. unguiculata* sub-species *dekindtiana* is potentially cross compatible with cowpea (*V. unguiculata*). In 2013, 280 accessions of cowpea landraces (*V. unguiculata*) including the 21 striga resistant wild *Vigna* genotypes from the previous trial were planted in a replicated trial on a *S. gesnerioides* sick plot at the same location as in 2012. Sixteen genotypes of the cultivated cowpea landraces planted for the 2013 trial were confirmed resistant to *S. gesnerioides* while others were susceptible to varying degrees.

Keywords: Cowpea, genotypes, *Striga gesnerioides*, germplasm

QTL detection for root-related traits in wild barley introgression lines under drought stress conditions

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Abstract

Barley (*Hordeum vulgare* L.) exhibits remarkable variation in root system across the boreal to equatorial regions of the world. We have identified an extensive root system in a unique wild barley accession 'ISR42-8' in comparison to cultivar 'Scarlett'. In the present study, we tested a set of barley introgression lines (ILs) having 'ISR42-8' wild introgressions in cultivar 'Scarlett' background to detect genome-wide association of donor introgressions with root-related traits under control and drought stress conditions. The phenotypic evaluation revealed wild accession 'ISR42-8' had better root trait performances, more tillers and spreading habit compared to 'Scarlett'. S42IL population revealed wide range of variation for root length, root dry weight, root volume, number of tillers per plant and growth habit. Based on the significant trait values and SNP marker defined positions, 41 QTL (quantitative trait loci) were identified considering both overlapping and unique wild introgressions across S42IL population. Root dry weight contributed maximum 11 QTL where root length and root volume bore 9 QTL for each. Most significant and strong QTL for root length, root dry weight and root volume was detected on 5H chromosome at 154.37 cM. This major QTL was validated in multiple introgression lines like S42-173, S42-125, S42-126 and S42-176 which share the common QTL bearing wild introgression. For numbers of tillers per plant and growth habit, highly significant and strong QTL were located on chromosomes 1H (134.43-152.29cM), 4H (5.42-26.58cM), 5H (203.85-231.75cM), respectively. QTL bearing ILs, S42IL-102, S42IL109, S42IL-124, S42IL-133, S42IL-143, S42IL-176 revealed significant associations for most of the studied traits and carried several QTL effects simultaneously. Therefore, considering global warming and climatic change these lines can be novel resource in drought-stress breeding as well as to isolate underlying genes via positional cloning.

Keywords: QTL validation, Introgression lines, Drought stress

1.3 Novel germplasm characterization techniques

How the Focused Identification of Germplasm Strategy (FIGS) is used to mine plant genetic resource collections for adaptive traits

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ICARDA
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Abstract

The agro-ecosystems that underpin our food security are being increasingly destabilized by interacting factors such as population growth, decline in water availability, climate change, large annual losses of arable land, destruction of background eco-systems, decline in soil fertility, emergence of virulent disease bio-types, increasing land use for bio-fuels, increasing energy costs, declining phosphorous production and under-investment in agricultural research. Thus the need to breed more robust and efficient crop varieties will become increasing important. This process is in-turn underpinned by ready access to novel genetic variation for useful traits. In fact, empirical models suggest that early identification of appropriate traits within genetic resource collections is of equal importance to the process of transferring these traits into improved genetic backgrounds. Since there are over 7 million accessions residing in genetic resource collections globally and resources are limited, it is impossible to evaluate them all for all useful traits; a fact that impedes the transfer of novel variation into breeding genepools. What is needed therefor is an efficient means to identify relatively small subsets of genebank material that will have a reasonably high probability of containing individuals with a specific trait. The Focused Identification of Germplasm Strategy (FIGS) uses information about germplasm collection sites to predict where selection pressures may have occurred within *in situ* populations for specific traits and thus allows for a more rational approach to evaluating germplasm collections. This presentation will present specific examples of how FIGS has been used to identify germplasm from genetic resource collections that exhibit adaptions (traits) to specific abiotic and biotic constraints in faba bean (*Vicia faba* L.) and wheat (*Triticum* Spp.).

Keywords: Focused Identification of Germplasm Strategy, germplasm, traits

Detecting climate adaptations in the wild pearl millet *Cenchrus americanus* for future breeding use

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Abstract

The cultivated pearl millet is a major crop in West Africa where arid conditions restricted the choice of crops to a few species. Interestingly, the pearl millet wild relative is found in a set wider environmental conditions especially more arid environments. Consequently, the wild pearl millet has the potential to carry adaptations to harsher climatic conditions: hotter temperature and drier months. Identification of useful genetic variation could be introgressed into the cultivated forms. It would allow the agriculture of the region to face future changes.

The objective of this study is to make use of new possibilities offered by next-generation sequencing to investigate and identify genes and polymorphisms that confer climatic adaptations to the wild pearl millet. The study aims at performing a wide-genome screening to detect signatures of selection along a climatic gradient.

We investigate the genome wide diversity of 48 populations of wild pearl millet distributed across the West African distribution area and along climatic gradients. At first, two NGS approaches were tested: Genotyping by Sequencing (GBS) and RNAseq on a subset of 95 samples. SNP (Single nucleotide polymorphism) markers obtained from both approaches are compared regarding to their genomic distribution, mutation type and discriminant power. Preliminary results and conclusions are presented in regard to the final objective of this study.

Keywords: NGS, detection of selection, population genomics

Comparative population genomics in crops and their wild relatives: assessing the impact of domestication on crop genetic diversity

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Abstract

Domestication strongly impacted phenotypic and genomic evolution in crop species. An increased knowledge of the impact of domestication on crop diversity would contribute to a better understanding of the genetic potential of the wild ancestor in breeding programmes.

We conducted comparative analyses of the effect of domestication on genome evolution in different crop species, mainly to quantify the loss/recovery of diversity associated with domestication and to investigate variations in domestication patterns among crop species based on their life history, domestication depth, or phylogenetic range.

In 15 crops displaying various life history traits and having various domestication histories, we studied quadruplets of species comprising a crop species, its wild ancestor, and two out-group species, used for phylogenetic analyses. Their transcriptome was sequenced with a high-throughput RNAseq technology. This resulted in a gross number of 13.3 billion reads of 75 to 100 bp.

The strategy revealed its efficiency since several thousands of genes were available. The basic comparison of nucleotide diversity between the wild and the cultivated forms confirmed that domestication is responsible for a genome wide loss of polymorphism. Some crops, such as the African rice, showed a particular high loss. The cost of domestication was also assessed. The strong demographic bottlenecks experienced by the initial crop populations are expected to promote the fixation of weakly deleterious mutations and to depreciate the fitness of the first domesticated plants. As an example of our results and their interest for the use of wild relatives in breeding, we found a strong excess of fixation of deleterious mutations in African rice, especially for the lowly expressed genes. This suggests that useful alleles are available in the wild and shows that wild relatives could be used in breeding program not only for specific traits but also more globally to compensate the load accumulated during domestication.

Keywords: Population genomics, Domestication, Diversity, Crops, Wild ancestors

Next-generation SNP genotyping platforms for characterizing potato germplasm

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Abstract

High-throughput, low-cost methods for generating genotypic data within potato breeding programs are necessary to help breeders develop improved varieties faster. With the availability of the potato genome sequence and the identification of numerous polymorphisms, new genotyping strategies and marker resources for potato research are now widely available. These genome-wide markers are available for comprehensive characterization of potato genetic resources and prediction of the value of exotic potato germplasm. Several genotyping methods have been evaluated at the Agriculture and Agri-Food Canada (AAFC) Potato Research Centre to identify single nucleotide polymorphisms (SNPs), characterize potato germplasm resources, generate genetic maps, and initiate genomic selection projects. These methods include whole genome re-sequencing, targeted sequence capture, Illumina SolCAP SNP arrays, restriction site associated DNA sequencing, genotyping by sequencing, and most recently with 2b-RAD genotyping. Each of these methods has some advantages in terms of genome coverage, genotype certainty, sample throughput, and cost per sample. Diploid and tetraploid potato germplasm from the AAFC potato breeding program, the Canadian Potato Gene Resources Repository collection, the International Potato Center (Peru) breeding program, and diploid *Solanum phureja* germplasm from Colombia have been genotyped using the SolCAP SNP array and / or genotyping by sequencing. Applications of these methods for SNP discovery, detection of marker-trait associations, characterization and comparisons of diversity within gene pools and future research on prediction of breeding values will be presented. Based on our experiences, the new genotyping tools will lead to better utilization of beneficial diversity in wild potato relatives and germplasm from South America.

Keywords: potato, single nucleotide polymorphism, genetic resources

Theme 2: Conservation strategies

This theme examines the development of systematic CWR and LR conservation strategies at global, regional and national and relevant management interventions that will secure and improve the in situ and ex situ conservation of European CWR and LR diversity, as a means of promoting CWR and LR use by breeders.

Abstracts under Theme 2 fall into four sub-themes:

- 2.1 International CWR Conservation
- 2.2 International LR conservation
- 2.3 National CWR conservation
- 2.4 National LR conservation

2.1 International CWR Conservation

Joining up the dots: a systematic perspective on crop wild relative conservation and use

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Abstract

Growing concern over the rapidly increasing human population and potentially devastating impacts of climate change on food security has highlighted the necessity for action if human well-being is to be maintained. Crop wild relative (CWR) diversity offers a potential means of mitigating the impact of climate change through trait transfer to crops, enabling continued or even increased production under changing environmental conditions, thus underpinning the maintenance of food security. However, current use of CWR in crop improvement is limited by their genetic erosion in the wild, their inadequate conservation and multiple barriers to utilization. Therefore, systematic CWR conservation and improved utilization are urgent priorities. To improve CWR conservation and use in the 21st century, an invigorated approach is required which implements a holistic approach to conservation at global, regional, national and local geographic scales, which ensures complementary *in situ* and *ex situ* conservation and which employs novel means of identifying the diversity required by farmers and breeders. Such a novel approach to CWR conservation and use is likely to include: (i) strategic conservation planning, (ii) geopolitical complementarity, (iii) predictive *ex situ* sampling, (iv) establishing *in situ* networks, (v) sequenced-based high throughput predictive evaluation, (vi) GIS-based predictive evaluation, and (vii) user-based informatics. Alongside improved technology application, there is a parallel need to address the policy framework to ensure systematic and holistic conservation of CWR diversity, clarify its governance and long-term financing, strengthen global partnerships and linkages, integrate CWR into biodiversity conservation, improved access to CWR diversity for the user community and set in place legislative protection. Such significant changes in the scientific application and policy environment for CWR conservation and use will be required if we are to feed the 9.07 billion people predicted to exist in 2050 and ensure food security for future generations.

Keywords: Crop wild relative (CWR), Food security, Complementary genetic conservation, *In situ* conservation, *Ex situ* conservation, Conservation planning, Predictive *ex situ* sampling, High throughput predictive evaluation, GIS-based predictive evaluation, User-based informatics.

A regional conservation strategy for European crop wild relative diversity

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Abstract

There is an imperative to develop and implement a comprehensive strategy for the conservation of the valuable crop wild relative (CWR) genetic resources native to Europe, because plant breeders are seeking greater diversity of traits and CWR contain a wide pool of genetic diversity that is of value for crop improvement. CWR are therefore an important resource for maintaining food security and for safeguarding the substantial economic gains to Europe through crop production in the region. Recent advances have been made in our understanding of CWR diversity in the region in terms of the number of taxa that exist and their locations, their Red List status, and which are priorities for conservation. There is also progress in planning their complementary conservation. These developments provide a solid foundation for a strategic approach to their conservation based on a range of commonly agreed and widely tested scientific concepts and techniques. However, fully achieving effective conservation and utilization of European CWR diversity will require a coherent, regionally coordinated policy as well as appropriate funds for their conservation, characterization and evaluation.

In this paper, we propose a regional CWR conservation strategy to guide European and national policy development—a blueprint to drive concerted actions throughout the region. This policy would substantially aid and secure the implementation of the wider EU strategy for the conservation of genetic resources in food, agriculture and forestry. Included in the strategy is a proposal for the designation of Most Appropriate Wild Populations—a new paradigm for CWR conservation, a description of the two core levels of strategy planning needed for the development of a comprehensive pan-European CWR conservation strategy, a vision of how an integrated strategy for Europe can be established and administered, and rationale for new policy required to establish and support its ongoing operation.

Keywords: Crop wild relative, Pan-European conservation strategy, Conservation of genetic resources

Developing strategies for *in situ* crop wild relative conservation on a global scale

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Abstract

Crop wild relatives (CWR) have the potential to contribute beneficial traits to crops, such as biotic and abiotic resistance leading to improved yield and stability. While climate change will directly impact CWR diversity itself, it will also undoubtedly alter the conditions under which our crops grow. It is likely that many current crop varieties will need to be replaced with stress tolerant varieties to ensure agricultural viability of the crop in the same locations. CWR are a valuable source of diversity in the face of this challenge; however they are currently suffering widespread genetic erosion and even extinction as a result of direct or indirect human-mediated environmental changes. Effective *in situ* maintenance of these genetic resources is vital if they are to continue to meet exploitation needs of current and future stakeholders, and thus help to maintain agricultural stability.

In situ CWR conservation efforts have yet to take a systematic approach, with populations mostly having been conserved where their conservation is coincident with other protected area priorities, such as when they are valued because they are recognized as a nationally important rare or threatened species. However, the "Adapting crops to climate change: collecting, preparing and protecting the crop wild relatives of crops" project has set out to conserve the World's most important CWR in a systematic manner. *In situ* gap analysis was carried out as part of this project for the priority CWR of 80 globally important crops as identified in the Harlan and de Wet Inventory. Distribution maps were made for the wild occurrence of each taxon and used to determine hotspots of CWR richness. Hotspots were further analysed to find the most suitable and efficient combination of areas to conserve maximum genetic diversity, whilst taking into account the predicted impact of climate change.

Keywords: crop wild relative, in situ conservation, food security, gene pool, plant conservation, plant genetic resources

The distributions and *ex situ* conservation of crop wild relatives: a worldwide approach

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Abstract

The wild relatives of crop plants are increasingly used in plant breeding as sources of novel traits that can help agriculture to become more productive and resilient under the expected consequences of climate change. Estimates indicate that their value reaches 120 billion dollars when used to produce future varieties, however, despite their potential, crop wild relatives are still underrepresented in genebanks, therefore they are less available for plant breeding programs that could use them as donors of beneficial traits. In order to determine how well represented are the closest wild relatives of 80 crop gene pools relevant for global food security and income generation in germplasm banks, and to identify geographical areas where these taxa occur in the wild, we applied the gap analysis methodology (Ramírez-Villegas et al., 2010) on 1187 crop wild relatives taxa, representing 21 unique families and 58 distinct genera.
A large proportion of the taxa analyzed (more than 70%) were ranked as high priorities for urgent collection and subsequent *ex situ* conservation. Crops as cacao (*Theobroma cacao*), faba bean (*Vicia faba*), bananas (*Musa* spp.) and bambara groundnut (*Vigna subterranea*) have a narrow count of close wild relatives in their gene pool which were also identified as inadequately conserved ex situ, hence the preservation of such genetic resources should be a priority. In contrast, crops as tomato (*Solanum lycopersicum*), and wheat (*Triticum aestivum*) where the use and research of its wild relatives have been more intense, emerged as better represented in seedbanks. Similarly, distribution models for each assessed taxa have been used to identify hotspots of CWR richness and areas where collections efforts should be directed. The results obtained are used in the project: "Adapting crops to climate change: collecting, preparing and protecting the crop wild relatives of crops" and made available through the projects' website.

Ramirez-Villegas J., C. Khoury, A. Jarvis, D.G. Debouck, and L. Guarino. 2010. A gap analysis methodology for collecting crop genepools: a case study with *Phaseolus* beans. PLoS ONE 5(10):e1349.

Keywords: CWR conservation, Climate change, Food security

The GRIN-Taxonomy crop wild relative inventory

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Abstract

In order to provide an informational tool for assessing and prioritizing germplasm needs for ex situ conservation in the U.S. National Plant Germplasm System (NPGS), the USDA Agricultural Research Service in 2008 initiated a project to identify wild relatives (CWR) of major and minor crops. Each crop's CWR were evaluated from a thorough review of the taxonomic and crop science literature, integrating taxonomic, phylogenetic, ploidy, reproductive biology, artificial and natural hybridization, and other data to determine their potential for hybridization with that crop. The degree of genetic relatedness of the CWR to a crop was thereby partitioned into three categories approximating the primary, secondary, and tertiary gene pools. A fourth category, for CWR used as rootstocks or in the breeding of rootstocks for grafting scions of a crop, was also recorded. We have now completed initial work on over 120 crops in 70 genera, documented the basis for our decisions, solicited crop specialist reviews, integrated the data into GRIN Taxonomy, and developed a public interface to query the resulting information in relation to other GRIN taxonomic and distributional data. Integration and consolidation of these data with those of the Harlan and de Wet Crop Wild Relative Inventory (http://www.cwrdiversity.org/checklist/) is planned. Both external reviews of existing CWR classification data and contributions of data on other crops are welcomed.

Keywords: gene pools, taxonomy, CWR classification

2.2 International LR Conservation

Landrace conservation, farmers and crop evolution

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Abstract

In contrast to wild species, for crops in situ conservation has been considered less crucial and reliable than *ex situ* conservation. Notwithstanding, on-farm conservation of landraces is widely distributed in many agricultural systems, in particular in crops' centers of origin. Derived from the *ex situ* conservation model, too much importance is given to preserve genetic resources for breeders as a main objective for *in situ* conservation of crops. However, this proposition is unpersuasive because even germplasm banks have had limited use, present gene transfer barriers have been broken by genetic engineering, and including on-farm landraces in breeding programs has high costs. The case of maize landraces in Mexico will be used to illustrate the need to broaden our objectives and justifications for supporting *in situ* conservation of crops. About three-fourths of maize seed planted in Mexico comes from farmers' own crops and more than two thirds of these seeds are landraces that have evolved without technical or institutional intervention. Success of formal cultivars of maize in Mexico has been limited to lowland environments with good rainfed conditions or irrigation and traditional landraces are dominant in the highlands and mid-elevations. Several explanations have been investigated for the presence of landraces in Mexico, ranging from better local adaptation to marginal environments to special characteristics and missing markets. Rather than expecting that institutional breeding is indisputable, there are inherent limits to establish formal cultivars for all conditions and purposes due to the complexity of natural and social environments. *In situ* conservation is done by farmers for their own needs and is the outcome of their successful participation in crop improvement. Benign neglect of farmers' landraces is no way forward, breeders should undertake the challenge to embrace and imagine future crop evolution as a complex interplay of actors where farmers continue as effective players.

Keywords: Landrace conservation, Crop evolution, Maize, Mexico

Towards a European on-farm conservation strategy for landraces

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Abstract

The PGR Secure project revealed that different options for on-farm conservation and different materials suitable for on-farm conservation exist at National and European level. In the Southern and extreme Northern parts of Europe on-farm conservation is based on extant landraces due to the value of the product that is obtained from them, local culture and/or link with educational activities. In other parts of Europe, in general, extant landraces are often extinct or, whether still existing, the geographic/cultural link with them is not as strict. There, on-farm conservation activities are based on introduced (from different areas) or reintroduced (from gene banks) landraces or on variable populations from wide crossing and are mostly purposely developed to satisfy the demand of a more environmentally friendly agriculture.

While for Southern and extreme Northern parts of Europe there is the need to widen the demand for products obtained from landraces, in other parts of Europe there is the need to base introduction, reintroduction of landraces and the development of variable materials suitable to the on-farm conservation purposes on materials suitable to the local conditions. Since inventories of on-farm maintained materials are incomplete as well as incomplete/inconsistent/mis-recorded data about materials suitable for on-farm conservation exist in National and European genebank databases, as a first step to achieve an effective and efficient on-farm conservation complete, fully documented and congruent inventories at European level are needed.

An efficient and effective on-farm conservation through use can rely on the development from landraces and 'diverse' varieties of typical local products, of new (e.g. environmentally friendly) farming systems, of local food supply systems, including community and home gardens, of companies purposely dedicated produce and sell seed/propagation material and of participatory plant breeding programs.

Keywords: Landraces, On-farm, Conservation strategies

The use of spontaneous sexually-produced new landraces of a vegetatively propagated crop of the Andes (*Oxalis tuberosa* Mol.) to enhance in situ conservation

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Abstract

Unconscious incorporation of sexually-produced new genotypes into the cultivated germplasm of oca (*Oxalis tuberosa* Mol.), a vegetatively-propagated crop of the Andes, has been demonstrated as highly probable. Farmers would voluntarily seek spontaneous plants in previously cultivated fields and use their tubers as seeds, thinking of these plants as vegetative propagules of the landraces they possess. But an active sexual reproduction is also the source of those spontaneous plants and new genotypes can therefore be incorporated into cultivated landraces. Such incorporations would enhance the dynamics of the conservation of genetic resources of oca. Interviews have been realized with 38 farmers of 4 communities of the Candelaria district (Colomi, Bolivia) in order to assess the extent of such practices and the farmers' knowledge on the sexual reproduction of oca. Half of the interviewed farmers use tubers from spontaneous plants as seeds. Frequency of use varies between farmers. Utilization as seeds of tubers of spontaneous plants is usually due to seed shortage. The new seeds are assigned to existing landraces based on the color criteria, which is poorly selective. Only 7 of the 38 interviewed farmers are aware of the sexual reproduction of oca, having observed pods, seeds or plantlets. Only one of them is aware of the potential of those seeds for propagation or breeding purposes. During a group restitution phase organized with each community, farmers expressed their interests in obtaining new landraces by means of sexual reproduction, as they already sporadically use this technique to obtain new potato landraces. This could be encouraged by local institutions in order to enhance the creation and conservation of genetic diversity for this species.

