Report of Workshop 4:
Population Management Methodologies
21-24 April, 2004, Mahón, Menorca, Spain

L. De Hond, J.M. Iriondo and S. Kell, compilers

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Fifth Framework Programme for Energy, Environment and Sustainable Development
Coordinated by: University of Birmingham, UK
Report of Workshop 4:
Population Management Methodologies
21-24 April, 2004, Mahón, Menorca, Spain

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Hosted by the Universidad Politécnica de Madrid
Location: Hotel Port Mahón, Menorca, Spain

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José M. Iriondo
Lori De Hond
Shelagh Kell
Nigel Maxted

Front cover: *Vicia bifoliolata*
Photographer: David Draper
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1. PROLOGUE

PGR Forum (European Crop Wild Relative Diversity Assessment and Conservation Forum) is a Thematic Network funded under the EC Framework 5 Programme for Research, Key action 2 ‘Global change, climate and biodiversity’, 2.2.3 ‘Assessing and conserving biodiversity’. PGR Forum provides a European forum for the assessment of taxonomic and genetic diversity of European crop wild relatives and the development of appropriate conservation methodologies. The project brings together 23 partners from 21 countries: Belgium, the Czech Republic, Denmark, Finland, France, Germany, Greece, Hungary, Italy, Latvia, Lithuania, the Netherlands, Norway, Poland, Portugal, the Slovak Republic, Spain, Sweden, Romania, Russia, the United Kingdom, with the addition of partners representing IUCN -The World Conservation Union and the International Plant Genetic Resources Institute (IPGRI). Advisory and Stakeholder Panels provide additional input and feedback on project activities and deliverables. A broad cross-section of the professional European PGR community is represented, including conservationists, taxonomists, plant breeders, information managers, policy-makers and end-users. The project duration is 36 months, with a start date of November 1, 2002.

PGR Forum has created an information system providing access to European crop wild relative data. The database includes socio-economically important species with wild relatives in Europe and the Mediterranean; including food, fodder and forage, medicinal plants, condiments, ornamentals, forestry species, as well as plants used for industrial purposes, such as oils and fibres. One of the primary outputs of PGR Forum will be a conservation gap analysis and resultant recommendations for in situ and ex situ conservation of crop wild relatives. The development of population management methodologies, particularly for in situ conservation is also a major component of the project.

PGR Forum’s work programme is implemented through a series of five interrelated workpackages and associated workshops: 1) European crop wild relative assessment, 2) threat and conservation assessment, 3) data management methodologies, 4) population management methodologies, and 5) genetic erosion and genetic pollution methodologies. An additional workpackage coordinates thematic network product dissemination and exploitation, and the final dissemination conference.

Workshop 4, Population Management Methodologies was held in Mahón, Menorca, Spain, April 21-24 2004.

The primary objectives of Workshop 4 were to:

- Agree on population management methodologies appropriate for the in situ genetic conservation of crop wild relatives.
- Agree on population monitoring methodologies appropriate for the in situ genetic conservation of crop wild relatives.

Objectives relating to other workpackages were to:

- Review progress in Workpackages 1, 3 and 6.
- Review plans for Workshops 2 and 5, and the PGR Forum Final Dissemination Conference.
- Provide training in the application of IUCN Red List Criteria to European crop wild relatives.

This report summarises the workshop proceedings in chronological order, beginning with the general introductory sessions, including summaries of plans and progress reports for all workpackages and subsequent workshops. The presentations given by invited speakers are summarized and the results of working group discussions on issues of population monitoring and management methodologies are presented. Finally, the workshop resolutions are summarised, and resulting actions outlined.
2. OPENING SESSION

Chairs: Lori De Hond and Silvia Strajeru

2.1 Welcome / Press Conference

Speakers: Fina Casals Senent, Counsellor of Urban Planning and Environment, Consell Insular de Menorca, Balearic Islands, Spain

Nigel Maxted, PGR Forum Project Coordinator, University of Birmingham, Birmingham, United Kingdom

José Iriondo, PGR Forum Workpackage 4 Coordinator, Universidad Politécnica de Madrid, Madrid, Spain

José Iriondo introduced Fina Casals Senent to the PGR Forum Workshop 4 participants.

Fina Casals Senent welcomed the workshop participants to Mahón, Menorca. She explained that the island of Menorca was declared a Biosphere Reserve by UNESCO in 1993 and that Menorca was celebrating the 10th anniversary of this agreement of man with his natural surroundings. Therefore, it seemed particularly appropriate for PGR Forum Workshop 4 to be held on the island. The Counsellor mentioned a few crop wild relatives that can be found in Menorca. She also highlighted a few of the natural areas of particular interest and beauty, one of which participants would have the opportunity to visit on the excursion.

Nigel Maxted briefly summarized the scope and objectives of PGR Forum and José Iriondo translated the summary into Spanish for the Press.

Mahón, Menorca

The main characteristic of the Menorca Biosphere Reserve is the diversity found in its habitats. The most notable habitats are the gullies, caves, wetlands made up of ponds, lagoons and marshes, dune systems, coasts and islets. Approximately 220 species of birds, and 1000 species of plants, 60 of which are endemic, have been recorded. One of the most important landscape and geomorphic aspects of the reserve is the number of gullies that cross it in the direction of the south coast. Also important are the nesting sites of birds of prey and aquatic birds which nest close to small permanent or seasonal water sources. Menorca has a lot of natural land caves and underwater caves, situated in the north and south of the island. Among the coastal wetlands, there is the Natural Parc of Albufera de Es Grau (which is the core area of the Biosphere Reserve), as well as Addaia, Son Saura and Son Bou. The island has various species of thorny shrubs known as “socarrells” as well as Mediterranean shrubs. The rocky coast, mainly the limestone cliff, provides habitats for marine birds such as the Cory’s shearwaters, cormorants, seagulls and various birds of prey. Oak woods are abundant in the central part of the island and in a few gullies. The woods of wild olive trees, known on the island as “ullastrars”, appear in areas of thin soils, and is the dominating tree species on the island.
2.2 Introduction to Workshop 4

Speaker: José Iriondo, Universidad Politécnica de Madrid, Madrid, Spain

José Iriondo welcomed the PGR Forum Partners, their representatives, and the Advisory Board to PGR Forum Workshop 4. Thirty-four PGR specialists were present, representing 20 countries: Belgium, Czech Republic, Denmark, Finland, France, Germany, Greece, Hungary, Italy, Latvia, Lithuania, Norway, Poland, Portugal, Romania, Russia, Slovak Republic, Spain, Sweden and the United Kingdom, with representatives of IPGRI (International Plant Genetic Resources Institute) and IUCN - The World Conservation Union. All participants introduced themselves briefly to the forum.

2.2.1 Workshop 4 participants

<table>
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<tr>
<th>Dr. Aasmund Asdal</th>
<th>Dr. Stephen Jury</th>
<th>Ms. Maria Pohjamo</th>
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<tr>
<td>Mr. Damiano Avanzato</td>
<td>Ms. Shelagh Kell</td>
<td>Ms. Caroline Pollock</td>
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<td>Mr. Gábor Csizmadia</td>
<td>Dr. Helmut Knüpffer</td>
<td>Prof. Isaak Rashal</td>
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<td>Dr. Daniela Benedikova</td>
<td>Dr. Kell Kristiansen</td>
<td>Ms. Sabine Roscher</td>
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<tr>
<td>Ms. Lori De Hond</td>
<td>Dr. Juozas Labokas</td>
<td>Mr. Stelios Samaras</td>
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<tr>
<td>Ms. Sónia Dias</td>
<td>Dr. Emilio Laguna</td>
<td>Ms. Maria Scholten</td>
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<td>Dr. Ehsan Dulloo</td>
<td>Dr. François Lefévre</td>
<td>Dr. Tamara Smekalova</td>
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<tr>
<td>Mr. Dag Terje Endresen</td>
<td>Dr. Nigel Maxted</td>
<td>Dr. Zdenek Stehno</td>
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<tr>
<td>Dr. Brian Ford-Lloyd</td>
<td>Dr. Martine Mitteau</td>
<td>Dr. Silvia Strajeru</td>
</tr>
<tr>
<td>Dr. Lothar Frese</td>
<td>Mr. Jay Moore</td>
<td>Dr. André Toussaint</td>
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<tr>
<td>Mr. Craig Hilton-Taylor</td>
<td>Dr. Xavier Picó</td>
<td></td>
</tr>
<tr>
<td>Dr. José Iriondo</td>
<td>Dr. Wieslaw Podyma</td>
<td></td>
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</table>

(See Appendix II for contact details).

A moment of silence was held for Dr. Fabrizio Grassi, the Italian representative for PGR Forum who sadly passed away in the Autumn of 2003.

José Iriondo gave a brief introduction to Workshop 4 stating that the main objective of the meeting was to:

- Agree on population management and monitoring methodologies appropriate for the in situ genetic conservation of crop wild relatives.

The approach that was to be used in obtaining this objective was to:

- Use existing management and monitoring techniques as a starting point
- Resolve how these might be adapted to CWR (genetic rather than ecological goals)

The work procedure to be followed was parallel discussions in small groups of approximately 10 people to make recommendations and agree on further steps to be taken. Three parallel discussion sessions were outlined as seen in Figure 1.
Elements of discussion

Model for genetic reserve conservation (adapted from Maxted et al., 1997)

![Diagram of genetic reserve conservation model](image)

**Figure 1.** Workshop 4 discussion groups structured to develop methodologies for the different stages of genetic reserve conservation.

The main deliverable of this Work Package is a methodology for the generation of protected area management plans. The form this deliverable could take was considered. The population management methodologies could be published as a report by the International Plant Genetic Resources Institute (IPGRI) on behalf of ECP/GR (European Cooperative Programme for Crop Genetic Resources Networks). At a later date a more detailed methodology could be published by an independent publisher.
2.3 Workpackage Coordinator Updates

2.3.1 Workpackage 2: Threat and Conservation Assessment

Speakers: Craig Hilton-Taylor, Red List Programme, IUCN, Cambridge, UK; Kell Kristiansen, Danish Institute of Agricultural Sciences, Årslev, Denmark

The objectives of PGR Forum Workshop 2 are:

- To assess the extinction risk for a selected set of European crop wild relatives.
- Review the in situ and ex situ conservation status of the taxa.
- Conduct a gap analysis of the conservation needs.
- Produce a list of priority species for conservation action.

Craig Hilton-Taylor gave an overview of the Red List Programme, as an understanding of the Red List criteria and their application is essential to achieve the objectives this Workshop. Before Workshop 2 is held, a list of crop wild relatives will be selected for assessment and existing information on the conservation status of these taxa will be collated and databased. The last day of Workshop 4 was devoted to providing training in the Red List assessment of taxa through practical case studies. In this way as many assessments as possible can be completed before Workshop 2 itself.

A preliminary assessment has been made of 40 UK crop wild relatives. In most cases there was generally sufficient information to make an accurate assessment, although some follow-up details were needed for some taxa. The results coincided with the UK Red List, although some differences were found due to Regional Guidelines.

The types of information that are required to make an assessment of the conservation status of a taxon include distribution, the number of mature individuals, present and future population trends, number and size of subpopulations or locations, fragmentation, fluctuation and generation time. Threats to the populations and conservation measures are also considered.

Workshop 2 is being planned for Spring 2005. Kell Kristiansen explained that they are currently considering two possible locations. One would be at the Nordic Gene Bank in Sweden and the other would be in Denmark. According to the draft agenda, assessments of the conservation status of the selected crop wild relatives would be presented and reviewed on Day 1. Parameters for setting conservation priorities and a methodology for gap analysis would be discussed on Day 2, and gaps would be identified and a list of priorities would be compiled on Day 3.

2.3.2 Workpackage 5: Genetic Erosion and Pollution Assessment Methodologies

Speaker: Sónia Dias, Instituto Nacional de Investigação Agrária e das Pescas, Oeiras, Portugal

Workshop 5, jointly coordinated by Brian Ford-Lloyd, Sónia Dias and Eliseu Bettencourt, will deal with genetic erosion and genetic pollution methodologies for the genetic conservation of crop wild relatives. It will be held at the Regional Directorate of Agrarian Development on Terceira Island in the Azores, Portugal, from 8-11 September 2004.

A draft agenda was presented with the morning of Day 1 devoted to workpackage reporting and updates, and an overview of the objectives of Workshop 5. In the afternoon, Session 1 will provide a general overview of the measurement and prediction of genetic erosion and pollution followed by working groups which will discuss the generalities and realities involved in measurement and prediction and examine political and legal issues.

Day 2 will focus on practical aspects of measurement, monitoring and prediction examining the current indicators of genetic diversity and its loss, and the application of ecogeography, GIS and Red data methods to the conservation of CWR species. Working groups will discuss monitoring
at the taxonomic level, at and around the population level and at the gene level in order to
develop a hierarchy of monitoring techniques.

Case studies from the CWR list will be examined on Day 3 and working groups will discuss the
prioritising of the CWR list. Specific proposals regarding a hierarchy of methodologies, the CWR
species list prioritisation and future prospects will be presented.

A field trip is being planned to a Natural Park for the last day of the Workshop.

2.3.3 Workpackage 6: Thematic Network Product Dissemination and Exploitation

Speakers: Shelagh Kell, University of Birmingham, Birmingham, United Kingdom

The primary objective of Workpackage 6 is the organisation of the final European Conference
and dissemination and exploitation of the datasets generated by the project. Shelagh Kell
reported on the deliverables of the project which are a web site, a web-enabled CWR database,
the database on CD, the publication of dissemination conference proceedings and six
Newsletters. The first Newsletter was published in October 2003. Other publications will include
Workshop reports, peer-reviewed journal articles, other news items and commercial publications
parallel to the project.
2.4 Workpackage Progress Reports

2.4.1 Workpackage 1: European Crop Wild Relative Assessment

Speakers: Shelagh Kell, University of Birmingham, Birmingham, United Kingdom
Jay Moore, Plantkind.com Software Consultants, Warwick, United Kingdom
Maria Scholten, University of Birmingham, Birmingham, United Kingdom

The primary objective of Workpackage 1 is to create a European crop wild relative database, incorporating baseline biodiversity data with current conservation and threat status.

