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EIP-AGRI Focus Group

Genetic Resources

Cooperation Models

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1. Summary

This report is the result of the EIP-AGRI Focus Group on Genetic Resources: Cooperation Models, which was launched under the European Innovation Partnership 'Agricultural Productivity and Sustainability' (EIP-AGRI). The Focus Group brought together 20 experts with different backgrounds and experiences (scientists, farmers, advisers...) to disseminate and inform about transferable innovative solutions on the conservation and use of the EU genetic resources.

The Focus Group tasks were defined as:

- **Analysing** the different types of agreements between the stakeholders in the field and the successful factors in existing cooperation.
- **Proposing** models and strategies to motivate public and private stakeholders to engage in cooperation models.
- **Preparing** a gap analysis indicating where new solutions for cooperation models need to be found.
- **Documenting** priorities for further research actions: the main needs (i.e., pre-breeding and breeding priorities) concerning the generation of knowledge in order to maximise intra- and inter-specific variation for the benefit of agriculture and of society at large.
- **Identifying** the priorities for areas of work for the different stakeholders in order to maximise intra and inter-specific variation for the benefit of agriculture and of society at large.
- **Finding** ways to promote the use of locally adapted and under-utilised crops, varieties and breeds;
- **Suggesting** ways to broaden the genetic basis used in plant and animal breeding so as to strengthen the development of varieties and breeds particularly adapted to social, economic and ecological conditions, also in marginal areas suggest potential projects of practical operational groups and other project formats to test new methods for advancing cooperation in the area of Genetic Resources.

To address these tasks, eleven themes have been identified as key areas where innovative cooperation models could be implemented. For each of these eleven areas the experts were invited to develop a mini-paper to take stock of activities, practices and research, and to identify needs for cooperation among stakeholders. In the mini-papers, experts discuss challenges and constraints in cooperation activities as well as the (research) needs of each thematic area. Moreover, the Focus Group explores practical innovative solutions to problems or opportunities related to conservation and use of genetic resources for food and agriculture, draws on experience gained from related useful projects and shares experiences among actors involved in those projects (including farmers, advisers, agri-business, civil society and researchers, working at EU, national and regional level).

2. Introduction

Genetic resources of plants (both crops and forests) and of domestic animals can make an enormous contribution in addressing food and nutrition security, while ensuring resilience of the production systems. Genetic resources also offer solutions for coping with the impacts of future climate changes. Faced with an important loss of agricultural genetic diversity and variability, which is due to modern agricultural practices (use of mainstream varieties and breeds), there is an urgent need to reverse this trend.

In Europe, the extent of this loss remains unquantified for plant genetic resources (PGR), but it is considered to be significant (FAO, 2010); while for animal genetic resources (AnGR), it has been estimated that 481 mammalian breeds and 39 avian breeds have already become extinct and another 624 and 481 avian breeds are at risk (FAO, 2007).

There is a dire need to rationalise and harmonise collections and conservation efforts in broad terms as well as to improve the use of agricultural genetic resources by end users.

Organisation of the EIP-AGRI Focus Group

EIP-AGRI Focus Groups are composed of a key expert and 20 experts that are selected following a call for expression of interest. The selection is made on the basis of proven professional experience, motivation, potential contribution to the Focus Group topic and relevant (educational and) professional qualifications. Other criteria include a balance in different areas of expertise, geographical balance, and gender. In the EIP-AGRI Focus Group on Genetic Resources, the selected experts represent different fields of expertise, including gene bank managers, scientists on animal and plant genetic resources, university academics, researchers on molecular genetics and seed certification, farmers, breeders (both public and private), policy makers and non-governmental organisations. The members of the Focus Group served in their personal capacity rather than as representatives of the organisation to which they are affiliated.

3. Brief description of the process

In between the meetings, experts were asked to prepare a series of mini-papers on a number of key themes, which were identified during the first meeting. The aim was to provide more detailed descriptions of cooperation models relating to each of these themes. Each mini-paper has a common template with an introduction to the theme, followed by suggestions for the application of possible cooperation models (see Annex 1 for the list of the mini-papers).

Survey of key issues

Prior to the first meeting, a survey was carried out among members of the Focus Group, to determine the key issues for discussion. The results of this survey are shown in figure 1.

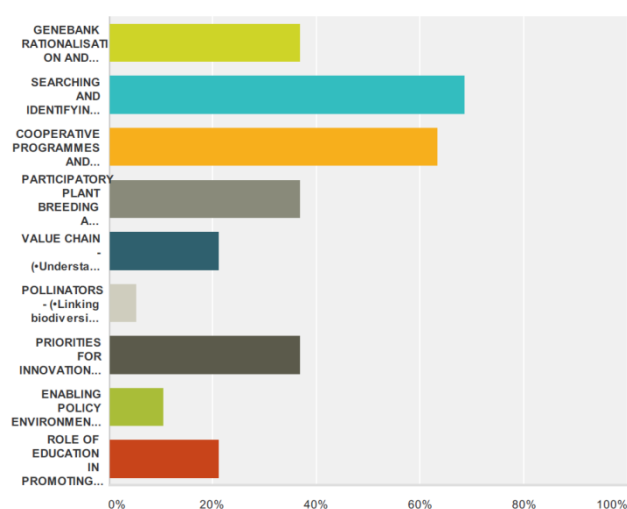


Figure 1 Key issues on genetic resources for discussion in Focus Group; results of a survey among members

The top priority topics are

- the **search for new traits for adaption to biotic and abiotic stresses in the context of climate change;**
- and **cooperative programmes and interdisciplinary approaches for the conservation and use of genetic resources.**

These topics are followed by

- the rationalisation and harmonisation of gene banks;
- participatory plant breeding;
- the use of Neglected and Underutilised species (NUS), local breeds, varieties and wild relatives
- and priorities for innovation actions.

The experts of the EIP-AGRI Focus Group on Genetic Resources also suggested that the following key questions be addressed in detail:

1. What is the role of plant/animal genetic resources in the adaptation to climate change?
2. What specific cooperation mechanisms are required for identifying desirable adaptive traits from genetic resources for crop/breed improvement?
3. How can interdisciplinary research and breeding programmes support and promote the use of locally adapted breeds and varieties?
4. How can best practices of conservation and use of genetic resources be mainstreamed in governments and what enabling policies are required?

The discussion during the first meeting (see [report of the first meeting](#)) focused on the analysis of existing cooperation models and the needs for research actions in relation to plant, forest and animal genetic resources. It was noted right from the start that the genetic resources issues for animal and plants are different in nature, and that different approaches for cooperation models may be required for these two sectors.

While discussing cooperation models for animal genetic resources, the expert group agreed that a key ingredient for success is the need to focus on the demand for the genetic resources, and on the creation of local businesses where farmers play a leading role. To ensure that the business is economically viable, branding is important, and an awareness and communication strategy based on whole product quality is needed. One example that was used to illustrate the key success factors was the rescue of an almost extinct local pig breed, the Schwäbisch-Hällisches Landschwein breed, which was transformed into a very successful business enterprise.

With regard to cooperation models on plant genetic resources, several experiences already exist in Europe. For example, the Public and Private Partnership (PPP) project in Nordic countries and the ECPGR platform are cooperation models that can stimulate the genetic resources community to work together at a European level. Members of the Focus Group discussed what did and did not work in these collaborative models (see table 1).

Things that made existing cooperation successful	Things that did not work well
<ul style="list-style-type: none"> • clear win-win situation among the stakeholders; • good understanding of the value of PGR and their products; in this respect roadshows proved to be very effective, but were limited by scarcity of funds; • good communication among members of the partnership; • certain threshold of trust among stakeholders. 	<ul style="list-style-type: none"> • different perspective among stakeholders in the public sector; • mismatch between the interests of large multinational companies and local community needs; • concerns about intellectual property rights, in particular with regards to royalty returns; • short time frame for the research projects.

Table 1: Experiences on cooperation models

The importance of farmers as drivers for attaining economic, social or environmental goals and for maintaining genetic diversity on-farm needs to be enhanced. There was awareness that genetic diversity was being lost, which may jeopardise the capacity for developing new improved varieties in the future.

It was noted that breeders (even those from smaller breeding companies) usually collaborate with the industry and only in some cases with farmers. Cooperation may take place between farmers, universities and administrations, as is the case in Tuscany, where a label to protect denomination helped in the conservation of some genetic resources. It was also noted that nowadays the characterisation and evaluation of genetic resources has become a trivial work. In that context, it could be useful to develop or adapt descriptors that could be used by gene banks but also by farmers.

It is also important to recognise the geographical differences within Europe – the Nordic region, Mediterranean region, Central/Western European region and Eastern European region – where each region has its own distinctive characteristics and different priorities and needs. For example, in Northern Europe disease resistance is a major issue, whereas the Mediterranean region has severe problems with drought. Therefore, it was suggested that while projects comprising all regions of member countries can make sense (for instance on the rationalisation of collections, of conservation infrastructures, etc.), there should be sub-regional projects that deal with the specific issues that are relevant for specific regions.

Two breeding strategies were identified, one geared to the market and another one geared to adapted varieties that can grow in specific locations. These two breeding strategies may conflict. Farmers' needs should be taken into account when varieties are being developed.

During the second meeting (see [report of the second meeting](#)), the Focus Group experts visited the organisation 'Schwäbisch-Hällisches Landschwein', a local enterprise where pure-bred pigs are managed in a sustainable way, with different approaches (in-stable, free-ranging in the open field, or organically). The organisation manages the whole chain and has outlet stores where their products are sold to the public.

4. Mini-papers

A number of key issues have been identified during the first meeting. They formed the basis of a more detailed discussion on the basis of mini-papers during the second meeting.

The links below give access to the mini-papers and the outcomes of discussions

[Annex 1. Information on gene bank accessions](#)

This mini-paper underlines the importance of proper documentation of gene bank accessions, to allow an effective and efficient use of germplasm. It discusses three types of information which are critical for the users (passport, characterisation and evaluation) and provides management information.

[Annex 2. Interdisciplinary approaches in conservation and use of plant genetic resources](#)

This mini-paper discusses the value (in terms of adaptation and resilience of cultivations) of on-farm crop conservation. It describes the role that farmers play in maintaining crops on-farm, discusses the different models of cooperation among farmers to collectively maintain diversity and the challenges they face. It shares the experiences from an international UN project (implemented in Latin America and South Asia) and from Italy.

[Annex 3. Tools for Characterisation and Use of Plant Genetic Resources](#)

This paper introduces some of the tools currently being used or developed in the characterisation of plant genetic resources, with some examples of the successful use of plant genetic resources in breeding programmes.

[Annex 4. Cooperation models on conservation and use of Crop Wild Relatives](#)

This mini-paper discusses the importance and role of crop wild relatives (CWR) as gene providers for crop improvement and their contribution to sustaining food security in the long term, especially in the wake of climate change.

[Annex 5. Harnessing plant genetic resources for enhancing resistance to abiotic stress in the genomics era](#)

This mini-paper discusses a multidisciplinary approach for enhancing crop resilience to climate change.

[Annex 6. Crop-pollinator interplay approach for the implementation of pre-breeding strategies on local breeds and varieties](#)

This mini-paper discusses the role of pollinators in the creation of novel populations through the crossing and recombination of genetically diverse materials selected by farmers and breeders.

Annex 7. Agro-Food Value Chain Cooperation

This paper analyses the role of genetic resources (both plant and microbial) on the agro-food value chain and presents some cases of successful valorisation of indigenous genetic resources.

Annex 8. Pre-breeding in crop plants

This mini-paper discusses pre-breeding of crop plants as a bridge between operations of plant genetic resource collections and modern plant breeding.

Annex 9. Public-Private-Partnership (PPP) in Plant Breeding

The paper provides several arguments for investing in public plant breeding research, and it describes some models of PPP initiatives in Europe.

Annex 10. Cooperation Platforms on Plant Genetic Resources and their Use in Europe

This mini-paper describes some of the most important European platform dedicated to plant genetic resources for food and agriculture.

Annex 11. Farm Animal Genetic Resources – Cooperation Models: Issues facing the local extensively farmed livestock breeds

This paper addresses issues specific to the traditional breeds of livestock species (pigs, cattle, sheep and goats) which are 'at risk', issues related to their utility for agriculture, along with relevant cooperation models for their conservation, characterisation and utilisation.

5. Ideas for cooperation projects and Operational Groups

During the working groups, the group of experts concluded that inter-multidisciplinary approaches involving economic, social, cultural, and nutritional aspects, tourism, and genetic resources, are needed to enlarge crops and breeds used in agriculture. Activities can be linked to the territory and should be driven by a business model.

There is also a need to build the capacity of the various value chain actors, using business and success stories. Existing varieties and breeds should be valorised and further developed using existing knowledge, habits and best practices.

Cooperation between ex situ conservation of genetic resources and on-farm management is needed to further enhance the development of more adapted crops and breeds through complementarity, reintroductions and best practices of crop management and animal husbandry.

The needs of farmers, industry, environment, consumers and breeders in terms of the genetic resources and their products were also examined. Farmers need good high-quality varieties and in general look for varieties with a good and stable yield that are resistant to biotic and abiotic stresses. They also care for certain agronomic traits of importance for the target crops (e.g. lodging and earliness are important traits for cereals).

Industries look for production of high-quality varieties in high quantities, at a low cost and with constant characteristics suitable to industrial processes. It is important that those (new) varieties are sustainable and that they use natural resources more efficiently, in particular that they are nutrient- and water-use efficient.

Integrated pest management approaches should be adopted, and varieties should also be resilient to future climate changes, in particular to water shortages, carbon dioxide, ozone and temperature.

Consumers, on the other hand, are seeking good quality and healthy food at affordable prices. They are increasingly looking for environmentally friendly products, and for easy accessibility to local products and production. They are also very concerned about ethical production systems.

For breeders, both adequate access to and the characterisation and evaluation of genetic resources are essential. There is a need for affordable technologies for the integration of phenotyping and genotyping, and a need for methods for incorporating adapted traits into varieties.

The experts suggested the relevance of a feasibility study on the interaction between local animal and crop genetic resources. Existing diversity should be identified and managed, and custodians of regional agricultural biodiversity could contribute to conserving territorial agro-biodiversity.

6. Ideas to increase human capacity, networking and dissemination

The group suggested the promotion of activities (for example, a Regional European Programme) that could develop the capacities in young people to become successful agriculture entrepreneurs. These should target local communities, and farmers of small- and medium-sized farms. The programme should be made attractive by proposing a new concept of agriculture in which genetic diversity, environment/nature, local identity (geographic indications) and economic opportunities play a central role. Such programmes should better integrate farmers into the eco-agrifood systems, to produce more healthy and nutritious food.

From a breeders' perspective, some kind of network involving farmers, consumers, and industries is warranted, to support cooperation activities in the field of genetic resources. It was argued that a network of private public and academic partnership (PPP) needs to be created to carry out pre-breeding activities, to deliver improved crop (and animal) genetic diversity.

To facilitate further action and use of the Focus Group results, the group has prepared a dissemination plan that aims to reach as many of the people concerned as possible.

The EIP-AGRI Focus Group experts expressed their willingness to further popularise the results of the work in their circles and at regional, national and international levels. The experts look forward to opportunities of taking action and being involved in Operational Groups and in research activities on issues that are related to cooperation in the field of genetic resources.

The EIP-AGRI Service Point will disseminate the Focus Group outcomes via targeted dissemination materials, via the EIP-AGRI webpage, and in future seminars and meetings in the EU Member States.

7. Summary of research needs

Research needs have been discussed for each of the sections above. The following is a summary of the main research needs identified by the members of the EIP-AGRI Focus Group:

Research needs for AnGR

- Evaluation of the risk of 'genetic drift' for the unique traits in traditional breeds and varieties.
- Methods/tools to encourage recording of pedigrees for the traditional breeds, as well as to improve management systems in the absence of pedigrees.
- Identification of genes that contribute to the ability to adapt to local conditions and to robustness, under low input and in extensive farming systems.
- Genetic improvement and enhancement, optimisation of genomic programmes.

- Market research is needed to demonstrate the sustainability of local breeds.
- Interdisciplinary initiatives that combine characterisation, enhancement and improvement of the genetic resource with business development and marketing, including the study of emerging consumer attitudes, needs and trends.
- Socio-economic aspects addressing opportunities for product innovation and differentiation.

Research needs for PGR

- Optimisation of ex situ collections;
- Strategies for in situ conservation; determination of conservation status and threats, policies and practices at priority sites for conservation, in situ conservation outside protected areas;
- Link between ex situ and in situ conservation;
- Coherent research programmes, to obtain genomic data on accessions in collections, and to link sequenced data with genetic and genomic information;
- Pre-breeding; identification, selection, evaluation of germplasm for important adaptive traits in CWR (Crop Wild Relatives) wild population, especially for disease resistance, drought tolerance, waterlogging, climate changes (CO₂; ozone; temperature), quality, and stability;
- stress interactions with crop growth and yield, better understanding of the rhizosphere, root functions and plasticity, reproductive failure under stress, epigenetic effects, perenniality, etc.
- Monitoring of changes in genetic diversity over time;
- Knowledge / technical transfer along the value chain in the agro-food sector.

8. Additional needs

Based on the discussions on the above mentioned issues relating to genetic resources, members of the EIP-AGRI Focus Group made the following suggestions:

- **Characterisation of genetic resources** – there is a need to improve descriptors lists of genetic resources and include nutritional, organoleptic and health as well as market traits to improve market value and contribute to the green economy. In addition, the characterisation of in situ populations to identify adaptive traits is especially important for climate change adaptation. For these purposes, the improved resource use efficiencies and resource stewardship for characterisation, mining of collections and safeguarding is warranted;
- **Creation of a pan-European network of farmers** - such a network is required to support on-farm conservation and management of genetic resources. It can also serve as a cooperation model both for allowing farmers to share their experiences and constraints, and for strengthening their capacity in the conservation and use of genetic resources. Finally, it can help them develop market access for their products. There is a need to create links with research (universities) and to use lead farmers as trainers, allowing them to share their experience and participate in training courses at EU level;
- **Research on yield improvement and yield stability** in changing and dynamic environments – with climate change as one of the major challenges. Research needs that target the potential of genetic resources to provide novel traits, taking into account environmental aspects and predictions for genetic potential in future environments. Pre-breeding for resilient plants, involving the development of new technology for the rapid transfer of traits from wild relatives to crops, for improved plant health and resilience (e.g. reduced use of fertilisers) is a priority.
- **Crop pollinators** – research should focus on elucidating the synergies between pollination and pollinators and local pre-breeding procedures, to develop win-win strategies (farmer-crop-pollinator). Mechanisms to

better connect farmers, breeders and gene bank managers with pollination biologists are very strategic and urgently needed;

- **Data management** of characterisation and evaluation, sequencing, phenotyping, genotyping; actions to link/mine/integrate phenotyping and genotyping data for core collection sets and functional diversity;
- **Value chain** - there is a need for a full market analysis to explore the potential value of genetic resources, especially for local crops and breeds, to ensure self-sustainability and market competitiveness/opportunities. Such an analysis needs to be done by farmers at local and regional levels. Incentives in the form of seed money are needed for farmers to implement this exploratory phase. The group recommends that a roadmap of the value chain (farm to fork) is required for each genetic resource, from the resource itself to consumption, to define the role of and the synergies between stakeholders in the chain. It is also important to analyse and draw lessons from success stories and failures at national, regional and international levels. Interdisciplinary research linking genetic characterisation, business development (downstream opportunities for innovation and product differentiation) and socio-economics.