Keywords: Reproduction system, *Oxalis tuberosa*, Traditional crop management, Genetic diversity

The Chirapaq Ñan Initiative: establishment of a long-term on-farm monitoring network for potato landrace diversity

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Abstract

A major shortcoming of on-farm conservation initiatives in centers of crop origin and diversity concerns the lack of functional long-term monitoring systems. Without such systems in place, no solid evidence can be attached to claims about genetic erosion, landrace loss or enrichment. CIP and partners in Latin America have recently started a regional network to facilitate in-depth baseline studies in selected hotspots to allow for future systematic comparisons of the temporal-spatial dynamics and conservation status of potato landraces. Initially, an applied methodology to determine contemporary landrace hotspots was developed, taking into account: (i) expert opinion, (ii) genebank passport data, (iii) geographical distance, (iv) inclusion of endemic species, (v) ethnicity, (vi) presence of conservation threats, (vii) presence of solid partnerships, and (viii) community interest. Baseline documentation of contemporary potato diversity is based on standardized methods and indicators that are replicable, comparable and robust at different system levels, and include: (i) genetic diversity, (ii) landrace diversity, (iii) geospatial diversity, (iv) collective knowledge. In 2012 baseline documentation started in two hotpots in Peru and in 2013 two additional hotspots, one in Chile and one in Bolivia, were added. The objective is to expand the network to at least eight complementary benchmark sites by 2016, including hotspots in Argentina, Ecuador and Colombia. Incentive systems and mechanism for recognition of custodian farmers are tested at the pilot level, including linkage of conservation to (formal) education, practical benefit sharing mechanisms and rapid open access sharing of research data and results. A major challenge for the initiative concerns future sustainability which is basically a function local participation at the hotspot level, national support and long-term commitment, and financial means.

Keywords: In-situ conservation, Andes, Chiloe Islands

2.3 National CWR Conservation

National Strategies for the Conservation of CWR

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Abstract

The design and implementation of national strategies are essential for the effective conservation of crop wild relatives (CWR). National strategies are usually developed to meet the conservation objectives posed for the CWR in each country according to its national interests. However, they should also take into account the goals and priorities emanated from wider regional and global international perspectives. The selection of the CWR species that should be considered for conservation assessment and implementation of management actions is the first and most critical step in the design of the strategy. Although this step has been carried out in various ways in different countries, in most cases, the main criteria used in the prioritization process are the socio-economical relevance of the crop, use potential of the CWR in crop improvement programmes, and Red List status. National strategies must first assess the conservation status of prioritized CWR both from an in situ and an *ex situ* perspective. Passport data associated with accessions stored in genebanks, along with chorological data and protected area data, provide the basic information on the current conservation status of each prioritized CWR. Because the aim of the strategy is not to simply conserve the targeted species but to allow their genetic diversity to evolve under the pressure of biotic and abiotic factors, conservation actions should be designed to protect a genetically representative sample of existing natural populations both in situ and ex situ. As the number of natural populations of the different prioritized CWR selected for active protection is likely to be large, national strategies should primarily try to identify 'hotspots' of natural populations of targeted CWR species for the establishment of multi-species CWR genetic reserves and seed collecting for *ex situ* conservation. Some examples of the development of National Strategies and an overview of progress in Europe will be provided.

Keywords: national CWR conservation, design and implementation of national strategies, conservation status of CWR, networks of genetic reserves, *in situ* conservation, *ex situ* conservation, management actions

Developing methodologies for the genetic conservation of UK crop wild relatives

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Abstract

Contemporary crops can be limited in terms of genetic diversity having passed through the genetic bottleneck of domestication and having been bred for uniformity and where possible, grown in monocultures. They can be seen as limited in their ability to adapt to diseases, pests and the often detrimental impacts of climate change, and in their ability to meet the ever-increasing production demands of the human population. Crop wild relatives (CWR), a provisioning ecosystem service, offer a largely untapped pool of genetic diversity holding the potential to improve crop varieties and their resilience through plant breeding. Little systematic or active conservation exists for these resources within the United Kingdom, despite their value being increasingly acknowledged in global, European and national policy documents.

Addressing similar issues, many countries have developed national CWR inventories and conservation strategies. Within the UK inventories of priority CWR have now been developed for England, Wales and Scotland separately and for the whole UK, with input from each administration's conservation agency. Based on the priority CWR identified, both *in situ* and *ex situ* gap analyses have been carried out to determine where to target conservation efforts. In addition, a genetic diversity case study of eight CWR has been carried out on the Lizard peninsula in the south-west of the UK. Using AFLP molecular markers, genetic diversity within and among CWR populations on the Lizard has been compared to genetic diversity of the same CWR elsewhere across the south-west of the UK. The study's aim was to establish how unique the Lizard populations are and the relative importance of designating it as the first UK genetic reserve with active CWR genetic conservation.

These approaches take the first steps towards ensuring active and systematic genetic conservation of CWR in the UK, contributing to European and global efforts in improving future food security.

Keywords: Crop wild relative, Conservation strategy, Plant conservation, Food security, Genetic Diversity, PGRFA Policy

Optimized site selection for the in situ conservation of forage and fodder CWRs: a combination of community and genetic level perspectives

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Abstract

Site selection for the in situ conservation of crop wild relatives can lead to the independent selection of sites for each of the prioritized CWR species. As this approach is not resource efficient there are methodologies that allow looking for 'hotspots' of CWR diversity – i.e., sites with high CWR species richness - where multi-species genetic reserves could be established. Forage and fodder CWRs have a tendency to grow together forming natural communities. The use of phytosociological associations as a unit for study and target for conservation allows to focus simultaneously on various CWR species. Traditionally, site selection for in situ conservation of CWR has been limited to selecting sites where a maximum of CWR species can be conserved using a minimum number of sites. However, the challenge of CWR conservation is to conserve not species but the genetic diversity of such species. Thus, the use of Ecogeographical Land Characterization (ELC) maps can help identify contrasting environmental conditions that are likely to be associated to genetic diversity derived from diverging selection pressures. We present a case study in which phytosociological associations and an ELC map were used to design an in situ conservation strategy for forage and fodder CWR species in Spain. Thirteen phytosociological associations that contained 33 prioritized species of forage and fodder CWR were identified and their chorological records were registered. Overlapping an ELC map for Spain over the geographic distribution of the phytosociological associations, each combination of phytosociological association-ecogeographic unit was used as a target conservation unit. A complementarity analysis was performed to rank the sites where genetic reserves could be established. Thirty-three priority sites were selected for protection and implementation of conservation actions. The conservation of these sites would provide protection to all 33 prioritized CWR species and 68% of the phytosociological association-ecogeographic unit combinations.

Keywords: Site selection for CWR, Phytosociological association, Ecogeographical Land Characterization (ELC) maps

Crop wild relatives, a conservation priority for Jordan

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Abstract

Jordan is located at the south western end of the Fertile Crescent. This region is well established as the cradle of agriculture origin, where two Vavilov centres of crop origin abut (Asia Minor and Mediterranean) and globally the region with the highest concentration of crop wild relatives (CWR) per unit area. An action plan for plant conservation in Jordan is thus needed and has been produced involving relevant Jordanian stakeholders. A point scoring procedure using eight different criteria was applied to the recent checklist of Jordanian Flora. One hundred species were identified as priorities for conservation, all of them CWR of global importance, such as *Triticum dicoccoides*, *Vicia galilaea*, *V. ervilia* and *Pisum sativum*. Gaps in *ex situ* and *in situ* conservation were identified at species and ecogeographic levels. Potential impact of climate change on species distribution was used for prioritizing species for conservation and as a criterion for selecting populations for *in situ* and *ex situ* conservation. A list of priority species for *ex situ* and in situ conservation was obtained and a network of priority populations for ex situ conservation and areas for establishing active in situ conservation was recommended. About 30% of the top 100 priority taxa are not conserved *ex situ*. Gap analysis with the predicted species distribution richness data shows the highest priority locations for collecting is the district of Al Balqa'. There is no active *in situ* conservation of CWR in Jordan but complementarity analysis identified 8 existing protected areas where 56 out of the top 100 priority taxa should be actively conserved. The remaining 44 priority species do not occur within any existing protected areas and new protected areas or informal in situ sites are proposed.

Keywords: *ex situ*, *in situ*, gap analysis, national strategies

Development of the national crop wild relative *in situ* conservation strategy for Lithuania

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Abstract

Lithuanian crop wild relative checklist, containing 1,670 taxa, was extracted from the CWR catalogue for Europe and Mediterranean (Kell et al., 2005) and used as the basis for prioritisation of CWR within Lithuania. The checklist was harmonized with the Vascular Plants of Lithuania (Gudžinskas, 1999), Dictionary of Plant Names (Jankevičienė, 1998), Flora of the Baltic Countries (1993–2003) and other sources. The following criteria were employed for CWR prioritisation: native status, socio-economic value, conservation policies applied, use by breeders and by growers, known cultivars. Three levels of priority could be identified based on socio-economic value of CWR. The 1st priority will mostly include food and forage species, the 2nd – medicinal and aromatic plants, and the 3rd – ornamentals and other uses. This prioritisation reflects the current situation and is subject to changes depending on agriculture policies, economic and demographic situations as well as globalisation. Multi-species approach will be the most common for the establishment of genetic reserves with the occasional mono-species reserves. The most appropriate framework for the genetic reserves is the existing network of protected areas, particularly – the state parks (total 35) and biosphere monitoring areas (total 28). All these fall under the category of integrated PA, where management activities are differentiated by functional zones and supervised by park administrations. In implementation of in situ conservation action plans, the state forest enterprises will play an important role, as they have available all capacities needed for practical reserve management. They also could provide in situ conservation in unprotected areas. One of the biggest gaps in in situ conservation is private lands, where reserve establishment is not foreseen by the current legislation. But the issue will be tackled with the upcoming amendment of the Law on Plant National Genetic Resources by setting up contracts between the state institutes and private land owners.

Keywords: crop wild relatives (CWR), national CWR in situ conservation strategy, CWR checklist, CWR prioritization, Lithuania, genetic reserve

Priorities and strategies for conservation of crop wild relatives at Indian National Genebank

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Abstract

Today the crop wild relatives of crop plants (CWRs) are becoming an increasingly important resource for improving agricultural production and for maintaining sustainable agro-ecosystems. This large natural gene pool is now under threat because of many reasons like habitat loss through the destruction and degradation of natural environment, deforestation, over grazing resulting desertification, and growing industrialization of agriculture leading to the depletion of CWRs within the traditional agro-ecosystems, thus their conservation is imperative.

Most of the world's genebank collections of the crop wild relatives are incomplete and the gaps in these collections represent limitations on the options available to researchers and breeders to introduce new diversity into their crop programs. Gap analysis is an important tool to assess the genetic as well as geographic diversity of the crop and its wild relatives, providing a more defined line of action with respect to collection and conservation strategies.

The gap analysis for collected and conserved CWRs in National Genebank (NGB) revealed that out of a total of 218 CWRs reported from India, only 94 species are conserved in NGB. During the analysis, areas were identified for future collection to enrich the genebank with CWRs which are either missing in the collections from diversity rich regions or are under-represented in the genebank. Thus, priorities and strategies for collection followed by their conservation will be defined based on the economic value of cultivated species, distribution of wild species and its potential use in crop improvement programme for enhancing the food and nutritional security. In this paper, we will be discussing the CWRs of high priority for conservation in order to fill the gaps in genebank collections at NGB.

Keywords: conservation priorities, developing strategies, wild species of cultivated crops

2.4 National LR Conservation

Landraces, Livelihood, and Community Biodiversity Management

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Abstract

The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture (PGRFA) recognizes community biodiversity management (CBM) as methodology to enhance the capacity of local communities to make their own decisions on conservation, and the use of biodiversity. It does this by appreciating innovations which are based on local knowledge, resources, and assets; recognizes farmers and local institutions, as legitimate managers of biodiversity; conditions and incentives local communities, to capitalize on assets that create diversifying biodiversity-based livelihood options; and leads to better governance of community-based approaches contributing to policy. However, the report also recognizes that many successful participatory practices have not yet been mainstreamed by national PGRFA programmes. This is due to CBM practices often being led by non-governmental organizations, which operate independently from national research institutions. Drawing upon in-depth experiences from Brazil, Ethiopia, India, France, Nepal, and reference cases from several other countries, this paper provides a global understanding of CBM. It highlights the participatory practices of CBM where farming communities, development organisations, and National PGRFA programmes can work together. Through strategizing with one another, CBM can contribute to the empowerment of farmers by enhancing their livelihoods through managing agrobiodiversity in a collective and more sustainable manner.

Keywords: Landraces, Livelihood, Community Management

Landrace Inventories and National *in situ* Conservation Strategy in Finland

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Abstract

In Finland agriculture and horticulture are today mainly based on the use of bred cultivars. However landraces and local strains are cultivated to some extent, especially landraces of cereals, forages, fruits, berries and some vegetables. There are no comprehensive statistics on landrace cultivation in Finland. Since 2000 the Decree for the conservation varieties, their seed production, approval and marketing has been applied to cereals, forage, pulses and some other arable land crops. There are 17 registered conservation varieties. Furthermore, 5 local strains of forages and one landrace potato are accepted to the National List of Plant Varieties.

The need for landrace in situ inventories has been stressed by international policies and strategies for a sustainable use of Plant Genetic Resources for Food and Agriculture, beside by many papers specifically referring to Europe (e.g. Veteläinen et al., 2009). In Finland the first collecting missions were organized by professional plant breeders who collected and studied an extensive amount of landrace samples for breeding material during the early 1900s. The Nordic Center for Plant Genetic Resources (NordGen) conducted its inaugural landrace collecting missions of cereals and forages during the late 1970s and early 1980s in Finland. Later in the mid 1990s and 2000s cereal landrace inventories were conducted by the Seed Testing Department and MTT Agrifood Research Finland (Heinonen & Veteläinen 2009). During 2011-2014 within the EC FPVII funded PGR Secure project and nationally funded the Native Apple –project, MTT Agrifood Research Finland has set up the nationwide *in situ* inventories on local apples, pears and potato onions as well as updates on landrace cereals, forages and some other arable land crops. The description of landrace inventory process applied will be provided. The general results of landrace inventories will be presented as well as the *in situ* conservation programme for conservation varieties. The National Landrace *in situ* Conservation Strategy for Finland (Heinonen 2014) will be also discussed.

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Assessment of Italian LR density and species richness: useful criteria for developing in situ conservation strategies

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Abstract

The landraces (LRs) are a key component of the agrobiodiversity, increasingly most threatened, which deserve immediate conservation actions. In Italy the risk related to their genetic erosion, and to the loss of agricultural biodiversity in general, was fortunately perceived earlier than in other countries and various studies to assess LR census have been conducted at local level. Within the PGR Secure project, the working group of the Department of Agricultural, Nutritional and Environmental Sciences has compiled the First Italian Inventory of *In Situ* Maintained LRs. On the basis of this inventory a Landrace Density Index (LDI), which provides information on the LR density, and a Shannon Index H', that gives information on species richness, were calculated for the entire Italian territory using grids of 20x20 km2. The results show that highest LRs concentrations are in the regions of Umbria (16%), Calabria (12%), Sicily (11%), Basilicata (9%), Campania (9%), Latium (8%) and Molise (7%). By analyzing the species richness, it was found that the most important species in terms of conservation and biological value are *Prunus avium* L. (18%), *Malus domestica* Borkh. (17%), *Pyrus communis* L. (15%), *Vitis vinifera* L. (9%) and *Phaseolus vulgaris* L. (7%). LR density index and species richness can be useful instruments to identify Most Appropriate Areas (MAPAs) where to set or enhance political and economic actions and conservation strategies in favour of LRs and agrobiodiversity safeguard. These actions are also among the objectives of the CAP 2014-2020 that is strongly oriented to diversify crops, conserve and restore diverse agricultural systems and provides large funding for these activities.

Keywords: Landrace Density Index, Landrace Inventory, On-farm conservation

Using landraces in agriculture, food and cooking: the experience around a big city in Southern Europe

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Abstract
Many networks strategies and programmes have been established since the necessity of preserve plant biodiversity raised. The Madrid Community -Central Spain- created in 1995 a germplasm bank which currently contains 203 accessions, 91% of them horticultural landraces collected within 60 km around the big town of Madrid. The bank complies with a growing number of seed requests: for instance, more than 200 users have demanded 440 accessions in 2013. 66.4% of them, in the last decade, were farmers or hobby cultivators and 22.9% were public institutions. But there were other typology of users such as cooperatives, foundations, associations and, interestingly, chefs. The main destination of the plant material was its growing at home-garden for domestic consumption (62.3%), followed by research task (11.8%). Other confirmed uses were production in farm, education, cultivation at restaurants and last breeding. Therefore, the main destination of conserved landraces is own consumption and its use in gastronomy. Only 23.3% of the delivered germplasms were grown under organic agriculture system. Preservation of plant genetic resources is based on the main idea of keeping them for future generations, to be able to breed crop varieties and face new challenges. This proposal is still valid. But, in addition, our experience shows that today consumers, especially those living in European cities, are strongly demanding food quality, flavours and textures from those big collections of old varieties. These landraces are always linked with the tradition of farmers and the gustative memory of folks. They are characterized by a highly remarkable morphological and sensorial diversity. These are some of its strengths in present and future, which may turn these landraces into the basis of an important economic and sustainable activity.

Keywords: horticultural landraces, germplasm bank users, domestic consumption

Hungarian strategies for the conservation of crop wild relative (CWR) and landrace (LR) diversity

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Abstract

The Hungarian National Strategy for the Conservation of Plant Genetic Resources for Food and Agriculture 2014 – 2020 was endorsed by the Hungarian Minister of Rural Development in 2013. The document was prepared by the Ministry of Rural Development, the National Genebank Council and by different experts from relevant institutions. The vision and targets have been developed in line with the Convention on Biological Diversity (CBD) and the International Treaty on Plant Genetic Resources for Food and Agriculture. Target 13 of the CBD Strategic Plan 2011-2020 invites parties to maintain the genetic diversity of cultivated plants and of wild relatives, including other socio-economically as well as culturally valuable species and to develop and implement strategies for minimizing genetic erosion and safeguarding their genetic diversity by 2020. The Hungarian Strategy sets a vision for 2020 backed up by 14 targets, which provide a comprehensive background for the conservation of plant genetic resources for food and agriculture in the next 7 years in Hungary. Targets refer to enhanced institutional and financial background; the better implementation of international treaties, conventions, strategies and programs; the adoption of a national regulation on LRs in line with the relevant existing EU directives; the collection of LRs and CWRs and associated traditional knowledge, support of research programs and plant breeding, including participatory plant breeding programs based on CWRs and LRs. The Research Centre for Agrobiodiversity (RCAT, Tápiószele, Hungary) is the largest seed bank in Hungary. The institute is specialized for ex situ conservation of crops and vegetables and has collected their LRs and CWRs in the last 50 years systematically. In addition, the 5-year-long Pannon Seed Bank Life+ Project (“The establishment of the Pannon Seed Bank for the long-term ex situ conservation of Hungarian vascular wild plants”) started in 2010. The establishment of a joint seed bank for the agricultural and wild flora is a good and demonstrative example in Europe in line with the objectives of the CBD, 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 conserved at one place. Thus the conservation of these public assets is solved in a cost-effective way by using professional experience, existing knowledge and infrastructure and avoiding unnecessary parallel work. This valuable collection can be complemented by 2020 with further LRs and CWRs and the existing collection can be used for analysis, research programs as well as by plant breeders and farmers. The implementation of the Hungarian National Strategy for the Conservation of Plant Genetic Resources for Food and Agriculture 2014–2020 started by the Collecting

Program 2013-2014 of RCAT. 4 collection missions were organized in 2013 as a part of the two-year-program for collecting plant genetic resources in Hungary and its neighboring countries. During these trips the collecting team visited more than 30 villages and revealed a range of diversity of locally grown traditional varieties. These varieties and landraces are cultivated by elderly home gardeners and there is an urgent need to conserve their varieties in gene banks. Traditional knowledge still existing on landrace maintenance may also form a basis for on-farm conservation activities by local NGOs. The collected 250 seed samples (mostly LRs) are stored in RCAT and will be regenerated and analysed in 2014.

Keywords: Hungary, national strategy, crop wild relative, landrace, diversity, collecting

Crop wild relatives and landraces of Jordan: their integration to food security programs

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Abstract

Jordan has a diverse range of ecosystems which reflect high plant diversity. It is located in the Fertile Crescent region and it's the most likely centre of domestication of crops including cereals (wheat, barley, oat), food legumes (lentils, chickpeas) and forage legumes (*Vicia* spp., *Medicago* spp.). An updated checklist of about 2565 species has been produced by the Royal Botanic Garden and the Royal Botanic Gardens, Kew. These species occur in 13 vegetation types and include important and diverse crop wild relatives (CWR) that can potentially be integrated in food security programs. In addition, landraces of important crops have been maintained by farming communities due to the use of traditional farming methods and traditional knowledge. More than seven local varieties of wheat have been improved for drought tolerance and salinity by local farmers. *Ex situ* and *in situ* conservation programs have been carried out in Jordan, those including survey, documentation, conservation and use of CWR and LR diversity for food and agriculture. Conservation programs encourage the sustainable utilization of plant genetic resources for food and agriculture through integrating farmers and rural communities in management activities of these resources. Global collaboration is important to meet world food security through sustainable agricultural development. Jordan recognized that self-sufficiency of a country regarding plant genetic resources is unfeasible and depends on the genetic diversity in crops from other countries and regions. Jordan signed and ratified the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) and the multilateral system of access and benefit sharing for PGRFA of most important crops. The accessions of PGRFA conserved in Jordan genebanks are available under a standard material transfer agreement (SMTA) and expect to integrate food security programs.

keywords: CWR, ITPGRFA, *Ex situ* conservation, *In situ* conservation, SMTA, Multilateral system, Access benefit sharing, Wheat landraces, Genetic diversity

Regeneration and conservation of chickpea genetic resources of Georgia

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Abstract

In Georgia the chickpea *(Cicer arietinum L.)* is a traditional grain legume crop influencing the food supply chain especially in warmer and drier regions. This crop was a dominant legume species in Georgia agriculture during 30 centuries, but not now, where other grain legumes such as bean and soybean predominate. Nevertheless, demand for chickpea is growing here at the present time also due to the interesting nutritive value of seeds and recently changing climate creating favorable conditions for chickpea cultivation.