The deliverables of Workpackage 1 are:

- List of European crop wild relatives
- Agreed taxon conservation dataset
- European crop wild relative database
- Web enabled database available via project website

List of European Crop Wild Relatives

At Workshop 1 it was resolved to produce an initial list of European CWR taxa through a process of data harmonisation and cross-checking between a number of databases; primarily Euro+Med PlantBase and Mansfeld's World Database of Agricultural and Horticultural Crops. The first version of the list (CWR_Ver_1.0) was created during 2003. It contains the taxa in Euro+Med matching genera in Mansfeld. The total number of CWR taxa selected from Euro+Med was 23,072 containing 813 genera and 15,031 species.

Version (CWR_Ver_2.0) was created using an updated list of Euro+Med taxa and a revised list of accepted genera from Mansfeld. Added to this is a list of ornamental genera extracted from the Community Plant Variety List and a list of forestry genera extracted Schultze-Motel (1996) (Enumeration of cultivated forest plant species). This second version contains a total of 21,347 taxa including 870 genera and 13,711 species.

Future steps are to incorporate data from Heywood and Zohary and from the VIR database of CWR. Medicinal plant genera may also be incorporated. Utilization data will be added and it would also be of interest to verify the data at a national level.

Taxon conservation dataset

At PGR Forum Workshop 1 held in February 2003 a working group discussed an idealised data structure illustrating the minimum data required to develop comprehensive conservation strategies for European crop wild relatives. Two working groups were established to further investigate some aspects of the taxon conservation datasets and data standards:

- Working Group 1 to investigate and debate ecogeographic data types required in order to develop comprehensive conservation strategies for European crop wild relatives, chaired by José Iriondo, Universidad Politécnica de Madrid (UPM).
- Working Group 2 to investigate and debate the use of existing data standards and to develop new standards if necessary, chaired by Sabine Roscher, German Centre for Documentation and Information in Agriculture (ZADI).

The initial list of data types and standards discussed at Workshop 1 was published in the Workshop 1 Report (http://www.pgrforum.org/Documents/WS%20reports/WS1/WS1%20Report.pdf). Draft data types were produced and posted in the PGR Forum intranet (www.pgrforum.org/Partner_intranet/index.htm). The working group discussions are ongoing via e-mail and the online discussion forum.
Case Studies

At Workshop 1 participants agreed that in order to develop and test conservation methodologies, a subset of taxa was required for in-depth data gathering, which would result in the production of quality, detailed exemplar datasets. A minimum of 5-10 taxa would be selected by each PGR Forum partner for in-depth data gathering. The taxa would be selected according to data availability and data would be collected either on a country or taxonomic basis. A list of case study taxa was produced by means of a questionnaire circulated to PGR Forum participants, along with an interim methodology for collation of case study taxa. A total of 89 case study taxa was selected and 21 trial datasets were collated.

It was decided that the final list of taxa for in-depth data collection should include some taxa with a more or less pan-European distribution in order to fully test the methodologies. Two examples proposed were *Arnica montana* and *Arctostaphylos uva-ursi*. *Arnica montana* is a medicinal plant included in the Red Data Book of ten countries (Bosnia and Hercegovina, Czech Republic, Germany, Hungary, Lithuania, The Netherlands, Portugal, Romania, Kaliningrad and The Ukraine). Data has been collated for Lithuania and is available for Norway. *Arctostaphylos uva-ursi* is a woody evergreen plant of high medicinal value distributed extensively throughout Europe and included in the Red Data Book of at least six countries.

Participants were invited to contribute further case study taxa in view of the family and geographical coverage of those already selected. (See Table 2 and Annex 1 in WP1 Progress Report of 16.04.04. [link](http://www.pgrforum.org/Documents/WP1%20Documents/WP1_Progress_Report_16_04_04.pdf))

User requirement survey

**Phase 1:**

A user requirement survey was developed and distributed to PGR Forum participants to ascertain how the broad categories of data types will be queried in the system. In this first phase 10 information categories were identified:

1. Taxonomy/nomenclature
2. Current uses
3. Relationship of CWR to crop
4. Priority species for conservation
5. Current, historical and potential distribution, including:
   - Country occurrence/extent of occurrence
   - Number of populations
   - Record of extinctions
   - Mapping function/GIS layers
6. Ecology and habitat
7. Threat status
8. Conservation measures, including:
   - Occurrence in named protected areas and genetic reserves
   - *Ex situ* holdings in gene banks
9. Reference to specific research projects
10. Contacts

**Phase 2**

In Phase 2 the revised online user requirement survey was tested by PGR Forum participants. The following results were obtained:

1. Research interests
   - Research interests and institutional activities are broad, and include:
In situ and ex situ conservation
- Population biology
- Plant genetics, evaluation, breeding and crop production
- Agricultural and crop research, including agrobiodiversity, agroecology, nutrition and medicine
- PGR documentation technology and information management
- Geographic Information Systems
- Gene bank management
- Seed conservation methodologies
- Production of the IUCN Red List of Threatened Species
- Archeobotany and ethnobotany
- Research in a wide range of specific taxonomic groups

2. Information of interest

Respondents were asked to indicate which categories of information were of interest to them and/or their research institutes. There were two sections: information related to a taxon (8 information categories - e.g. degree of relatedness, economic importance/use value, biological data, ecogeographic data) and information related to specific populations of a taxon (13 information categories - e.g. location, size, structure, habitat, geomorphology, management/conservation measures). Respondents were asked to indicate level of interest for each information category. The complete list of categories and the analysis of the responses obtained can be found in the Workpackage 1 Progress Report (16.04.04) ([http://www.pgrforum.org/Documents/WP1%20Documents/WP1_Progress_Report_16_04_04.pdf](http://www.pgrforum.org/Documents/WP1%20Documents/WP1_Progress_Report_16_04_04.pdf)).

The responses will aid in setting priorities during the development of the CWR database. Database development will also be guided by the other types of information of interest provided, and the list of typical database queries users might want to ask the information system.

Phase 3

In this third phase PGR Forum participants are invited to continue testing the current version of the user requirement survey and comment on its content and structure in the online discussion forum.

PGR Forum participants can also invite potential users to complete the online survey in order to conduct more extensive local surveys of user requirements within their own country (either through direct contact or via coordination).

Web-enabled CWR database

Jay Moore, PGR Forum data management consultant, reported on the progress on the Crop Wild Relative Information System ([www.pgrforum.org/cwris.htm](http://www.pgrforum.org/cwris.htm)). The database aims to capture all relevant data, to link to pre-existing databases and to respond to queries. Jay presented a development plan with future deadlines for task completion. Significant progress has been made in building the database and progress to date is on schedule.

The database platform is based on the mySQL database management system, the leading open-source high-spec database. The platform will include Active Server Pages web application as well as open source packaged applications. The database architecture has a snowflake schema with a data loading (extract/translate/load) tool, a browser to navigate the snowflake structure and a query and modelling tool to ask questions about the data and to generate hypotheses. A forthcoming requirement will be to decide on the number of pieces of data and the dimensions of the data.
UK CWR database

Maria Scholten shared her experience in the construction of a crop wild relative database for the UK currently being developed at the University of Birmingham, funded by the Department of Environment, Food and Rural Affairs, U.K.

The starting point for this project was the PGR Forum first match of Mansfeld’s and Euro+Med database filtered for taxa occurring in the UK. Harmonisation of European and UK taxonomies was carried out, UK ethnobotanical literature was consulted on uses, occurrence data was collated from botanical surveys and conservation data was collated. It was found that 20.3% of the total UK taxa is a crop wild relative for agriculture and food.

With regard to the structure of the database, occurrence data is based on botanical surveys. Occurrence is represented by the number of 10 x 10 km squares where the taxa occur and frequency categories indicate the number of taxa within the 10 x 10 grid squares. Conservation related fields in the database include threat assessment (IUCN categories), legal conservation status (UK legislation) and conservation action (Biodiversity Action Plan).

2.4.2 Workpackage 3: In Situ Data Management Methodology

Speaker: Sabine Roscher, German Centre for Documentation and Information in Agriculture, Germany

The deliverables of this Workpackage are:

- Identification of appropriate in situ genetic conservation data types
- Identification of appropriate data(base) structures and data visualisation tools
- Identification of in situ genetic conservation data management and analysis techniques
- Publication of data management methodology

The data management methodology currently being developed includes:

- List of data types (spatial data and non spatial data)
- Meta-data for these data types
- Methodology for data management
- Methodology for analysis techniques
- Visualisation tools
- Data structure for exchange
- Organisation structure for exchange

Data Interoperability and GeoDataInfrastructure (GDI)

- Data interoperability - IT-architecture and languages like XML and GML to combine geo-referenced data from different sources
- National GDI developed
- Metadata (Catalogue Service) - appropriate data items and structure for a meta-database developed
- Mapserver established
- Testbed for the implementation of WMS (web-mapping services) and WFS (web feature services)

Next steps

The next steps to be taken include setting priorities for the data types as well as continuing the documentation of data sources.
2.5 Presentation: Genetic Reserve Conservation of Crop Wild Relatives: Establishing the Context

**Speaker:** Nigel Maxted, University of Birmingham, Birmingham, UK

**Notes from powerpoint presentation:**

*In situ conservation*

In recent years the CBD (1992) [GPA (1996), GSPC (2002) and ITPGRFA (2003)] have refocused PGR conservation towards *in situ* conservation:

"*In situ conservation* means the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticates or cultivated species, in the surroundings where they have developed their distinctive properties." Article 2 CBD (1992)

This leads us to the conservation of wild populations in genetic reserves. Maxted et al. (1997) defined Genetic Reserve Conservation as "the location, management and monitoring of genetic diversity in natural wild populations within defined areas designated for active, long-term conservation".

PGR Forum should ask itself if this definition acceptable. Not cultivated species on-farm!

Synonyms: genetic reserve management units, gene management zones, gene or genetic sanctuaries, crop reservations, etc.

**Wild species vs. crop wild relative conservation**

Within the context of protected area conservation is there a difference between wild species and crop wild relative conservation?

- A crop wild relative is a taxon related to a species of direct socio-economic importance, a member of the same gene pool (GP1 and GP2) or genus (TG1, TG2, TG3, TG4), Not tertiary relatives in GP3 or TG5

Europe is an important centre for crop wild relative diversity.

- Major crops: oats (*Avena sativa*), sugar beet (*Beta vulgaris*), apple (*Malus domestica*), annual meadow grass (*Festuca pratensis*), and white clover (*Trifolium repens*) have wild relatives in Europe.
- Minor crops: arnica (*Arnica montana*), asparagus (*Asparagus officinalis*), lettuce (*Lactuca sativa*), and sage (*Salvia officinalis*).

These species are threatened = Need to improve efficiency of conservation of CWR

**Protocol for the genetic reserve conservation of CWR**

There is clearly a need to develop protocols for genetic reserve conservation of CWR. In theory there is existing experience in: Ammiad, Israel, the Turkish GEF project, the Fertile crescent project and other projects in various countries (Heywood, 2003). However, if we apply the definition of Maxted *et al.* (1997), the answer is no. However, ecologists, foresters and protected area managers may be able to provide us with some relevant information. Some questions need to be considered before formulating population management and monitoring guidelines.

- Ecosystem versus target taxon focus and emphasis on breadth of genetic base
- Demography versus genetic diversity
- The population management and monitoring methodologies formulated within the forum
must fit within the overall model of genetic conservation.

**Conservation issues:**

Some issues regarding pre-conservation measures include:

- Is there a need to understand patterns of genetic diversity in the target taxon prior to designating reserve sites?
- How many reserve sites are required to conserve a CWR using genetic reserve conservation?
- What impact will target taxon genetic diversity as opposed to ecosystem conservation have on reserve design?
- How can we attempt to ensure genetic reserve sustainability?
- What level of socio-economic compromise is acceptable without compromising the genetic reserve project?

When establishing a model, the forum should ask if the model for genetic reserve conservation proposed by Maxted *et al.* (1997) is appropriate. In order to manage the reserve it is necessary to understand the autecology or target taxon’s ‘niche’, synecology or community relationships, and population genetics and dynamics. The management plan should also include interventions and the target populations need to be monitored to ensure that the management plan is working.

**Conservation Objectives**

The conservation objectives of a genetic reserve must be clearly defined. One possible definition is:

- “To ensure that for the target taxon the maximum genetic diversity is represented within the minimum number and size of genetic reserves.”

The Forum should ask itself if this is a good statement of the objectives and consider if a reserve should conserve a single target taxon or multiple species (Heywood, 2003).

**Functions of Management Plans**

Functions of the management plan (adapted from Hirons *et al.*, 1995; Pirot *et al.*, 2000):

1. Describe the physical and biological environment of the reserve, as well as the local social and exploitation context.
2. Articulate the objectives and purpose of the reserve.
3. Analysis of opportunities and threats associated with the target taxon and reserve.
4. Describe management practices required to achieve the objectives, incorporating biological, social and economic actions at local and broader levels.
5. Identify key research activities.
6. Highlight expected outcomes of management.
7. Describe ecological monitoring practice specifying indicators, periodicity and methods.
8. Describe genetic monitoring practice specifying sampling, indicators, periodicity and methods.
9. Organise decision making, human and financial resources.
10. Specify means of involving and informing various stakeholders.
11. Act as a training guide for new staff.
12. Ensure consistency between reserve, national and regional conservation plans.
13. Ensure site management reflects the policies of parent organisations.
14. Facilitate reporting, communication and collaboration among genetic reserves.
A management plan should also allow for change, as communities are intrinsically dynamic and change is ‘natural’:

- Stochastic - drought, floods, fire, cyclones, hurricanes and epidemics
- Successional - directional, halted by management intervention
- Cyclical - density-dependent interactions, dramatic but their effects do not persist (genetic drift)

Changes due to human activity are even more dramatic, having permanent effects, often resulting in ‘islands’ of biodiversity. Human activity may create habitats, e.g. agriculture land and roadsides, the favoured habitat of the relatives of several important crops. Do such demographical changes equate to changes in genetic diversity?

**Genetic Management**

Some questions to be addressed by PGR Forum are:

- Is it possible to manage genetic diversity without also managing the broader community and ecosystem?
- What is the size and structure of the community and population to maintain diversity?
- How should the ecological and genetic dynamics of the system be monitored?