9. References

- FAO. 2007. *The State of the World's Animal Genetic Resources for Food and Agriculture*, edited by Barbara Rischkowsky & Dafydd Pilling. Rome.
- FAO. 2010. *The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture*. Rome

10. Annexes – Mini-papers

Annex 1: Mini-paper: information on gene bank accessions

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Introduction

Gene banks have a dual objective. They must first ensure that the genetic integrity of the accession is adequately safeguarded and secondly they must make them available to users of germplasm, such as curators, breeders, farmers, researchers and other users. The proper documentation of gene bank accessions is essential in good gene bank management, to allow efficient and effective use of germplasm (Visser and Engels, 2003). Germplasm use can best be promoted if their accessions are properly characterised and evaluated and if their information is made available. Indeed, the value of a germplasm collection is largely determined by the quality of its documentation.

Germplasm conserved in gene banks are of little use if their characterisation and evaluation data are not adequately documented and incorporated into an information system through which information can be shared worldwide and which can make the accessions available to potential users. Three types of information can be distinguished: Passport data, characterisation and evaluation data and management data (Perry et al. 1994).

- Passport data - These passport data include information such as taxonomy, accession name, country of origin, location and collecting site, cultural practices, the history of the accession, their origin, uses, etc. (FAO, 2013). Passport information should be documented using multi-crop passport FAO / IPGRI descriptors (Alercia et al., 2001).
- Characterisation and evaluation data - These are used to describe the genetic resources. Historical and cultural information provided by farmers, botanists, curators, horticulturists and collectors during expeditions also provides valuable information.
- Management data - These are essential for maintaining the viability of the genetic resources and their distribution to users.

Application for cooperative model

The proper documentation of gene bank accessions requires that information is described in a harmonised manner. Over the years, a wide range of internationally agreed crop descriptor lists have been developed by organisations such as Bioversity International, UPOV, OIV, and USDA -ARS NPGS (FAO, 2013). The development of these descriptors has involved many experts who have collaboratively worked with gene bank curators to produce crop-specific descriptors. The use of these international standards for characterisation data has proved to greatly increase the utility of the published data.

Other important areas of cooperation relate to the development of methodologies for data analysis and dissemination, aimed at better utilisation of plant genetic resources, as well as sharing of information about accessions. These are important for promoting the evaluation and utilisation of conserved material and in raising awareness on the importance of conservation activities.

As most traits are environment-dependent, evaluation must take place in the appropriate environment, and preferably in several different locations (multi-site evaluation). This calls for cooperative models for effectively carrying out evaluation activities among research scientists and gene bank curators. Molecular tools are often used to confirm the identity of the accession and conformity to type, to identify duplications of the same cultivar and synonyms in different collections or to identify mistakes in accessions from several germplasm repositories (FAO, 2003). These analyses are restricted to those countries where the expertise and technologies are

available. Thus the use of molecular technology still remains out of reach for some institutions because it is expensive and requires advanced laboratory facilities and technical capacity. Cooperation with laboratories that have the necessary facilities for these techniques is essential.

On a broader scale, combining data from many national and / or international germplasm collections for a crop can provide the basis on which to plan international genetic resources activities in order to reduce duplication of effort in the areas of conservation, regeneration, multiplication and collecting. To this end, common databases have been developed for several crops at several institutes (Visser and Engels, 2003). Lipman et al. (1997) consider that different actors are involved in the Central Crop Data Bases (CCDB) of gene bank accessions.

- Primary users. The curators and crop-specific working groups seeking to secure the conservation of a genepool in the most effective way. For these users, the CCDB will remain an essential management tool for the identification of duplicates and omissions in the collections, as well as a basic source of information for the development of collaborative activities such as the establishment of core collections, the planning of collection missions, etc.
- End users - Including breeders, researchers, growers, educational establishments and other users who wish to access the CCDBS to obtain specific information about the collections, frequently as an entry point to the collections themselves.

In Europe, a single web portal (EURISCO) provides access to all information on ex situ plant genetic resources. Further in order to avoid duplication across gene banks, a European Genebank Integrated System (AEGIS) has been established under the European Cooperative Programme for Plant Genetic Resources (ECPGR), to ensure the sharing of conservation responsibilities among European countries. AEGIS contains genetically unique and economically important accessions of all relevant crops in Europe. These accessions will be maintained in gene banks by the individual countries as part of their long-term commitments, applying agreed standards and ensuring that the material will be readily available to the members (Engels et al., 2012).

Most gene banks were used to play national or regional roles or else have well defined users. However, as a consequence of globalisation and the advance of information technology, new users from distant locations increasingly approach gene banks for material. Requests for germplasm may originate from the public, private or civil sectors. Users may want germplasm for breeding, for searching for specific genes, for basic research or for introduction and reintroduction material into farming systems. Whereas breeders and researchers will be interested in adaptive traits to incorporate them into their breeding materials, which may be present in anything from elite lines to wild relatives, including information on molecular and biochemical details, farming communities generally will be more interested in agronomic properties, requiring adapted varieties from comparable agroecosystems.

Problem and constraints

Two main problems can be considered: financial and physical constraints and lack of information.

- Many gene banks face serious financial constraints. This may be the result of a failure to appreciate their relevance and their costs of operation. The most expensive tasks of a gene bank are those of characterisation, evaluation and regeneration of accessions (Frison et al., 2003). Depending on the crop (trees), a big surface is needed to maintain the collections and more budget is required.
- Some descriptors are not harmonised and not all accessions in the collection are well documented. The missing or incomplete documentation reduces the value of an accession to the point of making it impossible to be used. Gene bank documentation is often low quality, incomplete and unreliable. This is particularly true of evaluation data. This greatly reduces the value of the accession.

Research / Activities needs

Different activities are proposed to try and solve the problems and constraints mentioned above:

- To develop cooperation and share information between and within all groups that are working on the genetic resources aspects of a particular crop. Crop networks should be coordinated by a committed

curator, who may also maintain a central crop database, and who should have the possibility to convene meetings on an annual or biannual basis for all curators involved.

- To organise training courses and short visits of scientists, with the idea to promote information and knowledge exchange between gene bank collections' curators.
- To publish the information from specific studies of gene banks in reports, catalogues or journals. Distribute this information not only between researchers, but also within the civil sector (growers, educational institutions, etc.).
- To create a well designed database, which is easy to handle, and a search database of phenotypic evaluation, so it can help users to target their germplasm requests.
- To establish security measures to protect information on germplasm against damage and loss, and ensure smooth functioning, easy access and unrestricted availability.

Discussion in plenary

The value of passport data was questioned saying that gene banks should focus and dedicate more time on traits rather than on passport data. However, other argued that passport data is important to identify and distinguish different gene bank accessions. In addition, passport data that includes information on geographical origin of accessions can be used to predict if accessions have useful trait expression (see more at <http://www.icarda.cgiar.org/tools/figs>). It is of paramount importance that all accessions have at least passport information in order to make their gene bank management possible. Characterisation and evaluation should focus on those traits that would enhance the use of genetic resources stored in the collections. In this context, a big ongoing project on characterisation of animal genetic resources was mentioned. An innovation in the documentation of gene bank accessions would be to further develop descriptors so as to include traits that are potentially useful for the market and can be used by value chain actors.

References

- Alercia, A.; Diulgheroff, S.; Metz, T. 2001. FAO/IPGRI. Multi-crop passport descriptors (available at http://www.biodiversityinternational.org/index.php?id=19&user_biodiversitypublications_pi1).
- Engels, J.; Visser, B. 2003. enebank management procedure. In: A guide to effective management of germplasm collections. (J.M. M. Engels and L. Visser, eds.) IPGRI: 60-79p. Rome, 2003.
- Engels, J., Freudenthaler, P., Landbo, L. and Latorre, F., 2012. Strategy Paper on the ECPGR Relationship with the European Union/European Commission. Rome, Italy, ECPGR.
- FAO, 2013. Genebanks Standards for Plant Genetic Resources for Food and Agriculture. Rome, 2013.
- Frison, E., Mitteau, M.; Sharrock, S.; Visser, B. 2003. Sharing responsibilities. In: A guide to effective management of germplasm collections. (J.M. M. Engels and L. Visser, eds.) IPGRI: 107-121p. Rome, 2003.
- Lipman, E.; Jongen, M.W.M.; van Hintum, Th.J.L.; Gass, T.; Maggioni, L. 1997. Central Crop Database: Tools for Plant Genetic Resources Management. Report of a Workshop, October, 1996, Budapest, Hungary. IPGRI, 100p.
- Perry, M.C.; Serwinsky, J.; van Hintum, Th.; Hazecamp, Th.; Knüpffer, H. 1994. Plant genetic resources, documentation and eastern Europe: history, current constraints and new perspectives. Proceedings of a joint FAO/IPGRI workshop on *ex situ* germplasm conservation. October, 1993. Prague, Czech Republic. 17-22p.
- Visser, B.; Engels, J. 2003. Setting objectives for genebanks. In: A guide to effective management of germplasm collections. (J.M. M. Engels and L. Visser, eds.) IPGRI: 20-42p. Rome, 2003.
- EIP-AGRI Focus Group 4: Genetic Resources – Cooperation Models

Annex 2: Mini-paper: Interdisciplinary approaches in conservation and use of plant genetic resources¹

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Introduction

Agricultural biodiversity is vital in sustaining humankind today and in the future. Its plant genetic resources are the raw material needed to produce food and many other products that make our life possible. The conservation of crop genetic resources either through seed or field gene banks was initially developed by N.I Vavilov in the early part of the twentieth century (Pistorius 1997). This type of conservation defined as *ex situ* conservation received a major boost during the so-called plant genetic resources movement which started in the early 1970s and led to the establishment of large gene banks around the world, including those of the CGIAR focusing on the conservation of the diversity of main food crops of the world. Calls for alternative ways of conservation, outside the *ex situ* method, started throughout the middle of the twentieth century, and increased during the 1980s. Scholars such as Altieri and Merrick (1987), and Brush (1989) have been advocating greater attention to '*in situ* conservation', as a highly complementary method to *ex situ* conservation to allow the maintenance of useful species either in their natural habitat ('*in situ* conservation') or in the production systems where they are grown ('on-farm conservation'). The conservation of crops on-farm has several advantages compared to *ex situ* conservation as it allows the evolution of crops through continued natural and human-driven selection which contributes to greater adaptation and resilience of cultivations, it makes possible the maintenance of crops whose seeds cannot be stored at the low temperatures of gene banks and support the maintenance of traditional knowledge associated to their use. Its disadvantages include the limited access to germplasm for breeders and other users, the vulnerability of crops to natural disasters and the fact that less diversity can be stored in any single location.

In reality, the on-farm conservation has been the oldest agrobiodiversity method of conservation ever practiced by humankind since the discovery of Agriculture. Farmers maintain crops through their continued cultivation and although they may not be aware that they are harbouring important biodiversity in their farms, they contribute with their work to serve as an informal gene bank for safeguarding crops that meet the needs of both their families and their communities as a whole (Mekbib 2009). Farmers may be also organised among themselves so as to create the so-called community gene banks, through which some leader custodian farmers maintain the diversity on behalf of all others members. Some of these community approaches are further structured and include multiple objectives in their work, as in the case of the 'gene-seed-grain' banks which are practices in some regions of India. Another type of on-farm conservation is represented by home gardens. These are reservoirs of diversity that contribute to the conservation of agrobiodiversity and at the same time serve as bench work to farmers and their families for testing out the value of species with regard to their livelihood needs before growing them out extensively in the field (Eyzaguirre and Linares 2004). They also contribute to environmental regulations, the generation of occasional income and the aesthetic value of the farming landscape (Sunwar 2006).

Unfortunately, attempts to create a cohesive on-farm conservation system that would strategically complement *ex situ* conservation efforts have so far been very scarce and this is a great limitation for both the effective conservation and the use of crop diversity. It is widely acknowledged that the largest amount of agrobiodiversity is maintained on-farm and it is also widely recognised that only a very small portion of this wealth of crop diversity (wild or cultivated) is conserved in *ex situ* gene banks (Padulosi 1999, FAO 2010). Moreover, traditional crops maintained by farmers are being rapidly lost because of their low economic potential due to the lack of technology, infrastructure and value addition methods. This low competitiveness with respect to commodity crops is also due to changes in traditional agricultural practices, urbanisation trends, changes in people's

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lifestyles and unanticipated effects of climate change. According to FAO², an estimated 75% of the world's agrobiodiversity has already been lost in the course of the 20th century, and what is left is likely to 'silently' disappear within the next few decades if no urgent and consistent efforts are set out for its rescue.

To halt this process of erosion and fully mobilise agrobiodiversity, it is today of paramount importance to develop an effective complementary conservation approach that blends synergically *ex situ* with *in situ* methods. This is what is also described as a 'conservation-through-use' approach because it aims at linking all stakeholders involved in the value chain of target crops. The level of complexity in linking conservation with use is also determined by the need of tackling multiple objectives, closely inter-linked to one another, such as income generation, nutrition security and health, maintenance of crops' evolutionary capacity, resilience, ecosystem services or empowerment of vulnerable groups. How to build this new collaborative model, what are the challenges and the needs to move towards this model is what we shall address in this short contribution, sharing lessons from an international UN Project implemented in Latin America and South Asia and from Italy.

The cooperative model

Lessons from a UN Project on minor crops

This cooperative model which covers the entire spectrum of conservation and use activities 'from farm to fork' has been tested out successfully in various international projects supported by IFAD (the so-called IFAD NUS Projects) which have been running in various regions, including Latin America and South Asia for more than a decade since 2001. These projects focused on the use enhancement of minor crops also defined as 'neglected and underutilised species' (NUS), a category of crops which more than any other require a holistic, multidisciplinary and inter-sector approach for their promotion (Padulosi et al 2013, Padulosi et al 2014). The stakeholders who have been involved in the implementation of these projects ranged from scientists engaged in surveying, collecting, studying and conserving diversity of target species in *ex situ* gene banks, to farmers contributing to their maintenance *in situ/on-farm*, from breeders and experts working to develop better varieties and value addition technologies and user groups, including women's associations (engaged in their promotion in households and in the market). Nutritionists, school teachers and media experts were also active partners in the projects by contributing to raising public awareness on the role of target crops in nutrition, income generation, adaptation to climate change and other livelihood domains. The key lesson learnt from these efforts is that the promotion of agrobiodiversity requires first and foremost the adoption of a new R&D paradigm, directed towards cultural-sensitive objectives and not solely towards economic benefits. The promotion of agrobiodiversity – in any country, regardless its state of development – is an opportunity to promote and make use of the crop diversity and associated food traditions present at the local level, which are the unique expression of the work of generations of farmers and users. Safeguarding such a heritage is an important contribution to protecting the identity of local communities and reinforcing their self-esteem and confidence to counteract threats of standardisation of local food culture arising from globalisation trends and changes in lifestyles. The role of multi-stakeholder platforms for promoting agrobiodiversity (and especially NUS) was also found highly strategic.

A key role in promoting such a multi-stakeholder cooperation is entrusted in the coordinator of the project at national level who has to play its 'trade union' role by facilitating the development of a common framework and its implementation through the harmonisation and leveraging of expertise among the various stakeholders. Building trust among actors is essential and this is a process that is greatly facilitated by bringing actors together during the project design workshops as well as during those meetings within the implementation. Key thematic areas in this collaborative framework include the joint conservation and characterisation of crop diversity (farmers, *ex situ* gene bank operators, breeders and processing/marketing actors), the participatory selection of better varieties and the production of high quality seeds (farmers, public breeders, private seed companies), the development of improved agronomic practices (farmers and researchers from public and private sectors), improved harvest/post harvest and processing (farmers and researchers from public and private sectors) and marketing (farmers, public and private sectors).

² FAO. 1999. Women: users, preservers and managers of agrobiodiversity (www.fao.org/FOCUS/E/Women/Biodiv-e.htm).

2.1.1 Issues and constraints

Impact assessment studies have shown that these multi-stakeholder collaborative efforts have been very successful, though challenging with regard to maintaining effective and cohesive collaboration across so many different actors and groups with diverse interests. This is an aspect that can be taken care especially by the agency playing the 'hub role' in the networking platform.

Another area that requires special attention is that regarding actions for strengthening on-farm conservation through establishment/or strengthening of community seed banks or the conservation implemented through custodian farmers, community-based participatory monitoring, custodian farmers' networks and crop diversity fairs to promote sharing of seeds and knowledge (including gastronomic recipes highly strategic for promoting uses).

The cooperative model: lessons from Italy

This example focuses on seed systems in Italy. In this country, like anywhere in the world, public organisations should be playing a stronger role in promoting cooperative programmes and interdisciplinary approaches that support conservation and use of genetic resources. This is highly relevant also in the context of seed production and trading phases so as to make the preservation of the landraces more effective, and to ensure that these will be available when a renewed economical interest in them may arise. In addition, the public intervention would also become a guarantee for seed companies, because public control would play a crucial role in differentiating and separating the marketing of conventional varieties from that of landraces, which should be exclusively aimed at the valorisation of genetic resources.

2.2.1 The Italian Regional System

The experience with the Regional Laws highlights the importance of the local context in addressing the question of the sustainable use of genetic resources. In particular, combining territorial development with agricultural biodiversity appears to be an appropriate strategy for harmonising local incentives and global objectives in pursuit of the common good deriving from the sustainable use of genetic resources for food and agriculture (Helfer, 2005).

Local and regional authorities are, by their knowledge of the territory, public bodies in a position to coordinate the principle actions for conservation and valorisation of biodiversity. The "Italy case" of Regional Italian Legislation on protecting local genetic resources (varieties and breeds) is one of the few operating examples for the protection and exploitation of PGRFA in Europe. Tuscany was the first region to enact a law in 1997 for the protection of agricultural biodiversity. Regional Institutions interact at various levels with different categories of stakeholders, depending on territorial dynamics:

- Scientific institutions dealing with the collection, inventory, characterisation, ex situ conservation and dissemination of collected information
- Other local institutions
- Farmers (custodian farmers)
- Groups, associations, organisations

The regional authorities take on the responsibility of safeguarding and enhancing genetic resources by means of a series of tools which are essentially based on the following points:

- Establishment of a voluntary, free-of-charge regional register for species, breeds, varieties, populations, cultivars, landraces and clones;
- Establishment of technical-scientific committees to assess the fact-sheets of the subjects listed on the regional register;
- Establishment of a network composed of farmers, associations, public and private bodies, research bodies, universities, gene banks to conserve and safeguard the varieties registered;
- Recognition of farmers as the stewards of the agriculture genetic resources or the Region itself as guarantor and manager of regional genetic resources.

Of these tools, the voluntary regional register, and the conservation network are the most effective and innovative means for pursuing the objectives of protecting and enhancing local varieties.