The chickpea genetic resources collection maintained in the Genebank of the Agrarian University of (AUG) as this institution is responsible mandatory for legumes in our country. A set of 46 chickpea accessions maintained in the collection (ex-situ) of the Genebank in 2011-2012 was regenerated (as winter and spring crop) using advance growing technology of seed pilling in accordance with Special Plan of regeneration, enhancement and protection. The level of genetic diversity and the effectively of new germplasm acquisition for the collection enrichment were evaluated. All of them collected last time needed regeneration for future breeding work, as well as for sending to genebanks of our collaborators and breeders in abroad. At the same time, by our group of scientists selected and officially released 3 new varieties: Zedazeni, Aragvi and Eliksiri.

In 2012 regenerated material was obtained from all the accessions special pilot plots of chickpea. Recently acquired new germplasm contributed all of new entire collection, i.e. almost 100% of collected diversity originated from the recently acquired accessions. Remarkable is also, that all accession carries a unique germination, not present in the remaining collection. Field and lab analysis revealed the importance of collecting missions for the enrichment of collections.

The overall of objective the food legume germplasm regeneration for future improvement program of Georgia (chickpea, lentil, bean, soybeans) is to increase the productivity and sustainability of the farming system in partnership with AUG and Georgian farmers. This objective is pursued through improving the methodologies for food legume breeding, training of AUG staff in renewal of germplasm, improvement of production practices and genetic stocks with resistance to various biotic and abiotic stresses, sharing of the improved germplasm with AUG and its evaluation under targeted environments for identification of improved lines for future use. During the same year regeneration process under report, all of 46 sort-populations and varieties of chickpea, were made to combine resistance to various biotic and abiotic stresses in varying agronomic backgrounds. The improved genetic materials were shared in the form of 3 different sets of trials for 3 different nurseries. Decentralization of breeding activities with ICARDA in South Caucasus and Central Asia resulted in identification of promising lines in chickpea. In accordance with IPGRI descriptors, safety cleaned and packaged new germplasm departed to Genebanks of AUG (Tbilisi, Georgia), ICARDA (Aleppo, Syria) and Svalbard Global Seed Vault (Spitsbergen, Norway) for the benefit of present and future generations.

Keywords: national, Georgian, resources, chickpea

Theme 3: Facilitating CWR and LR use

Theme 3 focuses on the utilization of CWR and LR on farm, *in situ* and in breeding programmes. It also examines the incentive mechanisms that motivate local communities to provide conservation services. Having an enabling policy environment is essential for facilitating conservation and use of CWR and LR. The theme also identify the strengths, weaknesses, opportunities and threats for the germplasm user community in increased use of CWR and LR diversity through dialogue with the stakeholders concerned.

Abstracts under Theme 2 fall into four sub-themes:

3.1 Community-based conservation/use
3.2 Improving breeders' access to PGRFA
3.3 PGR conservation/use policy

3.1 Community-based conservation/use

Rapidly increasing on-farm biodiversity through Evolutionary Plant Breeding: the Iranian experience

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Abstract
Rapidly increasing on-farm biodiversity is a matter of urgency in an era of climate change, yet farmers often have limited access to genetic resources. Evolutionary Plant Breeding (EPB) is a dynamic and inexpensive strategy that rapidly enhances the access of farmers to biodiversity and adaptation of crops to climate change. The method consists of deploying populations with large genetic variability in the hands of farmers and letting them gradually evolve and adapt to both climate and management changes. In 2008, five farmers in Kermanshah and Semnan provinces were provided with several kilograms of a mixture of 1,600 F2s of barley. This mixture included a wide range of germplasm: the wild progenitor, *Hordeum spontaneum*, landraces from several countries and modern breeding material. Based on the success of the barley population mixtures of populations of bread wheat were also developed. The EPB mixtures have been shown to produce higher yields and perform better in adverse conditions than their local or improved counterparts. There is evidence that the EPB populations are more resistant to weeds, diseases and pests. One of the most unexpected outcomes of the evolutionary population trials was that some farmers decided to sow all the seed they had harvested, multiplying and cultivating the seed as their main crop. The populations now cover several hundred hectares and are planted in 17 provinces by about 150 farmers. Future priorities include selecting adapted varieties from the populations for use in Participatory Plant Breeding programmes, developing products from the evolutionary populations of wheat (bread), assessing the potential impacts of seed laws and policies on farmers' ability to use evolutionary populations, and exploring options for monitoring the populations.

Keywords: On-farm, Plant breeding, Iran

Payments for Agrobiodiversity Conservation Services: Towards an instrument for environmentally effective, cost-efficient and socially equitable agrobiodiversity conservation

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Abstract

Following the development of a conceptual framework and the identification of variety-level conservation priorities for an Andean grain in Peru and Bolivia, competitive tenders (reverse auctions) were implemented across a number of communities in each country in order to determine willingness to provide conservation services. Selection criteria were developed in order to facilitate the identification of preferred farmers/communities to undertake such services based on efficiency, effectiveness and equity considerations. Findings to date indicate that farmers/communities were indeed willing to undertake a conservation services contract for threatened priority crop varieties and that participation costs vary widely between communities, thereby creating opportunities to minimize intervention costs by selecting least-cost providers. In-kind, community-level rewards were shown to provide sufficient incentives and suggest that a number of them could be provided through existing government agricultural and educational development programmes. Furthermore, targeting payments at a group-level are shown to be a potentially important means to enhance cooperation and build social capital, which is of crucial importance when conservation outcomes depend on collective action. The enthusiasm of the project participants to maintain the threatened crop genetic resources in future years, regardless of any further intervention and their interest in exploring market development opportunities for these varieties, suggests that the potential for PACS to support national biodiversity policy implementation and make a significant contribution to agrobiodiversity conservation and use goals, as well as to improve poor farmer livelihoods, once it is up-scaled, continues to appear promising. A number of future research and development issues are also identified.

Keywords: Payments for Agrobiodiversity Conservation Services, Payments for Ecosystem Services (PES), Cost-effectiveness, Social equity, Collective action

Conservation and utilization of genetic resources and heritage as a concept of rural sustainable economic development

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Abstract

Thanks to the unique diversity, the Balkan Peninsula could be considered as secondary center of genetic diversity for several fruit species, such as *Malus* x *domestica, Pyrus communis, Sorbus domestica, Prunus cerasifera, P. persica, P. armeniaca,P. cerasus, Prunus avium, P. fruticosa, P. amygdalus, P. nana, Juglans regia, Corilus colurna, Castanea sativa, Fragaria vesca, Cornus mas, Rosa* sp., *Sambucus nigra and Morus alba*. Conservation, utilization and sustainable use of natural resources in West Balkan countries could play central role in sustainable rural development and economic growth through wise use of natural resources. But, it has never been a field for dismantling the divide between indigenous and scientific knowledge. The main aim of the research was to connect in situ/on farm conservation and evaluation of minor and woody fruit species with ethno botanical heritage of nations and ethnic minorities, including possibility for enormous germplasm within local varieties in major fruit species to be included. The main outcome of the research is improved in situ/on-farm management and evaluation of genetic resources by the farming sector and derived products with enhanced health benefits for consumer as a foundation for economic benefits for farmers. Diversification of such products comes from the traditional ways of fruit processing in ethno botanical heritage of living nations and ethnic minorities. Socio-economic dimension have its relevance in farming innovations, diverse product outcomes as a foundation for regional networking between farms, within and between regions, leading towards a recognizable food chain. It has all attributes of organic agricultural practice including development of specialized farming systems. It is a precious possibility to improve the quality of life and economic well-being of people living in relatively isolated and sparsely populated areas.

Keywords: Genetic resources, Rural development, Woody fruit species, Ethno botanical heritage

3.2 Improving breeders' access to PGRFA

Improving breeders' access to PGRFA

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Abstract

Plant breeding plays an important role for global food security, by developing varieties with a higher yield, resistant against pests and diseases, better adapted to local conditions and more resilient to deal with climate changes. To be able to meet the demands for such new varieties, it is clear that breeders need access to the biodiversity that the world has to offer. However accessing genetic resources has only become more difficult these last years. In 1994 the Convention of Biological Diversity introduced the concept of sovereign rights of countries over their genetic resources. Consequently, permission is required before collecting genetic resources, whereby breeders are faced with many different, often unfeasible benefit-sharing conditions, if known at all. The entry into force of the International Treaty on Plant Genetic Resources in 2004 provided some relief, by introducing a multilateral system, as part of which access can be acquired upon the conditions of the Standard Material Transfer Agreement. But because the ITPGRFA only applies to 64 crops, not including most vegetable crops, breeders still need to negotiate the necessary permits for collecting genetic resources. These are time-consuming negotiations, facing the difficult task of finding the right person, authorized to grant permission and convincing this person to grant access upon reasonable conditions. Often, the authorities have insufficient knowledge of how plant breeding works, therefore demanding an unacceptably high form of benefit-sharing, not taking into consideration the time and money that needs to be spent by breeders to develop a new variety. And the fact that the new variety in itself is already an important form of benefit-sharing, as it is available for other breeders for further breeding, also when it is protected by a plant breeder's right under the so-called breeders' exemption. In order to improve breeders' access to PGRFA, creating a better understanding of how breeders work seems essential as well as harmonizing national ABS legislation.

Keywords: access and benefit sharing, Convention on biological diversity, International Treaty on Plant Genetic Resources for Food and Agriculture

Ways to unlock barley´s secondary gene pool for breeding with Next-Generation-Sequencing

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Abstract

Crop wild relatives (CWR) have been recognized as a source of beneficial traits to a given crop species and to overcome the erosion of genetic diversity resulting from domestication and small effective population size in elite breeding programs. The efficient utilization of crop-wild introgression lines for improving elite germplasm has largely been hampered due to the lack of suitable molecular tools for locating introgressed segments and decreasing their size during subsequent crosses. Marker development in CWR is mainly restricted by limited access to the genomic information of these species. We explored the usefulness of Next-Generation-Sequencing technology for developing and scoring molecular markers in a diploid introgression line of cultivated barley (*Hordeum vulgare* L.) containing chromatin from its wild relative *Hordeum bulbosum* L.. We used a recently developed whole exome capture assay in combination with a custom SNP genotyping assay as well as two-enzyme genotyping-by-sequencing to allocate the introgression interval and to genotype progeny segregating for the introgression. Both methods provided fast and reliable detection and mapping of the introgressed segment and enabled the identification of recombinant plants avoiding tedious and iterative steps of marker development. Furthermore, the study suggests that the same tools may be applied to high density genotyping and mapping of segregating populations of *H. bulbosum* and even more distantly related *Hordeum* species. This will ultimately pave the way for detailed comparative genomics within the genus *Hordeum*.

Keywords: *Hordeum vulgare, Hordeum bulbosum,* crop wild relatives, introgression line, genotyping-by-sequencing (GBS), exome capture, next-generation-sequencing, genotyping

Wild *Lactuca saligna* richness for lettuce breeding

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Abstract

Substantial progress in modern breeding of lettuce (*Lactuca sativa* L.) is supported by exploitation of wild related species, donors of valuable traits, e.g. resistance. Willow-leaf lettuce (*Lactuca saligna* L.), strategic species in lettuce breeding, is largely distributed over the world, but only a limited area of natural distribution is represented by accessions in world germplasm collections. Knowledge of its biodiversity is rather limited. Complex research activities were developed in the Czech Republic in cooperation with some other countries (e.g. Israel). 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. Large variation of morphological and phenological traits among samples originating from different eco-geographic conditions was recognized. New sources of resistance to economically important races of lettuce downy mildew (*Bremia lactucae*) and powdery mildew (*Golovinomyces cichoracearum*) were identified. Resistance against *B. lactucae* is considered as a nonhost resistance. Samples originating from various eco-geographical conditions (Near East *vs.* Mediterranean Basin) differ significantly in their molecular polymorphism (AFLP) and they are genetically different. There were recognized natural interspecific hybrids between *L. saligna* and some other related *Lactuca* spp. (*L. serriola*). F1 hybrids raised from the controlled hybridization of *L. saligna* with *L. sativa* were released, F1 progeny were identified by morphological traits and proved by isozymes. Recently, *L. saligna* is broadly used in commercial lettuce breeding.

Keywords: willow-leaf lettuce, *Lactuca sativa* L., geographic distribution, phenotypical variation, Bremia lactucae resistance, Golovinomyces cichoracearum, molecular polymorphism, interspecific hybridization

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A new selection tool to exploit genetic resources in durum wheat

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Abstract

A large wealth of genetic diversity is present in the diversity centers of durum wheat. However, modern breeding selection methods are mostly based on improvement of elite lines which have a narrow genetic base; this limits a lot the genetic pool which breeders can exploit for the production of new varieties ready to face the predicted climate changes or adaptation to new cultivation areas. The oncoming changing climatic conditions claim for the need of finding new adaptation traits to both abiotic and biotic stresses to be introduced in modern elite varieties. These traits are often found in landraces stored in germplasm collections. The Eurisco database reports a total of over 17,000 durum accessions, some 6,800 of which are traditional varieties and/or landraces: Besides their incontestable usefulness, their great number hampers the possibility to explore their genepool. A different approach to reduce the number of genotypes to screen for new useful traits to use in breeding programs while maintaining a good representation of the genetic background, is the constitution of a working durum wheat collection selected by mean of a single seed descent (SSD) approach. The working collection constituted by the SSD method, accounts for over approximately 300 genotypes representative of 44 countries mainly concentrated in the Mediterranean area and Horn Africa. In the present contribution we report on the constitution and the phenotypic and genotypic characterization of the working collection in order to share with the scientific community a new "genetool" for breeding and research.

Keywords: single seed descent, core collection, characterization

The use of crop wild relatives in public international breeding centres and implications for conservation

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Abstract

This study surveys all crop improvement centres under the Consultative Group for International Agricultural Research (CGIAR) to assess trends in the use of crop wild relative (CWR) germplasm, with particular attention paid to cultivars released with improved abiotic stress tolerance relevant to predicted climate change scenarios. Preliminary findings suggest that the rate of cultivars released from CGIAR crop improvement centres bred using wild lines has increased since last reported, as well as the proportion of those claiming increased resistance to drought, saline soils and temperature variation relative to other desirable traits such as pest and disease tolerance. This study updates earlier surveys, considering recent scientific advancements in the field of molecular biology that have allowed breeders to make increased use of species in secondary and tertiary gene pools (Brummer et al. 2011; Ford-Lloyd et al. 2011; Koebner and Ortiz 2013). The author explores the policy implications of increased use of CWR for species valuation and conservation investment, particularly the potential for their inclusion in market-based mechanisms for biodiversity conservation in the coming years. The growing recognition of use and potential use values of wild species will likely incite increased private investment in genetic diversity conservation as market-mechanisms are adapted to include their protection. Social and ecological concerns associated with biodiversity markets are identified as well as the opportunities they presented. Survey results are communicated with the help of the Crop Wild Relative Global Atlas interactive map (www.cwrdiversity.org).

Keywords: Use and potential use values, Conservation investment, Market-based mechanisms for biodiversity conservation, Abiotic stress tolerance

3.3 PGR conservation/use policy

Are we almost there yet? A backseat view of the 50 year voyage to develop international systems for PGRFA conservation and use

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Abstract

1965-present

For the last 50 years, members of the international community have devised interventions to support the conservation of plant genetic resources for food and agriculture. For much of that time there has been general agreement concerning many of the core components that an international PGRFA conservation system should include: virtually pooled PGRFA in ex situ collections around the world with common rules for facilitated public access; an international fund supported by developed country governments and or commercial users, based on recognition of farmers' contributions over millennia, to support capacity building in developing countries; and a complementary information system(s). The place of *in situ* conservation within the mix of components has been uncertain, and largely overlooked, until recently.

What have been controversial and dynamically changing are the 'deep rights of control' over PGRFA that countries and some stakeholders have insisted upon as pre-conditions for fully supporting the establishment of those core components. The paper will briefly review the controversies, compromises, and sea-changes over the last 50 years concerning the 'deep' legal status of PGRFA.

The paper will link the evolution of the legal status of PGRFA with the international community's ability to make progress developing/finalizing/implementing the Plant Treaty, which formalizes the 'core' components listed above. It argues that the collective political will to finally agree to international rules for pooling and sharing plant genetic resources and related information coincided with the abandonment of earlier concepts of PGRFA as public domain or heritage of mankind and recognizing instead the primacy of intellectual property rights and national sovereignty over genetic resources. It appears that countries and influential stakeholders were only willing to agree to rules for pooling (some of) their resources after their 'deeper' rights of exclusive control over these resources had been conclusively established. Subsequently, the international community has made a lot of progress, as evidenced in the adoption and coming into force of the Treaty.

However, there are still some challenges to be addressed to implement the Plant Treaty and to provide more focused support for in situ conservation.

Present and future

The second part of the paper will analyze challenges currently being experienced in the implementation of the Plant Treaty's multilateral system, in some cases linked to outstanding disagreements about the 'deep' status of PGRFA.

The 5th session of the Treaty's Governing Body launched an intergovernmental process, currently ongoing, to address this situation. The paper will describe the options being considered by the Working Group. It will provide an overview of the process, highlighting what appear to be potential areas of convergence within the working group, and some outstanding questions that the working group will consider in the lead-up to the Sixth Session of the Treaty's Governing Body.

The paper will also consider present opportunities and initiatives to promote in situ conservation as a much more robust component of the evolving international system.

Keywords: Plant Treaty, international community, PGRFA, in situ, access and benefit sharing

On the conservation and sustainable use of plant genetic resources in Europe: a stakeholder analysis

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Abstract

A wealth of plant genetic resources (PGR) is present in Europe, in gene banks, on farms and in natural and semi-natural environments. However, there are considerable constraints concerning both access and use of these valuable genetic resources. To analyse the constraints, PGR stakeholders from around twenty European countries were interviewed on the current status of conservation and use of genetic resources and about their visions for the future. The major stakeholders were identified as plant breeding companies, public research, gene banks, agro-NGOs and governments. Furthermore, a workshop was held on this issue, bringing together stakeholders from the European countries.

The result from these activities is a report describing the strengths, weaknesses, opportunities and threats of the European PGR conservation and use sector. Also a vision on how this sector should ideally function in the future is presented, as well as strategies on how to reach this vision. The report is publically available at http://www.nordgen.org/index.php/en /content/ view/full/2490/. Important problems identified were underfinanced gene banks, limited support from agrobiodiversity policies for on-farm and *in-situ* conservation, short term funding limiting pre-breeding and uncertainty with regards to international agreements (CBD, IT) limiting the use of plant genetic resources. In this presentation the background of the study, the methods used and the identified strengths, weaknesses, opportunities and threats, will be described. The vision and strategy will be addressed in a separate presentation ("Towards an improved European Plant Germplasm System").

Our main message is that it is possible to overcome the weaknesses and threats identified in the European gene bank system and that this can best be done via a concerted European effort. This is of vital importance, since an efficient use of genetic resources is essential for adapting our crops to an increasing human population and a changing climate, and thus ensuring food security.

Keywords: plant genetic resources, PGR, policy, SWOT, Europe, conservation

The work presented is carried within the framework of the PGR Secure project (www.pgrsecure.org), which is a collaborative project funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394

Towards an improved European Plant Germplasm System

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Abstract

Europe can capitalize on valuable assets of plant genetic resources (PGR), either occurring in the landscape or kept in genebanks, on existing plant genetic resources networks, on considerable opportunities for funding of PGR activities, on a diverse and innovative research and plant breeding sector, on engaged people and policy makers and on a favourable public opinion concerning biodiversity issues. The key message of this presentation is that it is possible to organise, on the aforementioned basis, a European/EU Plant Germplasm System (EU-PGS) ensuring a more effective and efficient conservation and sustainable use of plant genetic resources in Europe.

A SWOT analysis of stakeholder groups engaged in the conservation and use of PGR was performed to better understand how to achieve this goal. The results of this SWOT will be described in a separate presentation (On the conservation and sustainable use of plant genetic resources in Europe: a stakeholder analysis). We then identified desirable states to be achieved (=targets) and proposed strategies on how to reach the targets. Targets and strategies were presented in a report and reviewed by a large number of representatives from the genebank, public research, plant breeding, agro-NGO and policy sector during a European workshop held in Wageningen, The Netherlands, in November 2013. The suggestions of the participants have been considered in the revised report which provides the basis of this presentation.

A stronger European integration of PGR conservation and use actions is overdue. A good way forward would be to strive for a common system composed of sovereign, national plant germplasm units, sustained by jointly managed central infrastructure elements, coordinated by the European Cooperative Programme for Plant Genetic Resources (ECPGR) and co-funded by the European Union.

Keywords: Plant Genetic Resources, Conservation, Sustainable use, Stakeholder, Plant Germplasm System, Policy

The work presented is carried within the framework of the PGR Secure project (www.pgrsecure.org), which is a collaborative project funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394.