Jain (1975) notes that no primary crops or their progenitors are associated with climax vegetation. They are associated with disturbed open habitats (note: unlike forestry GR species). This implies that genetic reserves will require active management if we wish to avoid successions extinguishing our target taxon.

**Genetic Reserve Management Plan**

1. Preamble: conservation objectives, reasons for siting of reserve, place of reserve in overall conservation strategy for target taxon.

2. Taxon description: taxonomy (classification, delimitation, description, iconography, identification aids), wider distribution, habitat preferences, phenology, breeding system, genotypic and phenotypic variation, biotic interactions (e.g. pollinators, dispersal agents, herbivores, pests, pathogens, symbionts), local name(s) and uses, other uses, present conservation activities (ex situ and in situ), threat of genetic erosion.

3. Site evaluation: evaluation of populations of the target taxon, reserve sustainability, factors influencing management (legal, constraints of tenure and access), externalities (e.g. climate change, political considerations), obligations to local people (e.g. allowing sustainable harvesting) and anthropomorphic influences.

4. Site description: location (latitude, longitude, altitude), map coverage, photographs (including aerial), physical description (geology, geomorphology, climate, hydrology, soils), human population (both within reserve and around it), land use and land tenure (and history of both), vegetation and flora, fauna, cultural significance, public interest (including educational and recreational potential), bibliography and register of scientific research.

5. Status of target taxon in the reserve: distribution, abundance, demography, and genetic structure and diversity of the target taxon within the site, autecology within the reserve, interaction with associated fauna and flora, specific threats to population(s).

6. Site objectives and policy: site objectives, control of human intervention, allowable sustainable harvesting by local people and general genetic resource exploitation.

7. Prescription: details (timing, frequency, duration etc) of management interventions that will need to be carried out, schedule of ecological and genetic monitoring, population mapping, staffing requirements and budget, project register.
8. Genetic Reserve Management Plan

PGR Forum should ask if this is an appropriate formulation for a genetic reserve management plan. It should be kept in mind that each reserve is likely to require a unique management plan involving experimentation and evolution to attempt to maintain site dynamics and a “healthy” target taxon population that approximates the MVP. MVP and MDA will need to be larger for genetic conservation. The success of the management plan will be assessed by monitoring.

Monitoring a Genetic Reserve

Reserve Utilization

Genetic reserve conservation should be linked to utilisation, as genetic reserve conservation and on-farm projects are not ends in themselves. How can genetic reserve conserved diversity best be utilised?

Reserve Users

- Traditional users
  - Reserves are not established in an anthropogenic vacuum
  - Continued local use = project support
  - Compromise scientific management regime
  - Dana Nature Reserve, Jordan

How can local development aspirations be integrated into genetic reserve conservation activities?

- General users
Local, national or international population
Require their support
Encourage site visits
Example: Qa’at Al Hosn & Al Sala Hadeen, Syria

How can the general public be encouraged to use and support genetic reserve conservation activities?

- Professional users
  - Plant breeders
  - Pharmacologists
  - Characterise and publicise
  - Complement to ex situ conservation

How can professional germplasm users gain access to and be encouraged to use genetic reserve conserved diversity?

Some questions that should be considered before formulating the methodologies are:

- Is the definition of genetic reserve conservation acceptable?
- Is there a difference between wild species and crop wild relative conservation?
- Is there existing experience in genetic reserve conservation of CWR?
- Is the model for genetic reserve conservation proposed by Maxted et al. (1997) appropriate?
- What are the conservation objectives of genetic reserve conservation?
- How should a population be managed, what interventions are required?
- What monitoring regime is most appropriate?
- How can genetic reserve conserved diversity best be utilised?
  - How can local development aspirations be integrated into genetic reserve conservation activities?
  - How can the general public be encouraged to use and support genetic reserve conservation activities?
  - How can the professional germplasm users gain access to and be encouraged to use genetic reserve conserved diversity?

In conclusion there is a growing interest in biodiversity conservation, particularly in applying in situ techniques. However, in situ genetic conservation is still in its “infancy” (Jain, 1975; Hawkes, 1991; Heywood, 2003). It is time to establish protocols for CWR conservation in genetic reserves as a complement to ex situ seed storage activities.
3. POPULATION MANAGEMENT METHODOLOGIES FOR THE IN SITU GENETIC CONSERVATION OF CWR

Chairs: Tamara Smekalova and Shelagh Kell

3.1 Presentations

3.1.1 Population management methodologies for in situ conservation of CWR: an introduction

Speaker: Ehsan Dulloo, IPGRI, Rome, Italy

Notes from powerpoint presentation:

In situ conservation

According to the Convention of Biological Diversity, in situ conservation can be defined as "...the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated or cultivated species, in the surroundings where they have developed their distinctive properties."

Populations

When considering the in situ conservation of a population, we must remember that all levels of biological organisation (Ecosystem - community - species - population - individual - gene) are interdependent.

Populations can be defined as "geographical entities within a species distinguished either ecologically or genetically". From a genetic perspective, a population is "a group of individuals evolving independently of other groups because of limited gene flow and genetically distinguishable from other populations. Genetically distinct populations are important components of biodiversity. Hughes et al. (1997) estimate that there are 1.1 - 6.6 billion populations globally, 16 million of which are being destroyed annually in tropical forests alone.

Information for the management of populations

- Genetic
- Population dynamics (demography)
- Ecology

Based on these factors, approach and methods of management can be determined.

Role of Genetic Variation

- In situ conservation - mechanism by which the evolutionary systems that are responsible for the generation of variability are conserved.
- Genetic variation is essential for long-term survival of endangered species (Frankel & Bennet, 1970).
- Necessary for adaptive change and evolution.
- Lack of adequate genetic variation - risk of extinction.

Genetic considerations

- Different levels of organisation
- Ecosystem conservation - non selective
- Distribution of variation within species
- Implications for management: Ensure that the best individuals are conserved.
Genetic structure

The genetic structure between and within populations is influenced by several factors:

- Mutation, Selection, Migration, Gene flow
- Breeding System
- Dispersal system - pollen and seeds

Population dynamics

Population dynamics will also influence the conservation approach and methodologies.

- Annual rate of increase $\lambda$
- Net reproductive rate $R_0$
- Density dependence/independence
- Seed bank
- Regeneration
- Age structure
- Life tables
- Distribution - metapopulation

Ecological considerations

- Environmental parameters - climate, edaphic factors, aspects, altitude
- Habitat characteristics
- Competition - biological threats
- Pollinators and dispersers

In situ conservation methods

The table below summarises some of the current in situ conservation methods:

<table>
<thead>
<tr>
<th>Category</th>
<th>Purpose</th>
<th>Influence</th>
<th>Kind of intervention</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protected areas</td>
<td>Whole ecosystem</td>
<td>Natural/limited management</td>
<td>Legal Protection; monitoring</td>
</tr>
<tr>
<td>Genetic Reserve</td>
<td>Target species/ecosystem</td>
<td>Natural/Limited management</td>
<td>Legal protection; monitoring target species</td>
</tr>
<tr>
<td>Managed Genetic Reserve</td>
<td>Target species/ecosystem</td>
<td>Natural / More intensive management</td>
<td>Sustainable exploitation of target species</td>
</tr>
<tr>
<td>On farm</td>
<td>Target species</td>
<td>Human</td>
<td>Agricultural practices; selection by farmers</td>
</tr>
<tr>
<td>Home Gardens</td>
<td>Target species</td>
<td>Human</td>
<td>Household gardening</td>
</tr>
</tbody>
</table>

It should be remembered that a large number crop wild relatives occur in non-protected areas such as roadsides, wastelands, degraded habitats and disturbed areas.
Phases in *in situ* conservation of reserves

1. Formulation of objectives and priorities
2. Reviews, surveys and inventories
3. Selection of target species populations and sites
4. Assessment of conservation status, uses and threats
5. Development of management plan
6. Management of selected sites
7. Monitoring and evaluation

**Formulation of objectives and priorities**

When formulating objectives and priorities, the lead organisation should first consider the feasibility of the project and stakeholders should be identified. Examples of stakeholders are Ministries of Agriculture, Forest and the Environment; Forest and Agricultural research institutes; universities; extension workers; NGOs; farmers groups and women motivators. A project team should then be constituted to develop specific objectives.

Successful *in situ* conservation ultimately depends on the cooperation, support and participation of local communities. People should be empowered to mobilize their own capacities and to be social actors rather than passive subjects. They can participate by gathering information on useful species, priority uses, local indigenous knowledge and local rules. They can also participate in decision making, initiating action and evaluation.

**Reviews, surveys and inventories**

Current knowledge needs to be compiled through exploration and surveys. Workshops or stakeholder meetings could be held involving experts in the field and policymakers as well as grass root organisations and local people. This work should be linked to National development objectives and requires investment in staff, infrastructure, research and training.

**Selection of target species and conservation status**

Target species and populations can then be selected based on reviews and the criteria for selection and the conservation status of the target species can be assessed through ecogeographic studies and the identification of actual and potential threats.

**Selection of sites**

When determining the number of conservation areas, we must take into account the extent of diversity between populations and the ecogeographic distribution of the target species as well as understand their ecological amplitude, land tenure, etc.

When determining how many populations or individuals should be conserved, we should consider the following genetic factors:

- 5 populations - capture 90 - 95% common alleles (Brown & Briggs, 1991)
- Collecting 50 individuals from 50 populations considered as benchmark (Brown & Marshall, 1995)
- 172 plants capture all polymorphic genes from a population (Lawrence, 2002)
- 53 - 93% populations needed common allele standard (Neel & Cummings, 2003)

**Reserve design**

When designing a genetic reserve, we need to consider:

- Number, size and shape
- Human and cultural impact
- Politico-economic constraints
- Metapopulation models - habitat fragmentation
• Minimum population size

Reserve management
• All reserves should have a management plan; in situ conservation has a long term objective.
• The main purpose is to ensure that there is continuity and stability of management of the reserve.
• A management plan is a planning tool that contains a description of the reserve, evaluation and objectives (scientific dimensions) and a set of prescriptions and interventions to meet the objectives of the reserve area.
• Management plans should not be construed as a rigid framework for action but rather should be flexible to adapt to changes at the site.
• A feedback mechanism should be incorporated into the plan.

Elements of a minimum management plan
• Stage 1 Description
  o Location (name, status, area, grid ref., etc.)
  o Tenure (type of holding, agreements, legislation, right of access)

• Stage 2 Evaluation and objectives
  o Site description (habitat type, geology, ecology, flora and fauna)
  o Operations likely to damage the special interest (fragility and impact)
  o Evaluation (size, diversity, naturalness, rarity, recorded history, potential, intrinsic appeal, etc.)
  o Identification of important features
  o Ideal management objectives
  o Rationale
  o Identification of operational objectives, selection of management options and outline prescription

• Stage 3 Prescription
  o Project register and description (records, rsk, management, administration)
  o Project groups (according to objectives of the MP)
  o Work programme / Annual work plan

• Appendix 1 Maps
  o Owners / Occupiers
  o Habitat: existing state
  o Habitat: desired state
  o Management required

• The management plan should have control mechanisms that allow revision of the Plan for short, medium and the longer term.
3.1.2 Strategies and methodologies for the in situ genetic conservation of *Populus nigra*, an example CWR in forestry

**Speaker:** François Lefèvre, INRA, Avignon, France.

National programme for *Populus nigra* conservation (Marc Villar, coord.)

EUFORGEN Network for *Populus nigra* & *P. alba* (Sven de Vries, chair; Davorin Kajba, vice-chair)

**EUFORGEN Network**

EUFORGEN is a collaborative mechanism among more than 20 European countries to promote the conservation and sustainable use of forest genetic resources. It was established to implement Resolution 2 (Conservation of forest genetic resources) of the First Ministerial Conference on the Protection of Forests in Europe, held in Strasbourg in December 1990.

The first EUFORGEN *Populus nigra* (black poplar) Network meeting was organized in Turkey in October 1994 in parallel with the 37th meeting of the Executive Committee of the International Poplar Commission and after that, the Network activities have continued through both Phases of EUFORGEN. The Network has made considerable efforts to integrate ex situ and in situ conservation efforts for black poplar and developed guidelines for in situ conservation and a standardized list of descriptors for inventories of natural stands as well as established a database of black poplar clones, to name some of the achievements.

**Objectives of in situ conservation:**

1. Ensure the regeneration in sufficient quantity
2. Ensure the genetic quality of the regeneration
3. Preserve the ecological and genetic characteristics

**Integrated approach to the conservation of genetic resources**

Many factors such as habitat, human impact, the interaction between the domestic resource and the wild relative, etc., should be considered in conserving a target species.

**Integrated approach to genetic resources**

- Habitat monitoring (pop. management)
- Indirect human impact
- Population management
- Wild relative
- Domestic resource
- Interaction
- Environment landscape

**Restoration projects** (B. Heinze, F. Lefèvre)

- Actively plant *P. nigra* where? - suitable sites (river flooding regime, ...)

[Diagram of the integrated approach to genetic resources]
how ? - suitable techniques specific for P. nigra
what ? - suitable sources of plant material

• "Restoration genetics"
  how many individuals? - Ne equivalent

• Restoration management
  how to maintain viable populations in the long term

Monitoring genetic diversity (F. Lefèvre, D. Kajba)

• ecological indicators: hydroperiod, area pioneer vs. mature stage & tendency, …
• demographic indicators: occurrence of regeneration, number of adult trees, sex ratio, …
• genetic indicators: genic diversity, differentiation among cohorts, introgression…

=> inform on the processes of evolution: stochasticity, drift, mating system, gene flow, selection

Inventory of stands (N. alba)

A database has been specifically developed for P. nigra conservation and includes:

• “passport” data: code, location, river, tributary, protection status, …
• demography of current population: occurrence of regeneration, number of adult trees, sex ratio, …
• ecology & current management: soil, climate, hydroperiod, river and forest management, …

From research to recommendations

EUROPOP (B.C. van Dam coord)

• gene flow (seed & pollen)
• mating system
• clonal propagation
• introgression
• ongoing processes of evolution

1. Conservation sites

Research results show that genetic diversity is not evenly distributed:

• Differentiation among populations within each country
• Differentiation among populations within river-system
• No accumulation of diversity down the rivers
• Variable amount of diversity among populations
• Variable amount of clonal redundancy

Recommendations:

• should be distributed over the range of the species map of cpDNA lineages ecological conditions (altitude, latitude)
• eventually more than 1 site per river-system
• preliminary estimate of genetic diversity among adult trees

2. Introgression

Research results show that gene flow with cultivated poplars is scarce but not null:

• P. deltoides genes are sometimes detected at the seedling stage especially on isolated P. nigra females
Older introgressed individuals are rare over Europe.