2.2.2 The National Plan for Agricultural Biodiversity (NPAB)

The Italian Plan for Agricultural Biodiversity is another model for cooperation between various scientific stakeholders and regional authorities. Under the coordination of the Ministry of Agriculture and Forestry, a Standing Committee on Genetic Resources was established. The aim is to coordinate the actions that are to be implemented at the local level, to transfer the information needed to protect local agricultural resources to local operators and all interested stakeholders. The actions are divided into three phases:

1. Operational guidelines for agricultural biodiversity
2. Interregional projects
3. Establishment of a National Register of varieties, breeds and local populations

In 2009 a specific project was launched, to establish a working group for defining operational requirements. The project produced National Guidelines for the conservation and characterisation of plant, animal and microbial genetic resources, for food and agriculture. On 24 July 2012, the Italian Ministry of Agriculture, Food and Forestry adopted the National Guidelines for the *in situ*, on-farm and *ex situ* conservation of plant, animal and microbial biodiversity of agricultural interest. This is the first significant interdisciplinary work for the protection of biodiversity, for food and agriculture.

2.2.3 Reflections on the EU Seed Legislation

Seed from the main agricultural and vegetable species has to be certified before it can be marketed. In order to be marketed and entered for certification, the species or variety has to be listed on a National List or in the EU Common Catalogue. To be added to a National List or EU Common Catalogue, a variety must be distinct, sufficiently uniform and stable (DUS) and, for agricultural crops, have satisfactory value for cultivation and use (VCU).

The recent EU legislative developments (i.e. Commission Directives 2008/62/EC 20 June 2008, 2009/145/EC 26 November 2009 and 2010/60/ EU 30 August 2010) on seed production and marketing opened a new way to safeguard landraces, as well as other variable populations, because they are aimed "to ensure *in situ* conservation and the sustainable use of PGR".

Seed production and commercialisation of local varieties in Europe is now regulated by specific laws for "*conservation varieties*" and "*amateur varieties*" (with no intrinsic value for commercial crop production). Conservation variety is defined as a landrace or plant variety that is naturally adapted to local and regional conditions and is threatened by genetic erosion. Conservation varieties can be listed in the catalogues if there is a specific interest for a sustainable use for plant genetic resources, with some derogation to DUS standards (distinct, sufficiently uniform and stable), varietal denomination, acceptance of unofficial tests, fees charged for registration.

The main aim of Directives is to safeguard the local plant genetic resources through the production and marketing of a very limited quantity of seed only in their area of origin. Local farmers and seed companies can sell small quantities of seed from conservation varieties to the farmers of the original area. The Directives on conservation varieties certainly are an opportunity to promote landrace on-farm conservation through commercialisation of their seed, but several actions are still needed to enlarge the registration of landraces as conservation varieties.

Conclusions and research needs

More attention is needed to understand how agrobiodiversity is maintained and used on-farm today, how on-farm conservation efforts can be better linked with *ex situ* (e.g. joint organisation of seed fairs, joint maintenance of diversity by farmers and gene banks, participatory monitoring of crop and cultural erosion in the fields, establishment of a red list for cultivated varieties).

Public bodies should play an important role with regard to the access to genetic resources, their conservation and valorisation. To that regard, a "bottom up" process is needed, whereby local Authorities and Agencies, present on the territory, would work closely with local communities in collecting data and information on the

status of landraces, the assessment of their market opportunities and interest by people in their enhanced use. This information will then be used to prepare national inventories of landraces eligible to be registered as conservation varieties based on recorded interest by users.

In the case of landraces that are threatened by genetic erosion and that do not have a current interest from people in terms of market, nutrition, agritourism or other uses, their rescue and continued conservation on-farm can be pursued by promoting farmers' networks or ad hoc through farm conservation projects. These interventions seem to be the most viable means to provide continued seed supply to farmers of such landraces. In those regions where landraces have been developed and are being maintained, it will be important to include aids targeting custodian farmers that are playing a major stewardship role for these resources in rural development policies.

More research is needed on the front of the policy frameworks that are needed to facilitate seed exchange among actors, with respect to both the farmers' right to freely exchange seeds as well that of breeders to continue developing improved varieties and commercialise them. More research is also needed to develop policies that facilitate the linkage between farmers and ex situ gene banks for maximising the complementary roles of both groups of actors.

Discussion in plenary

Reference was made to the several EU initiatives, e.g. the ECPGR on-farm conservation working group, which has developed an on-farm conservation strategy and Solibam EU project, which is another example of a collaborative project among farmers. This project's final conference was held in the second week of July 2014. It was argued that breeders have a limited timeline and cannot engage in long-term pre-breeding programmes. However, it is important that such programmes are developed to provide new traits to breeders. Other regions in Europe contemplated the Tuscany model of regional legislation to protect local varieties and breeds. The model could also be replicated in the UK or at a regional level.

References

- Altieri, M. A., and L.C. Merrick. 1987. *In situ* conservation of crop genetic resources through maintenance of traditional farming systems. *Economic Botany* 41:86-96.
- Bravi R., Porfiri O., Negri V. 2002 – La salvaguardia della biodiversità e la produzione di sementi di specie ortive. *Sementi Elette* n.2
- Brush, S. 1989. Rethinking Crop Genetic Resource Conservation. *Conservation Biology*. 3.1: 19-29.
- EU Commission. 2008. Directive 2008/62/EC of 20 June 2008 providing for certain derogations for acceptance of agricultural landraces and varieties which are naturally adapted to the local and regional conditions and threatened by genetic erosion and for marketing of seed and seed potatoes of those landraces and varieties. OJ L 162, 21.6.2008, pp. 13–19.
- EU Commission. 2009. Directive 2009/145/EC of 26 November 2009, providing for certain derogations, for acceptance of vegetable landraces and varieties which have been traditionally grown in particular localities and regions and are threatened by genetic erosion and of vegetable varieties with no intrinsic value for commercial crop production but developed for growing under particular conditions and for marketing of seed of those landraces and varieties. OJ L312, 27.11.2009, pp. 44–54
- EU Commission. 2010. Directive 2010/60/EU of 30 August 2010 providing for certain derogations for marketing of fodder plant seed mixtures intended for use in the preservation of the natural environment Text with EEA relevance. OJ L 228,31.8.2010.
- Eyzaguirre, P.B. and O.F. Linares eds. 2004. *Home Gardens and Agrobiodiversity*. Smithsonian Books, Washington, (USA), 256 pp.

FAO. 2010a. Second report on the state of the world's plantgenetic resources for food and agriculture. Commission on genetic Resources and Agriculture. FAO, Rome, Italy.

Lorenzetti F., Negri V., 2009. *The European seed legislation on conservation varieties*. In: Negri V., Vetelainen M. and Maxted N. eds., *European landrace conservation*, Bioversity International publ., Rome, Italy.

Marino M., Bravi R., Porfiri O. 2012. Linee guida per la conservazione e caratterizzazione della biodiversità vegetale d'interesse per l'agricoltura. Dal seme. 4,34-40.

Mekbib F., A. Bjørnstad, L. Sperling and G. Synnevåg. 2009. International Journal of Biodiversity and Conservation Vol. 1(2) pp. 045-059 June, 2009

MSSRF 2010. Community based agrobiodiversity conservation. <http://www.mssrf.org/bd/ch-agrobio.html>

MIFAAP. 2002. National Plan for Agricultural Agrobiodiversity- Guidelines for the conservation and characterization of plant, animal and microbial genetic resources for food and agriculture. Executive Summary - October 2012. MIPAAP-INEA . ISBN978-88-8145-278-1. <http://www.reterurale.it>

Negri V. (2003) Landraces in central Italy: where and why they are conserved and perspectives for their on farm conservation. *Genet Resour. Crop Evol* 50:871–885

Padulosi S. 1999. A comprehensive vs. limited list of crops: the role of underutilized crops and opportunities for international centres, donor communities and recipient countries. In M. Broggio ed. Exploring options for the list approach - Proceeding International Workshop: Inter-dependence and food security which list of PGRFA for the future multilateral system? Istituto Agronomico per l'Oltremare, 1-2 October 1998, Firenze, Italy.

Padulosi S, J. Thompson and P. Rudebjer. 2013. Fighting poverty, hunger and malnutrition with neglected and underutilized species *(NUS): needs, challenges and the way forward. Bioversity International, Rome. 56 pp. ISBN 978-92-9043-941-7.

Padulosi S., K. Amaya, M. Jäger, E. Gotor, W. Rojas and R. Valdivia (2014). Holistic Approach to Enhance the Use of Neglected and Underutilized Species: The Case of Andean Grains in Bolivia and Peru. *Sustainability* 2014 (6). XX pp. ISSN 2071-1050

Pistorius R. 1997. Plants and politics: a history of the plant genetic resources. Bioversity International, 134 pp.

Porfiri O., Costanza M.T. and Negri V., 2009. *Landrace Inventoring in Italy: the Lazio Regional Law Case Study*. In: Negri V., Vetelainen M. and Maxted N. eds. *European landrace conservation*. Bioversity International publ., Rome, Italy.

Sunwar S, Thornström CG, Subedi A, Bystrom M. 2006. Home gardens in western Nepal: opportunities and challenges for on-farm management of agrobiodiversity. *Biodiversity and Conservation* 15:4211-4238.

Annex 3: Mini-paper: Tools for the Characterisation and Use of Plant Genetic Resources

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Introduction

The world's ex situ collections of plant genetic resources (PGR) are extensive and represent a vital resource for plant breeders as they develop the new and improved crop varieties required to fulfil the need to produce more food in a sustainable manner. Over seven million accessions are conserved in ~1700 different gene banks. The challenge of understanding and accessing the genetic diversity in this germplasm, as well as developing efficient management procedures, cannot be underestimated. Rapid developments in technology can play a vital role in the efficient characterisation and evaluation of the many collections of PGR. This will enable users of PGR, namely plant breeders, researchers and farmers, to enjoy facilitated access to collections and to understand and incorporate novel traits into crop varieties. Given the scale of the global PGR collection, high throughput approaches are required which achieve a good balance between cost and the amount of data obtained. Putting the conserved crop diversity to use for an economically efficient and sustainable agriculture is also a key challenge that will validate conservation efforts. The development of more sophisticated approaches for the characterisation and targeted transfer of novel genetic variants into breeding lines is progressing and could vastly expand the use of plant genetic resources. New techniques for molecular marker-assisted selection, genetic modification and targeted mutagenesis alongside phenotypic selection, enable plants to be selected which possess only the desired allelic or other variant. Minimising the quantity of the rest of the donor genome which is introgressed is important as it means that breeding programmes can proceed more rapidly, particularly when non-target traits (e.g. from crop wild relatives) would be deleterious to the agronomic performance of the breeding line. This paper introduces some of the tools currently being used or developed, with some examples of the use of PGR in breeding programmes. It is by no means an exhaustive list, and examples have been selected to illustrate particular tools and techniques.

Tools to Characterise and Facilitate the use of PGR

Phenotyping and morphological characterisation

Conventional morphological characterisation was previously the only means available to both assess genetic diversity in collections of PGR and provide potential users with the means to select material for testing. Growing material out is relatively slow and resource-intensive. However, basic descriptions of crop phenotypes can be valuable to users who do not have the capacity to grow out and describe large numbers of accessions themselves. PGR accessions can also be evaluated in more detail for particular traits of interest to researchers and breeders, such as pest and disease resistance, or agronomic traits such as yield and environmental resilience.

Users of PGR sometimes supply non-commercial phenotypic information to the providing institution; this is required under the Standard Material Transfer Agreement mandated by the International Treaty on Plant Genetic Resources for Food and Agriculture. In practice however this may not occur routinely, nonetheless the provision of information from users is one way for gene banks to accumulate phenotypic data to provide to other users.

The formation of consortia between gene banks in different countries, breeding companies and researchers has had some success at phenotyping larger numbers of accessions than can typically be handled by a single Gene bank / provider. Recent examples include the various GENRES projects (established under EC 870/2004). Project CT99-105 involved 8 partners and carried out multi-site morphological characterisation of cultivated and wild carrots; other similar projects were carried out on other crops such as brassicas, leafy vegetables and alliums.

The development of new phenotyping technologies allowing extremely detailed characterisation of plants in a controlled environment will further aid the collection of phenotypic data and its provision to users. Facilities such as the National Phenomics Centre in the UK (<http://www.plant-phenomics.ac.uk>), Plateforme de Phénotypage Haut Débit (PPHD) in France and the IPK Automated Plant Phenotyping Platform in Germany are now available to carry out such work. In addition, other phenotyping approaches are currently being developed, from tools to image root growth over time to automated phenotyping robots being developed to collect data on field trials. The development of automated tools for image analysis of plants is a vital area which should enable users to access desired phenotypes via searches of databases.

Another form of phenotyping analysis of increasing importance is the screening of proteins and metabolites (proteomic and metabolomics) in collections of PGR. This enables the discovery of potentially interesting variation related to nutritional profiles, agronomic performance and new bioproducts. These data must be curated and aligned with the accession-level information in order to understand where useful variation in proteomic and metabolomics variation lies in the crop gene pool to permit efficient exploitation.

Characterisation of PGR by Genotyping and Sequencing

The potential of molecular markers to aid collection management and utilisation was recognised early on, but technical and resource limitations meant that investigations were often on a relatively small scale involving relatively small numbers of both markers and accessions. Recent developments in massively parallel sequencing technologies (“next generation sequencing”) have vastly reduced the cost of these types of studies (Kilian and Graner, 2012). The need to deploy genotyping and sequencing to aid the management and use of PGR was emphasised by McCouch (2013), who noted the potential of sequence information to facilitate the uptake of relatively exotic allelic variation in key genes from sources such as crop wild relatives and landraces, where such techniques can minimise the introgression of non-desired portions of the genome into target breeding lines.

Various approaches can be taken depending on the depth of genetic information required, and the genomic resources already available for the crop in question. Approaches range from molecular marker genotyping, sequencing of the expressed portion of the genome (transcriptome sequencing), sequencing based on only the variable or non-repetitive parts of the genome and sequencing and assembly of whole genomes. Genotyping is now most frequently carried out through the use of SNP markers (single nucleotide polymorphisms, which are abundant in eukaryotic genomes), and this is the least costly approach, yet variation at thousands of markers can be assessed. When these markers are ordered on a genetic linkage map and combined with suitable phenotypic data, it allows the identification of regions of the genome which are involved in the control of the trait of interest. This type of information is of particular interest to breeders, and such marker data can aid selection of individuals in breeding programmes to reduce time and cost-intensive phenotyping and selection trials.

New Tools for Accelerating the Use of PGR

There are many examples by which the diversity in collections of PGR has provided vital traits to researchers, plant breeders or farmers to ensure healthy and affordable food production. For example, in Africa, resistance to a devastating viral disease (the Cassava Mosaic Disease, CMD) could be introgressed from the wild (inedible) species *Manihot glaziovii* into cultivated cassava (*Manihot esculenta*) and helped reverse a CMD pandemic. A similar example is presented in maize where a Mexican variety contributed a source of resistance to southern maize leaf blight that attacked the maize crops in the USA in the 1970’s causing a 15% fall in yields.

Broadening the genetic base of crops is a key aspect of a balanced approach to crop improvement. PGR collections are reservoirs of natural genetic variation. Yet, surprisingly recent estimates show that only a few gene bank accessions (less than 1%) have been utilised in crop improvement programmes such as wheat, maize, soybean and others (Sharma et al., 2013). Therefore, the vast diversity of PGR collections is presently only marginally utilised.

Plant breeding encompasses a variety of tools and approaches to improve crops: (i) crosses between sexually compatible species that can inter-mate; (ii) mutagenesis techniques (chemical or radiation) to create new diversity; (iii) in vitro tissue culture procedures for e.g. embryo rescue or protoplast fusion; (iv) induced

polyploidy (chromosome doubling); (v) the use of bridging crosses. The latter techniques were all developed to overcome barriers for gene transfer between sexually incompatible plant species.

Several factors explain the limited use of gene bank materials in crop improvement programmes:

- (i) The breeders' preference for working collections which require less time and fewer resources for developing new cultivars
- (ii) The large size of the germplasm collections: how to select the appropriate genetic diversity?
- (iii) The need to remove undesirable traits ('linkage drag') when utilising wild or unknown germplasm
- (iv) Sexual incompatibility between donor and recipient germplasm preventing transfer of traits of interest

Pre-breeding involves the transfer of traits from unadapted exotic or wild germplasm into well-adapted genetic backgrounds and results in intermediate material that can then be used to develop new varieties (described elsewhere) and can be used as a strategy to tap into the genetic diversity of PGR. Recent innovations in crop improvement provide researchers and plant breeders with new tools that can also expand or speed up the use of the genetic diversity present in PGR collections. A few illustrative examples are presented.

For example, in the 1980s, a new source of CMD resistance was discovered in African cassava landraces. This resistance trait could be located on the cassava genome through genetic mapping, and closely linked molecular markers were identified (Akano et al, 2002). Using molecular marker techniques in combination with phenotypic selection, this important trait can now be more rapidly introduced into other cassava varieties, diversifying CMD resistant cassava germplasm.

Other innovations in crop improvement, such as Genetic Modification (GM) in combination with in vitro tissue culture techniques allow to transfer traits from wild species into cultivated varieties which are very difficult, very slow or impossible to cross, and which could greatly enhance the use of PGR. An example from the public sector is the development of a late blight-resistant potato whereby a resistance gene from a wild potato relative was transferred into a cultivated potato variety (van der Vossen et al, 2003). Field tests in several European countries have demonstrated that the GM product is resistant under field conditions and drastically reduces the number of fungicide sprayings for effective control of late blight compared to conventional methods. This is one example of the use of plant genetic resources in conjunction with a biotechnological approach where environmental and competitiveness concerns can be reconciled.

An example from the private sector concerns the development of lettuce varieties resistant to the aphid pest *Nasanovia*. In this case, the resistance trait originates from a wild relative of lettuce (McCreight, 2008). This trait has been introduced into commercial lettuce varieties using closely linked molecular markers that allowed to break the undesirable linkage drag contributed by the wild relative.

A range of new genome editing techniques for plant breeding are being developed that will further expand the (molecular) toolset for plant breeders and researchers and that will allow to tap into the richness of genetic diversity of PGR collections (Lusser et al., 2011; Hartung and Schiemann, 2014).

Overall, these examples illustrate how PGR in conjunction with innovations in plant breeding can be used by the public and/or private sector to develop new crops with improved economic and environmental sustainability traits.

Models of Cooperation

Various models of cooperation between providers and users can be seen in the context of the development and application of tools for the characterisation and use of PGR. Generally, the providers in this context are gene banks and other institutions rather than farmers themselves. A variety of other organisations may also be involved, from academic institutions, plant breeding companies and international scientific organisations and NGOs. An additional layer of complexity is added when one considers the size, resources and technological capacity of all stakeholders in the provider/user group. Large, well resourced gene banks often have some capacity to develop and deploy these types of tools themselves. Although the technology is developing rapidly, it has not yet reached the stage where it can routinely be used on often variable and heterozygous accessions in gene bank collections.

Two examples of international collaborative activities are the African Orphan Crops Consortium, a partnership aiming to obtain the genome sequences of 100 traditional and underutilised crops from Africa which have hitherto not attracted such research investment, and to deploy this information in breeding programmes to speed up crop improvement activities (see <http://www.mars.com/global/african-orphan-crops> and Fox, 2013). Consortium partners include the Mars Corporation, UC Davis, the Beijing Genomics Institute and the World Agroforestry Center. A nascent consortium involving genome researchers and ex situ collections (DivSeek) is currently under development, and this grouping is aiming to facilitate the linking of sequence data and ex situ germplasm collection data to make such data more useful for users and managers of PGR collections.