Impact of the genetic resources policy landscape on food security

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Abstract

Challenges of securing future food supply are enormous. Climate change is one of the most serious threats ahead of us. Sustained growth of global agriculture is needed. Crop research must be strengthened. Plant breeding must have clear goals and priorities. Access to and best use of genetic resources for new cultivars adapted to future climate and environmental conditions is necessary. Expanding the range of crops in farmer's fields will be important, demanding for innovations in breeding, particularly for new/niche markets. International conventions and bio-science development have led to new conditions for access to GR and knowledge. CBD and requirements under WTO/TRIPS have caused stricter control and new regimes for protection of bio-innovations. FAO-ITPGRFA has contributed to easier and efficient flow of genetic material across national borders. Breeders' exemption in UPOV provides mechanisms for facilitated access to germplasm in consistency with the ITPGRFA.

Daily management of PGR has become more complicated. Trade relations, IPRs, biosafety, indigenous communities and public–private relations are some issues in need of consideration. This new environment has created both threats and opportunities for countries, especially in the South. In order to capture benefits and protect GR and knowledge countries must formulate efficient policies and engage in international debates.

SLU and SEI organized since 2003 an international training program on Genetic Resources and Intellectual Property Rights. The aim of GRIP has been to provide guidance in policy formation of IP and innovation-systems, assist policy makers, researchers and practitioners to understand the regulatory and policy landscape related to IPRs and exchange of genetic resources and contribute to processes of change and development.

Result from an assessment of the GRIP program's impact on implementation of GR related international regimes in participants' countries, how this has influenced research and innovation capacities and remaining gaps and needs will be presented.

Keywords: Food security, Genetic Resources, Access and Benefit Sharing, Intellectual Property, Capacity building

The strategic action plan to strengthen the conservation and use of Mesoamerican plant genetic resources in adapting agriculture to climate change (SAPM)

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Abstract

The Strategic Action Plan to Strengthen the Conservation and Use of Mesoamerican Plant Genetic Resources in Adapting Agriculture to Climate Change (SAPM) is a ten-year road map to strengthen conservation, access and use of plant genetic resources for food and agriculture in Mesoamerica, as a strategic element for food security and agricultural adaptation to climate change and other threats. The SAPM comprises six thematic components: (1) conservation that includes, a) on-farm and in situ conservation of plant genetic resources, through the creation and recognition of integrated biocultural territories within existing conservation programmes, and support to local seed systems, and, b) a new ex situ conservation system for optimal services to users; (2) the sustainable use component identifies the measures to facilitate availability of diverse varieties with adaptive potential to changing climate conditions, to encourage on-farm crop diversification and to promote the dissemination of improved varieties; (3) the institutional and policies component includes measures to support the conservation and sustainable use, steps towards the implementation of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) in Contracting Party countries, and measures to implement farmers' rights; (4) the education and capacity-building component describes actions for ensuring the full and effective participation of famers' organizations, decision makers, and academic and other professionals in implementing the SAPM; (5) the operational component identifies regional coordination frameworks and mechanisms needed for implementing the SAPM; (6) the financial component identifies actions needed for resource mobilization to support SAPM implementation. The SAPM was formulated using a methodology that combines the analysis of scientific evidence on the current state of 26 crop species and their 358 wild relatives in the region, and of climate change challenges and opportunities, and a broad participatory process involving regional stakeholders. The SAPM was financed by the ITPGRFA through its Benefit-Sharing Fund.

Keywords: conservation, use, policies, Mesoamerican, PGRFA, regional plan

Theme 4: Informatics development

In order to ensure an effective and efficient conservation and use strategies for CWR and LRs on farm and in the wild, it is important we know what diversity exist where, what important traits are contained that are value for crop breeding and how these resources are changing over time. This theme examines how data are gathered, organized, described, managed and made available to germplasm users. It also examines the the type of data necessary for monitoring changes in diversity and what IT tools are needed for a better characterization, and conservation management.

Abstracts under Theme 4 fall into two sub-themes:

4.1 Characterization informatics
4.2 Conservation informatics

4.1 Characterization informatics

Plant Breeding Data Management, Analysis, and Integration

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Abstract

Plant Breeding Data Tsunami
All scientific disciplines are facing an enormous data tsunami. More importantly, we need to be able to analyze these data in an integrated manner, in order to be able as a plant breeder to reach the goals, as set by the FAO, to produce twice as much with twice less input. Two aspects are important: 1) We need to develop tools and databases, which are able to analyze these data in an integrated manner, and 2) we need make our data interoperable! Until now, most attention has gone to the first aspect. Research data have been stored in databases worldwide. There are several examples in which storage of research data has been combined with tools for analyzing this data. One of such examples is BreeDB, which has been developed within Wageningen UR Plant Breeding. BreeDB has been used to store data from the EU funded project (EU-SOL), in which a collection of > 7000 tomato cultivars, landraces and wild species were phenotyped and genotyped (https://www.eu-sol.wur.nl). A core collection was selected and has recently been part of the 150 tomato genome re-sequencing project (http://www.tomatogenome.net). Concepts developed within this resource will be discussed. However, the aspect of data interoperability is not yet used regularly within the Plant Breeding domain. This will require that (different) communities will start talking the same vocabulary (ontologies). For researches, this will mean that 1) They will need to provide metadata of datasets they generated and 2) Datasets needs to be made available using standard formats and descriptors accepted by the community. As a research community, it is already important to invest effort in the formulation of these standards. The EU (H2020, except most of the life science calls) will require that research data will be made available and will enforce minimal descriptors of datasets. The benefit for the research community will be that 1) data can than be integrated easier and might lead to the detection of "implicit knowledge", using automated reasoning processes and/or statistical approaches, and 2) data does not need to be aggregated anymore in one large database, but up-to-date datasets can be made available at the site of the (research) organization.

Keywords: tomato landraces, tomato resequencing, breeding data management, semantic web

New predictive characterization methods for accessing and using CWR diversity

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Abstract

Novel approaches to enhance characterization of plant genetic resources are being developed, as traditional phenotypic characterization techniques have shown to be insufficient to fully harness crop wild relative (CWR) and landrace diversity. These are genomics, transcriptomics, metabolomics, high-throughput phenotyping, as well as less resource intensive predictive characterization techniques. The latter build on the hypothesis that the environment influences gene flow and natural selection, and thus spatial genetic differentiation of organisms. CWR populations growing in a specific environment will possess a suite of adaptive traits shaped by selection pressures unique to these environments. Thus information about a CWR occurrence site can be used to approach the utilization of genetic resources in a more rational way. Two predictive characterization methods for CWR were developed within the PGR Secure project, using an agro-ecological approach for optimizing the search for populations and accessions with targeted adaptive traits: The ecogeographical filtering method combines spatial distribution of the target species with the ecogeographical identification of those environments that are likely to impose selection pressure for the selected trait. Edaphic, geophysic and bioclimatic variables most relevant for adaptation are identified and used together with ecogeographic land characterization maps to identify promising occurrences. The calibration method bases the criteria to filter accessions on existing evaluation data for the trait of interest. Ecogeographical data specific to the environment at collecting sites evaluated for the trait are used as input to identify existing relationships between trait and environment. This relationship is then used to calibrate a model through which other non-evaluated accessions can be assessed. The methods were applied to the four project genera, *Avena*, *Beta*, *Brassica* and *Medicago* to identify subsets of potentially interesting accessions or occurrences, investigating the following abiotic stress factors:

aluminium toxicity for *Avena*, drought for *Beta*, drought and salinity for *Brassica*, and frost for *Medicago*.

Keywords: predictive characterization, crop wild relatives, *Avena*, *Beta*, *Brassica*, *Medicago*, Conservation and use

Plant Genetic Resources Diversity Gateway – a way forward

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Abstract

Data and information for plant genetic resources (PGR) is not readily available, due to many factors including: lack of institutional capacity, scarce data mobilization, outdated or inappropriate documentation and standards, limited free or easy tools, lack of long-term holistic management strategies, rare continuous data assessments, and barriers for sharing and publishing scientific data by institutions or individuals.

The data generated globally are constantly increasing in size, complexity and heterogeneity. The availability of the data to users of germplasm, especially breeders, is increasingly unfit for purpose. While there are great advances being made for collecting and managing *ex situ* conservation data, there is currently no information system for *in situ* conservation and on farm management. There is an urgent need for a system with the capacity to store *in situ* conservation data, provide common and diverse methods, allow for linking, annotation and an easy way to query and retrieve information from different locations, and in multiple types, formats and sources that meet the requirements of the end users. Challenges include: 1) How to build a system allowing constant adaption and flexibility? 2) How to develop a suite of technologies that are technically powerful and challenging and at the same time user friendly? 3) How to drive the system based on easy solutions – allowing and facilitating data sharing, publishing, query and retrieval?

The PGR Diversity Gateway vision is to facilitate access to *in situ* and on-farm, crop wild relatives (cwr) and landrace information. It has a trait information system at its core, but also includes: characterization and evaluation data, QTL data, national inventories, country crop and cwr checklists, national and European conservation strategies and links to other sources of related relevant information. The Gateway will enable breeders to identify the most likely sources of their priority traits and how they can access that material for utilisation. The PGR Diversity Gateway, while facilitating and assisting countries in meeting national and international commitments and responsibilities, also promotes PGR conservation and sustainable use of cwr and landrace diversity. In addition, it strengthens networks and the conservation of biodiversity, which is required if successful variety development is to continue in the face of the challenges posed by climate change, ensuring food security worldwide.

Keywords: CWR, LR, in situ, on farm, Information system, Traits, Inventories, Checklist, Conservation strategies

The work presented is carried out within the framework of the PGR Secure project (www.pgrsecure.org), which is a collaborative project funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394.

4.2 Conservation informatics

Information technology to assist in conserving and using crop wild relatives and landrace diversity

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Abstract

Information technology (IT) provides possibilities to increase the efficiency of tasks and processes. Based on a rudimentary analysis of the of tasks and processes involved in the conservation and use of crop wild relatives (CWR) and landrace diversity, the supporting IT tools will be described.

Regarding the CWR, the first step is the identification of the species that can be considered CWR. In this context a brief look at the Harlan and de Wet Crop Wild Relative Inventory will be taken, and issues regarding compatibility of taxonomies will be discussed. The second step the localisation of these species in and *ex situ*, involving several information sources to identify the natural distribution and the representation in genebanks, including GBIF and GeneSys. Also bioclimatic niche modelling approaches to predict occurrence of species in locations not yet surveyed will be described, giving examples from the MaxEnt models that are currently used for this purpose. These niche models can also play a role in identifying threats to CWR due to climate change, and planning in situ conservation measures or ex situ rescue activities. Other types of geographic information systems play a role in assessing the conservation status of species that need protection, and in monitoring in situ conserved populations. Finally, in regards to the use of CWR in research and breeding, developments in bioinformatics play a central role, especially where it comes to the in silico identification of potential traits.

Regarding landrace diversity the situation is more complex. Objectives are less well defined, and therefore the strategy is difficult to analyse and supporting IT-tools difficult to describe.

In the presentation, an inventory of the state of the technology will be made, what tools exist and what tools should be developed to optimally support the conservation and use of crop wild relatives and landrace diversity.

Keywords: bioinformatics, information technology, genetic resources management, methodology, bioclimatic niche modelling, crop wild relatives, landrace diversity

CAPFITOGEN tools. Facilitated spatial and ecogeographical germplasm analysis for efficient PGR conservation and utilization

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Abstract

We present seven tools to facilitate the use of spatial and ecogeographical germplasm analysis among curators and the plant genetic resources community. These tools are the main component of CAPFITOGEN, a technology transfer and building capacity program, which constitutes an effort to bring scientific and technological advances to the PGR technical community. This program has focused its efforts on Latin American national entities on conservation and sustainable use of plant genetic resources building capacity.

These tools are designed to make accessible a number of useful methodological approaches that have, in most cases, been presented and validated in scientific publications. CAPFITOGEN tools have been selected to operate under scarce economic resource conditions and to help in decision-making processes in countries rich in plant genetic resources. Consequently, these methods are based in Geographic Information System (GIS) technology and ecogeographic approaches.

Computer tools have been programmed in R (R Core Team, http://www.r-project.org/) and a user-friendly interface has been developed using Java and html code and a Java web server. The list of available tools and their main function is the following:

GEOQUAL: Evaluation of the quality of georeferentiation in passport data

ELCmapas: Generation of ecogeograpical land characterization maps

Representa: Assessment of the ecogeographical representativeness of a species in a germplasm collection.

ECOGEO: Ecogeographical germplasm characterization.

DIV mapas: Development of ecogeographic, phenotypic and genotypic variability maps.

ColNucleo: Development of ecogeographical core collections.

FIGS_R: Application of ecogeographical filters to optimize potentially valuable germplasm for specific crop breeders' interests.

Through various workshops, CAPFITOGEN tools have been distributed to more than one hundred Latin American curators and plant genetic resources researchers. CAPFITOGEN program is an initiative of the International Treaty on Plant Genetic Resources for Food and Agriculture. Spanish and english version of the tools is freely available, more information at http://www.planttreaty.org/capfitogen.

Keywords: Geographic information systems, Environment, Spatial analysis, Informatics tool, Documentation, Technology transfer, Capacity building

Thoughts and experiences building an *in situ* /*ex situ* information system

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Abstract

Motivation: Development of the first central point for crop wild relative (CWR) and landrace information that includes: national inventories, national crop and CWR checklists, national and European conservation strategies, QTL summary data linking to other data resources, mapping and environmental layers. All these are advances on capacity to use, re-use and discover the data for research and breeding.

To develop this system, it was necessary to use community-agreed standards and develop a comprehensive ontology component advancing the search, publication, integration of resources and user demands, still being consistent with machine readable and discovery systems. The system uses a document database, MongoDB, and a graph database, Neo4j, for the ontologies. The system is capable of producing and retrieving useful information, storing and retrieving many diverse data types, discovering relations which, without an ontology, would simply not be possible.

Results: PGR Diversity Gateway is an innovative system that has both a general search and ontology for informatics operations (tool or workflow functions), types of data and identifiers, application domains and data formats. The system supports semantic annotation of diverse entities such as traits, methods, units, international standards, data schemas and search forms. It includes over 17,000 defined concepts.

Availability: The latest stable version is available from http://pgrdiversity.bioversityinternational.org

Keywords: *In situ*, *Ex situ*, Information system, Ontologies

The work presented was carried out within the framework of the PGR Secure project (www.pgrsecure.org), which is a collaborative project funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394.

Implementation of a PGR Global Documentation System in Portugal

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Abstract

Genetic resources conservation programs generate a large amount of data. Thus, the need for a storage and retrieval system that integrates the data from surveys, collecting and conservation work and related research activities, namely morphological and agronomical evaluation, molecular and biochemical characterization and nutritional analysis, allowing for a proper management and facilitating access to genetic material and related data information.

At present, the Banco Português de Germoplasma Vegetal (BPGV) and ISOPlexis/ Germobanco together conserve 90% of the total volume of the seed collection maintained in Portugal.

BPGV and ISOPlexis Genebanks, agreed to implement the new documentation system - GRIN-Global (GG) as their genebank platform. This system is a free flexible, easy-to-use plant genetic resource information management system that enables genebanks to either set the system individually or in a network setup. Besides guarantying a high quality management system it also includes a web publishing site where for the first time in one go collection will deliver information globally.

The implementation process in Portugal was done in four phases with several key steps: 1) System evaluation training (SET):

First training to become familiar with the tool
Evaluation of system capacity to genebanks needs

2) Functionality analysis (FA);

Detailed platform functionalities analysis
Analysis of procedures in both of the genebanks

3) Implementation decision (ID)

Reasoning for implementation
Result analysis
Decision on implementing this solution

4) Planning next steps (PNS).

New functionalities needs
Indexing of data

Load the inventory of accession-level passport data for all collections maintained in both of the genebanks,

Public launching in 2014.

Portugal has decided to implement this system, as is provides us with the opportunity to increase data quality, to have long term sustainability for data curation, integrate all collections in one management system optimizing the costs and staff resources allocated to the genebanks.

Keywords: Genebank, Plant Genetic Resources, Conservation, Data quality

What do we have to lose? Generating crop diversity and threat monitoring information to support poor farmer livelihoods and public good ecosystem services

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Abstract

It is said that “you can't manage what you don't measure”. The unprecedented global loss of agricultural species, varieties and associated traditional knowledge is of increasing concern, threatening the provisioning, regulatory, supporting and cultural ecosystem services of importance to the livelihoods of the poor as well as the welfare of broader society. Such services include such public goods as maintaining agroecosystem resilience and future option values.

Unfortunately, although many crop genetic resources (CGR) are widely recognised as being threatened, there is only limited information available regarding actual status. Only isolated efforts at monitoring have been undertaken. Conventional monitoring efforts, where they exist at all, have been subject to limitations due to ad hoc approaches that lack rigorous survey and sampling approaches, do not adequately account for search effort costs or systematically involve the participation of local-level actors, and are usually based on collections instead of direct observations in the field. Furthermore, the links between specific CGR conservation levels/configurations and the provision of specific ecosystem services are poorly understood.

There is thus an urgent need for the development of a systematic approach to the monitoring of CGR. This paper draws on the outcome of a recent Bioversity/CIP international expert workshop aimed at the development of such an approach. The proposed multi-scale approach builds on a wide range of existing monitoring experiences and a review of the literature related to agricultural biodiversity-relevant ecosystem services. A number of proposed indicators that could be used to assess CGR threat levels, be used for monitoring purposes and/or assist in evaluating ecosystem service public/private good trade-offs arising from agricultural intensification are presented, with a view to supporting the potential for prioritizing, designing and implementing on-farm/in situ conservation measures that actively involve farmers, support livelihoods, complement existing ex situ conservation efforts and facilitate access and benefit sharing.

Keywords: Agrobiodiversity-relevant ecosystem services, Monitoring, Indicators

Part 2
Poster presentations

Part 2. Poster Presentations

Theme 1: Characterization techniques

Introgression lines of wild *Pisum fulvum* / *P. elatius* into cultivated pea (*P. sativum*) genetic background, as a tool to broaden genetic diversity

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Abstract

Plant evolution under domestication has altered numerous traits, including self-pollination which reinforced fertility barriers between wild and cultivated populations, facilitating fixation of the desired genotype. Consequently, domestication bottleneck has resulted in high degree of relatedness between varieties, which was further pronounced in modern breeding programs, leading to narrower genetic base of cultivated germplasm, prone to pests and diseases. The study of genetic diversity preserved in pea collections showed that although wide diversity is captured among cultivated material, wild material provides yet broader diversity. Highly variable germplasm is found in the secondary and tertiary pools of crop plants, including pea. However, the transfer of genes from wild species, is often accompanied by inevitable genetic drag of undesirable wild material related traits and this has prevented its broader use. To avoid this, the synthesis of exotic libraries, such as introgression lines, near isogenic lines and chromosome substitution lines, containing molecularly defined chromosome segments from wild species in a constant genetic background of the cultivated species has been applied to make the use of alien genomes more precise and efficient. Here we report development of the set of chromosome segment substitution (CSSL) lines, containing genomic segments of wild pea (*Pisum fulvum* WL2140/P. *elatius* L100) in the cultivated pea (*P. sativum* subsp. *sativum* cv. Terno/Cameor) genetic background, monitored by molecular markers covered all seven linkage groups of pea genome at 2 to 82 cM spacing. These lines have been preliminarily phenotyped for 8 traits (including branching, height, node, pod and seed numbers) showing often transgression. Establishment of such permanent introgression libraries will allow phenotypic characterization of unlimited number of target traits, which, coupled together with higher density markers, will provide means for QTL and gene identification and subsequent incorporation in desired genotypes ultimately leading to better performing pea varieties.

Funding from Czech Ministry of Agriculture ME10062 project and European FP7 project Legato (613551) is greatly acknowledged.

Keywords: introgression, germplasm, legumes, pea, *Pisum*

Conditions that optimize individual plant performance boost the chance to qualify and beneficially utilize the within a landrace genetic variability

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Abstract

Landraces of self-pollinated species consist of genetically homogeneous individuals, and constitute valuable sources to isolate single-plant progenies targeting pure-line varieties. However, the negative relationship between yield and competitive ability may constitute an insurmountable obstacle to recognize the outstanding genotypes. Indeed, the performance of one vetch (*Vicia sativa*) and two wheat (*Triticum aestivum*) landraces showed a perfect match to this speculation. They significantly lagged behind a homogeneous check at the dense stand (by 29 % for vetch, and 64 and 38% for wheat), but the reverse was true with spaced plants to preclude interplant competition (landrace superiority of 32% in vetch, and 58 and 73% in wheat). Thus, landrace qualification as potential gene pool is a matter of absence of competition. Further, the hypothesis was verified through single-plant selection in the absence of competition within dry bean (*Phaseolus vulgaris* L.) and lentil (*Lens culinaris* L.) landraces. To simulate heat stress in case of bean breeding was performed at a greenhouse besides the normal open field conditions. Progeny-line testing in open field and greenhouse trials revealed yield improvement up to 75% in the absence of competition and up to 38% at the farming density. Note of worthy is the hearsay evidence, drawn from growers, of exceptional performance even during fairly hot seasons. Breeding in lentil prioritized genotypes that escape infection from seed-born and insect-transmitted viruses. Ultra-low densities may not favour aphid plant-to-plant movement, however, favour insect landing and infections originating from outside sources, uncovering thus the susceptible genotypes. Second generation sister lines originated from healthy and highest yielding plants yielded up to 136 and 23% more than the source landrace as ultra-spaced and in dense stand, respectively. It was concluded that selection in the absence of competition improves the health status of the seeds produced and further results in potentially virus-tolerant varieties.