*P. trichocarpa* genes can also introgress *P. nigra*.

*P. nigra 'italica'* cannot hybridise local resource in Northern Europe, but can in other regions.

Recommendations:

- There is no need to completely forbid all poplar plantations around the conservation units.
- Estimate the amount of introgression for adult trees only.
- Further check introgression from *P. trichocarpa*.
- Pay attention to 'italica' only in Southern Europe and if the number of local pollinators is limited.

### 3. Population size

Research results show that mating does not occur at random:

- Female trees preferentially mate to few particular males (distance, phenology).
- Half-sib progenies from a single mother tree only involve a few pollinators.

Gene flow follows the model of isolation by distance:

- Effective gene flow ≠ potential gene flow, seedling establishment is a limiting factor.
- Gene flow is symmetrical, wind dispersal pollen and seeds.

Recommendations:

- Number and spatial distribution of females is critical, effective population size requires a balanced sex ratio.
- Seed-set and seedling establishment should be favoured to restore populations, unrelated clones should be preferred to seed progenies.
- Assisted regeneration should be achieved on several scattered plots rather than a single large one.
- Rely only on poplars located 5 km apart to contribute significantly to the population size.

### 4. Monitoring local evolution

Research results show that drift effects are observed at the local scale (within stand):

- Differentiation among cohorts.
- Differentiation among seedling patches.
- It can affect the fitness of the populations.

Recommendations:

- Focus attention on all practices that have an impact on:
  - the flowering habit.
  - the regeneration process.
- Ecological and demographic indicators most relevant:
  - hydroperiod.
  - structure of habitats.
  - number and distribution of male & female trees.

Further information on the conservation of forest genetic resources in Europe (EUFORGEN programme) can be found at: http://www.ipgri.cgiar.org/networks/euforgen/euf_home.asp.
3.1.3 Rationale for *in situ* management of wild *Beta* species

**Speaker:** Lothar Frese, BAZ, Braunschweig, Germany

**Taxonomy, genepool concept, geographic distribution**

The wild species of the genus *Beta* are native to Europe and adjacent areas. The section *Beta* is mainly distributed along the shores of the Mediterranean basin and along the Atlantic coast from the Canary Islands as the most southern outpost to the South of Sweden. Section *Corollinae* frequently occurs in Turkey and the adjacent Caucasus region with outposts in Dagestan and the Talysh mountain (Iran/ Azerbaijan). The only species of section *Nanae* is endemic in Greece. The *Procumbentes* section has its major distribution area on the Canary Islands but can also be found in Southeast Spain and along the coast of Morocco.

In 1979 the first *Beta* germplasm collecting mission was funded by IPGRI and a number of additional missions followed with the objective to sample wild beets and landraces in the Mediterranean area. Between 1980 and 1990, large geographic gaps were closed by IPGRI and USDA/ARS funded missions (South Italy, southern part of France, West Atlantic coast, British Islands, Ireland and Denmark) (Doney et al., 1995) and the collecting data were entered into national databases. On the initiative of the ECP/GR programme an European inventory of *Beta* collections was established in 1987, and in view of the effective collaboration achieved with the NPGS (USA) it was recommended to assume an international role. The International Database for *Beta* (IDBB) (Frese and Van Hintum, 1989) contains information provided by 28 germplasm holdings in 24 countries. This central crop database currently stores, besides data on cultivated germplasm, passport data on 4022 wild beet accessions. The geographic coordinates of collecting sites were used for plotting distribution maps to visualise smaller geographic gaps in the world holding. Subsequently the German-Dutch Cooperation on Beta Genetic Resources (Iberian peninsula, East Caucasus region), and the Turkish genebank (explorations within the country) organised collecting trips to purposefully complete the world holding. Today, for wild beets only smaller geographic gaps need to be closed in Europe such as for *B. vulgaris* subsp. *maritima* in Northwest Spain. In West Asian countries additional populations may exist.

**Selected demographic data**

There are individual large populations of *B. macrocarpa* which, according to criteria developed by animal genetic resources experts, are not threatened (EPS > 1,000 individuals). The average population size of *B. macrocarpa* in Spain is close to this value while the average value of the Portuguese material would indicate the “observation status” (EPS 200 to <1,000 plants) of a population (if we consider all Portuguese plants of this species as one population). With a total number of about 17,000 observed plants in the western part of the distribution area of *B. macrocarpa* the survival and evolution of the species seems to be guaranteed (if we take 5,000-10,000 individuals as the minimum viable population size - MVPS). We must, however, keep in mind that the data are about 15 years old, and secondly with the modernization of a single sea salt winning area in Portugal or land cleaning activities in Spain several thousand plants can be wiped out.

The total number of plants for *B. vulgaris* subsp. *maritima* (Portuguese distribution area) is 7,300 individuals, for *B. macrorhiza* 1,190 in the Caucasian area, *B. lomatogona* 3,600 in Turkey, *B. nana* 140 in Greece, and *B. patellaris* 600 individuals in Morocco. These figures indicate that we need to assess the threat of genetic erosion for *B. macrocarpa* (by region), *B. macrorhiza*, *B. lomatogona* (by region). Such need does not exist for *B. nana* because this species is already known to be highly endangered.

Whether these figures really indicate a threat of genetic erosion in the species *B. vulgaris* subsp. *maritima* in Portugal can be debated, as there are areas in Europe (France, British Islands) where the species forms very large populations. Nevertheless, with the decrease in population sizes in Portugal we might lose valuable traits such as variation for cytoplasmic male sterility in the area around Cascais close to Lisbon.
According to www.floraweb.de, operated by the Federal Office of Nature Protection, the species *B. vulgaris* subsp. *maritima* is not endangered in Europe and world-wide. The subspecies is not included in the FFH-regulation and the currently only way to safeguard populations is the habitat protection. In Germany the Federal Nature Protection Law according to §30 allows the protection of cliffs, salt meadows, silting zones etc. close to the coast. But who in the local communities and administrations knows that this species is a CWR and who cares about if construction activities are planned and conducted as it happened in the Netherlands in the 1950s? The species once was fairly common at the Dutch coast. Due to coast protection measures the abundance of the species drastically dropped to almost zero. Hence, FFH-regulations and derived national laws may not be effective enough to protect populations of CWR with economically important traits.

**Structures of genetic diversity in Beta**

Section Procumbentes forms part of the relict flora of the Canary Islands. Its small, remote distribution area as well as its surprisingly low homology with the *B. vulgaris* genome indicates that it has most likely reached its final evolutionary stage (Jung et al. 1993). The section is divided in diploid species which are closely related if not identical (*B. procumbens*/*B. webbiana*) (Wagner et al. 1989) and a tetraploid species (*B. patellaris*). The diploid species can only be found on the Canary Islands.

Section Corollinae is considered the second oldest group of *Beta* species. Genetic as well as morphological differences exist between *B. macrorhiza* plants from Dagestan and the Turkish distribution area. *B. corolliflora* was more polymorphic and heterozygous than *B. lomatogona* and *B. macrorhiza* (Reamon-Büttner et al., 1996; Shen et al., 1997).

Due to the lack of sufficient germplasm only few studies on *B. nana* have been published. The species lacks the EcoRI satellite DNA which is common in the rest of the genus (Schmidt et al., 1991). It contains unique isozyme markers and was essentially monomorphic for almost all investigated enzyme systems (Nagamine and Ford-Lloyd, 1989).

*B. macrocarpa* is more distantly related to *B. vulgaris* than is *B. vulgaris* subsp. *adanensis* (Letschert, 1993; Shen et al., 1997) while *B. patula* is closer to *B. vulgaris* subsp. (Letschert, 1993). *B. macrocarpa* can be divided into a western group mainly distributed on the Iberian peninsula (synonym *B. bourgaei*) and an eastern group in the East Mediterranean region. A tetraploid type of *B. macrocarpa* possibly of an alloplloid nature occurs solely on the Canary Islands (Lange and de Bock, 1989).

The annual and predominately inbreeding species of section *Beta* (*B. macrocarpa*, *B. patula* and *B. vulgaris* subsp. *adanensis*) are less polymorphic at the population (accession) level than the wide-spread *B. vulgaris* subsp. *maritima* (Letschert, 1993; Shen et al., 1996). Within *B. vulgaris* subsp. *maritima* the macrogeographic allozyme distribution patterns were investigated by Letschert (1993) who concluded that more variation was shown to be concentrated in the Mediterranean accessions while the Atlantic accessions seemed to be less polymorphic. This is supported by the concordance of results presented by Kraft et al. (1997) investing genetic diversity in wild beets with RFLP. Letschert further concluded that genetic diversity is more or less equally divided among individual plants in a population and among neighbouring populations. With respect to allozyme diversity it should, therefore, be sufficient to extensively sample one large population within a geographical region to capture most of the variability present in the region.

However, where does a geographic region begin and where are the limits of *B. vulgaris* subsp. *maritima* populations which are generally colonizing a linear habitat? Genetic material of the sea beet is distributed by wind (50% of the pollen is still present 100 m from the source, Levin and Kerster, 1974 cited in Boutin-Stadler et al. 1989), tide movements and sea currents (seed balls) and by human activities (road construction etc.). Within the sea beet Desplanque et al. (1999) found differences between material collected on the French Mediterranean coast and populations from the Biscay region. There were non-significant genetic differences between Biscay populations and populations from the Channel probably due to the limited number of investigated plants.
Gene flow in the natural habitat

*B. vulgaris* subsp. *maritima* is homed in a linear habitat. Raybould et al. (1996) were the first who investigated the genetic structure of a population distributed along the coast line of Furzey Island amongst others “to better understand the major ecological processes such as colonization, invasion, succession and extinction” (Avise, 1994 cited in Raybould et al., 1996). Based on isozyme and RFLP data they found strong evidence that the structure of the investigated population was determined largely by founder effects and not by isolation by distance arising from limited pollen and seed flow diminishing with increasing spatial distance between patches of plants. Raybould *et al.* (1996) continued this kind of research with 10 populations collected at the Dorset coast and found highly significant decrease in gene flow with distance when using RFLP markers but not for isozymes. They explained this finding by uniform balancing selection that may operate to maintain approximately equal allele frequencies among populations at the isozyme loci. Isozymes may therefore be unsuitable for modelling the spread of neutral genes and for analysing the gene flow in the habitat. Further analysis revealed that the effects of isolation by distance are habitat dependent and play only a role in cliff-populations while in the drift-line populations in the perimeter of the harbour founder effects are a significant source of variation between populations.

The application of genetic markers in research has improved our understanding of the structures of genetic diversity at the section, species, subspecies and population level. In addition, today we know better than in the past that samples taken from populations in nature can contain useful genes. However, we do not know how these useful genes are distributed. Such information would be useful if we had to take a decision on maintenance priorities. Are identical genes conferring resistance to Rhizomania widely common distributed in *B. vulgaris* subsp. *maritima* at different frequencies within populations, contain the known sources (e.g. Bretany / Demark/ Italy) different genes, is the occurrence of the (specific) resistance gene(s) restricted to specific areas ? We don’t know.

Distribution of traits of economic importance

In the 1980s breeders were rather reluctant to use exotic germplasm in sugar beet breeding programs. They feared that the introgression of resistance genes from wild species into the sugar beet would deteriorate their elite breeding genepools and that the gain in terms of higher resistance would not pay off the efforts required to select high yielding and high quality elite material from exotic cross progenies.

In addition, there was little knowledge on the great potential of exotic material as a source of novel genetic variation. This attitude towards genetic resources began to change dramatically with the start of systematic screening programs in the United States and the detection of economically important characters such as the Rizomania resistance in *B. vulgaris* subsp. *maritima*. Additional screening work was conducted in Europe in the framework of a EU funded GENRES project. Today, there is much detailed information on the occurrence and distribution of traits useful to agriculture.

Accessions collected after 1979 often have complete passport data including the geographic co-ordinates of the collection place. We can, therefore, present local communities/landscape managers etc. with economic arguments why a specific population should be maintained in an area.

Potential for co-operative actions

During a ECP/GR meeting, a task force on a *Beta* core collection discussed the *in situ* management issue (France, 2000, [www.ecpgr.cgiar.org/publications/IBCCRep.pdf](http://www.ecpgr.cgiar.org/publications/IBCCRep.pdf)). It was suggested to:

- maintain core collection entries of sections Corollinae, Nanae and Procumbentes *in situ*,
- add a database module for *in situ* management to the International Database for *Beta*
• use official channels to approach the institutions, local communities, or persons involved in in situ management of *Beta* species or of sites sustaining *Beta* populations and involve them in this effort.

The *in situ* management issue will be on our next ECP/GR working group /World *Beta* Network meeting agenda. We also need to initiate discussion on *in situ* management programmes with the International Institute for Beet Research, an organisation with experts in many parts of Europe and overseas. However, the respective IIRB members can only mediate contacts and motivations between local officials who are legally responsible for the management of an area and the *Beta* genetic resources community.

**Urgent needs for *in situ* management**

**Highest priority: *B. nana***

Since 1980 there have been only few attempts to monitor the species. For biological reasons *ex situ* conservation is no alternative and we have to determine whether the species still exists at all. One might argue that such a distantly related species is of little use to breeding. Until recently nobody would have expected that another “cinderella” species, *B. patula*, is a source of resistance. Hence, *B. nana* should also be considered as a potentially valuable source for breeding.

*B. macrorhiza* is for sure endangered in the East Caucasus area by overgrazing, and there is astonishingly little left of section Corollinae species in Armenia and Georgia. Overgrazing is the main factor of genetic erosion in the whole Caucasian and Transcaucasian region. In Azerbaijan and Northern Iran (Talysh mountain), at the margin of its distribution area, *B. lomatogona* is very probably endangered and almost extinct. The reasons are overgrazing and modernization of agriculture.