In terms of smaller national level activities, the Genetic Improvement Networks developed in the UK such as VeGIN (vegetable crops – see www.warwick.ac.uk/go/vegin) and OReGIN (rapeseed – see www.oregin.info) in the UK offer pipelines for the uptake of PGR by plant breeders into new commercial varieties with improved sustainability traits. These government-funded networks aim to include representatives from all elements of the supply chain, and have developed further genetic resources such as core sets of germplasm and other research populations to facilitate the uptake of novel allelic variation in pre-breeding material. The networks have proved popular, and have directly led to public/private partnerships which will allow the commercial exploitation of research results.

For effective use and adoption of new varieties in farmer fields, a multi-stakeholder approach is required. In the case of CMD cassava for example, the active participation of many stakeholders including NGO's, government agriculture offices, farmer organisations and farmer training centres and support by multilateral donors was key to the successful monitoring and management of the CMD pandemic. Involving a wide range of stakeholders from the onset had the twin advantages of fostering ownership of the initiative at the local level and ensuring continuity after the project had finished. In case of plant varieties or products generated by innovative plant breeding techniques, especially GM plant products, it will be critical to engage end users and consumers for successful deployment and acceptance.

Problems and Constraints

Germplasm characterisation. The main issue is the level of resources available for the routine sequencing of accessions in ex situ collections. Such activities, although vastly reduced in price from when the human genome cost \$3 billion to sequence and assemble, are beyond the resource limits for most gene banks. McCouch (2013) estimates that complete sequencing of all unique accessions in the world's gene banks would cost around \$200 million dollars – a lot of money for gene banks but relatively small in the light of other research and public spending. The development of strong consortia to link curators (who have the expertise at the crop level), genomics researchers, bio-informaticians and end users will also take some effort. Particular efforts must be paid to the curation of the huge amounts of data which will result from these types of activities and to ensure that users can access and understand them. Large multinational breeding companies have their own expertise in utilising genomic information but efforts will have to be made to assist smaller companies so that they too can benefit from the massive amounts of genetic and genomic data which will be generated. The development of (mini)core collections that capture the majority of genetic diversity is a strategy to select appropriate genetic diversity for breeding programmes. Additionally, accessions may need to be purified to move them from variable populations to homozygous lines, particularly for outbreeding crops. The issue of whether gene banks themselves produce and curate this type of derived material is also not resolved.

Ownership. The use of the genetic diversity in PGR collections is impacted by the various intellectual property (IP) regimes applicable to crop varieties (e.g. patents or plant variety protection) and by restrictions on the free exchange of plant genetic resources. IP rights impact the use of improved material by other companies, plant breeders and also farmers. Further, several countries have restricted access and exchange of especially indigenous plant species or crop (varieties), sometimes within their national borders, in the absence of access and benefit-sharing measures. Therefore, the concept of plant genetic resources as a general public good with free (inter)national exchange/use has declined in recent times.

Regulatory systems. The regulatory regimes surrounding the field testing and commercial deployment of GM plant products are lengthy and costly in many countries, especially in Europe. While these innovative techniques could greatly expand the use of plant genetic resources, the complex regulatory systems currently limit applications to a few major crops and traits, dominated by some six multinational companies. The low understanding and acceptance level by the general public, particularly within Europe, further means that market opportunities and public initiatives for other crops/traits are limited at this time – although this is less of an issue in other regions of the world.

Phenotyping and trait screening. The deployment of genetic diversity from PGR collections will eventually be limited by the cost and effort involved in phenotyping and trait screening. Such experiments will need to be correctly designed and replicated in order to statistically link sequence and genotype data to agronomic traits and should preferably be carried by or in close cooperation with the end users of the germplasm, e.g. plant breeders or farmers. These data will also have to be correctly managed and curated to allow for efficient future access as well.

Research Needs

The most pressing needs are the development of coherent programmes to obtain genomic data on accessions in collections of PGR. This will require the development of frameworks and consortia using common standards of data curation to ensure that data are available in a format that is accessible by users and collection managers.

Activity is well under way on the major staple crops (maize, wheat and rice) but other crops, including traditional crops and fruits and vegetables of nutritional significance have been less well-studied. Developments in technology will make it much easier to obtain genomic information on a wide range of crops regardless of the level of previous investment. Particular targets should be clonally propagated crops, for example fruit trees. As they are heterozygous and have long breeding cycles, the application of new technologies could potentially have an impact of a greater magnitude. Technological and bio-informatics advances should also be pursued to allow efficient analysis of heterozygous material, as well as the development of sets of homozygous lines which represent gene pool diversity (the latter is time and resource intensive). Additionally there needs to be a recognition that DNA sequence diversity is important, but that other factors can affect crop traits and phenotype – for example epigenetic variation, pleiotropic interactions and differing effects of alleles in different genetic backgrounds to name but a few. Sequencing should be used as a tool to better understand collections and to prioritise efforts but there must be an understanding that PGR collections cannot be reduced to DNA sequences.

In terms of phenotypic characterisation, experimental design is going to be crucial in order to link such data with genetic and genomic information. It is likely that phenotyping will become a limiting step rather than the collection of sequence data so advances in data collection and automated approaches will become more important in order to fully exploit the diversity in PGR collections and provide users with the information they need to best select material.

Discussion in plenary

Among the 7 million accessions which exist in gene banks, about 70% are duplicates. Tools for identifying duplicates from collection are needed. There is also the need to characterise the diversity found on-farm and not only in seed banks. There are new genomic technologies, such as high throughput DNA fingerprinting, Next Generation Sequencing (NGS) which can help to characterise germplasm in a much cheaper way and more quickly.

References

Akano A, Dixon A, Mba C, Barrera E, Fregene M (2002) Genetic mapping of a dominant gene conferring resistance to the cassava mosaic disease. *Theoretical and Applied Genetics* 105: 521-525

Fox, J (2013) *Nature Biotechnology* 31: 867 doi:10.1038/nbt1013-867a

Lusser M, Parisi C, Plan D, and Rodriguez-Cerezo E (2011) New plant breeding techniques. State-of-the-art and prospects for commercial development. JRC Scientific and Technical Report. ISBN 978-92-79-19715-4. ISSN 1018-5593. Doi:10.279/54761

Hartung F and Schiemann J (2014). Precise plant breeding using new genome editing techniques: opportunities, safety and regulation in the EU. *Plant J.* 78: 742-752

McCouch (2013) Feeding the Future. *Nature* 499:23-24

McCreight (2008) Potential sources of genetic resistance in *Lactuca* spp. the lettuce aphid *Nasanovia ribisnigri* (Mosely) (Homoptera: Aphididae). *Hortscience* 43: 1355-1358

Sharma S, Upadhyaya HD, Varshney RK, and Gowda CLL. 2013. Pre-breeding for diversification of primary gene pool and genetic enhancement of grain legumes. *Frontiers in Plant Science.* 4: 1-4

Van der Vossen E, Sikkema A and Hekkert BTL (2003). An ancient R gene from the wild potato species *Solanum bulbocastanum* confers broad-spectrum resistance to *Phytophthora infestans* in cultivated potato and tomato. *Plant Journal* 36, 867-882

Annex 4: Mini-paper: Cooperation models on conservation and use of Crop Wild Relatives

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Introduction

Crop Wild Relatives (CWR) are wild plant species that are related to cultivated plants, based on a genepool or taxonomic relationship (Maxted et al., 2006). As such they are an important constituent of plant genetic resources for food and agriculture, and they have a key role to play in sustaining food security in the long term, especially in the wake of climate change. They represent an important reservoir of genetic resources for users of germplasm, especially breeders, because they contain the widest diversity in adaptation to changing biotic and abiotic conditions, and they may possess beneficial traits that are useful for breeding. Many useful traits from CWR, such as pest and disease resistance, abiotic stress tolerance or quality improvements, have been used to produce today's crops (Hajjar and Hodgkin, 2007). Like other wild plant species, CWR are currently suffering genetic erosion in the wild and are poorly represented in both *ex situ* collections and *in situ* reserves (Maxted and Kell, 2009). A recently published Red List assessment of 571 native European CWR species (Kell et al., 2012) has shown that over 15% are considered as threatened, while a study by Vincent et al. (2013) revealed Southern Europe as the region with the highest CWR diversity.

The successful conservation and use of CWR requires a concerted collaborative action on the part of gene bank curators, environmental scientists and breeders, to ensure that CWR are adequately conserved in their natural habitats as well as in gene banks for safety backup and for facilitating access to the CWR germplasm to breeders and other users of the germplasm. Often, the greatest challenge is to ensure that relevant national authorities give adequate attention to *in situ* conservation of CWR within their territories, given that in many countries there is no single agency that has responsibility for their conservation—they are outside the remit of established nature conservation agencies, and agricultural ministries have no conservation remit. There is a need for promoting the collaboration between the agriculture and environment sectors, for building local and national

capacities for *in situ* conservation of CWR as well as for educating younger generations about the importance of CWR and their conservation and potential use.

Application for cooperative model

A good example of a cooperative research model on the conservation and use of CWR and local landraces in Europe is provided by the EU FP7 funded project on “Novel characterisation of crop wild relative and landrace resources as a basis for improved crop breeding” (PGR Secure) which is a collaborative project bringing together 10 European organisations. The aim of this collaborative project is to research novel characterisation techniques and conservation strategies for European CWR and landrace diversity, and further to enhance crop improvement by breeders, as a means of underpinning European food security in the face of climate change.

The main actors of the collaborative action and their respective role are given the table below:

Partner	Country	Role
University of Birmingham (coordinator)	United Kingdom	Coordinator and main principal investigator and responsible for work packages on conservation strategies for CWR
Dienst Landbouwkundig Onderzoek (DLO)	The Netherlands	Work package leader on phenomics and genomics
University of Nottingham	United Kingdom	Partner on transcriptomics
Bioversity International	Italy	Work package leader for the informatics and predictive characterisation and work package on dissemination
University of Perugia	Italy	Workpackage leader on on-farm conservation strategies
Julius Kühn- Institut, (JKI)	Germany	Co-leader of the work package on engaging user community
Nordiskt Genresurscenter, (NORDGEN)	Sweden	Partner in work package on engaging user community
MTT Agrifood Research, (subcontracting Finnish Museum of Natural History University of Helsinki)	Finland	Partner on work package on CWR and landrace conservation
Universidad Rey Juan Carlos,	Spain	Partner in work packages in the predictive characterisation, and CWR and Land race conservation
Service XS B.V.	The Netherlands	Partner in work package on phenomics and genomics

The consortium has been working together during the past three years and has made good progress in coordinating their respective research activities. DLO and the Universities of Nottingham and Birmingham and the Service XS B.V. have been working together to demonstrate how novel phenomics, genomics and transcriptomics technologies can be used to speed up plant breeding, using brassica as model plant. The application of a novel high throughput method for phenotyping gene bank accessions of *Brassica* spp. has led to the identification of resistance to the cabbage aphid and to the cabbage whitefly in local races and crop wild relatives accessions of several different species, and some novel sources of whitefly resistance for breeding

have been identified. Bioversity International, in collaboration with the University of Rey Juan Carlos, Spain, on their part collaboratively developed a predictive characterisation method using distribution data and environmental profiles of the habitats of CWR and LR that are likely to favour selection for specific abiotic resistance traits, or that can identify sites that are most likely to favour development of the resistance traits. The University of Birmingham worked in a number of national PGR programmes in Finland, Italy, Spain, UK, Albania, Bulgaria, the Czech Republic, Cyprus, Norway and Sweden and the developed conservation strategies for CWR. Land race conservation strategies have also been developed in Finland, Italy and the UK. An approach to an integrated European CWR conservation strategy has been developed. It combines national CWR conservation strategies and a regional CWR conservation strategy for priority taxa at European level. CGN, NORDGEN and JKI carried out a SWOT analysis of European PGR conservation and use community needs, to promote CWR and LR use (Frese et al., 2013). They organised a stakeholder workshop and generated a web-based map of stakeholders, PGR-COMNET (www.pgrsecure.org/pgr-comnet). The application will facilitate stakeholders to establish contacts which will in turn promote the use of CWR and LR through improved cooperation. Online databases have been screened for interesting accessions which for *Avena* and *Beta* breeding/breeding research programmes and results circulated to private breeders and public researchers. As a result, at least one *Beta* researcher has ordered accessions from gene banks for further evaluation and another researcher has started to develop new project ideas. Finally, Bioversity International has also been developing a web-based information system 'Plant Genetic Resources Diversity Gateway for the conservation and use of crop wild relative and landrace traits' (PGR Diversity Gateway) to provide trait and conservation information to users of germplasm in Europe and beyond.

Within Europe, besides the PGR Secure project described above, there are also many national initiatives aimed at inventorying CWR and at developing action plans for their conservation and use. In Bulgaria for example, a CWR project fund by the Ministry of Environment aims at creating a database of CWR, including the morphological description of the plants, natural habitats, conservation status and potential use of the species.

Problem and constraints

The main constraints experienced by the project, from a cooperative perspective, relate to the exchange of information and data between the stakeholders. Access to information has been a major challenge. For example in the predictive characterisation exercise, the absence of distribution data of whitefly, a major pest of brassica, has not allowed the identification of the potential CWR population of Brassica with resistance to the whitefly. Feedback from breeders on the PGR Diversity gateway has also been poor. There has also been a lack of information on diversity of local crop varieties maintained on-farm, limited access by farmers to available diversity and to information on different varieties. Another important constraint has been the delays that occur when researchers share their data with other partners, before they have published the information.

Research needs

There is a research need to support and enable cost-effective and efficient local, national and global in situ conservation-and-use strategies for targeted crop wild relatives. There are more than 50,000 CWR species worldwide (Maxted et al. 2012a), and it is not possible to conserve all these species in situ. Research is needed to choose not only which species deserved the highest priority for conservation, but also where. Strategies are needed, in the following three areas:

1. To determine the conservation status of CWR and threats to them, and develop long-term indicators and risk threshold levels ;
2. developing policies and practices to conserve CWR in priority sites in the most effective and cost-effective manner.
3. to determine priority sites through the participation and strengthening of local institutions and stakeholders;
4. identifying adaptive traits in CWR, how they are being used or can be used, and the consequences of use;

The conservation of CWR outside protected areas is also more problematic. Many CWR of major crops are commonly found in disturbed, pre-climax plant communities, and are therefore located outside protected areas (Heywood and Dulloo, 2005). Such sites are not managed for biodiversity conservation and the occurrence of CWR populations is incidental, making them particularly vulnerable to adverse management changes.

Generally it is considered that CWR are poorly represented gene banks. Ex situ collections of CWR should be seen as complementary to their in situ conservation (Dulloo, 2011). Often the biology of CWR species is not well known. Elucidating the seed storage behaviour of CWR species, for example, is necessary to improve the best practices for their ex situ conservation. Significant progress has been made in in-vitro slow-growth conservation and cryopreservation research over the past twenty year.

Discussion in plenary

The level of awareness about conservation of CWR by national authorities was discussed. The UK has developed a national strategy on CWR. A plant genetic group was established, involving gene bank managers, who provides technical advice to government, and to policy makers. This committee meets twice per year and discusses issues relating to breeding and biodiversity. There is also a committee on AnGR in the UK. This model should be replicated in other countries, especially in Eastern Europe where there is little awareness and less energy to act.

References

- Dulloo M.E. (2011). Complementary conservation actions In Crop Wild relatives A manual of in situ conservation (eds. Hunter D and Heywood VH). Chapter 12 Pp. 275-294 Earthscan, London, Washington DC.
- Frese L., Kik C., and Palmé A. (2013). On the sustainable use and conservation of plant genetic resources in Europe. Input paper for the Stakeholder workshop of PGR Secure WorkPackage 5 held in Wageningen, November 2013.
- Hajjar R, Hodgkin T (2007). The use of wild relatives in crop improvement: A survey of developments over the last 20 years. *Euphytica* **156**: 1-13.
- Kell, S., Maxted, N., and Bilz, M. (2012). European crop wild relatives threat assessment: knowledge gained and lessons learnt. In Maxted N., Dulloo M.E., Ford-Lloyd B.V., Frese L., Iriondo J., Pinheiro de Carvalho, M A.A., (2012). *Agrobiodiversity Conservation: Securing the diversity of Crop Wild Relatives and Landraces*. CABI Publishing, Wallingford
- Maxted, N., Ford-Lloyd, B.V., Jury, S.L., Kell, S.P. and Scholten, M.A. (2006). Towards a definition of a crop wild relative. *Biodiversity and Conservation*, **15(8)**: 2673–2685.
- Maxted, N., Kell S, Ford-Lloyd B., Dulloo E., and Toledo Á. (2012). Towards the systematic conservation of global crop wild relative diversity. *Crop Science* **52**, 774–785.
- Maxted, N. and Kell, S.P. (2009) *Establishment of a Global Network for the In Situ Conservation of Crop Wild Relatives: Status and Needs*. FAO Commission on Genetic Resources for Food and Agriculture, Rome, Italy.
- Vincent, H., Wiersema, J., Kell, S.P., Fielder, H., Dobbie, S., Castañeda Alvarez, N.P., Guarino, L., Eastwood, R., León, B. and Maxted, N. (2013). A prioritised crop wild relative inventory as a first step to help underpin global food security. *Biological Conservation*, **167**, 265-275

Annex 5: Mini-paper: Harnessing plant genetic resources for enhancing resistance to abiotic stress in the genomics era

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Introduction

Food security in the 21st century will largely rely on the release of climate-resilient cultivars that are better able to perform well across a broad range of environments. In terms of impact on crop growth and productivity, the two most important features of climate change are an increased unpredictability of the prevailing weather patterns in any particular location and an increased frequency and intensity of extreme weather conditions. Consequently, as compared to the cultivars released in the past century, the genetic make-up of climate-resilient cultivars will require greater functional plasticity and resistance to abiotic stress, particularly drought, the most important environmental factor curtailing crop yield worldwide. In 2008, widespread and prolonged drought and the consequent yield losses and sharp increase in rice and wheat prices sparked social unrest and riots in several developing countries, while in 2010 the reduced availability of wheat in Russia consequent to excessive heat and drought caused a sharp increase in the price of wheat. Notably, the spectacular increase in maize productivity during the last century has largely been attributed to an increased resistance to drought and other abiotic stresses that all contribute to curtail yield (Duvick 2005). This notwithstanding, the present rate of increase in crop yield (ca. 1% but varying according to the crop) achieved via conventional breeding is increasingly unable to meet the needs of a burgeoning and more affluent population (Mba et al. 2012). Translational genomics provides novel opportunities to enhance the yearly rate of gain in crop yield (Langridge and Fleury 2011; Varshney and Tuberosa 2013) while advancing our understanding on the functional basis of abiotic stress adaptation, a feature controlled by many quantitative trait loci (QTLs). A major factor that has delayed and limited the contribution of translational genomics to improve crop resistance to abiotic stress is the unpredictability of QTL effects across a broad range of environments (Collins et al. 2008), with few notable exceptions (Maccaferri et al. 2008; Vikram et al. 2011). Importantly, genomics allows for a powerful and targeted survey of the allelic richness of genetic resources (Frison and Demers 2014), a treasure-trove that breeders will need to harness at its fullest in order to counteract climate change more effectively. Accordingly, cloning loci that control abiotic stress resistance provides a new paradigm for tapping into non-elite and wild germplasm, particularly for quantitative trait variation (Zamir 2001; Uga et al. 2013).