Keywords: competition, competitive ability, genetic homogeneity/heterogeneity, yield potential

This research has been co-financed by the European Union (European Social Fund – ESF) and Greek national funds through the Operational Program "Education and Lifelong Learning" of the National Strategic Reference Framework (NSRF) - Research Funding Program: **THALES**. Investing in knowledge society through the European Social Fund.

Spatial heterogeneity within lentil landraces is better sampled by the honeycomb rather than the classical-plot arrangement

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Abstract

Breeding effectiveness for quantitative traits is subject to errors due to the environmental heterogeneity. In order to overcome the problem the honeycomb designs have been invented that allocate entries systematically and evenly across the whole experimental area. The objective of this study was to investigate whether this kind of experimentation tackles the spatial heterogeneity. Three lentil (*Lens culinaris* L.) landraces, named 'Evros', 'Elassona' and 'Englouvi', were tested at a particular NR-0 honeycomb experiment (1000 plants allocated at about 900m2). Severe virus infection was recorded depicted by the very high CVs of single-plant yields, particularly for 'Englouvi', i.e. 129, 123 and 162%, implying huge environmental heterogeneity. Each experiment was analysed as either R-7 or R-13 honeycomb arrangement including 7 and 13 simulated entries, respectively, as well as divided towards two directions to form 7 or 13 classical plots. It was hypothesized that the entire heterogeneity would have been tackled whether comparison of the simulated entries would not reveal significant residuals from the overall mean (z-test for independent means and standard deviations). The latticed 7 and 13 plots of honeycomb design in no case gave significant residuals. The same was true for the classical 7-plot settlement of 'Evros' and 'Elassona', however, their yield gap was greater than the respective of the honeycomb pattern. For 'Englouvi' the 7 classical plots of a particular orientation gave 5 out of the 7 residuals to be significant and yield gap >900% vs 32% of the R-7. Significant residuals were also observed when 'Elassona' and 'Englouvi' were analysed on the classical 13-plot for a particular orientation (3 and 8 out of the 13, respectively). The conclusion was that the triangular plant arrangement of honeycomb designs samples environmental heterogeneity in a more effective way compared to the classical plot configuration.

Keywords: experimental error, mean residual, objective evaluation

This research has been co-financed by the European Union (European Social Fund – ESF) and Greek national funds through the Operational Program "Education and Lifelong Learning" of the National Strategic Reference Framework (NSRF) - Research Funding Program: THALES. Investing in knowledge society through the European Social Fund.

New ways of screening of genofund of wheat to Leaf and Stripe rust in Kazakhstan

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Abstract

In present days in Kazakhstan wheat is growing on 12 million hectares about. Spring wheat previously is growing in North and Central regions. Winter wheat previously growing in South and Southeast regions (about 700 000 hectares). The rust diseases on this crop are obligate parasites and can fatly attack it and yield losses can be up to 60-80%. Leaf rust caused by fungus Puccinia recondita Desm. (synonym *P. tritici* Eriks.). This disease is widespread everywhere in Kazakhstan on wheat. Yellow or stripe rust caused fungus Puccinia streeformis West (syn. *P. glumarum* Eriks. et Henn previously attacks winter and spring wheat in South and Southeast Kazakhstan.

FAO 2050 predicts that the world population will increase to 9 billion. Therefore, to satisfy the needs of the global population by 2030 is necessary to mutilate the potential yield by 30-40%. For this purpose, it is necessary to increase the potential of 1.6-1.8% annually, including 1% due to breeding and genetic methods. Achieving the latter goal can be in attracting the genetic resources of wild relatives. In present days the main direction for in improving the capacity of this culture laid in increasing resistance to abiotic (drought, Heat-resistant, salinity,) and biotic stresses (diseases and pests). In present days the currently distant hybridization remains is the most effective method of introduction of foreign genetic variability in the wheat genome. Synthetic diploids, including the genomes of different species of grasses, can greatly facilitate the transfer of the properties of the genetic material of wild species to cultivated plants. They also open up the possibility of recombination between genomes isolated at the diploid level. Rust diseases caused by aggressive an obligate parasite of wheat. That's why the best way for control of these diseases is a breeding for resistance. In autumn 2013 we sowed new nursery of new material synthetic hexaploid wheat of breeding of Kyoto University of Japan and CIMMYT. For the first time in Kazakhstan we are going to evaluate this nursery for resistance to leaf and stripe rust in the soil and climatic conditions of the Northern, Central, Southern and Southeast Kazakhstan. Will be held on selective study of the experimental

material of synthetic hexaploid wheat breeding Kyoto University of Japan and CIMMYT. (100-120 samples) to identify adapted to this areas lines. Will screened samples of synthetic hexaploid wheat for resistance to common bunt. Will studied the character of the inheritance of disease resistance in crosses with synthetic wheat varieties zoned based on a comparison of the first generation and their parents. Will be identified new sources of resistance synthetic hexaploid wheat diseases.

Keywords: screening of genofund, resistance to rusts hexaploid synthetic, wheat

New ways of screening of genofund of winter wheat to Common Bunt in Kazakhstan

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Abstract

Actuality, FAO 2050 predicts that the world population will increase to 9 billion. Therefore, to satisfy the needs of the global population by 2030 is necessary to mutilate the potential yield by 30-40%. For this purpose, it is necessary to increase the potential of 1.6-1.8% annually, including 1% due to breeding and genetic methods. Achieving the latter goal can be in attracting the genetic resources of wild relatives. In present days the main direction for in improving the capacity of this culture laid in increasing resistance to abiotic (drought, Heat-resistant, salinity,) and biotic stresses (diseases and pests). In present days the currently distant hybridization remains is the most effective method of introduction of foreign genetic variability in the wheat genome. Synthetic diploids, including the genomes of different species of grasses, can greatly facilitate the transfer of the properties of the genetic material of wild species to cultivated plants. They also open up the possibility of recombination between genomes isolated at the diploid level.

Winter wheat is a wide spread cereal crop in South and southeast Kazakhstan. The most harmfulness disease of winter wheat with seed infection is a Common Bunt (caused by *Tilletia caries* (DC) Tul. (synonym *T. foetidia* Liro) and *T. levis* (synonym *T. tritici* Wint). If wheat was sowed by untreated by treatment seed, yield losses can be from 3-4 to 62%. Infected grain cannot be used for forage and bread production. In present days screening of forms and cultivars of winter wheat with resistance to Common Bunt is one of main direction of wheat breeding. This fungus is an obligate parasite. That's why the best way for control of these diseases is a breeding for resistance. In autumn 2013 we sowed new nursery of new material synthetic hexaploid wheat of breeding of Kyoto University of Japan and CIMMYT. For the first time in Kazakhstan we are going to evaluate this nursery for the soil and climatic conditions of the Southern and Southeast Kazakhstan. Will be held on selective study of the experimental material of synthetic hexaploid wheat breeding Kyoto University of Japan and CIMMYT. (100-120 samples) to identify adapted to this areas lines. Will screened

samples of synthetic hexaploid wheat for resistance to common bunt. Will studied the character of the inheritance of disease resistance in crosses with synthetic wheat varieties zoned based on a comparison of the first generation and their parents. Will identify new sources of resistance synthetic hexaploid wheat diseases.

Latent traits of *Oryza longistaminata* could contribute to the realization of a sustainable culture system in rice

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Abstract

Current high-input agriculture systems have caused negative impact to the global environment, though they have undoubtedly realized the drastic increase of crop yield through the adoption of the semi-dwarf feature. Therefore, there is global demand to change to sustainable agricultural systems for food security, safety and conservation of the harmonized environment. One possible way to achieve this is to breed low-input adaptable (LIA) crops. LIA crops should carry the large biomass trait under low-input conditions because the plant significantly decreases biomass, resulting in low yields, under these conditions. *Oryza longistaminata*, a wild species of rice native only to Africa, possesses several latent useful traits including a vigorous biomass observed in low input conditions. This is an important trait for LIA rice. Hence, this study's objective was to characterize and detect QTLs for several important traits for large biomass introduced from *O. longistaminata* collected at Mombasa, Kenya. LIA candidates selected from selfed pedigree of the cross between *O. longistaminata* and T-65, a japonica variety, under non-fertilized conditions showed important traits for high productivity in low-input conditions such as large biomass, large panicles and very thick culm-base diameter. Genotyping using genome-wide SSR markers demonstrated that LIA-1 selected carries several chromosome segments of *O. longistaminata*. QTL analysis for several important traits for large biomass conducted in F2 of the cross between LIA-1 and Norin 18 detected 32 QTLs. More than 50% of the QTLs detected were derived from LIA-1 and had positive contribution to the specific traits. Majority of the QTLs detected were located in *O. longistaminata*-introgressed chromosome regions. These results suggest that *O. longistaminata*-derived chromosome segments locate QTLs for important traits which could be utilized for breeding low-input adaptable (LIA) rice varieties.

Keywords: *Oryza longistaminata*, low-input adaptable (LIA), sustainable

Agroecological characterization of the wild sunflower from three sunflower crop regions of South America and Europe

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Abstract

Sunflower (*Helianthus annuus* L.) wild relatives provide genes valuable for breeding. We studied natural populations of *H. annuus* in two European regions (Iberian (IBE) and Balkan (PAN) peninsula) and South America (AME). By field trips between 2010 and 2013, the habitat environment, population size and plant morphology of natural populations were characterized.

Twenty-six populations in Argentina (9), Serbia (9), Spain (7) and Romania (1) were observed. The estimated total area and population dimensions were >60 ha and >4 10^6 individuals. Natural populations of *H. annuus* grew between 31-45° latitude and 57-616 mosl. Overall, environmental determinants of *H. annuus* distribution overlapped in AME and IBE, but differed from PAN. AME and PAN populations grew on ruderal or riparian habitats and differed from IBE, where they appeared as weed (agrestal). In IBE, sunflower was the most frequently invaded crop with *H. annuus* populations. In AME and PAN, these populations developed near but outside sunflower, corn and wheat. Twelve quantitative traits, measured under natural growing conditions and analysed by PCA, differed among the geographic groups. The PC1 explained 62.1% of variance and was mainly determined by ray flower characteristics. All groups showed over 99% of acuminate bract tip, a trait used in *H. annuus* taxonomic determination. The AME populations showed the highest frequencies (>90%) of traits typical for wild *Helianthus*. IBE and PAN populations showed >20% of plants with traits such as anthocyanin pigment absence and yellow ray flowers, indicating introgression of cultivated sunflower genes. The high morphological variability and wide geographic distribution of *H. annuus* natural populations observed in our study, demonstrated their high value as potential source of agronomically important traits. Appearance of traits introgressed from cultivated sunflower in these populations proves that crosses with cultivated sunflower are possible, thus fulfilling the basic pre-requirement for their successful use in sunflower breeding.

Keywords: sunflower, natural population, pre-breeding, characterisation

Acknowledgements: This work is part of the Projects TR31025 and III46008 supported by Ministry of Education, Science and Technological Development of R. Serbia and PICT 3854 support by AgenciaNacional de PromociónCientífica y Tecnológica of Argentina.

The French Genetic Resources Centre on Small Grain Cereals: a tool-box for pre-breeding

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Abstract

The small grain cereals Genetic Resources Centre (GRC) gathers accessions of major species of agricultural interest belonging to genus *Triticum* (wheat), *Hordeum* (barley), *Secale* (rye), *Triticosecale* (triticale), *Avena* (oat), and there wild relatives. About 25 000 accessions composed by patrimonial genetic resources as landraces, breeding lines, registrated cultivars, are held in INRA Clermont-Ferrand. All these genetic resources constitute a useful genebank as well, for basic, genomic studies and applied breeding approaches.

Different genetic analyses have contributed to describe the genetic diversity of the GRC collections. The main result was the definition of a core collection (F. Balfourier, *et al.*, 2007) which is now highly genotyped for more than 120 000 SNP and phenotyped for a hundred of agronomical and technological descriptors (Bordes *et al.*, 2008, 2011, 2013). A part of the bread wheat collection is also evaluated in precompetitive national project "Breedwheat" and in the European project "Whealbi".

Genetic Resources Centre is a part of different kind of network at national level, in the national networks for cereal crop genetic resources, and at European level, in ECPGR Cereals Networks.

The implementation of a quality management system is in progress, with a first quality-label from a French organization IBiSA in 2013 and CRG engages itself in a certification process.

A part of small grains cereals collection is available online on SIReGal database (http://urgi.versailles.inra.fr/siregal) and request of seeds samples can be done directly by SIReGal or by mail. This database is a part of a global portal (GnpIS) which allows crossing and exchanging data from genomic, proteomic and phenotypic evaluations.

Balfourier *et al.* 2007 TAG 114:1265-1275
Bordes *et al.* 2008 JCS 48(3): 569-579
Bordes *et al.* 2011 JCS 54:137-147.
Bordes *et al.* 2013 TAG 126 (3): 805-822

Keywords: Genetic resource centre, Cereal crops, Diversity analysis, Evaluation Network, Databases

Genetic and phenotypic variability in rocket germplasm

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Abstract

Rocket, which includes several species within the Brassicaceae family, is widely spread all over the world with multiple uses as salad, cooked vegetable, medicinal plant and oil crop. The consumption as leafy vegetable has rapidly risen in many countries during the last decade because of its use in processed products, such as mixed salad packages. However, to such growth does not correspond an increase in the number of cultivars, as a result of limited variety selection activities. Plant genetic resources are fundamental for breeding new genotypes, the assessment of genetic and phenotypic diversity among accessions being a useful tool to facilitate the more efficient use of germplasm. In the present study, one hundred genotypes from 25 countries belonging to *Diplotaxis* (*D. tenuifolia* L., *D. eruicoides* L., *D. muralis* L., *D. harra*, *D. acris*, *Diplotaxis* spp.), *Bunias* (*B. erucago* L.), *Erucastrum* (*E. virgatum* C. Presl, *Erucastrum* spp.) and *Eruca* (*E. sativa* Mill., *E. vesicaria*) genera have been collected from germplasm banks and farmers. Several agronomic traits have been recorded including: growth habit, growth rate, leaf type, leaf pubescence, leaf and flower colour, bolting time, pungency, root type. A preliminary approach to detect genetic variation for nitrate accumulation has been conducted. Results allow identifying different types and several promising accessions in terms of late flowering time and aptitude for mechanical harvesting which are two desirable traits for the cultivation of rocket. Molecular markers analysis is underway with the aim to develop markers for species discrimination and authentication. Since for all genera studied specific codominant markers such as CAPS (Cleaved Amplified Polymorphic Sequence) and SSR (Simple Sequence Repeat) are not available, molecular markers developed in other Brassicaceae, including *Brassica napus*, *B. oleracea*, *B. nigra* and *Arabidopsis thaliana*, were chosen. To our knowledge such efforts have not been done in rocket, yet. Moreover, in order to enhance the use of genetic resources for breeding programs, glucosinolate content will be assessed in selected genotypes.

Keywords: rocket, agronomic traits, molecular markers

Screening Helianthus species for resistance to diseases in field conditions

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Abstract

Besides collection and conservation, characterisation is essential to promote and enable the use of plant genetic resources by breeders. Evaluation of PGR genetic diversity for economically important traits should be one of the basic activities of each gene bank.

The collection of *Helianthus* species at the Institute of Field and Vegetable Crops in Novi Sad comprises 8 annual and 21 perennial species with 189 accessions of annual and 316 accessions of perennial species. It was founded in 1980 and has since been used in sunflower pre-breeding programs. Main reason for the establishment of the collection was the susceptibility of cultivated sunflower to different pathogens and the possibility of acquiring resistance from wild relatives.

The aim of this research was to determine response of *Helianthus* species to infection in the field, as there are not many references on the reaction of wild sunflowers in ex-situ conservation conditions. Disease incidence and severity was recorded in a naturally infected field during seven years. Total of 29 *Helianthus* species (505 accessions) were included in the survey, while an addition were F1 interspecific hybrids between the cultivated sunflower and perennial species (10 species, 23 genotypes).

Powdery mildew (*Erysiphe chichoracearum*) was the most frequently observed disease. While its development and severity varied due to climatic conditions, it was most abundant in 2011. Symptoms of other diseases like necrotic spots on leafs (*Alternariaspp.*), stem necrosis (*Phoma macdonaldii*) and head and stem rot (Sclerotinia sclerotiorum (Lib.) de Bary), were observed. One parasitic plant - broomrape (*Orobanche cumana* Wallr.) was also registered in traces.

The obtained results were used to select accessions for inoculation trials on head rot and black stem disease resistance.

Keywords: characterisation, disease resistance, ex-situ, *Helianthus*

Next-generation sequencing and genome characterization of red clover and its wild relative zig-zag clover

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Abstract

The genus *Trifolium* is classified taxonomically into the agronomically outstanding Fabaceae family. It comprises species known as clovers, both wild and cultivated. Red clover (*T. pratense*) is an important forage legume and its breeding is aimed at improving traits like persistency, resistance to biotic and abiotic factors and forage quality. Recently, interspecific hybridization of tetraploid red clover with related wild octoploid zig-zag clover (*T. medium*) has been used for the introgression of useful traits into red clover. Currently, our study has been aimed at using novel techniques of molecular genetics for characterization of the both genomes and key traits transferred into improved variety Pramedi. Techniques such as next-generation sequencing and high-throughput DNA marker typing systems can increase the speed and precision with which traits may be selected.

De novo assembly of the *T. pratense* genome after Illumina sequencing was achieved. The current assembly comprises ~314.6 Mbp of draft nucleotide sequence. Overall, 47398 protein coding genes were annotated from 64761 predicted genes. Resistance genes, genes for leghemoglobins and nodule-specific cystein-rich peptides were identified. Sequencing data of T. medium were obtained with average genome coverage 20.7x (x = 3.5 Gbp). Species-specific SNP calling for coding sequences was performed and over 924837 SNPs between parental genotypes used for hybridization were discovered. Species-specific DNA markers for *T. pratense* (23299) and T. medium (1177) was gained. Detailed SSR catalogue is available for coding sequences and exons.

The presented genomic data constitute a resource for assessment of genome introgressions from zig-zag clover into red clover and for red clover improvement through molecular breeding.

Keywords: Fabaceae, clovers, interspecific hybridization, next-generation sequencing, genome annotation, single nucleotide polymorphism, simple sequence repeat

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Commercial success of introgressing wild relatives, landraces, and exotic germplasm into elite breeding populations in barley

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Abstract

Intermating among elite lines is the source of most new cultivars. This eventually leads to loss of diversity through selection and loss of desirable alleles through drift. New alleles must be introduced into the elite breeding population from wild relatives and land races without ''polluting'', or diluting, the elite gene pool with undesirable alleles and repulsion linkages. Exotic germplasm may also disrupt the essential epistatic allele combinations which give adaptation, quality, and agronomic performance. New desirable alleles from exotic germplasm can be introgressed into an elite population in a systematic way through limited backcrossing with a minimal disturbance to the finely tuned elite background. Combining recurrent selection within elite germplasm with a systematic introgression from exotic germplasm in the recurrent introgressive population enrichment (RIPE) system, based on efficient management of genetic male sterility, has led to an open-ended, continually improving, and sustainable elite population breeding system, which is simple, effective, and a regular source of superior new commercial cultivars. This system allows a much broader range of germplasm to be maintained in a dynamic, adapted, and continually evolving gene pool rather than stagnating in gene banks. It is ideal for exploiting the vast reservoir of quantitative genetic diversity in *H. spontaneum* and land races that is virtually untapped at this time. The success of the RIPE system, as applied to barley breeding in Ontario, Canada, will be presented and discussed. This concept is applicable to breeding programs in most domesticated crop species.

Keywords: introgression, recurrent selection, male sterility, barley, *Hordeum spontaneum*

Crop Wild Relatives (CWR) of cultivated fruit species: Rootstocks for sustainable production

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Abstract

Fruit growers and researchers have always paid attention to the exploration of wild species related to cultivated ones, for interesting characters to be used in breeding programmes, both for new cultivars, and rootstocks. The latter are expected to improve adaptation of the cultivars to soil or climate, to reduce their susceptibility to biotic and abiotic stresses, to control tree size, to enhance yield and fruit quality while improving economic return and reducing environmental impact. Concerning temperate zone species, interest in Europe is mainly oriented to wild relatives of stone fruits (*Prunus* spp.), pear (*Pyrus* spp.) and Hazelnut (*Corylus* spp.) which are native or naturally spread in the region.

P. mahaleb L., the Saint Lucie cherry, native to Central and Southern Europe, is the most widely used wild rootstock in sweet and sour cherry (*Prunus avium* L., *P. cerasus* L.) orchards, but investigations are being intensified on *Prunus cerasifera* Ehrh., the Myrobalan, native to South-Eastern Europe and the Near East. Other wild species of interest as cherry rootstocks comprise *P. canescens*, *P. tomentosa* and *P. fruticosa*. The Myrobalan is also used in breeding rootstocks which are compatible with plum, apricot and peach, as well as wild plum species *P. insititia* and *P. spinosa*. Most pear cultivars are grafted on wild *Pyrus communis* seedling rootstocks, or on quince (*Cydonia o*blonga Mill.). Currently, the few other wild species employed in pear rootstock research are *P. pyraster* Burgsd. and *P. syriaca* Boiss. *Corylus colurna* L., the Turkish hazelnut, is native to South-eastern Europe and interesting as rootstock, since it is non suckering and improves water efficiency in cultivars. The present work analyses current trends in the use of wild relatives as rootstocks for cultivated fruit species, aiming to provide an overview on their strengths to be further exploited in future research and breeding.