**Second priority: *B. macrocarpa* and Procumbentes species**

*B. macrocarpa* is a source of useful genetic variation. I am not aware of any monitoring activities in Portugal, the western continental outpost of this species, since our collecting mission in 1989. The species survival is linked to traditional management of salt winning areas and can get lost with the modernisation of sea salt production. The tetraploid type of *B. macrocarpa* was considered fairly secure occupying a very ruderal habitat on some of the Canary Islands in 1981 (Ford-Lloyd et al., 1981). Is this assessment still valid after more than 20 years? We just don’t know.

Little is known on the lot of Procumbentes populations on the Canary Islands, but with a yearly influx of roundabout 9,000,000 visitors (Francisco-Ortega et al., 2000) one can imagine the impact of tourist industry on nature and natural sites in and around villages and roads. However, we just do not know whether the populations sampled in 1981 have survived, increased or decreased at the collection sites.

**Conclusions**

- Reviews of the taxonomy of *Beta* has removed much of the confusion existing 20 years ago.
- An on-line taxonomic key to the species is available (first draft, www.fal.de/bgrc/eu9542/default.htm).
- Research has increased our knowledge on the genetic relationship between species.
- We have some understanding of the macrogeographic distribution patterns of genetic diversity at the molecular marker level (mainly section Beta).
- We start to understand the mechanisms causing gene flow in *B. vulgaris* subsp. *maritima*.
- We know the distribution of species and their populations.
- Passport and evaluation data are contained in databases including the geographic coordinates of the majority of material collected after 1979.
• We know economically important populations and their growing places.
• There are European / international organisations dealing with the crop. Hence, potential for co-operation is present.
• We know causes for genetic erosion in *Beta* and some of the areas where genetic erosion is currently taking place.
• We can define priorities.
• We need to combine knowledge and forces to develop an *in situ* management programme for *Beta*, a group of CWR native to the European region and of world-wide economic and scientific importance.
3.2 Working Group Discussions

The purpose of group discussions was to make the best use of workshop time by establishing small working groups to discuss different subjects related to management methodologies for the *in situ* genetic conservation of CWR.

The workshop participants formed two parallel working groups to discuss and present issues on "Genetic reserve location and design. Integration of PGR conservation in Protected Area management" and "Identification of milestones for *in situ* genetic conservation. Minimum baseline information for the development of a management plan". One and a half hours were allocated for each parallel group discussion. The findings of each group were presented for discussion with the Forum at the beginning of Day 2.

**Overall objective:**

Agree on population management methodologies appropriate for the *in situ* genetic conservation of European crop wild relatives.

**Work description:**

The working groups examined existing techniques for the generation of management plans as a starting point for the discussion and then debated and resolved how these might be adapted to genetic rather than the traditional ecological goals.

**Reference Material:**

**Available Guidelines or Planning Documents relating to various aspects of *in situ* conservation of wild species.**

**General**

Endangered wild species


Forest genetic resources


Thomson, L. 1998. SPRIG: South Pacific regional initiative on forest genetic resources. Forest Genetic Resources No 26


Crop wild relatives


Genetic resources in protected areas


3.2.1 Group A: Genetic Reserve Location and Design. Integration of PGR Conservation in Protected Area Management.

Facilitator: Ehsan Dulloo

Discussion points:
- Criteria for selection of genetic reserve locations among taxon localities present in protected areas
- Criteria for delimitation and design of genetic reserve within selected protected areas

Reference material:

Criteria for selection of genetic reserve locations among taxon localities present in protected areas

- **Basic terminology:**
  - Genetic reserve conservation: the location, management and monitoring of genetic diversity in natural wild populations within defined areas for active, long-term conservation (Maxted, Hawkes, Ford-Lloyd and Williams, 1997).
  - Genetic reserve, site, population.

- **Number and size of reserves** will depend on the characteristics of the target species (Soulé and Simberloff, 1986).
  - Large reserves especially suited for low-density species
  - Small multiple reserves more appropriate for annual plant species.
  - Minimum Viable Population (MVP) estimates to provide a lower limit in the size of reserves. Lawrence and Marshall (1997) suggest the number of 5000 individuals although this estimate depends on intrinsic features of the taxon and habitat.

- **Criteria**
  - Taxon sustainability. It is assumed that the taxon has previously been assessed for its suitability for conservation over an extended period in an *in situ* genetic reserve (e.g. a highly mobile species may not be suitable).
  - Ecogeographical surveys. Genetic reserve locations are chosen within the taxon's distribution area in order to gather the most representative combinations within the ecogeographical range of the taxon. It is assumed that ecogeographical variation will be somewhat correlated to genetic variation, especially in genes that play a role in adaptation.
  - Genetic surveys. Genetic reserve locations are chosen after a characterisation of genetic diversity is made in a representative sample obtained throughout the taxon's distribution area.
  - Location and type of protected areas
  - Political and socio-economic factors
  - Reserve sustainability
Criteria for delimitation and design of genetic reserves within selected protected areas

- **Model for reserve design** (from Cox, 1993, modified from Batisse, 1986, obtained from Hawkes, Maxted and Zohary, 1997):

- **Reserve shape**: the edge to be kept to a minimum (round shape, best)
- **Habitat heterogeneity**: to include as much as possible
- **Minimum dynamic area**: smallest area with a complete, natural disturbance regime (Pickett and Thompson, 1978).
- **Political and economic factors**.
- **Users' needs**: reserve visitors, scientific community
Results

1. **Definition of protected area**
   - According to IUCN categories
   - Flexibility in the definition in terms of extent/type of protection (legal, local community protection, etc.)

2. **Genetic reserve**
   - Genetic reserve concept refers to a network of key locations of target CWR genepools.

3. **Inventories**
   - Identification of protected areas at national level
   - National inventory of CWR
   - Identification of Protected Areas with CWR (Use of GIS technology)

4. **Hotspot Areas**
   - Identification of hotspots (multiple CWR species) within Protected Areas

5. **Criteria**
   The group agreed with the criteria presented in the reference material:
   - Taxon sustainability
   - Ecogeographic surveys
   - Genetic surveys
   - Location and type of protected areas
   - Political and socio-economic factors
   - Reserve sustainability
   Sustainable utilisation must also be considered.

6. **Highly mobile species**
   - Develop simulation models to study movements and delimitations of populations

7. **Sustainability of reserves**
   - Consider adding public and decision makers awareness

8. **CWR outside Protected Areas**
   - Recognise that many CWR occur outside Protected Areas and different guidelines should be produced for these.

9. **Next steps**
   - Guidelines should be as generic as possible, but could consider developing different guidelines of similar groups of CWR in terms of life forms, etc.
   - Seek comments on draft guideline from wider audience of experts
   - Need to test guidelines on pilot case studies
   - Project funding proposal
   - Test existing/ongoing projects
Discussion

In the general discussion following this group's presentation PGR Forum participants raised additional issues for consideration.

1. The term "genetic reserve" should perhaps be "translated" for the general public. "Genetic reserve" is not a "friendly" term and the general public may not understand what it implies. Perhaps a more user-friendly term could be found to make it easier for the public to understand and aid in increasing public awareness.

2. A hierarchy of filters is needed to end up with a genetic reserve. It was proposed to establish a hierarchy of filters which could be generally applied as criteria in designing and establishing a genetic reserve.

3. Genetic survey vs. ecogeographic survey. When carrying out surveys to determine genetic reserve location and design, ecogeographic surveys are much more practical as they are less expensive.

4. The question of how many populations should be conserved for a target species was raised. Literature has cited varying numbers of populations and there are conflicting views concerning available information.

5. Conservation of genetic diversity vs. conservation of interesting traits (resistance genes). The Forum addressed this question and generally agreed that the goal is to conserve useful genetic traits. In many instances, these traits are conserved in ex situ collections. It was also noted that GIS techniques can be a useful tool in the prediction of the occurrence of particular traits.
3.2.2 Group B: Minimum baseline information for the development of a management plan. Contents and structure of a management plan. Identification of milestones for *in situ* genetic conservation.

**Facilitator:** Nigel Maxted

**Discussion Points:**

- Identification of genetic reserve objectives
- Minimum baseline information that needs to be collected for the development of a management plan
- Minimum contents and basic structure of a management plan
- Development of a sequential list of steps that need to be taken for the design and implementation of a conservation and management plan.

This working group was divided into subgroups to deal with different aspects of the discussion points.

**Reference Material:**

Identification of genetic reserve objectives

**Main objective for *in situ* conservation of particular CWR taxon:**

- To ensure that the maximum possible range of genetic diversity is represented within the minimum number and size of genetic reserves

**Main objective within a particular genetic reserve:**

- Conservation of the target taxon population(s)
- To maintain or enhance the target population(s) in the quality and quantity of their genetic diversity

**Specific objectives:**

1. **Identification of specific values inherent to the population(s)**
   - relative location, latitude, longitude, altitude
   - environmental adaptations (tolerance, resistance,...)
   - recreation, agrotourism, local culture value
   - other

2. **Diagnosis of the status of the population(s)**
   - assessment of threat of extinction
   - evaluation of biotic and abiotic environmental factors associated with the population
   - study of genetic structure, diversity and particular adaptations
   - identification of threats, problems and conflicts associated with the viability of the target population
     - No relevant threats to population viability:
     3. **Maintenance of population size and genetic diversity**
     - Threats to population viability:
       4. **Elimination of threat causes**
       5. **Population recovery in genetic and demographic terms**
Results

Subgroup 1: Definitions (Brian Ford-Lloyd, Stephen Jury and Nigel Maxted)

This group examined the conservation objectives of genetic reserves and the definition of crop wild relative presented by Nigel Maxted in his overview. Additions and conclusions arrived at by the group are underlined.

Conservation Objectives:

- “To ensure that for the target taxon (within the CWR list) the maximum genetic diversity is represented sustainably within the minimum number and size of genetic reserves.”

- Within the context of protected area conservation is there a difference between wild species and crop wild relative conservation?

There is a difference between wild species and crop wild relative conservation because:

- there is potential for genetic pollution of CWR from related crops.
- the conservation focus is likely to be more genetic rather than demographic

What is a crop wild relative?

- A crop wild relative is a taxon related to a species of direct socio-economic importance, a member of the same gene pool (GP1 and GP2) or genus (TG1, TG2, TG3, TG4)

- Where there is no other prioritising information, then a crop wild relative is a taxon related to a species of direct socio-economic importance, i.e. a member of the same gene pool (GP1 and GP2) or genus (TG1, TG2, TG3, TG4)

Where TG = Taxonomic Group

- TG1 same species
- TG2 same section / series
- TG3 same subgenus
- TG4 same genus
- TG5 different genus = tertiary taxon
Subgroup 2 - Management Plan Format (Shelagh Kell, Maria Pohjamo and Silvia Strajeru)

This group examined the contents and structure of a management plan presented by Nigel Maxted in his overview at the end of the Opening Session. Additions and conclusions arrived at by the group are underlined.

1. **Preamble**: conservation objectives, reasons for sitting of reserve, place of reserve in overall conservation strategy for target taxon.

2. **Taxon description**: taxonomy (classification, delimitation, description, iconography, identification aids), wider distribution, habitat preferences, phenology, breeding system, means of reproduction (sexual or vegetative) and regeneration ecology, genotypic and phenotypic variation, biotic interactions (e.g. pollinators, dispersal agents, herbivores, pests, pathogens, symbionts), local name(s) and uses, other uses, present conservation activities (ex situ and in situ), threat of genetic erosion.

3. **Site evaluation (or justification)**: evaluation of populations of the target taxon, reserve sustainability, factors influencing management (legal, constraints of tenure and access), externalities (e.g. climate change, political considerations), obligations to local people (e.g. allowing sustainable harvesting) and anthropomorphic influences.

4. **Site description**: location (latitude, longitude, altitude), map coverage, photographs (including aerial), detailed physical description (geology, geomorphology, climate, hydrology, soils), human population (both within reserve and around it), land use and land tenure (and history of both), vegetation and flora, fauna, cultural significance, public interest (including educational and recreational potential), bibliography and register of scientific research.

5. **Status of population of target taxon in the reserve**: distribution, abundance, demography, and genetic structure and diversity of the target taxon within the site, autecology within the reserve, interaction with associated fauna and flora (particularly pollinators and dispersal agents), specific threats to population(s) e.g. (potential for gene flow between CWR and domesticate).

6. **Site objectives and policy**: site objectives, control of human intervention, allowable sustainable harvesting by local people and general genetic resource exploitation.

7. **Prescription**: details (timing, frequency, duration etc) of management interventions that will need to be carried out, schedule of ecological and genetic monitoring, population mapping, staffing requirements and budget, project register. Impact assessment of target taxon prescriptions on other taxa at the site.

   Research recommendations for population(s) at the site e.g. genetic diversity analysis, breeding system, pollination, characterisation and evaluation.

NB: Results of monitoring leads to review of management interventions, and management plan is updated accordingly (Sections 4-8).
Subgroup 3 - Model for Genetic Reserve Conservation (Stelios Samaras, Tamara Smekalova and Juozas Labokas)

This group was assigned the task of reviewing the model for genetic reserve conservation as presented by Maxted et al. (1997).

Original model:

Phase 1

Reserve Planning and Establishment

Site Assessments

↓

Assessment of Local Socio-economic and Political Factors

↓

Reserve Design

↓

Taxon and Reserve Sustainability

↓

Formulation of the Management Plan

Phase 2

Reserve Management and Monitoring

Initiation of Reserve Management Plan

↓

Reserve Monitoring

↓

Community Inter-relationships

Phase 3

Reserve Utilisation

Traditional, General and Professional Utilisation

↓

Linkage to Ex Situ Conservation, Research, Duplication and Education
Revised model:

The results of the group were presented for general discussion. After some active exchange of ideas, it was decided that the discussion should continue online or within a smaller working group.
Subgroup 4 - Management Prescription (Françoise Lefèvre, José Iriondo and André Toussaint)

The goal of this group was to focus on the stage of prescription of management interventions and to identify the different types of prescriptions that may be available.

The group decided it could be interesting to differentiate the interventions that had a direct effect on the target taxon from those that had an indirect effect and were not specifically focused on the target taxon. Within each category it was found useful to group the interventions according to the objectives pursued. Some examples were included in this categorization, but there was not time to gather a complete list of possible types of interventions.