A multidisciplinary approach for enhancing crop resilience to climate change

As compared to other categories of traits, the genetic dissection of abiotic stresses benefits more from a multidisciplinary approach. Identifying the main morphophysiological factors that regulate the adaptive response of crops to unfavourable conditions provides valuable clues on the traits to be targeted as yield “proxies” in order to improve yield itself (Reynolds and Tuberosa 2008). Along this line, a number of multidisciplinary, integrative projects have been completed or are in progress in the public domain and/or by means of public-private partnerships. One of the largest public projects specifically aimed to improve our understanding of abiotic stress resistance towards the release of climate-resilient pre-breeding materials and cultivars is the Generation Challenge Programme (GCP: <http://www.generationcp.org/>). The GCP main mission has been to use genetic resources and advanced plant science to improve crops for enhancing food security in the developing world. The GCP website reports many accomplishments at all levels and products that have been obtained during the project. Given the inherent functional complexity of the traits governing growth plasticity and adaptation to climate change, engaging a broad range of expertise is an essential prerequisite in order to successfully leverage genetic resources toward the release of climate-resilient cultivars.

The role of phenotyping and modeling

In the past few years, there has been increasing awareness of the critical role played by accurate, relevant and high-throughput phenotyping (Tuberosa 2012). Digital technologies allow for the collection of large amounts of data in both controlled and field conditions (Araus and Cairns 2014). Aerial infrared thermography of drought-

stressed nurseries allows for an accurate and relevant evaluation of the water status of field plots. High-throughput phenotyping is an essential component for the application of crop modeling based on genetic effects at single loci, an integrative approach that attempts to simulate/predict yield of different genotypes across sites and years in order to define the most beneficial allelic combination to be selected. Importantly, while models allow for (i) testing *in silico* across an almost unlimited range of climatic scenarios and (ii) ranking the yield performance of a large number of genotypes, the results indicate that these differences have a small impact on yield prediction of a reference genotype because errors on the effects of different traits tend to compensate each other (Parent and Tardieu 2014). Nonetheless, large-scale simulation will be increasingly feasible because model parameters corresponding to each genotype can now be measured in phenotyping platforms for large plant collections that will in turn allow us to predict parameter values from the allelic composition of genotypes, as is presently being attempted in DROPS (<http://www.dropsproject.eu/>), a modeling project funded by the EU. It is expected that crop models will increasingly be adopted to simulate the allelic effects in different climatic scenarios where water or heat stresses occur (Parent and Tardieu 2014) while helping to advance our understanding of abiotic stress resistance of crops.

Problem and constraints to optimise the conservation and use of plant genetic resources

The main constraints towards the release of climate-resilient cultivars are insufficient beneficial allelic variability and low heritability of yield. The recent breakthrough in genetic fingerprinting and sequencing have ushered in a paradigm shift for optimising the conservation of genetic resources and have shifted the main focus from the whole plant phenotype to the single loci and/or haplotypes. This has been made possible by the use of SNP-based platforms that allow for robust, high-density profiling at low cost even in polyploid species with complex genomes (e.g. wheat; Trebbi et al. 2011). Genotyping-by-sequencing (GBS) offers the ultimate profiling approach for surveying genetic resources. The impressive scale-up in the number of accessions that is now possible to analyse facilitates the assembly of mini-core collections well representative of each species while facilitating the identification of rare, novel haplotypes at target loci. These rare haplotypes will be instrumental in enriching the pool of novel, beneficial alleles to be introduced in pre-breeding programmes and will eventually contribute to the final make-up of climate-resilient cultivars. Both linkage mapping and association mapping (AM) contribute to the discovery of loci for abiotic stress tolerance. However, as compared to biparental mapping where the frequency of each allele is usually balanced, AM is less effective in detecting a beneficial allele when its frequency is low, from 2 to 10% according to the size of the entire collection of accessions, usually at least 200 to avoid an excessive level of false positives. An example is provided in Maccaferri et al. (2008, 2011) where two major epistatic loci for grain yield in durum wheat under broadly different water regimes were detected in a biparental study, while AM failed altogether to identify the same two loci because the frequency of the key parental haplotype was too low.

Research needs toward the release of climate-resilient varieties

Only a limited number of QTL studies have provided a tangible contribution toward the improvement of crop productivity under abiotic stress. The main reasons for this have been critically reviewed (Collins et al. 2008; Xu and Crouch 2008). This notwithstanding, notable examples of genomics-assisted breeding for enhanced resistance to abiotic stress have been described, and have in some cases led to the release of cultivars with significantly improved performance. Additionally, major QTLs for abiotic stress tolerance have been cloned, thus enhancing our understanding of the adaptive response of the plant to environmental cues. Compelling examples are those reported for tolerance to submergence in rice (*Sub1*; Xu et al. 2006), salinity in wheat (Munns and Tester 2008), aluminum in maize (Maron et al. 2013) and drought in rice (Uga et al. 2013).

Research priorities for further enhancing crop performance under constrained conditions are plentiful. A major issue that so far has been marginally addressed is how stress interactions affect crop growth and yield. Many interactions are possible not only among abiotic factors but also between biotic and abiotic factors (e.g. nematodes and drought). Important contributions to reduce crop vulnerability to climate change will be provided by a better understanding of the rhizosphere, root functions and plasticity, reproductive failure under stress, epigenetic effects, perenniality, etc. Ultimately, sustaining the selection gains required to secure a sufficient and stable supply of food under increasingly challenging climatic conditions will require a more effective integration

between conventional and genomics-assisted approaches. In this context, sequence-facilitated mining of plant genetic resources (Tuberosa et al. 2014) will provide the allelic diversity required for effectively sustaining the breeding/genomics pipeline towards the release of climate-resilient cultivars.

References

Araus JL, Cairns JE (2014) Field high-throughput phenotyping: the new crop breeding frontier. *Trends Plant Science* 19: 52-61

Collins N, Tardieu F, Tuberosa R (2012) Phenotyping for drought tolerance of crops in the genomics era. *Frontiers in Plant Physiology* 3, 347: 1-25

Duvick DN (2005) The contribution of breeding to yield advances in maize (*Zea mays* L.). *Advances in Agronomy* 86: 83-145

Frison E, Demers N (2014) Building a Global Plant Genetic Resources System. In: R Tuberosa, E Frison, A Graner eds. *Genomics of Plant Genetic Resources, Volume 1: Managing, sequencing and mining genetic resources*. Springer, Dordrecht, The Netherlands, 3-27

Langridge P, Fleury D (2011) Making the most of 'omics' for crop breeding. *Trends in Biotechnology* 29: 33-40

Maccaferri M, Sanguineti MC, Corneti S, et al. (2008) Quantitative trait loci for grain yield and adaptation of durum wheat (*Triticum durum* Desf.) across a wide range of water availability. *Genetics* 178: 489-511

Maccaferri M, Sanguineti MC, Garcia del Moral L, et al. (2011) Association mapping in durum wheat grown across a broad range of water regimes and yield potential. *Journal Experimental Botany* 62: 409-438

Maron LG, Guimaraes CT, Kirst M, et al. (2013) Aluminum tolerance in maize is associated with higher *MATE1* gene copy number. *PNAS* 110: 5241-5246

Mba C, Guimaraes EP, Ghosh K (2012) Re-orienting crop improvement for the changing climatic conditions of the 21st century. 1:7 <http://www.agricultureandfoodsecurity.com/content/1/1/7>

Munns R, Tester M (2008) Mechanisms of salinity tolerance. *Annual Review of Plant Biology* 59: 651-681

Parent B, Tardieu F (2014) Can current crop models be used in the phenotyping era for predicting the genetic variability of yield of plants subjected to drought or high temperature? *J Experimental Botany*, in press

Reynolds M, Tuberosa R (2008) Translational research impacting on crop productivity in drought-prone environments. *Current Opinion in Plant Biology* 11: 171-179

Trebbi D, Maccaferri M, de Heer P, et al. (2011) High-throughput SNP discovery and genotyping in durum wheat (*Triticum durum* Desf.). *Theoretical Applied Genetics* 123: 555-569

Tuberosa R (2012) Phenotyping for drought tolerance of crops in the genomics era. *Frontiers in Plant Physiology* 3, 347: 1-25

Tuberosa R, Graner A, Frison E (2014) *Genomics of Plant Genetic Resources*. Springer, Dordrecht, The Netherlands, (two-volume set) 1154 pages

Uga Y, Sugimoto K, Ogawa S, et al. (2013) Control of root system architecture by *DEEPER ROOTING 1* increases rice yield under drought conditions. *Nature Genetics* 45: 1097-1102

Varshney RK, Tuberosa R (2013) *Translational Crop Genomics*. Wiley, London, (two-volume set) 684 pages



Vikram P, Swamy BP, Dixit S, et al. (2011) *qDTY_{1.1}*, a major QTL for rice grain yield under reproductive-stage drought stress with a consistent effect in multiple elite genetic backgrounds. *BMC Genetics* **12**: 89

Xu K, Xu X, Fukao T, et al. (2006) *Sub1A* is an ethylene response-factor-like gene that confers submergence tolerance to rice. *Nature* 442: 705-708

Xu YB, Crouch JH (2008) Marker-assisted selection in plant breeding: From publications to practice. *Crop Science* 48: 391-407

Zamir D (2001) Improving plant breeding with exotic genetic libraries. *Nature Reviews Genetics* 2: 983-989

Annex 6: Mini-paper: A crop-pollinator interplay approach for the implementation of pre-breeding strategies on local breeds and varieties.

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Introduction

The incorporation or dynamic gene pool management approach to breeding programmes on local varieties, in combination with farmer-participatory population improvement, seeks to produce a long-term genetic improvement of diversified populations. This approach better meets farmers' needs for varietal adaptation to variable environments as well as for site-specific requirements. The aim is to create new broad-genetically based populations through crossing and recombination of genetically diverse genetic materials, selected by farmers and breeders (Hausmann et al. 2004). Diversity, crossing and recombination have to be maximised. Open-pollinated varieties (OPVs) are demanded for low-input and organic (LI/O) farming, to avoid the dangers of genetic uniformity and to make the beneficial effects of heterosis available to low-income farmers in a timely manner (Nandety 2010).

For animal-pollinated crops, creating OPVs based on local germplasm and using pollinators as agents of crossing should be considered. In that sense, pollinators are natural breeders of highest importance. Open pollination is seldom used by breeders for making crosses but it is a method of crossing that is well adapted to farm management (Weltzien et al. 2005). Two basic approaches are used to manage pollination by farmers at field level: a) in Farming for Alternative Pollinators (FAP), the approach targeted at pollinators has focused on appropriate semi-natural habitats management along field margins (Christmann and Aw-Hassan 2012), that is pollinator-friendly practices; b) in Crop-Design systems, breeders and farmers develop, by participatory plant breeding (PPB), cultivars with enhanced heterosis-mediated yield and resilience, as a result of the provision of floral resources within the crop, for supporting insect pollinator populations to be used as agents of crossings to increase heterozygosity (Palmer et al. 2009), i.e. pollinator-friendly crops. Additionally, this approach could be a promising strategy to develop crop environmental services and to link breeding and ecosystems services (ecological and food production). This approach requires the understanding and management of complex crop-pollinator-farmer interactions.

Problems and constrains

Summarised as a series of bullet points

- **Knowledge gaps**
 - **Lack of knowledge** on the factors that shape the amount and distribution of genetic diversity and consequently the lack of appropriate protocols, location and species based, to maintain the heterogeneity and heterozygosity level.
 - **Lack of knowledge** on efficient pollination managements technologies on a species-specific base
 - **At accession level information:** identification, characterisation and evaluation data of 'useful' traits related to the crop-pollinator inter-play. Even when some data exists, low quality or reliability of data limits the usefulness of the data.
 - **Constraints in germplasm availability.** We face a situation where we need to recover functional floral traits, which may have been lost through extended breeding for conventional systems.
- **Insufficient participation and communication**
 - **Insufficient PPB** development. Considering that farmers have local knowledge on pollinator habitats, their contribution is especially valuable.
 - **Lack of translational progress in the pollination biology field.** Huge gains in basic reproductive biology knowledge, obtained by using mainly wild populations, have not led to the development of novel

germplasm management and pre-breeding improvements. Researches in floral biology tend to be confined in their field. There is a gap between biologists interested in floral biology and those interested in the application of this knowledge to germplasm management and pre-breeding. The proposed strategy should bridge the gap between floral biologists and curators and breeders.

Research needs

Summarised as a series of bullet points

- **Reduce knowledge gaps**
 - **Observation and data collection:** Assessing how pollinators and crops interact to shape the specific environments in which breeders and farmers make breeding decisions.
 - **Strategies for management:** Practices to maintain and enhance insect-aided crossing technologies suited to specific situations.
 - **Untangling the linkages:** Elucidating synergies between pollinators and crops for food production and ecological services enhancement to develop a win-win strategy (farmers-crops-pollinators).

- **Information flows. Interaction with relevant European and world-wide initiatives**
 - The implementation of the proposed strategy will gather support from the following initiatives: a) at European level, a Cost Action FA1307 on Sustainable Pollination; and b) at world level, the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES) on the assessment of pollination and pollinators associated with food production.

Discussion in plenary

The case of pistachio in the Middle East was mentioned. Farmers plant wild *Pistacia* species in the orchard for providing pollen which, according to them, contributes to improving the success of pollination among male and female cultivated varieties. A similar situation is recorded in the oases of North Africa where date palm growers select specific male trees as donors of pollen used for pollinating specific female trees (according to the farmers, this 'matching' provides date fruits of larger size and better shapes – a poorly known phenomenon, known to scientists as xenia or metaxenia). Farmers' knowledge on how to manage pollination (operated by the wind or by insects or both) is thus extremely relevant in crop production and warrant thus further studies. Additionally, it was suggested that there is a gap between pollination biologists interested in floral biology and those interested in the application of this knowledge to germplasm management and pre-breeding. A new EIP-AGRI Focus Group to strengthen the links between pollination biologists, gene bank managers and farmers, to better use pollination and pollinators in PGR conservation, has been proposed.

References

Cost Action FA1307, 2014. Sustainable pollination in Europe: joint research on bees and other pollinators (SUPER-B). Available at: http://www.cost.eu/domains_actions/fa/Actions/FA1307>[Accessed 21 April 2014].

Christmann, S., Aw-Hassan, A.A., 2012. Farming with alternative pollinators (FAP) - an overlooked win-win-strategy for climate change adaptation. *Agriculture, Ecosystems & Environment* 161, 161-164.

Hausmann, B.I.G., Parzies, H.K., Presterl, T., Susic, Z., Miedaner, T., 2004. Plant genetic resources in crop improvement. *Plant Genetic Resources* 2, 3-21.

IPBES, 2013. Report of the second session of the Plenary of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. United Nations Environment Program. Available at: <<http://www.ipbes.net>>[Accessed 21 April 2014].



Nandety, A., 2010. Recurrent selection for increased outcrossing rates of barley from semi-arid regions of Syria and Jordan. Dissertation. University of Hohenheim, Stuttgart, Germany. pp. 1-76.

Palmer, R., Perez, P., Ortiz-Perez, E., Maalouf, F., Suso, M., 2009. The role of crop-pollinator relationships in breeding for pollinator-friendly legumes: from a breeding perspective. *Euphytica* 170, 35-52.

Weltzien, E., vom Brocke, K., Rattunde, F., 2005. Planning plant breeding activities with farmers. In: Christinck, A., Weltzien, E., Hoffmann, V. (eds), *Setting breeding objectives and developing seed systems with farmers*. Margraf Publishers, Wageningen, The Netherlands.

Annex 7: Mini-paper: Agro-Food Value Chain Cooperation

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Introduction

In recent years, the increasing demand for agro-food products has imposed a selective pressure upon a small part of the available genetic resources to assure productivity and product standardisation, which has led to the erosion of genetic resources. Such genetic erosion is a major problem as biodiversity is essential to the sustainability of agricultural production. Indeed, the hidden genetic variability is believed to be the key to secure the adaptability and resilience of agro-ecosystems to environmental and social challenges, as global warming, water shortage and the increasing population and food demand. The Millennium Ecosystem Assessment (MEA, 2005) concludes that human activity is having a significant and escalating impact on the biodiversity of world ecosystems, reducing both their resilience and biocapacity.

Ecosystem services are defined as the benefits people obtain from ecosystems (MEA 2003). Agriculture and ecosystem services are interrelated in at least three ways: firstly agro-ecosystems generate beneficial ecosystem services such as soil retention, food production and aesthetics; secondly agro-ecosystems receive beneficial ecosystem services from other ecosystems such as pollination from non-agricultural ecosystems; and thirdly ecosystem services from non-agricultural systems may be impacted by agricultural practices (Dale and Polasky 2007).

Therefore, the variability of genetic resources is of significant value to drive innovation, to tackle the challenges to ecosystem services and consequently to boost the competitiveness of the European agro-food sector. In order to understand how genetic resources can add value to the agro-food chain, it is important to analyse its entire value chain, and then to identify which bridges should be built to promote effective and value-adding cooperation. Herein we carry out a brief analysis of the role of genetic resources on the agro-food value chain and present some cases of successful valorisation of endogenous genetic resources.

The integrated agro-food value chain

Despite dealing with biological production factors, where endogenous genetic resources can be of high value, the players on the principal value chain of the agro-food sector deal with an already reduced variability of genetic resources – as most of them are provided by the complementary chain suppliers, who offer a reduced sub-set of biological resources – only those that can be industrially produced. Nevertheless, it is important to note that, most commonly, these are actors that bridge the research to innovation divide, by supplying innovative services and/or products to the principal value chain, which can then leverage innovation downstream.

Indeed, genetic resources (GRs) play important roles along the typical agro-food value chain – from farming to the consumer (Figure 1). Therefore, when developing R&D programmes on the variability of GRs and on their potential applications, it is important to have a clear view of the stakeholders on all the associated value chains. Of the entire value chain, the GRs (both plant and microbial, PGR and MGR, respectively) play a major role on two particular stages:

- To *farming* the GRs are critical as they are the primary source to agricultural production, and to its ecosystem. Also, farming is the stage with more suppliers of GRs, which can be used directly on production, or indirectly on modulating the ecosystem. Nevertheless, this stage is the bottleneck for genetic variability, as the tendency is to reduce variability on biological production factors to better control the production field, and hence, to increase production. At this stage it is important to understand how can genetic variability brings innovation to farming: How can GRs allow for process

and product innovation? Will PGRs produce new products? May MGRs, in particular beneficial microorganisms, allow for process innovation? How can the ecosystem services contribute to a more sustainable process?

- GRs are also important in *transformation*, particularly for those industries in the agro-food sector that involve food processing. Indeed, these processes may involve the use of MGRs – as fermenting microorganisms; or biotechnological derivatives of GRs – as enzymes, protein extracts or mannoproteins, amongst others. Also, it is important to note that innovation in food processing may lead to product innovation. Therefore, the genetic variability of GR should be further explored to allow for process innovation.