Keywords: wild species, fruit cultivation, breeding, rootstocks

Screening resistance against pea weevil (*Bruchus pisorum* L.) in the primary gene pool of Ethiopian field pea (*Pisum sativum* var. *sativum* L.) accessions

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Abstract

Field pea (*Pisum sativum* L.) is an important agricultural crop worldwide, as a main source of protein in human diet and as animal fodder. In Ethiopia, it is the second most important legume crop, next to faba bean (*Vicia faba* L.). However, its production is suffering from a devastating pest, the pea weevil (*Bruchus pisorum* L.), which is rapidly spreading to areas throughout the country where field pea is currently grown since its introduction three decades ago. During June-October 2011 a total of 602 pea accessions from Ethiopia were screened for pea weevil resistance at three field sites, where pea weevil is a major pest problem. From this trial, accessions with low mean percent seed damage were selected and evaluated during the following season (June-October 2012), in replicated trials. Some genotypes from selected accessions were also screened in the greenhouse for three consecutive generations. Both in the field trials and greenhouse experiments, a significant level of variation in seed percent damage was observed among accessions/genotypes. In the field trial, accessions GL8440, GL0840 and GV4710 showed a moderate level of resistance with less than 30% seed damage during the F2 while released varieties like Adet, scored nearly 80% seed damage. A similar pattern was also observed in the greenhouse experiments where genotypes 37-3 -VOK-par, 37-3-LGRK-par and 37-3-LGRK-pro-1-1 recorded very low or no pea weevil damage. This work is a first step in finding resistance to pea weevil in the gene pool of field pea in Ethiopia.

Keywords: resistance, *Bruchus pisorum*, field pea, pea weevil, *Pisum sativum*

Wild relatives in breeding to improve wheat cereal

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Abstract

Wild cereal is the best reserve and resource to improve crops (bio-resistance and abiotic stress, lack of micronutrients, efficient photosynthesis, etc.) for use in breeding programs.

We studied a set of wild species (*T. timopheevi*, *T. militinae*, *T. kiharae*, *T. dicoccoides*, *Ae. cylindrica*, *Ae. triaristata*) and 15 constant hybrids samples between wild species and winter, spring wheat. Iron, zinc, serum and cadmium in the grain determined using inductive plasma-atomic emission spectrometry (ICPAES). Several wheat breeding lines developed with various of wild wheat relatives showed high grain Fe concentration, especially the lines WAH x *T. kiharae*, WAH x *T. militinae*, Zhetisu x *T. kiharae* which can be exploited in breeding programs aiming at improving Fe concentration of modern wheat grains.

This forms combine technological and nutritional properties in one genotype. The level of S accumulation in the wild relatives grain of cultivated forms significantly limit: Ae. triaristata 2404-2565 mg/kg; *Aegilops cylindrica* 2164-2404 mg/kg; *T. militinae* 2190-2330 mg/kg; *T. timopheevi* 1841-2443 mg/kg; *T. kiharae* 2124-2205 mg/kg in comparison with the cultivars in the range of 1452-1836 mg/kg. Constant line by crossing wild relatives was characterized by S containing, intermediate between wild and cultivated forms N: S ratio in these forms is optimal for wheat bread (no more than 17:1). We have also found that gluten content of cereal wild-relative crosses line declined in following order: *T.kiharae* (up to 44,0 %) > *T. timopheevi* (up to 36,0 %) > *T. militinae* (up to 35,2 %). Lines 1675, 1671, 1723 allocated as high level of grain Fe and Zn (55, 59 and 44, 48 mg / kg), also “K” 4584 - 4858 mg/kg; phosphorus - 3860 - 3894 mg/kg; the S content 1999 -2017 mg/kg, Ca - to 665 mg / kg, which indicates a high productive and adaptive capacity.

Keywords: Wild wheat, iron, zinc, serum, gluten content, grain quality

Identification of allelic variants present in durum wheat (*Triticum turgidum* L. var *durum*) landraces able to confer salt tolerance

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Abstract

In the climatic changes framework, the water resources will be more and more important not only in terms of availability, but also of quality, considering that these led to an increase of water salinity. Landraces are often a reserve of important adaptive allele variants useful to be inserted in pre-breeding activity focused to face the climatic changes. Wheat modern varieties, cultivated over 210 Mha, in spite of its importance and diffusion, has not a specific salt tolerance traits to be introduced in the improved variety. The mechanisms developed by plant to tolerate salinity stress are not simple involving complex and elaborate signaling networks, which could be summarizing in three main strategy adopted by the plants: (i) osmotic tolerance, (ii) tolerance to Na+ and (iii) Na+ exclusion in the tissues. In order, to identify allelic variants able to confer tolerance to water stresses, conserved domains of transcription factors involved in salt tolerance have been multialigned and specific primers of DREB1, WRKY1 transcription factors (TFs) and HKT-1 have been designed. Full-length cDNA extracted from durum wheat accessions treated with solutions containing different salt concentrations were amplified with HRM (High Resolution Melting) technology in order to identify allelic variants revealed by differences in melting temperatures. The different amplicons obtained, have been sequenced and SNPs variants have been identified. Some of them were non-synonymous (nsSNPs) causing changing in peptide sequences. Several SNPs mutations identified, have been found in the highly tolerant durum landraces Jennah Khetifa, treated with the maximum salt concentration (1.5 M). Present results underline the value of these landraces and their mutants, which carry advantageous characteristics never identified before, that are of interest for stress tolerance breeding activities in durum wheat.

Keywords: durum wheat, salinity tolerance, HRM, SNP

Looking for Insect resistance in *Brassicas*: Combining physiology with plant transcriptomics to identify new sources of resistance and candidate genes

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Abstract

Brassica crops are grown worldwide for oil, food and animal feed, and constitute a significant economic value due to their nutritional, medicinal, bioindustrial, biocontrol and crop rotation properties. Insect pests cause enormous yield and economic losses in Brassica crop production every year, and are a threat to global agriculture. Worldwide losses caused by insects are at least 30% and perhaps 50% when no insecticides are used. However the use of pesticides can be hazardous to the environment and is usually not very durable as insects may develop resistance very rapidly. Additionally in 2009 the European Parliament proposed legislation placing controls on crop spraying, banning 22 pesticides. Therefore crop production is in need of alternative control measures, of which resistant varieties are most promising. This project has aimed to identify plant resistance factors against the cabbage aphid in varieties of Brassica (*Brassica oleracea*) and its crop wild relatives. These insects are phloem feeding herbivores and cause serious problems in *B. oleracea* crops across Europe. Host plant resistance towards insects can be based on different mechanisms, for example in phloem feeding pests we can distinguish between phloem location and phloem acceptance. Using a combination of different resistance mechanisms could result in more durable resistance. This study elucidates the different resistance mechanisms present in genetic resources of brassicas. The EPG (Electrical Penetration Graph) method has been used to determine the underlying mechanisms of resistance by comparing insect feeding behavior across the different plant genotypes. At the same time, whole genome transcriptomics analysis has been carried out using Affymetrix gene chips to assess gene expression variation across different accessions/CWRs to determine within species variation and response to insect attack.

Keywords: Insect-Plant interaction, Aphid resistance, Electrical penetration graph(EPG), Gene expression profiling

Mapping and validation of QTLs for resistance to whitefly in cabbage

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Abstract

In previous studies the white cabbage cultivar Rivera was identified as resistant against the cabbage whitefly (Aleyrodes proletella) (Broekgaarden et al. 2010). Adults died within a week and nymphs were not able to develop on this cultivar (Broekgaarden et al. 2012). An intraspecific F2 population, obtained from a cross between the susceptible white cabbage cultivar Christmas Drumhead and Rivera as pollen donor, was grown in the field and scored for whitefly adult survival and ovipostion rate, as well as several morphological characteristics, including wax layer, leaf toughness and head formation. In total 179 F2 plants were phenotyped, including both parental accessions. Clear differences in whitefly performance were seen in the population and between the parents. A genetic linkage map based on 140 SNP markers was calculated and association between markers and phenotypic traits were identified. QTL were found for adult survival (Chr. 9) and oviposition rate (Chr. 4), as well as a major QTL for wax layer presence (Chr. 3) and minor QTLs for leaf toughness (Chr. 1 and 6) and head formations (Chr. 2 and 5). None of the morphological characteristics was linked to adult survival or oviposition rate. Seeds were collected from the 11 most resistant and susceptible F2 plants but only of these, five resistant and four susceptible, produced F3 seeds in sufficient quantity and quality for validation of the QTLs. A no-choice field experiment was carried out in late summer in which 20 plants per F3 line were screened for adult survival and ovipostion. The markers with the highest LOD score in the QTL mapping performed in the F2 population were significantly correlated with the resistance among the F3 plants. The F3 lines derived from F2 plants that carried the Rivera alleles of the resistance related markers in either homozygous or heterozygous form were significantly more resistant than those homozygous for the Christmas Drumhead alleles. Fine mapping is needed to narrow down the regions of interest to assign candidate genes for adult survival and ovipostion in cabbage.

Keywords: Aleyrodes proletella, Brassica oleracea, host resistance, age dependent resistance

Crop wild relatives as a source of insect resistance: example of thrips resistance in pepper (*Capsicum annuum*)

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Abstract

Thrips are small insects but may cause big losses in pepper cultivation. Direct damage results from feeding on leaves, flowers and fruits, while indirect damage is caused by the transmission of viruses especially TSWV. We developed bioassays for resistance to two thrips species (*Frankliniella occidentalis* and *Thrips parvispinus*) and showed that non-choice, detached leaf and leaf punch assays correlated well with whole-plant assays. Based on both whole-plant assays and detached leaf and leaf punch assays we identified several accessions with strong and medium resistance to these species (Maharijaya et al, 2011). The strong resistance in two wild *Capsicum annuum* and one *C. baccatum* accessions was shown to reduce oviposition by adult *F. occidentalis* females and to almost completely block the development of L1stage larvae into L2 and further stages (Maharijaya et al, 2012). Finally we produced an F2 cross population based on one of the resistant *C. annuum* accessions and mapped a major QTL on pepper chromosome 6. This resistant wild accession and markers closely linked to the QTL will enable the breeding of thrips-resistant varieties. Maharijaya A, Vosman B, Steenhuis-Broers G, Harpenas A, Purwito A, Visser RGF & Voorrips RE (2011) Screening of pepper accessions for resistance against two thrips species (*Frankliniella occidentalis* and *Thrips parvispinus*). Euphytica 177: 401-410. Maharijaya A, Vosman B, Verstappen F, Steenhuis-Broers G, Mumm R, Purwito A, Visser RGF & Voorrips RE (2012) Resistance factors in pepper inhibit larval development of thrips (*Frankliniella occidentalis*). Entomologia Experimentalis et Applicata 145: 62-71.

Keywords: pepper, *Capsicum annuum*, thrips, *Frankliniella occidentalis*, *Thrips parvispinus*, Resistance, QTL

Hungarian sunflower landrace ISZCS (*Helianthus annuus* L.) as a source of fertilizing ability of central flowers of disk (FACFD) to drought-heat stress resistance

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Abstract

In Hungary, the drought and heat stress is a serious problem nowadays. The climatic change causes water deficiency and high temperature at flowering time of sunflower almost every growing season. The sunflower has a good tolerance to drought and heat stress separately, but it is not true when they occur together. The high potential oil hybrids show significant yield losses due to drought-heat stress frequently. The typical symptom is that the central flowers of the disk don’t able to fertilize, or the zygotes are aborted. In this case there are no seeds in the centre of disk, which may cause yield reduction up to 20% on the field.

ISZCS is an ancient Hungarian landrace maintained by Feed Crops Research Institute. This germplasm was selected at the central region of Pannonia (Western Hungary) before Second World War. Typical traits of ISZCS are the color and brightness of achene, the excellent hullability, high protein content of seeds, and specific size and shape of achene. Furthermore, the fertilizing ability of central flowers of disk (FACFD) is highly good and stable.

This landrace has several disadvantageous features too, for example: self-compatibility, sensitivity to several diseases and other pests, low yield potential.

Our aim was to build the FACFD character into our new inbred lines and hybrids.

The breeding process was started at 1999 from elite individuals of ISZCS. During the breeding cycles has become clear that FACFD is controlled by partial dominant alleles. In this case the trait has to build into both parental lines of hybrids. In S4-S6 generation of third breeding cycle we could select new elite lines (restorers and maintainers) which were homozygous for FACFD alleles and had high level of resistance to drought-heat stress.

Yield of our new sunflower hybrids with FACFD alleles from ISZCS landrace, will be more resistant to drought-heat stress.

Keywords: sunflower landrace ISZCS, drought-heat stress resistance, fertilizing ability of central flowers of disk

Morphological and molecular characterization of a barley composite cross derived population

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Abstract

There is a need for the development of new cultivars that better tolerate biotic and abiotic stresses and that realize high performances in low-input conditions for the improvement of barley productivity. This requires a good understanding and management of the genetic diversity existing in both landraces and cultivated barley. However, with the rapid disappearance of landrace populations from their primary and secondary centers of diversity, heterogeneous populations might offer a realistic alternative by producing a modern equivalent of landraces or "reconstituted" landraces. Composite cross derived populations (CCP) can be useful materials to exploit genetic diversity in environmentally friendly agricultural systems and provide experimental material for studying effects of natural selection and as a source of locally adapted new varieties. In 1997, barley CCP was produced by crossing seven different F8 progenies, derived from seven crosses of cultivars, landraces and promising lines that were good performers under low-input conditions in Central Italy. The population was then multiplied for 13 years under a low input management system and without any conscious human selection. In 2011, 91 seeds from the CCP were randomly chosen and grown in the field as single plants that were characterized using morphological and molecular markers ("neutral" an EST-derived SSR). Data from the molecular analysis underlined that genetic diversity was mainly conserved in the CCP after 13 years of multiplication and, according to the different multilocus genotypes identified, that the population is composed of a minimum of 60 different genotypes. Evidences of selection for key genome areas, known to be involved in abiotic stress response in cereals, were also detected. In addition, results from the morphological characterization indicated that the population contains interesting lines that overcome the best varieties for traits of agronomic relevance like spike weight, number of seeds per spike and kernel weight.

Keywords: barley, composite cross, genetic diversity evolution, SSR molecular marker, molecular characterization, morphological characterization

Proline related genes expression in *Hordeum vulgare* response to water-deficit stress

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Abstract

Osmotic stress severely limits plant growth and agricultural productivity. In response to drought and salinity stress, many plant species accumulate high levels of proline, which is thought to function in stress adaptation. It has been suggested that proline protects plant tissues against osmotic stress because it is an osmosolute, a source of nitrogen compounds, a protectant for enzymes and cellular structures, and a scavenger for hydroxyl radicals. It was reported that constitutive production of proline could confer osmotolerance in transgenic plants. But somehow, the mechanism by which osmotic stress induces P5CS gene expression and proline accumulation is still not understood. In the present study, two P5CS genes (HvP5CS1and HvP5CS2) were isolated for the first time from barley. Expression analysis revealed that the transcript of HvP5CS1 and HvP5CS2 in leaves was significantly up-regulated in four barley cultivars exposed to osmotic stress. The results suggested that HvP5CS genes might play a critical role in barley adaptation to osmotic stress and the over expression of HvP5CS genes, in particular, over expression of HvP5CS2 by genetic engineering method, might be an effective way to enhance the drought tolerance of sensitive barley.

Keywords: gene expression, P5CS, proline accumulation, osmotic stress

Exploration of underutilized crop diversity of *Capsicum* peppers in their primary center of diversity in Bolivia and Peru

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Abstract

The genus *Capsicum* is a highly diverse complex of domesticated and wild species that displays abundant variation in its main center of domestication and diversity in Bolivia and Peru but that remains under-researched. New collecting expeditions undertaken in 2010 by the Instituto Nacional de Innovación Agraria (INIA) in Peru and the Centro de Investigaciones Fitoecogenéticas de Pairumani (CIFP) in Bolivia have significantly increased the size of the collections. INIA Peru now maintains 712 accessions of the five domesticated species, making it one of the largest and most diverse national collections of native *Capsicum pepper* varieties in the world. The collection in Bolivia contains 492 accessions, including the five domesticated species, four wild species, and one wild botanical variety of a domesticated species. We report on the identification of promising native Capsicum germplasm for potential use in the development of differentiated products. Identification of promising material representative of native Capsicum diversity in both collections followed several steps: (1) Identification of a core collection of nearly 100 accessions per country representing the different species and their geographic distribution. Dried samples of these accessions were biochemically screened for commercially interesting attributes including capsaicinoid content, polyphenols, antioxidant capacity, carotenoids, lipid content and color; (2) Based on results of the biochemical screening, sub-sets of 44 Bolivian and 39 Peruvian accessions were selected, representing the different species and variation in biochemical attributes; and (3) The selected materials were grown in different environments to identify the agro-ecological conditions were they best express the special properties of commercial interest. The biochemical screening and agromorphological characterization and evaluation revealed that Capsicum accessions from Bolivia and Peru have unique combinations of functional attributes, confirming that a wealth of commercially valuable properties can be found in *Capsicum*'s primary center of diversity. This study was financed by GIZ.

Keywords: *Capsicum*, Peru, Bolivia, Biochemical screening, Agromorphological characterization, Germplasm selection

Interspecific introgression of resistance to reniform nematode from *Gossypium barbadense* L wild photoperiodic accession GB713 into upland cotton

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Abstract

Rotylenchulus reniformis Linford and Oliveria, *reniform* nematode, is a major pest of cotton. There are no known upland cultivars or wild accessions of *Gossypium hirsutum* L, highly resistant to this pest. A wild photoperiodic *G. barbadense* accession GB713 was identified as highly resistant and molecular markers indicated two QTL, Renbarb1 and Renbarb2, on chromosome 21 and one QTL Renbarb3 on chromosome 18 were associated with resistance. A single resistant plant of GB713 was crossed with elite cultivar SureGrow 747 and the F2 generation of 800 plants was grown in the field at Mississippi State, MS and all (204) flowering plants were genotyped with selected DNA markers, GH132_201, BNL3279_106, and BNL569_131. Fifteen F2 flowering plants homozygous for markers for the three QTL were backcrossed to SureGrow 747. The 15 BC1F2 populations were grown in the field and at least 100 plants in each were genotyped with the selected markers and 32 plants from 10 populations were backcrossed to SureGrow 747. The 32 BC2F2 populations were grown in the field and 16 populations were screened for markers. From these BC2F2 populations, two plants homozygous for three QTL and one plant homozygous for two QTL were selected, self pollinated, and in BC2F3 they were evaluated for resistance to reniform nematode and agronomic performance. These three lines, M713 Ren1 and M713 Ren2 (homozygous for markers for Renbarb1 and Renbarb2 and Renbarb3) and M713 Ren5 (homozygous for markers Renbarb1 and Renbarb2) were released in BC2F4 as productive germplasm with genes for resistance to *reniform* nematode. Commercial cotton seed breeding companies are incorporating these QTL into their breeding programs using marker assisted selection to produce resistant cultivars.

Keywords: Use of wild species, Marker assisted selection, Cotton, *Gossypium hirsutum*, *Gossypium barbadense*, *Reniform nematode*, *Rotylenchulus reniformis*

First reports on the local landraces of chickpea (*Cicer arietinum*) in Serbia and results on their breeding value

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Abstract

Chickpea (*Cicer arietinum*) originated in Near East and is one of the most ancient crops in the world. The material evidence on the presence of chickpea on the territory of present Serbia goes as far back as sixth millennium BC. However, today it is not considered a genuine crop and is completely imported, being used mostly as a snack. In May 2011, several local landraces of chickpea were discovered in the villages of Klinovac, Klenike and Sveta Petka in the County Pčinja in the deepest south of the country. Along with the seed samples, useful data were gathered from the local farmers related to cultivating. Each household grows its own landrace for its own needs, without exchanges and rarely selling them on nearby village or town green markets. All local landraces are sown in March and are usually intercropped with maize in small fields together with other crops. The collected local landraces from the Pčinja villages were included in the only chickpea collection in Serbia, maintained by the Institute of Field and Vegetable Crops in Novi Sad, with about 100 accessions of exclusively foreign origin collected from 2001 onwards. A preliminary evaluation of the Pčinja chickpea populations was carried out during 2012 and 2013 in the field conditions near Novi Sad, 500 km to the north from their native environment. It demonstrated higher grain yield and more prominent earliness in comparison to the cultivars present at the Serbian market, mostly of Turkish origin. This provides a solid basis for establishing the first Serbian chickpea breeding programme aimed at developing cultivars well-adopted for local conditions and use.