**Direct prescription acting on target taxon**

Objective 1: Increase number of individuals
- reinforcement (demographic rescue)
- reintroduction from gene bank (local origin)
- controlled burning
- etc.

Objective 2: Improve genetic quality
- reinforcement (genetic rescue)
- translocation among populations
- migration of propagules among populations
- re-introduction from another site
- introduction

Objective 3: Improve reproductive success
- introduce pollinators

Objective 4: Improve survival and sustainability
- chemical treatment
- biological control
- remove parasites / predators / competitors
- introduce beneficial species (mychoriza, etc.)
- fire prevention / controlled burning

B. Impact of any indirect activity in the reserve area (including prescriptions for other taxa)
(No examples were given)

Subgroup 5 - Genetic IPA or IPGRA? (Jay Moore, Daniela Benedikova and Xavier Picó)

This group discussed the concept of important plant areas versus important plant genetic resource areas, and provided some ideas about the management of these areas.

- Where are taxa?
  - Ecogeography
  - Hot Spots of species richness
  - Looking for multiple target taxon sites
  - Extant reserves
  - Gap analysis
  - Areas of ecogeographic diversity
  - Areas of traditional practices
  - ‘Deep rural’ locations
  - Locations near related crops
  - Linked to ecological, phyto-sociological regions

- IPA are unlikely to be linked to IPGRA
- Management of IPGRA
  - Trade-offs
- Experimental approach
- Close monitoring
- Prioritise taxa at site
- Core and peripheral taxa
- Native and indigenous
- Identify valuable alleles
- Looking to maintain diversity / heterogeneity
- Political / economic impacts
- Climate change
- Disease resistance
3.3 General Discussion

The next steps to be taken were discussed. It was suggested that on-line discussions could be used to make progress, and that a core group could prepare the outline or rough draft.

At some point the issue of how to deal with multi-species genetic reserves (genetic reserves with more than one target taxon) was raised. It was considered that it would be interesting to take this situation into account at the time of generating management methodologies.
4. POPULATION MONITORING METHODOLOGIES FOR THE IN SITU GENETIC CONSERVATION OF CWR

Chairs: Aasmund Asdal and Kell Kristiansen

4.1 Population Monitoring Methodologies

4.1.1 Introduction to Population Monitoring

Speaker: José Iriondo, Universidad Politécnica de Madrid, Madrid, Spain

Surveying and Monitoring

Surveying gives us a picture of the status of a population at a particular time, providing information on the demographic and genetic structure of the population as well as habitat structure and environmental interactions. All of this information is essential in the initial assessment of suitable sites for genetic reserves and in the preparation of a management plan.

Regular surveys show the progress or evolution of a population and its habitat through time (population and habitat dynamics). This systematic series of surveys through time is referred to as monitoring.

Monitoring gathers baseline information for the formulation of management plans and the establishment of objectives. Monitoring also detects relevant changes that may require reassessment of the management prescription.

Monitoring design

Some considerations should be kept in mind when planning the monitoring design:

- Consistency
  - The same methods must be systematically applied in every survey.
- Monitoring design is important
  - Scientific considerations
  - Resource limitation
  - Compromise data quality - simplicity

Monitoring methodology

The monitoring methodology will vary depending on the specific characteristics of the target taxa:

- Elements in common vs. specificities
- Demographic monitoring
  - Life cycle & propagation
    - Annuals
    - Perennials
    - Vegetatively-propagated plants
- Genetic monitoring
  - Breeding system & propagation
    - Autogamous
    - Allogamous
    - Vegetatively-propagated plants

Demographic & Genetic Monitoring

A proper diagnosis of the situation of the population sometimes requires an integrated view. Data on reproductive success, mortality, and vigour and growth can indirectly provide us with information on the genetic diversity within the population. Genetic diversity, genetic
differentiation and inbreeding will, in turn, affect population size.

**Ecological monitoring**

Ecological monitoring is important as ecosystem dynamics also influence target taxa populations. Ecological monitoring provides information on:

- Abiotic components
- Biotic components
  - Vegetation (competition or facilitation)
  - Mutualists (e.g. specific pollinators)
  - Herbivory
  - Pathogens

**Multiple taxon monitoring**

With regard to multiple taxon monitoring, design is very important.

**Models**

- Monitoring provides information about trends or patterns
- Why is this happening?
  - Hypothesis
  - Experimentation
  - Proposal and validation of models
- Use of models
  - Projections to the future
  - Sensitivity analysis
  - Testing management alternatives

**4.1.2 Reference Material for Working Group Discussions on Demographic and Genetic Monitoring**

**Monitoring**

**Monitoring objectives:**

- To gather baseline information on target population demographic and genetic trends as well as community trends and successional changes needed for the development of a management plan
- To detect any detrimental changes in target population characteristics that may require a reassessment of the management regime.

**Demographic monitoring:**

- **Demographic parameters**
  - Number of individuals
  - Size/stage/age structure
  - Reproductive success
  - Spatial structure
- **Sampling method**
  - Where to sample (random, systematic, stratified random)
  - How to sample (plot methods, intercept methods)
  - How much to sample (number and size of quadrats)
  - How often to sample
- **Data analysis**
  - Population Viability Analysis (PVA)
    - Population trends
    - Extinction risks
    - Critical demographic parameters
    - Sensitivity analyses
Management recommendations

Ecological monitoring:
- Determination of taxa to monitor
- Parameters
  - Density
  - Frequency
  - Cover
- Sampling method
  - Where to sample (random, systematic, stratified random)
  - How to sample (plot methods, intercept methods)
  - How much to sample (number and size of quadrats)
  - How often to sample
- Data analysis

Genetic monitoring:
- Genetic parameters
  - Morphological characters of agronomic importance
  - Type of molecular markers
  - Estimates of diversity
  - Spatial structure
- Sampling method
  - Where to sample (random, systematic, stratified random)
  - How to sample (plot methods, intercept methods)
  - How much to sample (number and size of quadrats)
  - How often to sample
- Data analysis
  - Diversity estimates
  - Cluster analysis
  - Ordination techniques
  - Spatial structure

Selected references on demographic monitoring of plant populations

Monitoring:

Population Viability Analysis and Modelling:
Akcakaya, HR. 2000. Viability analyses with habitat-based metapopulation models. Population...


meets population genetics. Trends in Ecology and Evolution, 8: 234-239
Thomas, C.D. 1990. What do real population dynamics tell us about minimum viable population sizes? Conservation Biology, 4: 324-327
4.2 Demographic Monitoring Methodologies

4.2.1 Presentation: Demographic Monitoring: Field Sampling And Data Treatment

Speaker: F. Xavier Picó, Centro Nacional de Biotecnología (CSIC), Madrid, Spain

Notes from powerpoint presentation:

Field sampling

In field sampling, demographic plots are established as sampling units and the data gathered can provide us with accurate estimates of life-cycle traits.

Demographic monitoring is determined by life-history type

Life histories:

1. Annuals with and without seed banks.
2. Short-lived (with and without seed banks) and long-lived pluricarpic perennials.
3. Monocarpic perennials.

Key life-cycle traits that require specific experiments:

1. Seed survival in the soil seed bank.
2. Recruitment rates (i.e., No. of recruits at t per flowering plant at t – 1).

Data treatment

1. Analysis of spatio-temporal variation in life-cycle traits.
2. Assessment of the dynamics of plant populations.

Analyses to examine the spatio-temporal variation in life-cycle traits

0. Identification of outliers and graphical representation of variability in life-cycle traits.

1. Continuous variables (e.g., fecundity).
   ANOVA, Simple main effects test.

2. Binomial variables (e.g., flowering probability).
   Logistic regression.

3. Demographic transitions (e.g., survivorship, growth, stasis).
   Log-linear analysis.

Matrix analyses

   Change in the number of individuals over time.
   Confidence intervals using probability density functions.

2. Sensitivity and elasticity analyses.
   Contributions of vital rates to population growth rate.

   Contributions from the variance (covariance) in vital rates to the variance in population growth rate.

Stochastic simulations


2. Bootstrapping and re-sampling methods.

*The more information we have the better our knowledge will be inbreeding depression, density dependence, spatial structure, etc.*

Final remark

Long-term demographic monitoring is needed to:

1. fully assess the demographic behaviour of plants,
2. validate demographic models, and
3. perform experiments with artificial populations.
4.2.2 Working Group Discussions

The workshop participants formed three parallel working groups to discuss and present issues on the demographic monitoring of annual, perennial and vegetatively-propagated CWR. One hour was allocated for each parallel group discussion. The findings of each group were then presented for discussion with the forum.

Overall objective:

Agree on population demographic monitoring methodologies appropriate for the in situ genetic conservation of European crop wild relatives.

Work description:

The working groups examined existing techniques for demographic monitoring as a starting point for the discussion and then debated and resolved how these might be adapted to the peculiarities of CWR conservation.
4.2.2.1 Group A: Demographic and ecological monitoring methodologies for annual crop wild relatives

**Facilitator:** Zdenek Stehno

**Reporter:** José Iriondo

**Discussion points:**

Parameters, sampling method and data analysis to be considered in the monitoring of annual CWR. Special needs and problems.

**Results**

This group decided that it was also important to include biennial CWR in the demographic monitoring methodology. Recommendations were made considering both annual and biennial plants.

1. **Important parameters**

   - Number of individuals (multi-species target taxa)
   - Seed production
   - Seed dispersal: high mobility (ruderals, colonisers,...)
   - Seed dormancy: permanent seedbanks
   - Stage structure:
     - Annuals: no structure/ seeds + adults
     - Biennials: (seeds) + vegetative plants + adults
   - Permanent seedbank
     - Seedbank
     - Simulation of seed bank with seeds from genebank

2. **Sampling method**

   - Where to sample:
     - Random: annuals
     - Fixed plots: biennials (marked individuals)
   - How often: once a year
     - Seasonal monitoring to see how the different seasons affect population survival

3. **Data analysis**

   - Critical demographic parameters:
     - Reproduction
       - No permanent seedbank
       - Outbreeders
   - Critical life stages
     - Dormant seeds in permanent seedbanks

4. **Management recommendations**

   - *Ex situ:*
     - Experimentation with artificial populations
     - (Reintroductions)
4.2.2.2 Group B: Demographic and ecological monitoring methodologies for perennial crop wild relatives

Facilitator: Wieslaw Podyma

Discussion points:

Parameters, sampling method and data analysis to be considered in the monitoring of perennial CWR. Special needs and problems.

Results

1. Objective:
   Establish a monitoring methodology for perennial CWR

2. Preconditions:
   Collecting existing, or obtaining new knowledge on the life history of the target taxon

3. Demographic parameters
   - Size classes
   - Number of individuals

4. Reproductive success
   - Potential reproductivity
   - Dispersal range
   - Recruitment
   - Seed source

5. Flow of individuals from outside

6. Difficulties
   - Irregularity of life cycle
   - Dormancy
   - Plant habit
   - Widely dispersed species e.g. fruit trees (*Malus, Pyrus*)

7. Methodologies
   - Taxon and site dependent
   - Must be consistent!!

8. Ecological monitoring
   - Phytosociological description, including species composition and abundance
   - Keystone species
   - Phenology
   - Associated pollinators and dispersers
   - Environmental conditions
   - Sampling method
   - Case by case basis: dependent on many variables, both plant biology and environmental
   - Historical management practices and site data
   - Frequency of monitoring: case dependent
4.2.2.3 Group C: Demographic and ecological monitoring methodologies for vegetatively-propagated crop wild relatives

Facilitator: Isaak Rashal

Reporter: Stelios Samaras

Discussion points:

Parameters, sampling method and data analysis to be considered in the monitoring of vegetatively-propagated CWR. Special needs and problems.

Results

1. Objective

To gather baseline information on target population demographic, ecological and genetic trends as well as community trends and successional changes needed for the development of a management plan

2. Demographic monitoring

Demographic parameters

Number of individuals - define what an individual is before monitoring

"Individuals" may not always be clear in vegetatively-propagated plants. It is essential to establish criteria for determining individuals in each case to obtain valid information in monitoring surveys. This definition will influence the analysis of:

- Size/stage/age structure
- Reproductive success
- Spatial structure

Genetic analysis may be more important in these taxa.

The area covered by the plant is also a way to monitor the population.

3. Sampling method

Where to sample (random and systematic)
How to sample (plot methods)

Sampling methods and frequency need to determined for each specific case

4. Consistency

Due to the nature of vegetatively-propagated CWR, monitoring criteria must be established for each taxa to ensure the quality of monitoring data.
4.3 Genetic Monitoring Methodologies

Session chairs: François Lefèvre and Martine Mitteau

4.3.1 Presentation: Genetic monitoring methodologies

Speaker: Maria Pohjamo, University of Helsinki, Finland

The main goals of conservation genetics are to prevent the loss of genetic diversity so that the ability to evolve in response to environmental change remains (correlation between genetic diversity and population size) and to prevent the deleterious effects of inbreeding on reproduction and survival (inbreeding depression).

Additional goals include to prevent fragmentation of populations and reduction in gene flow, to prevent genetic drift overriding natural selection as the main evolutionary process, to resolve taxonomic uncertainties and to prevent deleterious effects on fitness possibly occurring as a result of outcrossing (outbreeding depression).

The level of genetic diversity can be explained by factors such as historical and current population sizes, population bottlenecks, breeding system, natural selection, different mutation rates and immigration and emigration among populations.

Genetic diversity can become threatened by the extinction of species, populations and subspecies, the extinction of alleles due to drift or directional selection and inbreeding reducing heterozygosity (alleles maintained but allocated to homozygotes → possibly inbreeding depression due to the homozygosity of deleterious recessive alleles).

Genetic diversity can be analysed through morphological traits which allow the interpretation of relationships between the genotype and environmental conditions or by using molecular marker techniques. These techniques allow direct investigations of variation at the DNA level, thereby excluding all environmental influences.

Measures of inbreeding

- The inbreeding coefficient (F) of an individual refers to how closely related its parents are
- In the case of selfing, F=0.5 in the offspring
- Inbreeding accumulates in isolated populations, and complete inbreeding can eventually be reached with repeated inbred matings (an F=0.999 reached after 10 generations of self-fertilization)
- The average inbreeding coefficient of all individuals in a population: Average F increases at a rate of 1/(2N) per generation in a randomly breeding diploid population of size N
- Levels of inbreeding can be determined from pedigrees or inferred from heterozygosities for genetic markers

Is the taxon suffering from inbreeding depression?