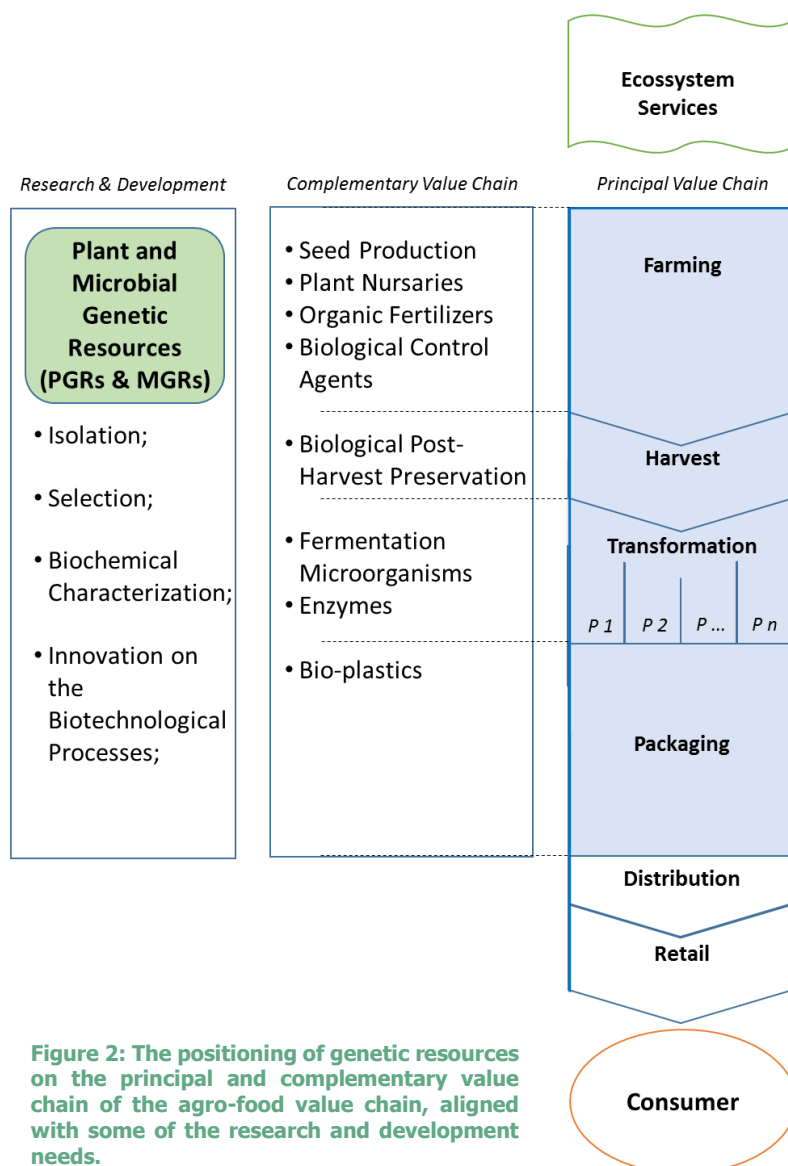


Figure 2: The positioning of genetic resources on the principal and complementary value chain of the agro-food value chain, aligned with some of the research and development needs.

Apart from farming and transformation, GRs do not play prominent roles in the agro-food value chain. However, it is worthwhile noting that they may play minor roles, as in harvesting, to tackle post-harvest challenges and, consequently, to increase the shelf-life of perishable GRs; or even in packaging, with, for instance, the development of bio-plastics.

In conclusion, both PGRs and MGRs play important roles in the value chain of the agro-food sector, and their genetic variability has the potential to drive both process and product innovation. However, the genetic diversity that is, in fact, available to the principal value chain is limited, as it faces several constraints and bottlenecks,

which ultimately result in genetic erosion. Therefore, all players, from the upstream academy to the downstream consumer, have a role to play in what concerns the valorisation of GRs, but there must be an active articulation between all the levels of stakeholders. It is also important to understand who in the chain has the power to drive innovation, and hence to pull the R&D on genetic resources.

Examples of cooperation models

CAMPOTEC, SA - Association of Fruit and Vegetable Growers, Portugal

CAMPOTEC, SA was formed in 1994. It buys and sells fruit (pomoideae and prunoideae), potatoes and pre-packaged agricultural produce (fourth generation preservation methods). It currently has 800 shareholders, and in 2011, sold roughly 26,000 tonnes of agricultural products, with a total value of EUR 19 million. Its flagship products are two autochthonous fruits: the Rocha pear, from the denominated region for Pêra Rocha do Oeste, and the apple variety produced within the PGI of Alcobaça. One of CAMPOTEC's first actions to value their autochthonous fruits was to protect the designation of origin, which was crucial for their activity. For this association, innovation and the valorisation of these PGRs is a priority, so that they were one of the first in their sector to have an internal certified innovation department, which is responsible not only for the internal innovation, but also for their integration in innovation networks and cooperation with the stakeholders.

At a pre-competition level, CAMPOTEC refers to its interaction with the *Centro Operativo e Tecnológico Hortofrutícola Nacional (COTHN)*, a private non-profit association focused on applied research on fruits and vegetables. COTHN represents the different stakeholders, from universities to Consumer Associations, and plays an important role in knowledge transfer and in the interaction with the state and policy makers. On the other side, the Innovation Department is responsible for developing those projects that are of direct interest to CAMPOTEC, and for networking directly with the other stakeholders, namely universities and their suppliers.

ADVID - the Association for the Development of Viticulture in the Douro Region, Douro Wine Region Cluster, Portugal

Wine production in the Alto Douro Wine Region has been done for more than 2,000 years, and has even received the World Heritage Status by UNESCO in 2001. Its wine producers have soon recognised the importance of their natural resources, and the challenge to modernise their practices, without impacting their unique environment. For this, they created ADVID in 1982, which is a non-profit organisation, with the aim of contributing to the modernisation of viticulture and, consequently, to an increased profitability of vineyards in the Demarcated Douro Region (DDR) and to the improvement of the quality of its wines through the implementation and support of related studies. Currently, it has 168 members, who are mainly grape and wine producers, but ADVID also counts with the membership of suppliers and R&D institutes.

The R&D component, which is mainly at the pre-competitive stage of the value chain, is mainly focused on the protection of their *Vitis vinifera* genetic variability – in Douro a total of 114 endogenous *V. vinifera* varieties are under production – and on the protection of their unique environment. ADVID has defined strategic R&D lines of action that were considered by its members, in a demand-pull form, critical for the sustainability of viticulture. These include, amongst others: impact of climate change on viticulture in the DDR; functional biodiversity in viticulture; assessing the oenological fitness of grapes; preservation of genetic biodiversity of the vine plants; and sustainable production in viticulture.

Indeed, their objective is not only to promote R&D projects, but also to act as a knowledge hub, to transfer knowledge, to provide innovative support services to their members, as well as to act as an interface with the regulatory agencies and policy makers.

Evening primrose and Scotia Pharmaceuticals Ltd., UK

Originally cultivated as a garden plant, evening primrose (*Oenothera* spp.) is now grown commercially as an oilseed crop as its seeds contain gamma-linolenic acid (GLA), an unusual fatty acid which is of use to the pharmaceutical industry (Fieldsend, 1996). Scotia Pharmaceuticals Ltd was an international, research-based

pharmaceutical company which was founded in 1979 and played a leading role in the development of evening primrose as a crop plant. In doing so, it added to the biodiversity of agriculture and the ecosystem services it provides.

To provide the genetic basis for its plant breeding programme, Scotia gathered over 2,000 'accessions' of evening primrose from across the world. Many of these were collected directly from the wild, but the majority were acquired from botanic gardens or from the extensive collections held by some academic institutes that were researching the plant's unusual genetic system. Without this cooperation between academia and the commercial sector, it is certain that the dramatic rate of progress in the development of the crop reported by Fieldsend (2007) would have been much lower.

There was also close cooperation between plant researchers, seed companies and farmers, to ensure that the crop was grown to its maximum potential in commercial agriculture. On the manufacturing side, the oil was extracted from the seed and packaged in gelatine capsules by specialist companies. Scotia also cooperated closely with medical researchers to conduct trials designed to evaluate the pharmaceutical benefits of evening primrose oil.

Problems and constraints

It is widely accepted that, notwithstanding the contributions of the type of cooperation models described in this paper, agriculture in Europe has a very narrow genetic base. Furthermore, as stressed in the value chain analysis, when moving downstream the value chain, a reduction of the use of genetic variability is observed. All of this can lead to low levels of biodiversity in farming systems and a loss of ecosystem services.

It is important to notice, that all three examples of cooperation models share two factors: they are driven by the industry, and the end product is economically viable. If this were not the case, the work done on the development of PGRs would not have taken place. This is a point that is frequently missed by those who champion plant (or animal) species that are suitable for agricultural production, and would thus contribute to agricultural biodiversity and potentially the enhancement of ecosystem services, without assessing their economic viability.

Also, in these cases, there is already the awareness of the need to promote continuous research on the entire value chain, in order to successfully innovate using the genetic resources. However, especially to the end-chain stakeholder, it is sometimes difficult to promote the necessary research and innovation to the logistics and distribution partners – which can be critical to preserve the original properties and quality of the products, and to increase their shelf life in the product cycle.

Another problem frequently pointed at is marketing, and the need to create a market – often GRs are initially explored in niche markets, but the need to go to the mass market will not be neglected, in order to be a sustainable and viable business.

Research needs

If it is accepted that an increase in genetic diversity is needed in European agriculture, more efforts are required to ensure that agricultural production using novel genetic resources is economically viable. While the introduction of subsidies that would recognise the value of the ecosystem services provided could be one option, as an alternative approach more attention should be given to cooperation models through which the various actors in the value chain work together to maximise the value added that can be generated from the utilisation of novel genetic resources in agriculture: from researchers to consumers.

As discussed, it is important to have a comprehensive view on the entire value chain, to thereafter define the research actions. Only then should it be defined what the concrete needs of each actor are, so the very first suggested action is to engage in a comprehensive analysis of the different value chains of the Agro-Food Sector, to understand the specific and value-adding research needs.

Discussion in plenary

The relationship between farmers and the industry was discussed. Farmers are considered as a part of the industry. In the UK and Portugal, "farmer- scientist" networks are being set up, where groups of farmers and researchers meet and talk through problems etc. Collaboration exists with policy makers, scientists etc.

References

Dale, V.H. and Polasky, S. (2007): Measures of the effects of agricultural practices on ecosystem services. *Ecological Economics* **64**, 286-296.

Fieldsend, A.F. (1996): Evening primrose - from garden flower to oilseed crop. *The Horticulturist* **5** (3), 2-5.

Fieldsend, A.F. (2007): The impact of plant breeding on seed oil content and quality in evening primrose crops. In: *Proceedings of the Joint International Conference on Long-term Experiments, Agricultural Research and Natural Resources*; Debrecen, Hungary, 31 May – 1 June 2007, 29-36.

MEA (2003): *Ecosystems and Human Well-being: A Framework for Assessment*. Washington DC: World Resources Institute.

MEA (2005). *Ecosystems and Human Well-being: Synthesis*. Washington DC: World Resources Institute.

Annex 8: Mini-paper: Pre-breeding in crop plants

Ahmed Jahoor

Introduction

There is currently a major gap between the operations of plant genetic resource collections and modern plant breeding, which is potentially a major restriction in the development of cereal varieties that are needed to meet novel agronomic and environmental challenges. This disconnect can be bridged through a process known as pre-breeding, which is based on the characterisation of genetic resources for traits of interest, followed by transferring these traits into suitable, agronomically adapted genetic backgrounds, to develop appropriate varieties with enhanced yield, yield stability and disease resistance for different agro-ecological zones.

Pre-breeding in crop plants in Europe for long-term goals must be undertaken in close collaboration between public research institutes, gene banks as well as private plant breeding companies, in order to be attentive, sustainable and successful. Such partnerships will ensure that targets are chosen that meet the demands for climate adaptation and environmental policies – changed crop production systems, extended cultivation areas, improved water and nutrient use efficiency, improved resistance to pests and pathogens, etc. – and also the demands on increased production in combination with specific quality requirements of the market. Such partnerships will also help to develop the capacity building for breeding, which is needed to counteract the competence erosion that has resulted from structural changes and low priority on this area in recent years. Such capacity will be of paramount importance for meeting the challenges that future agriculture has to meet, both in Europe and in developing countries.

Pre-breeding for disease resistance

Plant pathogens cause considerable yield losses in crop production, reducing crop quality and threatening food safety. The prevalence of different plant diseases is changing due to changing environmental conditions, including global climate change, but also changes in agricultural production systems. In such a changing environmental and economic context, plant diseases will certainly appear and compromise crop production in regions where they did not represent a problem before, as is already being seen for example with the emergence of a new strain of heat tolerant wheat yellow rust and increasing problems with *Fusarium* head blight in North Europe. To combat diseases in crop plants, fungicides are often used. The fungicide can create the environmental concern that they are also harmful for human health. Therefore, pre-breeding for disease resistance is the most environmentally friendly and human-friendly method to combat this problem in crop plants.

Many major race-specific resistance genes controlled by very few genes have been introduced in the recently released varieties. However, these major race-specific resistance genes are frequently overcome by newly developed pathogen races through mutations or recombination. Therefore, it is extremely important to search for new sources of resistance. Since major race-specific resistance does not always provide durable resistance, it is important to identify new race-specific major genes as well as race non-specific minor genes for disease resistance. The race non-specific resistance genes are mostly controlled by several genes with minor effect. While the major race-specific resistance genes provide complete resistance against a specific pathogen race, race non-specific resistance controlled by minor genes provides a wider spectrum of resistance and slows down the occurrence of mutation in the pathogen populations. In addition, the minor genes for disease resistance might also hinder the penetration of pathogen into the host. Due to these facts, it is important to develop strategies for sustainable use and management of resistance genes in pre-breeding programmes.

Following steps are needed in pre-breeding for disease resistance:

Identification of new sources of resistance: The new sources of resistance are often found in exotic material, land races or wild relatives of cultivated crops. The resistance genes can be identified with help of host-pathogen interaction. However, it is difficult, laborious and not always possible. Therefore, new tools have

to be developed for the identification of new resistance genes. Here, the DNA markers, together with the advanced methods in statistics, offer an excellent opportunity to identify the new resistance genes.

Mapping of new resistance genes: There are several kinds of progenies used for mapping resistance genes in exotic material. The most commonly used population is bi-parental populations, in which two parents, a resistant and a susceptible one are involved. In association mapping population, a large number of different lines are screened for disease resistance and genotyped with DNA markers. This will result in the identification of loci involved in disease resistance. A multi-parental advanced generation inter-cross, or so-called MAGIC population, in which 4 or 8 donor parents for a disease or for different diseases are included, can also be employed to map disease resistance genes in exotic material. In addition, a nested association mapping (NAM) population, in which a resistance donor line is back-crossed several times with adopted material, can also be used to localise resistance genes in exotic material. Here, all above mentioned populations offer the opportunity to map major race specific as well non-race specific resistance genes.

Transfer of new sources of resistance in adopted material: The above mentioned population can be used to identify closely linked DNA markers for disease resistance originating from exotic material, land races or wild relatives. The identified DNA markers can then be used for marker assisted back-crossing in pre-breeding programmes and the marker assisted selection in breeding programmes.

Discussion in plenary

In terms of capacity building, it was mentioned that Ghent University in Belgium and the Institut Polytechnique LaSalle Beauvais in France have set up a joint 2-year Master in plant breeding. Training programmes for future breeders have been established in France and there is an interest in working with the private sector and in providing internships.

Annex 9: Mini-paper: Public-Private-Partnership (PPP) in Plant Breeding

Ahmed Jahoor and Johan Van Huylenbroeck

Introduction

In Europe, plant breeding is based on research output in the field of plant genetics and breeding. In the past, the findings of basic research were immediately used in applied plant breeding. At present, basic research and applied research are moving far from each other. Consequently, the gap between basic research and applied research for plant breeding is increasing drastically. Therefore, it is necessary to build cooperation between plant breeders and plant researchers in the frame of a Public-Private-Partnership.

In a recent report, Van Elsen et al. (2013) described the potential of the public sector and public/private partnerships in the EU within the framework of plant breeding for a bio-based economy. Public plant breeding research significantly decreased during the last 30 years. This trend is more pronounced in the Western European countries. Arguments to invest in public plant breeding are:

- Scientific research in genomics and basic research should be public and accessible to all SMEs
- Public plant breeding should complement private breeding: germplasm development, new traits of interest, breeding on orphan crops
- Public plant breeding can initiate the take-off of private breeding efforts for crops/traits combinations that are not considered by companies to date

Focus for public applied breeding might be in minor crops, germplasm conservation and development, introduce and validate new genetic traits, enhance technology transfer, integration of new tools (i.e. high throughput phenotyping, bioinformatics), education...

Nordic Public-Private-Partnership

The Nordic public-private partnership for pre-breeding in plants (PPP) was established in 2011 by the Nordic plant breeding entities, the Nordic agricultural universities and the 5 Nordic ministries for food and agriculture of Denmark, Iceland, Finland, Norway and Sweden, as a response to the future challenges of crop adaptation to climate change, the need for resilient crops for sustainable intensification of food production and the need to meet future market demands with suitable crop varieties including disease resistance. The Nordic region represents large climatic and agro-ecological differences and plant production under the specific conditions of 16+ hours of day light in summertime, and under ambitious environmental goals of the Nordic countries causing strong pressure to reduce the environmental footprint of agricultural production. This requires access to high quality seeds of adapted cultivars with adequate performance concerning disease resistance, nutrient use efficiency, and stable quality traits. This requires a long-term engagement in pre-breeding and a correspondingly long-term funding.

The purpose of the PPP is to support pre-competitive pre-breeding collaboration between plant breeders and researchers, meeting the requirements of the Nordic societies and increasing access to adapted varieties for Nordic agriculture. Pre-breeding projects can include:

Base broadening; - broadening of the genetic base in a given crop by wide hybridisation and introduction of a new and wider genetic variation into the breeding gene pool of a crop.

Gene introduction;- introduction of specific traits of importance for a crop into an adapted genetic background allowing for plant breeding programmes to apply these traits in further plant breeding and variety development.

Development / Adaptation of tools and methods; - further developing and adapting state of the art tools, methods and technologies to a given crop in order to speed up the breeding process or in other ways providing a higher efficiency in the breeding programme.

The crop innovation Denmark – from genes to plants

The Danish plant breeding companies have been cooperating with universities in research projects for decades. However, so far no strategic pre-competitive collaboration dealing with applied breeding research as well pre-breeding has been conducted. In 2012, the Danish plant breeding companies joined forces and formulated "A Vision for Plant Breeding Research". This became a platform for a constructive dialogue between the private breeding companies and the public research institutes. This resulted in the formation of the Crop Innovation Denmark (CID). The CID is a public private partnership where the plant breeding companies have joined the forces with the research groups at the universities and with the Danish Agriculture and Food Council. The participating breeding companies are DLF-Trifolium, Sejet Plant Breeding, Nordic Seed, and LKF Vandel. The Copenhagen University as well the Aarhus University is participating in this partnership.