Key words: local landraces, chickpea (*Cicer arietinum*), breeding value

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In Vitro Conservation of Plant Genetic Resources in Jordan

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Abstract

Jordan has made significant achievements in conservation of plant genetic resources. Along with the in situ conservation and the seed gene bank, in vitro conservation has been experimented on various plant species especially the wild relatives and endangered species. Medium-term conservation has been used utilizing omoticums added to the media, low temperature and growth retardants. Long term preservation (cryopreservation) has also been applied on many wild relatives and horticultural species. Methods including encapsulation-dehydration, encapsulation-vitrification, vitrification and droplet cryopreservation were reported for many species. Genetic stability of in vitro conserved material was also tested to assure the fidelity of the stored plant material. The Royal Botanic garden is now approaching the conservation of red-listed plants using updated conservation methods. Capacity building is taking a great effort to have well trained people, infrastructure and instruments for in vitro conservation of wild relatives germplasm

Keywords: cryopreservation, *In Vitro* Conservation, wild relatives germplasm

Defining gene pools to enhance cultivated *Phlox*: Development and characterization of wild germplasm for use in insterspecific hybrization between an ornamental crop and its wild relatives

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Abstract

The North American native genus *Phlox* plays an important role as an ornamental in constructed landscapes. A collection of wild germplasm is being developed to support the genetic improvement of cultivated *Phlox*. The principal horticultural forms in this genus include the tall and long-blooming summer phlox (*P. paniculata*); the prostrate and intense-but-briefly blooming moss phlox (*P. subulata*); the low-growing and more dainty woodland phlox complex (*P. divaritaca, P. carolina, P. glaberrima*); and the intensely floriferous winter annual Drummond phlox (*P. drummondii*). The attributes that make these ornamental crops attractive are countered variously by significant limitations such as disease susceptibility, restricted adaptability, and short blooming periods. Because the genus consists of approximately 65 species distributed in diverse habitats, principally in the Eastern half and in the Central Texas/Rocky Mountain region of USA, there likely exists wide diversity in wild relatives that could be tapped for enhancement of the horticultural forms. The Ornamental Plant Germplasm Center has begun developing a collection of crop wild relatives for *Phlox* for use in germplasm enhancement. Approximately 180 accessions consisting of 16 species (31 taxa) have been collected thus far and a systematic process of characterization begun. Our initial focus has been on analysis of ploidy and DNA content using flow cytometry. This characterization has identified some populations with varied ploidy, although the majority of wild accessions are diploid. The potential for hybridization between these species to help define the gene pools is being systematically analyzed. Initial hybridization studies not surprisingly indicate members of a given subsection are more like to hybridize than those of different subsections, but some wide hybrids are possible. However, in many cases of intersectional and different-ploidy combinations, the interspecific hybrids had significant sterility, potentially limiting further breeding unless fertility can be restored by allopolyploidization.

Keywords: *Phlox*, wild species, germplasm, ploidy, flow cytometry, interspecific hybridization

Genetic Diversity and Association Mapping Studies in *Colchicum* L.

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Asbtract

Occurrence of the high frequencies of *Colchicum* L. species in Turkey and the elevated number of the endemics could be a strong indication that Turkey is a major center of diversity for *Colchicum*. In this study, genetic diversity among 49 species including 168 populations of large *Colchicum* genus was investigated by Random Amplified Polymorphic DNA (RAPD), Inter Simple Sequence Repeat (ISSR) and Amplified Fragment Lenght Polymorphism (AFLP) markers at molecular level. A high level of polymorphism was observed in the genotypic profiles of plants. Within the scope of the morphological analysis, 42 morphological parameters were examined according to The International Union for the Protection of New Varieties of Plants (UPOV) requirements. We observed extensive morphological variations among the natural populations of *Colchicum* L. collected from various geographic and climatic regions of Turkey. The results obtained from the DNA fingerprinting data will be associated with morphological characters for genome-wide association mapping study. These results will make a major contribution to analyze the taxonomic classification of the genus, understanding of evolution with the discovery of genomic structure and relations of a lot of species of *Colchicum* genus growing naturally in Turkey's flora using current morphological and molecular methods.

Keywords: *Colchicum* L., DNA markers, morphology, genome-wide association mapping

LEAFY as a Candidate Gene for Association Mapping in *Colchicum* L.

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Abstract

The high frequencies of species and of endemics in Turkey indicate that is major centers of *Colchicum* L. diversity and speciation. *Colchicum* L. is represented by 49 taxa of which 35 are endemic in Turkey and some of these species are autumn-flowering species, whereas the others are early-spring flowering species. In this study, we aimed to map and identify the genes which affect flowering *Colchicum* L. species by using candidate gene based association mapping. *LEAFY* gene plays an important role in regulating flowering in *Arabidopsis* and it encodes a plant-specific transcriptional factor. The primary function of *LEAFY* is to repress the development of vegetative organs and to promote the formation of flower meristem. In this study, 168 *Colchicum* L. populations contain 49 species and 17 new candidate species in the flora of Turkey were used. Flowers of autumn and spring *Colchicum* L. species were measured using different morphological parameters (number of flowers, shape of flowers, size of flowers, redolence, flower life, vegetation time, aspect of pendruncle, size of pendruncle, diameter of pendruncle, color of pendruncle, tepal size, shape of tepal, shape of tepal surface, color of tepal, tessellation, anther color, anther size, filament size, style size, number of style color and position of the stigma). Pairwise comparisons of measured morphological parameters and amplification profiles of *LEAFY* gene were detected up in 168 *Colchicum* L. populations. Primer pair was designed for *LEAFY* gene associated with the development of flowers and PCR amplifications were performed. Differences of DNA sequence of this gene associated with measured morphological data of flower will be evaluated with Tassel statistical program and association mapping will be done with candidate gene approach. This approach proved to be a valuable strategy for identifying genes implicated in key processes of flower development, which are therefore potential targets for genetic improvement of colchicum.

Keywords: *Colchicum* L., morphological characters, candidate gene association mapping

PGR management in Poland - SWOT analysis

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Abstract

About 60% of the total area of Poland, i.e. 18.7 million hectares, is used as agricultural land. Agriculture in Poland is characterized by a large fragmentation of farm holdings (on average 10.42 hectares). In the frame of PGR Secure project the interviews were carried out with representatives of the gene bank, public research organizations, NGOs and breeding companies. On the basis of these interviews a preliminary SWOT (strength, weakness, opportunity and threat) analysis was carried out to identify the crucial issues relating to the PGR management in Poland. The strengths points are: Poland is a country with considerable biodiversity, has clear governmental control on the PGR sector and the national genebank system is well organized. The access to germplasm is provided via the genebank website and the cooperation between all stakeholder groups is well developed. Threats for the PGR management were identified as: decreasing staff capacities in the public PGR sector, insufficient financial means required to improve the flow of characterisation and evaluation data between stakeholders, a too strong focus of breeding research, pre-breeding and breeding on major crops and lack of incentives to use LR and CWR in long-term in broadening programs of companies. The opportunity for the PGR management in Poland is increase of the efficacy of the Polish genebank system through the AEGIS process, development of market niches for native species / regional products, improvement of the public interest in agrobiodiversity issues through the support of agro-NGO sector and development of agrobiodiversity friendly (ecological) farming systems.

Keywords: PGR management, SWOT analysis, CWR LR conservation, Pre-breeding

Barley landraces as source of resistance to leaf rust and powdery mildew

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Abstract

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops in the world. In barley, many race-specific resistances to powdery mildew and leaf rust are available. However, in the last twenty years several sources of powdery mildew and leaf rust resistance have been overcome by virulence in the pathogen. Barley breeders are constantly looking for gene pools from which new genes can be introduced into existing cultivars in order to improve resistance to both these pathogens. Many of the powdery mildew and leaf rust resistance genes used commercially are derived from landraces. Based on many reports it may be assumed that barley landraces may possess powdery mildew and leaf rust resistance genes different from those which already have been introduced into barley cultivars.

The objective of this study was to determine the identity of powdery mildew and leaf rust resistance genes in lines selected from 908 barley landraces from ICARDA collection. These landraces were collected in West Asia and North Africa (Jordan, Egypt, Libya, Tunisia, Algeria and Morocco). Differential isolates of powdery mildew and leaf rust were used to recognize specific resistance genes.

Results of this study confirmed that barley landraces possess powdery mildew and leaf rust resistance genes different from genes present in cultivated varieties. As isolates used in this experiment had virulences corresponding to all major resistance genes used in Europe to date, it may be concluded that these lines had resistance to all powdery mildew and leaf rust virulence genes prevalent in Europe. These lines should be used as new sources of resistance to powdery mildew and leaf rust in barley breeding programmes.

Keywords: barley, landraces, pre-breeding, resistance, powdery mildew, leaf rust

Ecotypes as a source of diversity for perennial grasses recommended for conventional and low input agriculture

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Abstract

Permanent grasslands are a source of healthy forage 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. Biodiversity include biotic variation at intraspecific genetic variation level, species diversity and ecosystem diversity. 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. As an example is the most important species - perennial ryegrass. Based on the results obtained during evaluation of 169 population belonging to six groups - diploid and tetraploid commercial cultivars; clones and ecotypes it was possible to conclude that they formed a distinct group in terms of the most important agriculture traits. The range variability has been moving towards forms with the traits more important from the agricultural point of view. Because of this the aim of the study was to evaluate diversity in the perennial grasses species recommended for conventional and low input agriculture. Red Fescue, Meadow Fescue, Timothy-grass, Kentucky Bluegrass, Wood Bluegrass, Tall Meadow Oat and Redtop cultivars and ecotypes were investigated. Resistance for biotic and abiotic stresses and plant morphology traits were described. Based on the obtained results it was possible to conclude that from the marginal group of the grass species Redtop could be recommended for both type of agriculture.

Keywords: perennial grasses, ecotypes, cultivars, resistance, biotic and abiotic stresses, low input agriculture

Variability in cowpea germplasm assessed using phenotypic traits

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Abstract

Cowpea can be used for human food and livestock feed in developing countries. It is also used to enhance soil fertility. Information on genetic variability levels among the existing cowpea germplasm will potentially increase the efficiency in cowpea improvement programme in South Africa. Field experiments were conducted at the Roodeplaat Vegetable and Ornamental Plant Institute, South Africa, to estimate the level of phenotypic variability among 22 cowpea germplasm. The experiment was laid out in a randomised complete block design with three replications. Fifteen phenotypic traits were recorded. Analysis of variance for the phenotypic traits revealed that differences among genotypes were highly significant for all traits. This indicated the high level of genetic variability among the accessions studied. The pair-wise genetic distances based on phenotypic traits showed varying genetic distances. The principal component analysis showed that the first principal components (PC) contributed 74.75% of variability among the accessions. Cluster analysis of the phenotypic traits resulted in four distinct groups of accessions. Therefore, the phenotypic markers provide a useful measure of genetic distances among cowpea accessions to identify potential parental materials for future breeding efforts in South Africa.

Keywords: Accession, cowpea, phenotype, variability

Theme 2: Conservation strategies

National implementation of the conservation of plant genetic resources within Norway

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Abstract

We have a responsibility to conserve plant genetic resources native to Europe for the rest of the world to utilise. The populations and species of crop wild relatives (CWR) found in Norway are adapted to unique environmental conditions due to the great variations in climate, altitude and day length plus the recent glacial past. An important goal for plant genetic resource conservation is not to conserve whole species as such, but to preserve the genetic diversity within each species (Poulsen, 2009). This may mean the conservation of specific populations of common species which have developed in unique conditions. A national strategy for the conservation of CWR in Norway will not be a standalone procedure but will help the authorities meet conservation targets set out by the Convention on Biological Diversity (CBD), the Global Strategy for Plant Conservation (GSPC) and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITFPGFA). A preliminary report identified 174 priority CWR in Norway found within a network of 19 complementary in situ sites. Site 2 on the south eastern coast of Telemark appears particularly interesting. The two islands of Jomfruland and Stråholmen show high levels of CWR diversity and with the current plans of a new national park which will incorporate both islands and their current nature reserves; this presents a unique opportunity for the integration of Norway's first CWR genetic reserve. Further research on CWR conservation in Norway will involve detailed genetic diversity studies between crop species and wild taxa as well as establishing a threshold level for effective conservation of maximum genetic diversity within and between CWR populations.

Keywords: Convention on Biological Diversity, *In situ* conservation, Crop wild relatives, Norway, Plant genetic resources

Development of a national crop wild relative conservation strategy for Cyprus

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Abstract

Growing research interest in crop wild relatives (CWR) has highlighted their value for crop improvement, particularly to mitigate the impact of climate change and contribute to global food security. As most conservation activities are implemented at national level there is a requirement for each country to develop and implement a national CWR conservation strategy. This will contribute to regional and global CWR conservation actions and so help achieve CBD Aichi Targets 13 of improved genetic conservation of socioeconomically important taxa. Furthermore the Global Strategy for Plant Conservation (GSPC) Target 9 (CBD, 2010a) and the European Strategy for Plant Conservation 2008-2014 (ESPC) Target 7.1, 7.2 and 9.1 (Planta Europa, 2008), all stress the importance of the conservation of genetic diversity in CWR, with the ESPC highlighting the importance of in situ reserves. Cyprus has historically lacked systematic CWR conservation but is rich in CWR diversity being located in the eastern Mediterranean Vavilov centre and abutting the Fertile Crescent, it is also one of the countries with the highest concentration of CWR per unit area (Vincent et al., 2013) therefore a more coherent approach to CWR conservation is desirable. From an initial checklist of 1,722 Cypriot CWR taxa, 178 CWR were prioritized and eco geographic data was collated and analysed using GIS techniques. The Troodos and Pafos mountains are CWR hotspots and ten priority sites containing the genetic diversity of 74.7 % of priority CWR taxa were identified. These will form the basis of a national network of in situ genetic reserves. To complement in situ conservation 78 priority CWR taxa that have no accessions in the national Cyprus gene bank are highlighted for collection and ex situ storage.

Keywords: Conservation, Crop wild relative, Cyprus, *ex situ, in situ*, GIS, Prioritization

Cultural relict plants – living ancient monuments and how to conserve them

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Abstract

There are plants once cultivated, now naturalised and a sort of living ancient monuments. We call them cultural relict plants (CRPs).

CRPs were introduced by humans. CRP populations may have had little or no crosspollination from other populations, and may possess different and valuable traits, thus being of interest e.g. for breeding or other utilisation. In addition, they belong to our cultural heritage.

In the Nordic region, CRPs can be found within more than 200 species, once cultivated and used for food, medicine, flavour, fiber, and as ornamentals.

CRPs are often found in surroundings of ruins, old villages, manors, and church yards. One of the main threats to these populations takes the form of human activities. Sites of this type are often intensely managed, or managed in a, for the CRPs, unfavorable way.

A network of Nordic botanists, garden archaeologists, ethno-botanists, managers of historic sites and the Nordic Genetic Resource Center (NordGen) is established. A workshop in Egilsstaðir, Iceland, in
2012 discussed conservation strategies for CRPs. One conclusion was that first priority should be conservation *in situ* – a challenge as the locations are often private property. Hence, it is important to inform caretakers and managements about the existence of CRPs, and how to manage the sites in ways favorable to the survival of the CRPs. Conservation of threatened populations can also be done ex situ in genebanks.

A web page dedicated to CRPs and the Nordic network is found at NordGen's website. An information brochure aimed at caretakers and managements was recently released by NordGen. The first part informs about CRPs. The second part is a guideline, giving simple but effective advice on how to include CRP consideration in the management plans, examples taken from the management of the medieval ruin Hammershus and its surroundings on the island Bornholm, Denmark.

Keywords: cultural relict plant, cultivation, semi-natural, conservation, information, utilisitaion, management, *in situ, ex situ*, gene bank

Developing a crop wild relative conservation strategy for Finland

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Abstract

Crop wild relatives (CWR) are important plant genetic resources as they contain genetic variability for crop improvement. However, many crop wild relatives are threatened in their natural habitats and practical conservation actions are insufficient. National strategies targeted at CWR taxa provide bases for their conservation. To advance the conservation of the CWR genetic resources in Finland, a conservation strategy was developed as a part of the EU-funded PGR Secure project. The methodology for developing a complementary conservation strategy included following steps: (1) creation of the CWR checklist and national inventory, (2) prioritization of the checklist, (3) collecting ecogeographic data and identifying threats to the CWR taxa, (4) undertaking in situ and ex situ conservation gap analysis and (5) writing up the strategy. National agricultural, forestry and environmental agencies were included in the process. The national inventory and checklist revealed that a significant part of the Finnish flora belongs to crop wild relatives. Therefore, a workable list was created by prioritizing the taxa with the criteria of threat, value and use. As a result of the in situ gap analysis, five most species-rich areas within Finland were recommended as possible sites for genetic reserves. The ex situ gap analysis enabled specific recommendations for the future collection of CWR diversity. This presentation aims to show the process of preparing a CWR conservation strategy. Finally, it also stresses the importance of steps towards the implementation of the strategy and the promotion of the use of CWR diversity.

Keywords: crop wild relatives, CWR, plant genetic resources, national CWR conservation strategies

National programme for plant genetic resources – a platform of cooperation in Portugal

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Abstract

Since the 1970s, Portugal has been endeavouring systematic and coordinated efforts for *ex situ* conservation of plant genetic resources:

- National and international collecting missions with: France (forages,pasture, wild carrot), Spain (forages, cereals, food legumes, pasture, medicinal and aromatic plants), UK (forages, pasture, brassicas), Japan (garlic), United States (wild carrot;
- In1983, IBPGR, appointed Portugal-BPGV as the responsible for the Maize Mediterranean collection;
- Signed and rectified the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA);
- Portugal is a founding member (1980) of the European Cooperative Programme for Plant Genetic Resources (ECPGR);
- Within the framework of the ECPGR, Portugal participated in the development of the European Genebank Integrated System (AEGIS) and through the European Genetic Resources Search Catalogue (EURISCO) (12,193 accessions).

Today Portugal maintains ex *situ* a large seed collection of landrace crops and also national clone collections of olive, fruit trees and grapes. BPGV, among its collections, maintains 4,185 accessions of CWR belonging to 35 species from several botanic families. Considering Article 5 of the ITPGRFA, Portugal is developing and consolidating its National Programme for Plant Genetic Resources, with all national partners and stakeholders, directly or indirectly involved in PGR conservation and use.

The strategic priorities (SP) proposed in the National Programme are:

1. National Inventory on PGR;
2. Strengthening *ex situ* long-term conservation of cultivated plants and CWR;
3. Promote *in situ* conservation of agro diversity and CWR;
4. Consolidating the documentation system;

5. Establish participatory networks for characterization and evaluation;
6. Promoting the sustainable use of PGR;
6. Capacity building for conservation and sustainable use of PGR.

Portugal has to make crucial decisions concerning the conservation and use of plant genetic resources, to monitor progress towards improving the genetic resources availability to researchers and farmers and to give early warning of problems and responses to new challenges.

Keywords: Inventory, Conservation, Documentation, Sustainable use

Conservation of crop wild relative genetic resources in Lithuania

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Abstract

Plant breeding was started in 1918 in Lithuania. Accessions of plant genetic resources of local origin were involved in breeding programs of different species of grasses and many new cultivars were bred. There were 848 seed accessions in long term storage of Plant Gene Bank of Lithuania. These accessions belong to 49 different plant genera: 28 genera represent medicinal and aromatic plants and 21 – grasses. The highest number of *Festuca* (202 accessions), *Trifolium* (144 accessions), *Dactylis* (89 accessions), *Lolium* (81 accessions) and *Carum* (103 accessions) are preserved in long term storage. Accessions of *Malus sylvestris* (50 acc.), *Pyrus pyraster* (127 acc.) and *Oxycoccus palustris* (54 acc.) are preserved in field collections. The most of crop wild relative accessions were collected in Lithuania during the last two decades. They were evaluated for disease resistance, cold tolerance and other characters.

Keywords: grasses, fruit crops, long term storage

A gap analysis for *Brassica incana Ten*. and *B. montana* Pourr. present in Italy

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Abstract

Brassica Crop Wild Relatives (CWR) are native to the Mediterranean Basin and closely related to many important crops. In Italy there are 53 taxa and 19 species of Brassica. Actually no information on their real distribution and their status of conservation exist. To gather initial information we carried out an in situ and an ex situ gap analysis for *Brassica incana* Ten. and *B. montana* Pourr., which are strictly related to *B. oleracea* L.. We initially collected population location data from genebank records and from colleague personal communications. Some locations were then visited and actual population existence assessed. Also, location data were matched with area data relative to different protected areas. Inclusive of new records, 48 *B. incana* and 41 *B. montana* populations are recorded in Italy. Some of the *B. incana* and *B. montana* recorded populations could not be found anymore possibly because erroneously located in the past or because extinct. If most of the recorded populations of both species appear to be included in some type of protected areas and to benefit of some form of (at least passive) in situ protection, their actual status should be clearly assessed. While 41 *B. incana* are secured in genebanks, only 15 *B. montana* populations benefit of *ex situ* protection and should be possibly collected soon. Even for crops of great importance like *Brassica* sp. pl., little is currently known about their relic CWR/WHP populations, not all of them are adequately protected either *in situ* or *ex situ* and some may be extinct. The situations for other CWR/WHP Italian populations are also largely unknown.

Keywords: *Brassica*, CWR, GAP analysis

The work presented is carried out within the framework of the PGR Secure project (www.pgrsecure.org), which is a collaborative project funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394.

First steps towards an Italian conservation strategy for Crop Wild Relatives and Wild Harvested Plants

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Abstract

The Italian flora is rich in Crop Wild Relatives (CWR) and Wild Harvested Plants (WHP), which deserve to be protected in situ and ex situ at national and regional level. To develop conservation strategies, as an initial step, we inventoried all of the CWR and WHP species of Italy and annotated, for each of them, synonymies, uses, presence in the main areas of Italy (i.e. Peninsula, Sicilia and Sardinia) and eventual inclusion in the European and National lists of attention. Following both the taxon group and the genepool concepts, 7,128 CWR and/or WHP species were listed; some of them are often collected in the wild for medicinal, ornamental or food use. Considering this high number, as a second step, we created a priority list of CWR and WHP taxa. To the purpose the following prioritization criteria were used: importance of the related crop (in particular for food), authocthony and inclusion in European and National lists of attention. The priority list obtained includes 797 species of which 123 are of top priority. The prioritisation process was further developed at the level of Administrative Region, taking into account, as case studies, the two largest Italian Islands: Sicily and Sardinia. As an additional criterion for prioritization at the regional scale, we considered the inclusion of the species in the Regional Red Lists. Results show that in Sicily and Sardinia there are 74 and 43 species, respectively deserving the highest attention in planning a PGR conservation strategy. Main steps towards effective conservation were depicted on the basis of obtained results.