- Usually less of an issue in selfing species (about 40% of flowering plants can self and 20% may do so commonly)
- Typically higher in gymnosperms than angiosperms (could be related to a higher level of polyploidy in angiosperms)
- Direct evidence obtained (lowered fertility & viability?)
Inbreeding depression may be inferred from its correlation with reduction in genetic variation, assessed by genetic markers (e.g., microsatellites have the power to detect reductions in heterozygosity and allelic diversity)

Slow inbreeding generally causes less inbreeding depression than an equivalent amount of rapid inbreeding

Loss of genetic diversity and loss of self-incompatibility alleles

About half of all flowering plant species have self-incompatibility systems that reduce or prevent selfing

Self-incompatibility regulated by one or more loci, presumed to have evolved to avoid inbreeding depression

Small population → loss of diversity & self-incompatibility alleles → inbreeding → lowered fitness

A potential problem in threatened self-incompatible plants

Characterizing genetic diversity

Genotype frequencies, allele frequencies

Expected heterozygosity:
   a) single locus $h = 1 - (p_{12} + p_{22} + ... + p_{n2})$,
   b) mean across loci ($H$)

Hardy-Weinberg equilibrium: statistical testing to assess agreement between observed and expected numbers of genotypes; allows detection of inbreeding, population fragmentation, migration and selection

Linkage disequilibrium: non-random associations of alleles among loci

Diversity indices, e.g., expected heterozygosity, allelic diversity ($A =$ the number of alleles averaged across loci), the proportion of polymorphic loci ($P$), nucleotide diversity

Genetic distances between populations: based on allele or genotype frequencies, or DNA sequence differences

Analysis of molecular variance (AMOVA): the partitioning of genetic variation into within population and among populations components

- in inbred populations often a greater differentiation among populations than in outcrossing populations

- in fragmented populations often a greater differentiation among populations than in more continuous populations

Linkage disequilibrium (D)

This is measured as the deviation of haplotype frequencies from linkage equilibrium. It is common in threatened species due to their small population sizes and may be caused by population bottlenecks. Functionally important gene clusters exhibiting linkage disequilibrium are important to the persistence of threatened species.

Measuring inbreeding depression

A general measure of inbreeding depression ($\sigma$) is the proportionate decline in the mean due to a given amount of inbreeding:

$$\sigma = 1 - (\text{fitness of inbred offspring}/\text{fitness of outbred offspring})$$
The formula itself does not specify the level of inbreeding. Since many plants can be selfed, the usual estimate of inbreeding depression is obtained by comparing selfed and outcrossed progeny. This provides the impact of inbreeding due to an inbreeding coefficient of 50%.

**Recovering from inbreeding depression**

Recovery can occur by outcrossing the inbred population to another unrelated (outbred or inbred) population (through immigration). Fitness may recover as a result of natural selection removing deleterious alleles.

**Solving genetic problems**

Different methods can be used to attempt to solve genetic problems:

- Increase in population size (especially the effective population size Ne, averages ~10% of the census size)
- Establishment of populations in several locations (to minimize the risk of catastrophes)
- Maximize the reproductive rate by improving environment
- Genetic management of inbred/small populations, introduction of migrants from
  - outbred populations
  - inbred but genetically unrelated populations
  - from inter-fertile taxa (requires careful consideration, a risk of outbreeding depression)

**Genetic management for introduction**

Captive populations may provide a source of individuals to reintroduce and supplement wild populations of threatened taxa. However, the success of reintroduction is jeopardized by genetic deterioration in captivity due to inbreeding depression, loss of genetic variation, and genetic adaptation to captivity (leading to reduced adaptation to the wild environment). Therefore, individuals for reintroduction should have maximum genetic diversity and maximum reproduction fitness in the wild environment.

**Considerations in genetic monitoring**

- Is population size small or decreasing?
- Is the level of genetic diversity low or decreasing?
- What is the level and history of inbreeding, the amount of inbreeding depression?
- Is there population fragmentation (measured by AMOVA, partitioning of variation within and among populations) and what is its impact on genetic diversity and inbreeding?

**How large should a population be?**

The population should be large enough to avoid inbreeding depression and to retain the ability to evolve in response to changes in the environment.

Estimated effective population sizes (Ne, census size usually 10x) needed
- to retain reproductive fitness: Ne=50\(^1\)
- to retain evolutionary potential: Ne=500-5000\(^2\)

\(^1\) Franklin 1980, Soulé 1980
Measuring genetic diversity

- Continuously varying (quantitative) characters (genetic and environmental effects, e.g., seed set)

- Morphology (qualitative or quantitative)

- Chromosomes

- Proteins - Protein assays (enzyme electrophoresis)
  - Used to distinguish different forms of proteins and to measure the level of genetic variation for a particular protein locus
  - Co-dominant inheritance
  - About 30% of DNA base changes result in charge changes → electrophoresis underestimates the extent of genetic diversity
  - Coding genomic areas examined, not as much variation as in noncoding areas

- DNA (nuclear, chloroplast and mitochondrial)
  - PCR-based methods
    1) Sequence-arbitrary methods
       - Random amplified polymorphic DNAs (RAPDs)
       - Inter simple sequence repeats (ISSR)
       - Amplified fragment length polymorphisms (AFLP)

    2) Methods requiring *a priori* sequence information
       - Simple sequence repeats (SSRs)/short tandem repeats (STRs)/microsatellites
       - Sequence characterized amplified regions (SCARs)
       - Single nucleotide polymorphisms (SNPs)

  - Random amplified polymorphic DNAs (RAPDs)
  - Inter simple sequence repeats (ISSR)
  - Amplified fragment length polymorphisms (AFLP)
  - Sequence-dependent, PCR-based methods
  - Simple sequence repeats (SSRs) = short tandem repeats (STRs) = microsatellites
  - SSRs
  - Sequence characterized amplified regions (SCARs)
  - Single nucleotide polymorphisms (SNPs)

- Markers for ecologically important traits
  - Many studies concerning diversity and plant genetic resources have been based on neutral molecular markers.
  - However, studies of genetic diversity could benefit from targeting variation in such genes that exhibit ecologically relevant variation.
  - Procedure: to assess which traits matter, identify the genes that potentially affect such traits, and develop markers within, or flanking these genes → gene-targeted, multilocus profiles for the management of genetic resources.
4.3.2 Working Group Discussions

The workshop participants formed two parallel working groups to discuss and present issues on the genetic monitoring of autogamous and allogamous CWR. One hour was allocated for each parallel group discussion. The findings of each group were presented for discussion with the Forum at the beginning of Day 3.

Overall objective:

Agree on population genetic monitoring methodologies appropriate for the in situ genetic conservation of European crop wild relatives.

Work description:

The working groups examined existing techniques for genetic monitoring as a starting point for the discussion and then debated and resolved how these might be adapted to the peculiarities of CWR conservation.
4.3.2.1 Group A: Genetic monitoring methodologies for autogamous crop wild relatives

Facilitator: Brian Ford-Lloyd

Discussion Points:

Genetic parameters, sampling methods and data analysis to be considered in the monitoring of autogamous CWR.

Results

1. Target species

This group first raised the question of how many species need genetic monitoring. Approximately 21,000 CWR species have been identified in the PGR Forum project.

Which species need genetic monitoring?
Which target species should be conserved in reserves?

2. Genetic parameters

- Morphological/agronomic characters
  - Evaluate in-population where possible for:
    - Disease resistance
    - Abiotic factors
    - Morphological markers that are markers for other important traits
    - Intraspecific taxonomic markers (for genetic/taxonomic structure)
    - Possibly use information at the DNA sequence level to allow estimation of genetic diversity in important genes (need to have available information from genomic studies)

- Type of molecular markers
  - SSRs should be the choice of marker
    - (there will be considerable commitment needed to undertake genetic monitoring – use of sub-optimal marker systems will therefore be unacceptable – a co-dominant marker is needed)
  - DNA sequencing (possibly including SNPs) for specific purposes (variation in useful genes)

- Spatial structure
  - Needs to take account of taxonomic structure
  - Random sampling within target populations
  - Ecogeographically stratified sampling amongst populations

3. Sampling method

- Where and how?
  - Sampling method is governed by or directly related to spatial structure

- How much?
  - 50 plants per population to be sampled
  - Number of populations?
    - At least 10 – but could be many more

- How often to sample?
  - Once unless number of plants (N or \(N_e\)) changes substantially (refer to demographic monitoring)
4. Data analysis

- Diversity estimates?
  - Shannon’s, Shannon-Weaver (for morphological)
  - Nei’s (expected heterozygosity)

- Population genetic estimators?
  - $F_{st}/R_{st}$ for population differentiation and isolation
  - $F_{is}$ for inbreeding coefficient
  - Hardy-Weinberg
  - Linkage disequilibrium

- Cluster analysis and ordination?
  - Too late – needed for locating reserves!

5. Further needs - general

- SSRs for more species
  - How many species in CWR list have SSR markers available?
- Documentation system for Genetic Monitoring
- How to identify autogamous versus allogamous species?
  - autogamous – allogamous
  - partly autogamous – partly allogamous

6. Further steps needed to prepare guidelines

- Expansion of discussion and development of guidelines in WS5
- How to identify CWR species in reserves that need genetic monitoring?
  - This should be discussed in detail in WS5
4.3.2.2  Group B: Genetic monitoring methodologies for allogamous crop wild relatives

Facilitator: Sónia Dias

Discussion Points:

Genetic parameters, sampling methods and data analysis to be considered in the monitoring of allogamous CWR.

Results

1. Risk of loss of diversity
   - Measuring loss of diversity
     - Morphological characters evolution
     - Molecular tools for evolution
   - Loss of genetic diversity within a population leads to decreasing viability which may result in extinction.
   - Loss of interesting variation within populations

2. Genetic characterisation and genetic drift

For the study of the evolution of genetic drift, we need to use genetic diversity indices (indicators of overall diversity) or tools to monitor specific useful traits over time.

   - The use of molecular markers can provide data on:
     1. Diversity within and between populations
     2. Gene processes
     3. Fitness (related to specific traits)
        i. Demographic studies
        ii. Related to fecundity
     4. Differentiate between genetic and environmental stochasticity.
     5. Knowledge of heritability of molecular characters – use it as surrogate of genetic diversity
     6. Use list of descriptors as a base for CWR characterisation

3. Ex situ / in situ conservation

   - Link - ex situ and in situ conservation are closely linked
   - Coordination - conservation programmes should be coordinated to maximise efforts and resources
   - Ex situ bottleneck in characterisation/evaluation, useful for in situ conservation actions

4. Spatial structure (key point)

   - Distribution of individuals (further inbreeding)
   - Spatial structure, diversity of morphological characters
   - Genetic neighbourhood
   - Implication in restoration

5. Number of sample/periodicity

   - Annual crop wild relatives – every year
   - Perennial crop wild relatives – as often (generation time)
   - A greater number of samples is required for allogamous species
   - Sampling should be more frequent for allogamous species than for autogamous species
6. How to sample

- Allogamous species
  - Random / stratified
- Vegetatively propagated species
  - If knowledge is available – random
  - If knowledge is not available – random / stratified

RECOMMENDATIONS

1. Each genetic reserve should have a back-up ex situ collection

2. In situ / ex situ characterisation

  - To promote use

3. Carry out in-depth studies on CWR

  - Useful genetic information

4. Reinforce links with ex situ conservation

  - Documentation
  - Improve ecogeographic surveying

5. Development of primers

  - Sources
    - Genebanks
    - Breeding institutes
    - Universities
    - CG centres

  - At the National level – set priorities for developing primers
  - Transferability of primers is not easy

6. Policy issues, germplasm exchange required

  - Take into consideration international agreements, conventions, treaties,…
4.4 General Discussion

In the general discussion following the group presentations the following issues were discussed:

1. **Genetic characterisation.** Who will carry out the characterisation? The genetic reserve will not have the facilities. Genetic characterisation would have to be done by public institutions or private companies.

2. **Transfer of material between countries.** Bilateral agreements may be needed for sending samples of material for genetic characterisation.

3. **Basic vs. detailed monitoring.** The most limiting factor regarding genetic monitoring is the issue of cost. Molecular techniques cannot be applied on a regular basis, as they are still quite expensive. Knowledge on reproductive biology could provide some basic information on genetics. For example, IPGRI has a database on 7000 species and are presently working on the reproductive biology of these species. This information could be helpful in the determination of whether a species is autogamous or allogamous. Molecular techniques could be used in specific cases for more detailed monitoring.
5. SPECIES AND HABITAT RECOVERY TECHNIQUES. BACK-UP EX SITU STRATEGIES.

Chair: Stelios Samaras

5.1 Presentation: "From ex situ to in situ conservation: an assessment of the micro-reserve initiative"

Speaker: Emilio Laguna, Servicio de Conservación de la Biodiversidad, Generalitat Valenciana, Valencia, Spain

Emilio Laguna presented the Valencian policy on plant conservation which the regional government (Generalitat Valenciana) is developing based on ‘multispecific’ measures (those which simultaneously benefit a large number of species). The most remarkable activities are:

- *In situ* conservation through the plant micro-reserve network.
- *Ex situ* conservation through the regional germplasm bank (Botanical Garden of the University of Valencia) and the establishment of micropropagation protocols for the most endangered species (Valencian Institute for Agronomic Research)
- Establishment of a catalogue of *ex situ* and *in situ* protocols for germination, culture and plantation of target species (endemic, rare and dominant taxa for all types of natural habitats)
- Network of experimental plots for the monitoring of restoration practices – partially overlapping with the micro-reserve network
- New crops for sustainable development: Domestication of endemic species useful as scented plants, medicinal crops, etc.

These activities are all inter-dependent and as such are not considered isolated initiatives.

**Plant micro-reserves network: Projects LIFE93 NAT/E/000766 (1994-99) and LIFE99 NAT/E/006417**

In 1994 the Regional Wildlife Service of the Valencian Community created a new statutory protection figure for plant conservation named ‘plant micro-reserve’. The objectives were twofold:

1) Scientific monitoring of target species — ca. 600 taxa, 350 of which are Spanish endemics — and vegetation types to establish long-term trends.