The scope of the CID is to increase the activities dealing with applied plant breeding research and to promote the awareness of the need of such activities to public funding agencies.

The most important research activities that should be included are following:

Increase yield and yield stability

Reduced input of pesticides via increasing activities of pre-breeding for resistance

Enhancement of nutrition use efficiency

Production of healthy and high quality food and feed

Adaptation to climate changes

Germany – "Plant 2030"

In Germany, the national public and industry funded a research programme within "Plant 2030". In the PLANT 2030 projects, scientists are working closely with plant breeders and the industry. It connects the common goal to make crops for the future. Research themes are a.o. higher yield, disease resistance, or improved taste. New research results should lead to the development of new varieties. Technology transfer is a key issue in the platform.

www.pflanzenforschung.de/de/plant-2030

The Netherlands – Green Genetics and Better Plants for New Demands

In the Netherlands, the Technological Topinstitute Green Genetics (TTI GG) was founded in 2007 by the Dutch plant cultivation industry, to strengthen the knowledge base of the sector and promote capacity building. This is essential for the Netherlands to keep its prominent international position in the cultivation sector. TTI GG accomplishes this by stimulating breeding companies to cooperate with research and education institutions. By giving financial support to joint research projects, TTI GG also boosts the development of new scientific applications that benefit the sector as a whole. Plant genetics, plant physiology and plant pathology are core areas of attention for TTI GG. www.groenegenetica.nl. A new public private partnership was launched recently under the title "Better Plants for New Demands".

France – Breedwheat

The project BREEDWHEAT in France aims at strengthening the competitiveness of the French wheat breeding sector as well as to address the societal demand for sustainability, quality, and safety in agricultural production. This pre-competitive project, developed over a period of nine years for a total investment of 34 million Euros by 26 partners, has received a 9M€ grant from the French Stimulus Initiative. It brings together 13 public research units from various INRA sites and Universities across France as well as 10 partners from private companies and cooperatives, 2 technical institutes, and the competitiveness cluster Céréale Vallée. www.breedwheat.fr

UK – Crop Improvement Research Club

In the UK Biotechnology and Biological Sciences Research Council (BBSRC), the Scottish Government and industry have launched a Crop Improvement Research Club (CIRC). CIRC will support research on oilseed rape, barley and wheat and their uses in food production for humans and animals. Challenges are to develop a greater understanding of quality and yield traits and of the complex genetic and environmental factors affecting



them. 14 companies have agreed to join CIRC to date. CIRC will support research projects from a joint fund totalling £7.06M. www.bbsrc.ac.uk/publications/innovation/circ-brochure.aspx

Also in other European countries actions were taken to enhance collaborations between universities/research institutes and private breeding companies. In Belgium, SMEs collaborate with the Institute of Agriculture and Fisheries Research (ILVO). Also two grower associations finance public breeding and get the rights on developed material in return.

In general we see that most of these projects are dealing with more fundamental research, and concentrate on genomics.

Reference

Van Elsen A, Gotor AA, di Vicente C, Traon D, Gennatas J, Amat L, Negri V, Chable V (2013) Plant breeding for an EU bio-based economy. The potential of public sector and public/private partnerships.

Annex 10: Mini-paper: Cooperation Platforms on Plant Genetic Resources and their Use in Europe

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Introduction

Conservation of plant genetic resources is a precondition for their utilisation: the germplasm must be safely conserved and accessible for the users. In addition, the germplasm conserved in the gene bank collections needs to be well described and evaluated so that potential users can make their choice on what to acquire from the collections. Several international agreements and undertakings are dedicated to plant genetic resources for food and agriculture. These all link conservation of plant genetic resources to their use, and further improve food and feed security. In order to realise the goals of these agreements, European networks have been established as networking has been stressed as being essential in furthering their respective objectives. Networks may also serve as platforms for scientific discussions, sharing responsibilities and information, technology transfer and research collaboration (Maggioni and Engels, 2014). The most important European platforms are described in the following sections of this paper. Also their contributions to enhance the use of PGR are described.

Existing platforms in Europe

ECPGR - European Cooperative Programme for Plant Genetic Resources

In Europe the most prominent cooperation platform for conservation of plant genetic resources is the European Cooperative Programme for Plant Genetic Resources (ECPGR). It was founded in 1980 on the basis of the recommendations of the United Nations Development Programme (UNDP), the Food and Agriculture Organization of the United Nations (FAO) and the Genebank Committee of the European Association for Research on Plant Breeding (EUCARPIA). ECPGR is a collaborative Programme including most European countries, aiming to ensure the long-term conservation and facilitate the utilisation of plant genetic resources in Europe. The Programme, which is financed by the participating countries and is coordinated by a Secretariat, operates through Working Groups dealing with groups of crops or with general themes related to plant genetic resources. The stakeholders in the working groups represent mostly gene bank curators and database experts, researchers and plant breeders.

Since the start of the programme, the main focus of ECPGR has been on documenting the collections conserved in European gene banks. Documentation results in accurate information of gene bank material such as passport information and information obtained from characterisation and evaluation trials. Information from specific studies can also be included. Consequently, those who wish to utilise gene bank materials can use this information to retrieve suitable material for their own purposes. Today, after 30 years of ECPGR cooperation, one single web portal called EURISCO provides access to all *ex situ* PGR information in Europe. This means information on almost 1.1 million samples of crop diversity representing 5,586 genera and 36,356 species is available for users. In order to strengthen the efforts to make important and unique genetic resources available for breeding and research, ECPGR has established A European Genebank Integrated System (AEGIS). AEGIS will be a virtual European Genebank, where material will be maintained in accordance with agreed quality standards, and will be freely available in accordance with the terms and conditions set out in the International Treaty on Plant Genetic Resources for Food and Agriculture.

ECPGR has not only enhanced setting up an infrastructure for conservation and documentation, but also created opportunities for its working groups to exchange project ideas, discuss and investigate potential funding opportunities and form project partnerships. These opportunities have resulted in numerous germplasm evaluation and characterisation projects that have in turn yielded new information of the material preserved in the gene bank information systems. Also, ECPGR working groups have been successful platforms to develop joint project proposals for funding by the European Union e.g. 'GENRES' regulations (see project list at http://www.ecpgr.cgiar.org/fileadmin/www.ecpgr.cgiar.org/MISC/Secretariat_overview_finalc

[orr_280610.pdf](#)). Also the Seventh Framework Programme has been used as a source of funding and two projects have been realised (PGR Secure www.pgrsecure.org , FruitBreedomics www.fruitbreedomics.com).

ECPGR has currently 21 different working groups that involve experts from gene banks, research institutions, NGOs and breeding entities. These members and their national networks are provided with first-hand information on the utilisation possibilities of germplasm. However, the number of commercial plant breeders in the working groups has diminished, which can weaken the implementation of the activities that would strengthen the link between genetic resources and their use. Thus, activities and working forms that attract the user community should be built up in ECPGR in order not to lose this important link in the programme.

ECPGR with its vast network and technical and political expertise should be considered as an important actor when the European Commission is setting up research and innovation programmes and formulating a Common Agricultural Policy that concerns genetic resources as a basis for agricultural production and food safety.

National and regional programmes for conservation of plant genetic resources

A wide range of stakeholders are involved in the conservation and the sustainable use of plant genetic resources in individual European countries including farmers or growers who manage diversity on the farm or in gardens, breeders who use genetic resources in crop improvement programmes and gene bank curators. Also experts from the nature conservation sector have been involved, as *in situ* conservation of crop wild relatives has been gaining importance. To connect all these stakeholders and to realise the goals of FAO Second Global Plan of Action, national programmes have been implemented in various forms throughout the Europe since 1990's. The task of these programmes has been to plan, coordinate and promote conservation and use of genetic resources in the single countries. Sometimes even regional programmes have been established in order to strengthen and rationalise the work, e.g. The Nordic Gene Resource Center – a gene bank for five Nordic countries. In addition to ordinary national programme reports, outcomes of their activities are periodically published in the country reports of the State of the World of Plant Genetic Resources for Food and Agriculture - SoWPGR (FAO 1996, 2010).

In terms of utilisation of PGR, the second SoWPGR report (http://www.fao.org/docrep/013/i1500e/i1500e_brief.pdf) implies that the following issues are needed in order to increase the use of plant genetic resources:

1. Increase plant breeding capacity worldwide.
2. Characterise and evaluate gene bank collections to make the data more accessible to plant breeders.
3. Mainstream new biotechnologies for plant breeding and characterisation of plant diversity collections.
4. Increase the use of underutilised crops and CWR in breeding programmes. Establish effective and functional seed systems for farmers' access to quality seeds and markets.
5. Increase capacities for information exchange and implementation of seed policies and legislation in developing countries.
6. Promote awareness among policy makers, donors and others on the necessity of forging linkages between plant breeding and seed systems for increasing food production.

Most probably the main issues in Europe are 2, 3 and first item of 4. In addition, linkages between gene bank curators, researchers, breeders and farmers need to be strengthened. In the policy context, it is important that access to genetic resources should not be restricted.

The national programmes have enhanced the use of PGR originating both from national germplasm collections and elsewhere. It is beyond the scope of this paper to review all of the activities here, but the following activity categories can be mentioned: 1) Evaluation and characterisation projects, 2) breeding and genomic research, 3) pre-breeding activities, 4) database management, 5) various activities to raise public awareness on genetic resources and 6) enhancement of the use of landraces in traditional products along with on-farm conservation. These activities have been carried out with different combinations of partnerships between the various actors, as e.g. 1) projects between gene banks and plant breeders and/or researchers, 2) gene bank – gene bank cooperation projects 3) public-private partnerships, 4) gene bank – farmer/grower organisation projects and 5) between various NGO organisations and citizens. Putting projects together, the national programmes very often function as multi-stakeholder and multi-disciplinary platforms that have a possibility to enhance the use of

genetic diversity in many sectors of society. However, it should be kept in mind that their activities are often carried out with restricted and scarce resources. In many parts of Europe strengthening of these activities is highly required.

Project-based platforms

As explained in previous sections, many project-based platforms to enhance conservation and use of genetic resources have arisen, because of available funding mechanisms. They have undoubtedly been helpful in advancing and strengthening activities on the regional, national, European and international levels. An example on the project based platform is the former DIVERSEEDS project (<http://www.diverseeds.eu/>) which was designed to open the European networks to Asian research colleagues working in centers of crop origin, to establish a communication platform, and to promote knowledge exchange on genetic resources during 2006-2008. The funding was received from the European Commission's 6th framework programme.

Also the European INTERREG programme has provided possibilities to set up regional platforms for various aspects, to promote the use of genetic resources. As examples, two projects can be mentioned. DEVEPARK (Sustainable Historic Park Management and Development in Finland and Estonia 2009–2012) and 'Cross-border fruit tree genetic resources and biodiversity Management and development of Franco-Walloon fruit tree biodiversity'. These examples on project-based activities show that there has been a need to establish cross-border activities within Europe and overseas, too.

The project-based platforms that cannot be reviewed thoroughly here could probably be used as information sources to study the success of different cooperation models. What is important to keep in mind, however, it is that due to the nature of project activities the continuity of the work should be linked to more persistent structures in order to create sustainability. These issues are highly relevant when establishing Operational Groups within the EIP. This means that it is important that EU funding will support Operational Groups that will link their work to existing structures.

EUCARPIA – European Association for Research on Plant Breeding

In the user sector of plant genetic resources there are a couple of European organisations that deal with the enhancement of genetic resources. One of these is EUCARPIA (European Association on Research of Plant Breeding) established on 1956. It aims to promote scientific and technical cooperation in the field of plant breeding in order to foster its further development. To achieve this purpose, the Association arranges and sponsors meetings to discuss general or specific problems from all fields of plant breeding and genetic research. Activities with a predominantly commercial interest are excluded, as EUCARPIA is a non-profit organisation. During these meetings devoted to particular crops or cross-cutting topics, specialised up-to-date knowledge and methodology are exchanged among leading scientists and conveyed to practical plant breeders. Every four years, the General Congress is held together with the general assembly. These congresses are an opportunity for all EUCARPIA members to discuss subjects of a wider interest. They provide a forum for presentation of the problems and challenges which plant breeding faces today and in the future (<http://www.eucarpia.org/>).

ESA – European Seed Association

ESA is an organisation representing the European seed industry, and representing the interests of those active in research, breeding, production and marketing of seeds of agricultural, horticultural and ornamental plant species. Therefore, access to genetic resources as plant breeding is an item that ESA actively promotes, as plant breeding is strongly dependent on genetic variability. In addition, ESA has initiated a Working Group for Research and Innovation that deals with issues that enhance the use of genetic resources in plant breeding. The seed industry is at the forefront of research and innovation, with companies investing on average 15-20% of their annual turnover on R&D. Within the frames of ESA there is also the Working Group for Biodiversity that deals with all issues relevant to access and benefit sharing for genetic resources. At European level, ESA is a founding member of the European Technology Platform "Plants for the Future" within which it cooperates with plant science organisations and farmers' organisations, to identify joint research priorities and a common vision and strategy for plant research.

Links between existing platforms

The platforms presented here have many cooperations and links between each other. The collaboration can occur both on organisational and expert level. The main organisational links are presented in Table 1. The full details on national programmes for plant genetic resources and their collaborative platforms can be found on their respective homepages. The types of collaborators are described in Table 1.

Platform	Type/aim of platform	Cooperating platforms	Cooperating national programmes
European Cooperative Programme for Plant Genetic Resources (ECPGR)	Long-term conservation, and facilitating the utilisation of plant genetic resources in Europe	National programmes, project platforms, EUCARPIA, ESA	
National and regional programmes for conservation of plant genetic resources	Long-term conservation, and facilitating the utilisation of plant genetic resources in a European country or region	ECPGR	National research and breeding institutes, NGOs, farmer and grower organisations, ministries and regional authorities
Project-based platforms	Various: conservation, database management, characterisation and evaluation, research, pre-breeding, traditional uses, public awareness	Research and breeding institutes, European platforms, NGOs, farmer and grower organisations, ministries and regional authorities	
EUCARPIA	Scientific and technical cooperation in the field of plant breeding	Research and breeding institutes, ECPGR	
ESA	Cooperation in the seed sector	European Technology Platform "Plants for the Future, ECPGR, private and public breeding companies, EUCARPIA through common members	

Conclusions

There is an established network of platforms for the wide range of issues concerning plant genetic resources in Europe. Supporting the goals and already existing research strategies of these platforms should be the first priority in planning new actions to enhance the conservation and use of plant genetic resources in Europe, and in making these platforms more sustainable in the future.

Discussion in plenary

It was suggested to add *CIOPORA - the International Community of Breeders of Asexually Reproduced Ornamental and Fruit Varieties*. CIOPORA is the international association that groups together breeders of ornamental and fruit varieties of asexual reproduction, with a view to assist them in the protection of their Intellectual Property Rights.

References

FAO, 2010. The Second report on the State of the World's Plant Genetic Resources for Food and Agriculture – Synthetic Account
Maggioni, L. & J. Engels, 2014. Networking for plant genetic resources. Pan European Networks: Science and Technology, March 2014: 285-287.

Annex 11: Mini-paper: Farm Animal Genetic Resources – Cooperation Models: Issues facing the local extensively farmed livestock breeds

Coralie Danchin-Burge, Gintare Kucinskiene, Rudolf Buehler, Dianna Bowles and Georgios Banos

Introduction

In this paper we address issues specific to the genetic resources of 'at-risk' traditional breeds of livestock species (pigs, cattle, sheep and goats) and their utility for agriculture, along with relevant cooperation models for their conservation, characterisation and utilisation.

The need for the mini-paper has arisen from the very clear distinction between issues facing plant and animal genetic resources, recognised by this Focus Group at its first meeting. Such differences need to be clearly understood by policy makers on the EC Genetic Resources Committee.

Traditional breeds are endangered because of (1) numerical scarcity (cf. for instance Regulation (EC) No 445/2002, 26 February 2002) and (2) geographical concentration (many locally adapted breeds may exist in large numbers but only in a single regional area to which they are adapted (e.g. AGRI GENRES project HERITAGESHEEP http://ec.europa.eu/agriculture/genetic-resources/actions/f-040/index_en.htm)).

The genetic resources of locally adapted breeds are well recognised as important to agriculture because of their unique genetic profile and their potential to provide useful traits to benefit farming systems in the future.

These breeds often make use of marginal land that cannot be used for other forms of agriculture. Through their adaptation to harsh environments, such breeds may contribute to food security and generate value from land otherwise unusable to farming. Frequently, these breeds thrive in low-input, extensive farming systems, without the need for additional feeding or management.

As agricultural land becomes ever more limited and the costs of animal feed, supplements and energy increase, the genetic resources of locally adapted breeds offer an opportunity to achieve sustainable productivity in farming across the EU.

There are many challenges currently facing agriculture that will increase considerably due to climate change, water shortage, energy and food supply risks, and the need to feed an increasing world population.

We have a reservoir of genetic biodiversity in existing farm animals that can benefit society through providing food security and nutrition, and contributing to the health of the environment with appropriate farming management.

The value of these genetic resources must be recognised and protected. The only successful means of sustainable conservation is to identify and/or create markets for the local breeds and their products through the development of new holistic cooperation models.

The objective of this paper is to highlight the significance of the genetic resources of indigenous, locally adapted breeds of livestock in maintaining biodiversity and in promoting rural sustainability through stakeholder involvement and cooperation.

I. Interdisciplinary approach in conservation and use of animal genetic resources

The FAO guidelines (2010) provide useful insights into this topic. The first essential step would be to build a Working Group comprising all stakeholders and organisations involved in breeding, conservation and utilisation

of a specific farm animal genetic resource (species or breed). Four tasks are recommended by the FAO as critical to this process:

- Task 1: Establish an inventory of stakeholders and arrange a collective meeting.
- Task 2: Identify key stakeholders and representatives, and form the Working Group.
- Task 3: Discuss and agree a plan with the members of the Working Group.
- Task 4: Assign specific and auditable responsibilities to the members of the Working Group.

Ideally, each group will be run by a 'champion' of an individual breed or closely aligned group of breeds. This champion would normally be a breeder/farmer. It is important that decisions related to a breed are agreed by the people working in the direct area and making a living from the breed. Also, ultimately, breeders are the best representatives to explain fully to the market why customers should be interested in their products.

However, breeders already have a full time job and it is therefore important that these initiatives are provided with additional support. This ideally involves employees who are paid to contribute to the technical needs for the development of the breed. A common understanding from the technical and scientific members of the Working Group is needed and an agreement to involve some of the staff's time in the development of the breed.

As mentioned above, the first task is to identify and connect all stakeholders. This can be difficult due to a range of issues including lack of time on the part of farmers/breeders, their disinterest in teamwork and the likelihood that the stakeholders are spread over a wide geographical area making meetings difficult and costly to organise. This necessitates a funding requirement to 'kick off' the initiative as well as the involvement of 'outsiders' who have a good knowledge and expertise on how to start and handle such collective organisation.

Key analyses for each breed must involve the following issues:

- (i) The way the breed is marketed and promoted by its stakeholders.
- (ii) The type of breed-specific products and services that are or could be or used to be offered.
- (iii) A list of all relevant collective organisations that may already exist.
- (iv) A description on how the various collective organisations are established and their methods of working.