Keywords: CWR/WHP conservation, Italian inventory of CWR/WHP, Priority list of Italian CWR/WHP

The work presented is carried out within the framework of the PGR Secure project (www.pgrsecure.org), which is a collaborative project funded under the EU Seventh Framework Programme, THEME KBBE.2010.1.1-03, 'Characterization of biodiversity resources for wild crop relatives to improve crops by breeding', Grant agreement no. 266394.

Collection and exploration of crop wild relatives of grasses and herbage legumes in Estonia

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Abstract

Estonian Crop Research Institute (ECRI) executes the national programme on plant genetic resources, financed by the Ministry of Agriculture. The activities comprise the collection and ex situ preservation of crop wild relatives (CWR) of native grasses and herbage legumes. The collected seed samples are multiplied and studied in field experiments either for forage or ornamental purposes. The precious accessions are bred further into cultivars. Among 31 forage or turf cultivars released by the institute up to date, 24 are entirely or partly (in synthetic varieties) based on native material. Extensive collecting missions have been carried through in 1970s and restarted since 2002. Altogether 147 accessions for turf and 205 for forage purposes have been collected by 2013. Two lawn experiments (2004-2009 and 2009-2012) were performed with 15 grass species, 55 and 76 accessions, respectively. The screening has distinguished 5 ecotypes of *Festuca rubra*, one accession of *F. ovina*, Poa pratensis, and *Agrostis capillaris*, that have exceeded the local standards in visual merit. The screening of native forage grass accessions targets herbage yield improvement. The trials in 2010-2012 have revealed two CWRs of *Dactylis glomerata*, one *Festuca pratensis*, and *Lolium perenne* that attained the productivity of standards. As to native forage legumes, seeds of Medicago sp. and *Trifolium pratense* have mainly been collected and researched. Natural populations of these species were collected from old deserted hayfields, grazed lands or roadsides. 35 accessions were researched in 2003–2008. Forage productivity and quality were assessed from the perspective of their breeding value and prospective uses.

Since 2012 ECRI is collaborating in a Public Private Partnership programme for pre-breeding in perennial ryegrass, initiated and co-financed by the Nordic Council of Ministers.

Keywords: use of native germplasm, grasses, herbage legumes

Reintroduction of traditional Slovenian common bean landraces to facilitate their conservation and use

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Abstract

Common bean (*Phaseolus vulgaris* L.) has been cultivated in Slovenia for centuries, resulting in the development of numerous landraces, some of which are still grown today. The gene bank at the Agricultural institute of Slovenia (AIS) holds a collection of 1035 bean accessions collected from various parts of Slovenia in the last decades. A part of the collection was extensively evaluated using morphological, biochemical and molecular markers; special emphasis has been given to drought tolerance. The results revealed that during the centuries of common bean cultivation in Slovenia a diverse collection was formed that should be preserved for the future. Češnjevec, one of the most abundant and popular landraces grown in Slovenia has been studied in details; the genetic background was defined and genetic diversity changes within the landrace over the last 50 years were estimated. With the aim to reintroduce traditional landraces back to cultivation, 16 Češnjevec accessions and 23 accessions of landrace Lišček (another traditionally grown common bean type) were selected from the gene bank at AIS. Three cultivars were included as outgroups. Field studies were conducted in three successive years; plant growth, resistance to diseases and pests were evaluated and the yield was determined. The chemical composition of raw seeds was analysed, which included determination of macro and microelements, dry matter and starch content, crude proteins, crude fiber and polyphenols. Sensory analysis was performed as well as. Based on all the results obtained three landraces, one Češnjevec and two Lišček accessions were selected for inscription in the List of varieties as conservation varieties.

Keywords: common bean, landraces, conservation, use

Ex-situ conservation of genetic resources of crop plants in Saudi Arabia

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Abstract

The Kingdom of Saudi Arabia covers an area of nearly (2,200,000 km2), or about four-fifths of the Arabian Peninsula. Saudi Arabia is one of the most significant agricultural areas in Arabia, due to its diversity of crops including date palms, cereals, fruits and vegetables. Some of these crops have started disappearing from the farms as a result of damages caused by insects, viruses and other harmful pests such as the Red Palm Weevil, which eliminated several varieties of date palms (*Phoenix Dactylifera, Arecaceae*). In addition to the scarcity of ground water and low rainfall, high salinity, lack of labor and drought also have contributed to the degradation of agricultural lands thereby threating the existence of these crops. To avoid the loss of germplasm, rapid collection and preservation of seeds (germplasm) of these crops in plant gene banks is recommended. In the present study, 346 accessions of seeds representing 55 crops were collected from different regions of Saudi Arabia and stored in the Gene Bank of King Abdulaziz City for Science and Technology (KACST) at –18C, (Ex Situ Conservation). Eighteen of the 55 crops, *Coffea arabica*, *Triticum aestivum, Medicago sativa, Eruca* sp., *Cucurbita maxima, Oryza sativa, Cucumis melo, Cucumis sativus*, *Solanum melongena, Allium* sp., *Hibiscus esculentus*, *Cochlearia armoracia, Coriander sativum, Allium sativum, Illicium verum, Lactuca sativa* (elongated leaf)*, Sesamum indicum, Vigna unguiculata* are believed to be indigenous to Saudi Arabia. However, some of these crops such as *Eruca* sp, and *Cucubita maxima* have become extremely rare or endangered as a result of pest attack. In addition to the conservation of germplasm, KACST- GB also is involved in the production of seeds of some of the crops such as *Allium* sp., *Allium sativum, Solanum melongena*, etc. in order to conserve them in a field gene bank and also to substitute new seeds in GB, the old seeds in the GB with new ones. Further collections of seeds (germplasm) of crops from different regions in Saudi Arabia is an on-going effort of the GB.

Keywords: Saudi Arabia, *Ex-Situ* Conservation, 55 Crops, KACST-Gene-Bank, Genetic Resources, Indigenous crops

Establishment of a network of genetic reserves in Germany. The example of *Vitis vinifera* L. subsp. *sylvestris* (C. C. Gmel.) Hegi

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Abstract

In the German National Programme for the Conservation and Sustainable Use of Plant Genetic Resources of Agricultural and Horticultural Crops provision was made for identifying reserves in Germany, holding a high density of priority species, and additionally declaring them to be "genetic reserves". The goal is the designation of already-existing reserves (FFH areas) as "genetic reserves" for priority species; this is done by the formally-responsible organisational units, in coordination with the ongoing work of the Länder authorities. A prerequisite for active management of genetic diversity within species of plant genetic resources occurring in the wild in Germany, including the crop wild relatives (CWR), is a close collaboration between subject-specialists in agriculture and nature conservation respectively. In that context the occurrence of the wild species of grapevine *Vitis vinifera* L. subsp. *sylvestris* (C. C. Gmel.) Hegi, was the subject of data survey, inventory and genetic description; duplicate conservation of the material was obtained, genetic purity of the *Vitis sylvestris* population was assessed by molecular analysis and measures for in situ management were developed and tested. In 2013, the Information- and Coordination Centre for Biological Diversity (IBV) - of the Federal Office for Agriculture and Food -, organized a meeting. Responsible organizational units, as well as landowners, scientists, employees of the city of Kesch, the German Genebank for Grapevine and a private person dedicated to the conservation of the wild species of grapevine met in the Town Hall of Ketsch. As a result of the meeting a contract for a genetic reserve was developed by the Information- and Coordination Centre for Biological Diversity and send to the participants. The Network of genetic reserves of the wild species of grapevine *Vitis vinifera* subsp. *sylvestris* will be part of a national network of priority species, coordinated by IBV. What an appropriate infrastructure of conservation entails is not solely the conservation and expansion of a network of this nature - and thus the availability of genetic resources - but also the task of obtaining the necessary information about their characteristics and possibilities for their use (Characterisation and Evaluation).

Keywords: Network, genetic reserves, Germany, Vitis

Promoting the evaluation and accessibility of genetic diversity of underutilized crops in China

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Abstract

There are many underutilized crops in China, such as barley, buckwheat, millet, oat, etc. They have been playing very important roles in securing nutrition and food security in the country. Considerable genetic diversity has been collected and conserved in the national genebank in China. The majority of them are landraces, which contain various traits important for resistance to bio- and abiotic stresses, nutrition and adaptability to climate changes. The availability of useful diversity of these crops to users will be important for the livelihoods in the areas with short frost-free period and dry conditions. The efforts were made to identify accessions with important traits such as large grain, resistance to drought and salts, and chemical components such as protein. With phenotyping and genotyping approaches, many accessions with useful traits and genes have been identified from the collections of barley, buckwheat, millet and oat. By linking genebank to the communities, the useful diversity was made available to both breeders and local farmers. Bioversity collaborated with national partners in China and contributed to the evaluation and use of genetic diversity of underutilized crop for sustaining livelihoods and adapting to climate change.

Keywords: Underutilized crops, Traits, China

Theme 3: Facilitating CWR and LR use

Genebank ineractions with the seed sector in the Nordic and Arctic regions

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Abstract

Landraces and modern varieties of cultivated plants are not separate units, but rather connected by (at least partly) common alleles and a shared history. Selection in landraces was the dominant breeding method in the early 20th century, but was later replaced by crossings. In the Nordic and Arctic region farmers' access to varieties is restricted. A short growing season and extreme photo-period fluctuations are challenging and require adapted varieties and a regional plant breeding. We have studied seed catalogs and national variety lists over time to gain an overview of varieties available today and in the past. We have also conducted a targeted survey for the Arctic region. The results show a consolidation in breeding enterprises and breeding programs. With one exception, vegetable breeding has vanished from the Nordic and Artic regions. For pulses and for several minor crops breeding in the Nordic regions decreased or ceased completely, including for some important Artic crops. The survey showed that there is a general need for new varieties and increased variety testing. A Nordic or Circumpolar co-operation that offers an opportunity for gene banks' participation is described. From our perspective the chain "gene bank - breeding - seed companies – farmers" could be supplemented by other networks and linkages. One such initiative is the Nordic public private partnership, in which the Nordic ministries of food and breeding companies work together on pre-breeding projects. Other initiatives are farmers' and seed savers' networks for evaluation and local marketing of old wheat, pea and vegetable varieties. In Sweden and Norway the gene bank has listed more than 50 conservation varieties and varieties developed for growing under particular conditions. Cooperation with newly emerging non-for profit organisations to share know-how in diversity conservations and utilization is an important genebank activity in Canada. The relevance of participation of lay people and farmer's involvement in the seed system is increasing, especially in marginal regions of the world, such as the Nordic and Arctic regions.

Keywords: Genetic resources, Lay participation, Pre-breeding, Network

Improving and classification grain quality for oat breeding lines

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Abstract

For the wild oat relatives the oil content is found from 8.7% diploid to 9.8% in hexaploid. The highest oil content is characterized for the samples к-755 (*A. vaviloviana* Mord., 4n) to 13,0% and к-397 (*A. ludoviciana* Dur., 6n) to 14,2%. Finding of such sources is appropriate based on the study of world genetic resources.

VRIPI collection samples, reproduced by identical set in Aktobe and Almaty conditions varied by the oil content from 3.0 to 8.2% (K-14638 in both reproductions), K-14668 and K-14786. The oil quality for oat cvs determined by the content of monounsaturated oleic acid (37% for Alaman to 41% Zhorga). The ratio of linoleic to oleic acid as a biological activity ranged from 0.82 (Zhorga cvs) to 0.93 (Alaman, Baige cvs). In general, the ratio of the unsaturated fatty acids amount to saturated amount ranged from 3.00 to 3.43 (Zhorga cvs). Cluster analysis of Kazakhstan cvs, collection samples including wild oats on fatty acids content has allowed classifying genotypes on 2 clusters. In the first group with Kazakhstan cvs, in the second cluster the differentiation on subcluster is certain on the American cvs plus hexaploid type *A. sterilis* and separately wild species with different ploidy level.

Kazakhstans oat varieties characterized by fiber content in grain at the level of 10-20%. The Zhorga and Baige cvs are revealed with a maximum content (over 25%), mainly in the arid zones. The β-glucan content according to the amylose content as an indicator of starch quality the Zhorga, Arman and Alaman cvs are marked. The low number of avenin, which is perspective for "gluten free" was found in the cvs: Sinelnikovskiy 14, Altayskiy krupnozerniy and Shalkar.

Keywords: Oat, genetic resources, oil content, avenin

Wild *Lactuca serriola* richness for lettuce breeding

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Abstract

First attempts to use the prickly lettuce (*Lactuca serriola* L.) for its valuable traits (e.g. resistance) in lettuce (*Lactuca sativa* L.) breeding are reported since twenties of 20th century. However, the structure of world germplasm collections does not reflect prickly lettuce worldwide distribution and enormous infraspecific variation, and data on its natural distribution and biodiversity are missing. Research activities of authors include broad inventory of prickly lettuce representation in world germplasm collections, eco-geographical studies, descriptors development, morphological characterization, resistance studies and research of genetic polymorphism. Original data on ecology and distribution of *L. serriola* in Europe, North America and Near East were obtained, new seed samples were acquired for further studies. According to the relative DNA content *L. serriola* is grouped with *L. dregeana*, *L. angustana*, *L. perennis*. The composition of sesquiterpene lactones in leaves is similar to those in *L. sativa* and *L. dregeana*. Large phenotypical and 132 honological variation among samples related to their geographic origin was recognized. Enormous variation in the reaction patterns to downy- and powdery mildews were recognized and located new sources of resistance to economically important races of both pathogens. Samples originating from various eco-geographical conditions differ significantly in many characters, e.g. achene morphology and their molecular polymorphism, they are genetically different. Natural interspecific hybrids of *L. serriola* with some related *Lactuca* spp. were recognized. Progenies of *L. Serriola* × *L. Sativa* crosses are fully fertile, interspecific hybridization is used frequently also in recent lettuce breeding.

Keywords: prickly lettuce, *Lactuca sativa*, natural distribution, biodiversity, phenotyping, disease resistance, molecular polymorphism, interspecific hybridization

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The utilization of a Greek lentil (*Lens culinaris* L.) landrace diversity through selection for single-plant yield under low density

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Abstract

An ultra-low density has been suggested as ideal to recognize individual plants representing the most outstanding genotypes within a landrace. In predominantly self-pollinated crops the technique is of prime importance since just a single generation single plant selection might lead to good pure-line varieties. In this study the Greek lentil landrace “Englouvi” was evaluated in Larisa (Site 1) under two non-replicated honeycomb designs (NR-0) at two low plant densities (i.e., 4.65 and 1.81 plants m^{-2}). The 15 high-yielding genotypes of each trial (30 in total) were selected, having an average yield of 25.8 g plant^{-1}, (CV ranging from 13% to 18%) compared to the average population that was 4.14 g plant^{-1} (CV ranging from 140% to 160%). The above 30 selected genotypes, along with the mother population “Englouvi” as a check, were evaluated in two locations, Larisa (Site 1) and Orestiada (Site 2) in two R-31 honeycomb designs and under ultra-low density conditions (1.81 plant m^{-2}), with 90 replications per entry. The results showed that at both locations, a 10% of the tested lines showed higher yield compared to the check, by 31% (Site1) and 11% (Site 2). Also, on the basis of a prognostic statistic for crop yield potential assumed to incorporate yield potential and stability, named Line Crop Yield Potential (LCYP), it was recorded higher performance compared to the check by 95% (Site 1) and 66% (Site 2), respectively. The results are encouraging that the lentil landrace evaluation under very low density conditions could lead to efficient selections contributing to the landrace utilization.

Keywords: landrace, diversity, ultra-low density

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Effect of soaking and temparature on germination of two wild asparagus (Asparagus acutifolius L.) ecotypes

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Abstract

Aegean region is very rich in edible herbs. Culture of the local people to consume these herbs as vegetables is very old and widespread tradition. Asparagus acutifolius L. is a herb that is gathered and consumed by local people and price in the local market for wild asparagus is pretty high. Seeds were collected from two different locations in the region (Incirliova and Yenipazar) and germination trials were performed. Different soaking time and temperatures were applied, but the results were not very promising. Soaking the seeds at 350C for 24h gave the best result (7%). After the trial, plants in their habitat were observed at regular intervals to determine the natural germination period and conditions. Observing the flora it was found that germination began at the end of February. Most of the young seedlings were found under the canopy of golden wattle (Acacia cyanophylla) tree where the organic matter ratio was higher according to the analysis.

Keywords: Asparagus acutifolius, genetic resources, germination, gathering

Theme 4: Informatics development

Crop wild relatives and landrace resources stored in Genebank in CRI Prague

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Abstract

Conservation and characterization of crop wild relatives and landrace resources, considering they are valuable as donors of a broad genetic diversity used in breeding, have long been a part within Czech National Programme on Conservation and Utilization of PGR and Agrobiodiversity. In our Genebank we currently store 42,772 generatively propagated genetic resources available to the users, of which 15 % are crop wild relatives and landrace resources (6,840 accessions available). Almost one third of these accessions have been already evaluated by curators in field and laboratory tests. The characterization is carried out for each crop according to descriptor lists which are available on our database website: http://www.genbank.vurv.cz/genetic/resources/. There is also published not only all passport but description data as well.

The largest group of crop wild relatives (the total number is 4,520 accessions) forms 1,437 accessions of cereals where the highest part belongs to genus *Aegilops* (990 accessions), characterized in nearly 60 %. Other important groups of crop wild relatives stored in our Genebank comprise fodder (802 accessions), grasses (745 accessions) and aromatic plants (586 accessions).

From 2320 accessions of landrace resources kept in Genebank more than a half has been already evaluated. The most important group are again cereals with 1,143 accessions, where almost half of them rank among *Triticum* spp. Our collections of landrace resources are further well represented by groups like industrial crops (533 accessions), legumes (255 accessions) and vegetables (233 accessions).

Gene Bank secures an extra 1,500 accessions crop wild relatives and landrace resources that are not available to the users (working collection, protected material, etc.).

Keywords: crop wild relatives, landrace resources, accession, data

Acknowledgement: Supported by the project MZe ČR: National programme on Conservation and Utilization of Plant Genetic Resources and Agrobiodiversity.

Predictive characterization of *Beta* CWR using the ecogeographical filtering method

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Abstract

Sugar beet (*Beta vulgaris* subsp. *vulgaris*) and its wild relatives were one of the four target genera of the PGR-Secure project "Novel characterization of crop wild relative and landrace resources as a basis for improved crop breeding". Sugar beet is one of the top ten crops of the world in economic importance, and Europe has a leading position in sugar beet breeding. The centre of diversity of the beet gene pool is in Europe, with 10 out of the 13 species native to the region (two of which are single country endemics). *Beta* wild relatives are an indispensable source of novel, important traits for the European sugar beet breeding industry. Predictive characterization methods can support the identification of those traits. Predictive characterization techniques build on the hypothesis that the environment influences gene flow and natural selection, and thus spatial genetic differentiation of organisms. CWR populations growing in a specific environment will possess a suite of adaptive traits shaped by selection pressures unique to these environments. Thus information about an accession's collection or a CWR occurrence site can be used to approach the utilization of genetic resource collections in a more rational way. One important trait in sugar beet is drought resistance. Using a novel predictive characterization approach, the ecogeographical filtering method, we identified within the available European Beta genetic resources a small set CWR relatives originating from environments likely to favour the development of drought resistance traits.

Keywords: Predictive characterization, *Beta*, Crop wild relatives, Drought resistance

A DNA repository for germplasm collections

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Abstract

Long term monitoring of agrobiodiversity and the effects of climate change is one of the key issues of ecosystem research. Many national and international short term projects target questions in this highly important area, highlighting various effects of changes on diversity on the population level. Very often these studies are confined to certain countries – sometimes the analyses span various countries on the European level. Still, in order to put the individual study-results in a wider context over a longer time scale, access to data as well as (reference) samples used to produce these data are of utmost importance. Only where access to material (DNA, tissue) is available, analysis of agrobiodiversity over time will be possible. Therefore the DNA repository center at AIT offers access to samples and data from various national and international research projects on forest trees as well as orphan crops, managed by an automated storage unit at -20°C, as well as access to data at www.picme.at.

Keywords: DNA, repository, Austria

Ecogeographical Land Characterization (ELC) maps as a tool for optimized collecting and improvement on representativeness of a *Trichloris* genebank in Argentina

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Abstract

Studies on native wild plant genetic resources become important since they may be domesticated or useful for the identification of genes associated with tolerance to biotic and/or abiotic stress. In order to make available these interesting traits, germplasm collections must to capture species' genetic diversity as much as possible. Optimized collecting method is useful to improve the representativeness on germplasm collections through the inclusion of accessions from all type of environments where the target species occurs. Ecogeographical land characterization (ELC) maps make it possible to detect environmental gaps in germplasm collections and locate potential collecting sites where focusing collecting efforts. In Argentina, the genebank of the Facultad de Ciencias Agrarias of the Universidad Nacional del Litoral (FCA-UNL) holds the most important national germplasm collection for *Trichloris crinita* and *Trichloris pluriflora* (31 and 21 accessions, respectively) but due to that previous expeditions were not planned according to any collecting strategy, a low representativeness is expected. Both species are native forage adapted to arid and semi-arid environments. The present study shows how the application of optimized collecting method based on gap analysis and ELC maps can make more efficient collecting activities. In 2013, collecting trips were carried out covering a total itinerary of 4000 km. New accessions collected from key environments were introduced, and the ecogeographical representativeness of the FCA-UNL germplasm collection was contrasted (before and after collecting activities). Results show gains and improvement of the representativeness especially for T. crinita.

Keywords: Geographic Information Systems, spatial analysis, environment, wild pasture species, semiarid, salinity

Authors: Oral presentations

Authors: Poster presentations