This analysis will reveal the extent of knowledge and information that already exists. Once a comprehensive profile of the breed is established and understood, a SWOT (strengths, weaknesses, opportunities and threats) analysis should be undertaken regarding the possible product and service development and valorisation. Involvement of all stakeholders is crucial since perspectives will vary along different stages of the supply chain from the genetic resource (animals) through their products to consumers.

For farm animal genetic resources, a fundamental rule is that there is no single way to organise a local breed. Only a detailed analysis of the prevailing conditions can lead to successful progress and consensus on how the Working Group mentioned above can best serve the interests of a breed and its products. These roadmap events must occur before members of the Working Group undertake tasks 3 and 4.

II. Value chain cooperation and eco-system services

a) Starting with a niche market

The market must be ahead of production. At the start, the operation scale (and population size) may be quite small, making it essential to focus on niche markets. This will likely target no more than 10% (or less) of consumers who choose the product for quality and/or cultural reasons, and who have the financial capacity to make the purchase at a higher price than corresponding mainstream products. It is therefore useful to select outlets fulfilling such criteria (local hotels, local restaurants, local wholesalers, butchers, private buyers).

b) Marketing a local breed: the whole package

Unless the business is economically viable, there can be no sustainable success; therefore, the role of experts in advising how to realise the full economic potential of a new business must be emphasised.

It is essential that a product develops its own brand. The brand is based on the 'whole package' or 'enhanced product' concept, including the breed and its genetic resources, as well as the type of product (e.g. meat, milk, wool, breeding stock etc.). A mix of additional values such as animal welfare and health standards, taste and nutritional quality of the product, and cultural aspects of the breed or species will also contribute to the overall brand (see case study below).

Clearly, there are many different breeds with traditional qualities and endangered genetic resources but each breed on its own cannot always become a separate brand. Therefore ways should be investigated to bring breeds together in groups based on geography and/or farm management systems.

Case study of successful marketing a local pig breed

<http://www.besh.de/>

Rudolf Buehler, the originator of conserving, developing and marketing products from a local pig breed in Germany, described the process he had undertaken from the start of the enterprise through 30 years development to its current highly successful and profitable business.

Once markets started to become established, there was a need to recruit additional farmers. But for this to work sustainably and successfully, farmers had to earn more than they would by farming mainstream commercial breeds. Importantly, farmers were recruited into a complete concept – at the beginning, they received a guaranteed premium above the standard market place, but also had to conform to the 'commercial standards' for working with the breed. These were communicated through a specialised extension service specific to the breed, enabling the farming practices to be of the high standards required to achieve the 'product quality' that characterised the brand.

This case study may serve as a useful model for similar initiatives across a variety of breeds and species in the EU and beyond. Added value of the specific breed/species and market circumstances would determine the scale and success of the operation. In any case, the early start-up phase would require considerable commitment and support, both financial and otherwise. However, the ultimate goal should always be self-sustainability and sufficiency through success in the chosen market segment.

c) Building and financing technical support adapted to local breeds

Once the whole process starts, experience has shown that technical support is required to develop the various breeds further. For example, there is a need for appropriate tools to record animal performance. To achieve these developments:

- A Member State needs to support a technical programme where breed performance is recorded easily, at a cost affordable to the local breed's farmers or breeders' association.
- Performance recording needs to be adapted to the local breed's needs and conditions. In most countries, animal recording is designed according to circumstances relevant to intensive farming of mainstream breeds, which is not suitable for building on and developing further the strengths of the local breeds.

The issues of cost and availability of appropriate recording systems are hugely important for local breeds. Such systems should be tailored to the circumstances of local breeds and not mimic practices relevant to large intensive farming systems. It is important that farmers see the benefit of participating in recording schemes. For instance, in the UK, despite their great numbers, many commercially farmed regional sheep breeds do not participate in performance recording, since it is too costly for farmers and the traits recorded in intensively raised breeds are not suitable for these farming systems.

However, it is crucial for the future success of the local breeds and their contribution to agricultural output that information exists for all livestock. Importantly also, it will be difficult to attract new farmers into using local breeds if there is no explicit data on breed performance in an extensive, environmentally sustainable farming system.

d) Ecosystem services

There is a progressive acknowledgment by the research and regulatory governmental organisations that grazing by herbivores, when under control, is a successful tool to conserve wildlife and increase the environmental value of endangered resources (EAAP/ERFP/FAO symposium in 2011, "Environmental value of animal genetic resources").

General awareness of the following issues must be increased through outreach and extension:

- Many stakeholders in ecosystem services, such as landscape architects, local governments, national and regional parks and local communities, are not fully aware of the potential of grazing to sustain environmental biodiversity. To achieve the full potential of local breeds for this purpose, it will be important to offer training – both in the theory and practicalities of conservation grazing.
- It is also important that local breeds are used in the environment to which they are adapted. Often, “fashionable” exogenous breeds, such as Highland cattle or Hebridean sheep, are preferred over the use of better adapted local breeds of a region.

The appropriate synergies could be created by organising specific workshops held by ecosystem service specialists, such as those involved in regional parks, and inviting local breed associations as speakers, together with landscape architects and Wildlife Trusts that are already using local breeds.

If possible, these workshop should focus on practical issues, such as the type of species and breeds to be used according to the grazed ecosystem, basic training on animal handling, sanitary issues and welfare (e.g. parasite control and interaction with wildlife), and, importantly, security aspects (fencing, sharing a habitat with tourists, and protecting livestock from predators and theft).

III. Ex situ conservation – issues of concern

Ex situ conservation is often recommended as a key requirement to build a successful conservation programme. However, there can be major drawbacks in the processes leading to the establishment of these collections. For example, a principle constraint is that, for most animal species, sanitary requirements to collect and store frozen reproductive material follow European rules that were created to exchange (and commercialise) genetic material between countries.

Case study of long term cryo-conservation and commercial sanitary rules

The cryo-conservation objectives of reproductive material in germplasm (cryo-bank) collections are quite different from those for exchanging breeding material. Therefore, the existing regulations constitute significant constraints. For instance:

- Material from different species or different biological material (e.g. semen and embryo) from the same species cannot be stored within the same container.
- Biological material of an animal that does not originate from a certified flock free from certain diseases (e.g. scrapie in sheep) cannot be collected or stored.
- Certified material cannot be stored together with uncertified material, even when the uncertified status of the latter is due to administrative reasons; for instance, in France, embryos collected in a research facility with the same sanitary protocols as in a certified centre cannot be stored in the cryo-bank collection, because the research facility does not have the certification to collect embryos.

Reviewing and putting in place regulations that are specific for the ex situ cryo-storage and maintenance of gene banks for genetic variability and conservation is an exceptionally urgent issue warranting immediate action. This will also require a full cooperation between veterinarian institutions and gene bank managers.

IV. Raising public awareness

In parallel to farming the genetic resource, it is essential to create awareness and educate retailers, processors and consumers about this quality 'whole package' which is an integral feature of the breed and of the brand that the breed increasingly represents.

Our experience is that nowadays citizens in various countries have a very good opinion of local breeds and their products, when aware of their existence. However, we need to emphasise that their good opinion is frequently based more on how these breeds are farmed (usually in low-input and environmentally friendly systems, often organically) than the fact that these breeds are local and/or endangered. The sensitivity to the local aspect of the breed depends principally on attitudes in different countries or even regions within countries.

The awareness should be raised mostly through agricultural shows and communication (e.g. stamps on local breeds etc.). However, in our opinion, raising the awareness among citizens might not be as important an aspect

as increasing awareness among farmers and providing the necessary technical support. The survival of the breed depends on how many farmers are willing to raise such animals, and farmers will breed them only if they can make a living out of them. It will also help if national technical and policy-making bodies assist farmers to realise the importance and economic future of their local breeds, rather than advise them to change breeds and focus on intensive farming systems and on breeds developed for mainstream agriculture.

Therefore, we consider it to be essential that specific training be brought into farm and technical schools on how local breeds may provide a decent living and sufficient economic returns in a sustainable system.

V. Research and breeding programmes on local breeds - priorities

a) Breed characterisation: fitness traits

The genetics of local livestock breeds are currently attracting considerable interest due to their significant contribution to food security in marginal land areas of the world unsuitable for other means of agricultural production. Many of the breeds have also evolved to adapt and thrive under harsh environmental conditions such as drought, cold, or weather extremes (FAO, 2007 and 2009).

These characteristics strongly suggest that local, traditional breeds may have adaptive fitness traits that could become increasingly useful to the future sustainability of mainstream agriculture (Hoffmann 2013). Therefore their genetic characterisation becomes an increasingly important issue, together with a confirmation that they are genetically distinctive from mainstream breeds and an assessment of the biodiversity that each breed may contribute to future trait selection.

In this context, most Member States in the EU have a wide range of numerically scarce, rare local livestock breeds. Also of significance are the breeds (particularly sheep breeds) that are not rare and are commercially farmed but are recognised to be at risk because they are highly concentrated in specific geographical regions to which they are adapted.

A number of large-scale genetic studies have been conducted to characterise both the rare and locally adapted traditional breeds (e.g. Joost et al., 2007; Lawson et al., 2007; Toro et al., 2009; Groeneveld et al., 2010; Lenstra et al., 2012). This has been made possible by recent advances in a wide range of molecular, DNA-based tools and methodologies. The work has enabled an improved understanding of the origins and relatedness of the breeds, their distinctiveness; and their susceptibility or resistance to disease threats, whether currently relevant or projected to increase as climates change.

Literature examples of genetic characterisation and landscape genomics include the studies of Groeneveld et al. (2010) and Pariset et al. (2012) as well as the FAO guidelines of 2011.

For sheep and goats in particular, the following references illustrate the range of studies and strategies that have been undertaken: Peter et al. (2007), Chessa et al. (2009), Pariset et al. (2009), Kijas et al. (2009 and 2012), Bowles et al. (2014).

These references are only illustrative of the very many that exist in international, peer-reviewed publications.

Production traits are typically a key focus of the characterisation of commercial mainstream breeds, but, increasingly, recognition of the unique qualities of the local breeds are leading to studies to identify their 'adaptive fitness' traits. Of major significance is the development of landscape genomics in which the breeds and populations are placed within the holistic context of environmental and management data.

In addition to a thorough characterisation of farm animal genetic resources, research emphasis should be placed on their genetic improvement and enhancement, especially with regards to fitness, robustness, and health and fertility traits. Genomic and post-genomic technological developments including genotyping by sequencing, genotype imputation, genome-wide association studies and genomic predictions are very relevant to this effect. Research priorities should also include optimisation of genomic programmes which, in addition to improving the above traits, would allow monitoring of biodiversity and controlling inbreeding.

b) Breeds' marketing: proving that they are sustainable!

Given these traditional breeds are reservoirs of biodiversity of livestock genetic resources, it is also essential to prove their ability to adapt to local conditions and remain robust under low input and extensive farming systems. The FAO did an intensive work in this area, illustrating the case of developing countries (FAO 2010b).

An important issue is that success in increasing numbers of animals in a breed brings its own risks. As the size of a breed increases to that of a mainstream breed, there is a risk of a drift away from the traits that were unique to the traditional breed. This requires research to evaluate the risk and is dependent on issues which may be specific for each Member State.

In all cases, research priorities on breeding programmes for local breeds should be placed on interdisciplinary initiatives that combine characterisation, enhancement and improvement of the genetic resource with business development and marketing, including the study of emerging consumer attitudes, needs and trends. Socio-economic aspects addressing opportunities for product innovation and differentiation should also feature in research priorities.

Conclusion

This paper set out to discuss the significance of the genetic resources of indigenous, locally adapted breeds of livestock in supporting and promoting rural sustainability. The multi-faceted proposition presented will require cooperation amongst all stakeholders at the strategic, operational and research levels. Cooperation models should seek to enhance the continuity and coherence of the value chain through vertical integration and stakeholder involvement. Further cooperation should forge links between initiatives aiming at optimal utilisation of plant and animal genetic resources for the benefit of sustainable agriculture.

References

- Bowles DJ, Carson A, Isaacs P (2014) Genetic Distinctiveness of the Herdwick sheep breed and two other locally adapted hill breeds of the UK. PLOS One pone.0087823.
- Chessa B, Pereira F, Arnaud F, Amorim A, Goyache F, et al. (2009) Revealing the history of sheep domestication using retrovirus integrations. *Science* 324: 532–536.
- FAO (2007) The State of the world's animal genetic resources for food and agriculture. Pilling D, Rischkowsky B, editors. Rome.
- FAO (2009) Livestock keepers – guardians of biodiversity. Animal production and health paper no.167. Rome.
- FAO (2010a). Breeding strategies for sustainable management of animal genetic resources. FAO Animal Production and Health Guidelines. No. 3. Rome.
- FAO (2010b). Adding value to livestock diversity. Marketing to promote local breeds and improve livelihoods. FAO Animal Production and Health Paper. Rome.
- FAO (2011). Molecular genetic characterization of animal genetic resources. FAO Animal Production and Health Guidelines. No. 9. Rome.
- Groeneveld LF, Lenstra JA, Eding H, Toro MA, Scherf B, et al. (2010) Genetic diversity in farm animals – a review. *Anim Genet* 41: 6–31.
- Hoffmann I (2013) Adaptation to climate change – exploring the potential of locally adapted breeds. *Animal* 7: 346–362.
- Joost S, Bonin A, Bruford MW, Després L, Conord C, et al. (2007) A spatial analysis method (SAM) to detect candidate loci for selection: towards a landscape genomics approach to adaptation. *Mol Ecol* 16: 3955–3969.

Lawson Handley LJ, Byrne K, Santucci F, Townsend S, Taylor M, et al. (2007) Genetic structure of European sheep breeds. *Heredity* 99: 620–631.

Kijas JW, Townley D, Dalrymple BP, Heaton MP, Maddox JF, et al. (2009) A genome wide survey of SNP variation reveals the genetic structure of sheep breeds. *PLoS One* 4(3): e4668.

Kijas JW, Lenstra JA, Hayes B, Boitard S, Portoneto LR, et al. (2012) Genome-wide analysis of the world's sheep breeds reveals high levels of historic mixture and strong recent selection. *PLoS Biol* 10(2): e1001258.

Lenstra JA, Groeneveld LF, Eding H, Kantanen J, Williams JL, et al. (2012) Molecular tools and analytical approaches for the characterisation of farm animal genetic resources. *Anim Genet* 43: 483–502.

Pariset, L., Cuteri, A., Ligda, C., Ajmone-Marsan, P. and Valentini, A., 2009. Geographical patterning of sixteen goat breeds from Italy, Albania and Greece assessed by Single Nucleotide Polymorphism, *BMC Ecology*, 9, (doi: 10.1186/1472-6785-9-20).

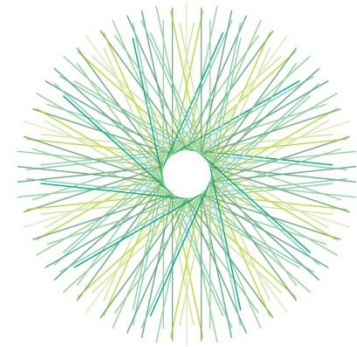
Pariset L, Joost S, Gargani M, Valentini A (2012). Landscape Genomics in Livestock. In: *Analysis of Genetic Variation in Animals*. INTECH, Rijeka, Croatia.

Peter C, Bruford M, Perez T, Dalamitra S, Hewitt G, et al. (2007) Genetic diversity and subdivision of 57 European and Middle-Eastern sheep breeds. *Anim Genet* 38: 37–44.

Toro M, Fernandez J, Caballero A (2009) Molecular characterization of breeds and its use in conservation. *Livest Sci* 120: 174–95

11. List of members of the Focus Group

Surname, first name	Profession	Country
Allender, Charlotte	Scientist	United Kingdom
Banos, Georgios	Scientist	Greece
Bowles, Dianna	Farmer; scientist	United Kingdom
Bühler, Rudolf	Farmer; agriculture organisation, industry or manufacturing	Germany
Danchin-Burge, Coralie	Agriculture organisation, industry or manufacturing	France
Fieldsend, Andrew	Scientist	United Kingdom
Contact this member		
Gomes, Ana Catarina	Scientist	Portugal
Ingelbrecht, Ivan	Scientist; other	Belgium
Jahoor, Ahmed	Agriculture organisation, industry or manufacturing	Germany
Koller, Beate	NGO	Austria
Kucinskiene, Gintare	Farm adviser; scientist	Lithuania
Contact this member		
Padulosi, Stefano	Scientist	Italy
Romana, Bravi	Scientist	Italy
Rovira, Mercé	Farm adviser; scientist	Spain
Suso, María Josefa	Scientist	Spain
Tisiot, Raphaël	Farm adviser; scientist	France
Tuberosa, Roberto	Scientist	Italy
Uzundzhaliyeva, Katya	Scientist	Bulgaria
Contact this member		
Van Huylenbroeck, Johan	Scientist	Belgium
Veteläinen, Merja	Agriculture organisation, industry or manufacturing	Finland



eip-agri
AGRICULTURE & INNOVATION

The European Innovation Partnership 'Agricultural Productivity and Sustainability' (EIP-AGRI) is one of five EIPs launched by the European Commission in a bid to promote rapid modernisation by stepping up innovation efforts.

The **EIP-AGRI** aims to catalyse the innovation process in the **agricultural and forestry sectors** by bringing **research and practice closer together** – in research and innovation projects as well as *through* the EIP-AGRI network.

EIPs aim to streamline, simplify and better coordinate existing instruments and initiatives and complement them with actions where necessary. Two specific funding sources are particularly important for the EIP-AGRI:

- ✓ the EU Research and Innovation framework, Horizon 2020,
- ✓ the EU Rural Development Policy.

An EIP AGRI Focus Group* is one of several different building blocks of the EIP-AGRI network, which is funded under the EU Rural Development policy. Working on a narrowly defined issue, Focus Groups temporarily bring together around 20 experts (such as farmers, advisers, researchers, up- and downstream businesses and NGOs) to map and develop solutions within their field.

The concrete objectives of a Focus Group are:

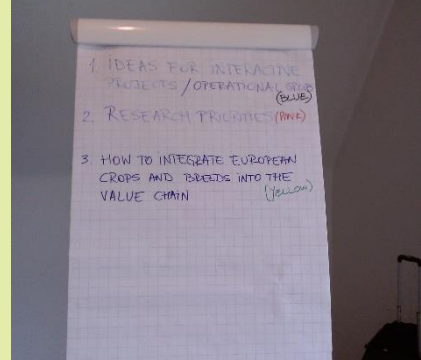
- ✓ to take stock of the state of art of practice and research in its field, listing problems and opportunities;
- ✓ to identify needs from practice and propose directions for further research;
- ✓ to propose priorities for innovative actions by suggesting potential projects for Operational Groups working under Rural Development or other project formats to test solutions and opportunities, including ways to disseminate the practical knowledge gathered.

Results are normally published in a report within 12-18 months of the launch of a given Focus Group.

Experts are selected based on an open call for interest. Each expert is appointed based on his or her personal knowledge and experience in the particular field and therefore does not represent an organisation or a Member State.

*More details on EIP-AGRI Focus Group aims and process are given in its charter on:

http://ec.europa.eu/agriculture/eip/focus-groups/charter_en.pdf



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