2) Development of experiences of active conservation: ecological restoration, population reinforcements, etc.

The micro-reserves are mainly focused on the protection of microhabitats, sites which concentrate a significant amount of target species in a small surface, i.e. Mediterranean temporary ponds, small islands, petrifying springs, coastal cliffs, relict forests, etc. This statutory protection figure was first established in public land. Subsequently, it included private grounds where landowners showed a patent interest in plant conservation.

Traditional activities (e.g. livestock grazing) compatible with plant conservation are maintained, so as to conserve rare or endemic species dependent on open vegetation (i.e. heliophytes that rely on vegetation clearing). Currently, 230 plant micro-reserves have been officially declared. They comprise a surface of 1,440 ha and include examples of natural and semi-natural habitats. Over 85% of the endemic species are represented in at least one population within micro-reserves.

The official declaration includes a management plan, which is published in the official gazette (together with the declaration of the protected site itself). The management plan of all micro-reserves includes at least 1 or more active conservation measures. For instance, the Regional Wildlife Service transfers seeds of the target species from the micro-reserves to the germplasm bank of the Botanical Garden of Valencia.
Experiences of habitat restoration and/or management of endangered species have been carried out in more than 30% of the micro-reserves during the 1999-2003 period in the framework of the LIFE project NAT/E/006417 ‘Conservation of priority habitats of the Valencian Community’.

**Micro-reserves and crop relatives**

Most micro-reserves shelter relatives of crop species, including neglected or abandoned crops such as:

- Remnants of old plantations or naturalized populations of tree crops, e.g. *Ceratonia siliqua*, *Prunus avium*, *Juglans regia*, etc.
- Wild relatives of formerly cultivated plants, e.g. *Crataegus gr. monogyna* (relative of *C. azarollus*)
- Wild relatives of currently cultivated trees, e.g. the only regional population of *Malus sylvestris* (micro-reserve ‘Barranco de la Pegunta, SCI Penyagolosa’)
- Wild relatives –often considered as ‘weeds’- of herbaceous crops, e.g., *Rapistrum rugosum*, *Beta maritima*, *B. patellaris*, *Atriplex patula*, *Malva* sp. pl., *Apium nodiflorum*, *Daucus* sp. pl., *Foeniculum vulgare* subsp. *piperitum*, *Pimpinella* sp. pl., etc.
- Wild populations of species formerly cultivated as medicinal plants – mainly Eurosiberian relict plants-, such as *Anethum graveolens*, *Conium maculatum*, *Ferula communis* subsp. *catalaunica*, *Laserpitium* sp. pl., *Smyrnium olusatrum*, etc.

**Micro-reserves: the meeting point for in situ and ex situ actions**

Micro-reserves bring together *in situ* and *ex situ* conservation actions. For instance, micro-reserves serve as:

- Preferred source of germplasm for seedbanks.
- Sites where reinforcement or re-introduction of endangered species are carried out. Most often plant material for reinforcements is obtained from propagules collected within micro-reserves, stored in the germplasm bank of BGs and reared in research centres or official nurseries.
- Places where practical applications of restoration ecology principles can be carried out.

**Quantifiable results of the LIFE99 NAT/E/006417 project (1999-2003)**

- 226 plots (over 966 ha) of 17 priority habitats (Directive 92/43/CEE annex I) managed
- 90,400 plantlets (168 species, 174 plots, 16 habitats) and 39,092 pre-treated seeds (20 spp., 17 plots, 5 habitats) planted; 7,611 plants (47 spp., 49 plots, 8 habitats) translocated from endangered to neighbouring safe sites for conservation.
- Eradication experiences of 6 alien invasive species in 85 ha (17 plots); vegetation clearing of 119 ha (34 plots); tree removal or the lowering tree density in 19 plots.
- 152 plots signalized, fencing experiences in 90 plots (5,540 posts, 15,1 km of rope), 17 explanatory boards.
Case studies

- Turning abandoned paddy fields into high-biodiversity lagoons
- Plant conservation in the Columbretes islands: the case of *Medicago citrina*

In addition, habitat restoration has been reinforced by raising public awareness through campaigns and educational activities, with the intervention of NGOs and the Botanical Garden of the University of Valencia.
5.2 Working Group Discussions

The workshop participants formed two parallel working groups to discuss and present issues on species and habitat recovery techniques, and back-up ex situ strategies. One hour was allocated for each parallel group discussion, after which, each group gave a presentation of their findings for discussion with the forum.

Overall objectives

- To identify the different species and habitat recovery techniques that are used in conservation and discuss whether they may be useful in the conservation of CWR in genetic reserves.
- To discuss relevant data sources with detailed information.

Discussion groups

1. Species recovery techniques. Back-up ex situ strategies
2. Habitat recovery techniques

Reference Material

Species and habitat recovery techniques. Back-up ex situ strategies.

Species recovery techniques:
- **Reinforcement**: Artificial establishment of new individuals in a natural population to increase the size of the population and make it more self-sustainable.
- **Translocation**: Moving a natural population from its natural location to a new site.
- **Re-introduction**: Establishment of a population in a historical location where the taxon is known to have occurred in the past.

Habitat recovery techniques:
- Controlled burning
- Fire protection
- Alteration of natural water regime
- Artificial perturbation (plowing, mowing, etc.)
- Fencing to prevent damage by stock, vehicles, etc.
- Elimination of invasive species (rabbit control, weed control, ...)
- Plague and disease prevention
- Supplementary planting or re-planting

Back-up ex situ strategies:
- Black-box collection in the nearest seedbank / national reference seedbank with a representative sample of the genetic diversity present at the genetic reserve.

Species recovery actions


5.2.1 Group A: Species recovery techniques. Back-up *ex situ* strategies.

**Facilitator:** Åsmund Asdal

**Discussion points:**

- Back-up *ex situ* collection for the genetic reserve.
- Identify the different species recovery techniques that are used in conservation and discuss whether they may be useful in the conservation of CWR in genetic reserves, including:
  - Reinforcements
  - Translocations
  - Re-introductions
- Relevant data sources with detailed information

**Results:**

1. **Species recovery techniques.**
   - Reinforcement: Establishment of new individuals into natural population
   - Translocation: Moving natural population to a new site
   - Re-introduction: Establishment in a historical site
2. **Objectives of a back-up collection**
   - Collection for reinforcement
     - Sampling intervals depend on seed physiology (storage behaviour of orthodox seeds, longevity of seeds of recalcitrant species) and reproduction mode (clone). Old samples could be replaced by new ones (black box principle)
   - Baseline collection for research
   - Careful documentation
   - For use, then kept as active *ex situ* collection. Samples taken from Genetic Reserves should be maintained using higher genebank standards i.e. prevent genetic bottleneck, use pair crosses (partial diallel).
3. **Sampling**
   - Collection of seeds or grafts should not add threat to the population. The natural reproductive capacity at the natural site must be ensured further.
4. **Long-term storage**
   - Back-up samples may be stored for a long time. Develop a memorandum of understanding signed by the genebank / botanic garden. Clear agreements with respect to the right and duties.
5. **Reinforcement / Re-introduction**

   Remove detrimental factors before reinforcement / re-introduction

   Compile existing guidelines and adopt them to the specific needs of a species. Develop cultivation methods.

   If possible maintain genetic integrity of population at the natural site (reinforcement). However, local material may not always be the solution.

   Manage population until the reproduction is self-sustainable. Observe trends by monitoring.

   Initiate reinforcement / re-introduction in several countries if required. Take all ecogeographic regions relevant to the species.

   Document all steps to enable data analysis

6. **Develop a priority list of CWR for species recovery plans**
5.2.2 Group B: Habitat Recovery Techniques

Facilitator: Juozas Labokas

Discussion Points:

- Identify the different habitat recovery techniques that are used in conservation and discuss whether they may be useful in the conservation of CWR in genetic reserves
  - Controlled fires
  - Fire prevention
  - Water regime
  - Perturbation
  - Enhancement of pollinators
  - Selective elimination of invasive species
  - Other
- Relevant data sources with detailed information

Results:

1. Habitat Recovery Techniques: Clarification
   - Two Types of Habitat Recovery Techniques:
     A. Preventive (e.g. Disease and Plague Prevention)
     B. Interventional (e.g. Supplementary Planting)

     Note: Ecosystem restoration should also be considered.

2. Standards and Classification
   - Use existing standards (e.g. EU ecosystem and habitat typology)

3. Habitat Recovery Techniques: Major Problems
   - Lack of management manuals
   - Disperse information on management techniques
   - Some available information is highly specific (e.g. island restoration)

     • Recommendation 1:
       - Make an inventory or list of references of habitat management techniques

     • Recommendation 1a:
       - Take existing bibliography of island habitat recovery techniques by Shelagh Kell as starting point

4. Habitat Recovery Techniques: General or (Species) Specific?
   - General techniques: translocations, alien eradication, some wetland techniques are general.
   - Specific techniques
5. Comments on the list of techniques given as reference material

- **Not exhaustive:** Additional techniques include soil removal, wild harvesting, environmental pollution clean-up, traditional management, introduction of pollinators, grazers (wild harvesting and grazing would be allowed if already established and monitored).

- **Wording:** ‘elimination’ of invasive species should be ‘control’. Should all alien/invasive species be controlled?

6. Habitat Recovery Techniques More Data Sources:

- EUROSITE coordinates Natura 2000 and has action plans and manuals at [www.eurosite.org](http://www.eurosite.org)
- EUROPARC (European Federation of natural parks (only large parks))
- European Centre for Nature Conservation
- IUCN/SSC Invasive Species Specialist Group
- Society for Ecological Restoration (USA)
- Dr. Emilio Laguna will provide a list of key contact persons


- Species recovery is more specific whereas habitat recovery is more open-ended. Each habitat requires specific techniques – no protocol can be produced.

- Position 1: No guidelines should be produced by PGR Forum. This is too much of a specialists’ task; a list of references should be produced instead.

- Position 2: References should be hierarchical, forming part of the general methodology.

- Outcome: Produce **metaguidelines**: guidelines to direct towards more specific guidelines
5.3 General Discussion

In the general discussion following the group presentations PGR Forum participants raised additional issues that should be kept in mind when preparing guidelines for species and habitat recovery techniques and back-up *ex situ* strategies:

- Hand pollination and other techniques could be applied in recovery plans.
- Back-up *ex situ* collections should be kept for both threatened and non-threatened CWR, but different procedures would need to be followed.
- Non-threatened populations could have seeds stored in the genebank with no active management, whereas threatened species should be actively managed with propagation, hand pollination, etc.
- Agreements may be needed between the genebank and the genetic reserve.
- The guidelines should be structured in a hierarchy of questions to know which procedure should be followed.
6. FINAL REMARKS AND FURTHER STEPS

Session chair: Daniela Benedikova

It was resolved that the further development of the population management methodology should be carried out in working groups.

Working groups

Four working groups were established:

1. Identification of milestones for *in situ* conservation. Genetic reserve location and design.
2. Minimum contents and basic structure of a management plan. Minimum baseline information for the development of a management plan.
3. Population monitoring methodologies

PGR Forum participants signed up for the different working groups. The members of each working group can be found in Appendix III found at the end of this document.

Working Procedure

1. Each working group elaborates a draft text including more detail and improves it through circulation among its members.
2. The different parts of the draft are put together and edited into a single text.
3. The draft is distributed to all PGR Forum members and it is discussed on-line.
5. The text is sent for publication.

Publication

The following resolutions were agreed upon with regard to the publication of the population management methodology:

1. **Workshop 4 Report.** The results of Workshop 4 will be presented in the Workshop Report and will be available on the PGR Forum web site.
2. **Population management methodology.** It was agreed to contact IPGRI for collaboration in financing the publication of the population management methodology.
3. **Book.** A more detailed version could be developed for publication by an independent publisher such as Cambridge University Press.
7. RED LIST TRAINING WORKSHOP

Organisers: Craig Hilton-Taylor and Caroline Pollock

This session was devoted to Red List training in preparation for Workshop 2: Threat and Conservation Assessment. The aim of the training workshop was to familiarise PGR Forum participants with the IUCN Red List Programme and how to apply the IUCN Red List Categories and Criteria to the conservation assessment of crop wild relatives.

Presentations were given on:

- Overview of the IUCN Red List Programme
- IUCN Red List Categories and Criteria
- Regional Application Guidelines

After the presentations, examples of how to apply the system were presented through case studies on Ancistrocladus robertsoniorum, Ficus faulkneriana and Ziziphus robertsoniana.

The Forum then broke into working groups to carry out case studies of some crop wild relatives such as Lupinus angustifolius and Galanthus koenanianus using data from the trial datasets compiled after Workshop 1. Groups were allotted one hour to carry out the case studies. The Working Groups then presented their Red Listing assessments to the Forum and the obtained results were discussed.

After the Red List Training Workshop, PGR Forum participants had the necessary information to carry out assessments of some crop wild relatives in preparation for Workshop 2.
APPENDIX I. Final Agenda

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<td><strong>09:00 Opening Session</strong></td>
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<td>Welcome / Press Conference</td>
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<tr>
<td>- Welcome from Menorca: Consell Insular, 10 min.</td>
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<td>- Summary of PGR Forum objectives: Nigel Maxted, 10 min.</td>
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<td>Introduction to Workshop 4: José Iriondo, 10 min.</td>
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<td>WP6 Update: Shelagh Kell, Ehsan Dulloo, 10 min.</td>
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<td>WP1 Progress Report: Shelagh Kell, Jay Moore, Maria Scholten, 30 min.</td>
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<td><strong>11:00 WP3 Progress Report</strong> Sabine Roscher, 15 min.</td>
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<td><strong>11:15</strong></td>
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<tr>
<td><strong>Discussion and Further Steps</strong></td>
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<tr>
<td><strong>12:00</strong> &quot;Genetic reserve conservation of crop wild relatives: an overview&quot; Nigel Maxted, 30 min.</td>
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<tr>
<td><strong>12:30 Lunch</strong></td>
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<tr>
<td><strong>Session chair:</strong> Tamara Smekalova</td>
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<tr>
<td><strong>1. Population management methodologies for the in situ genetic conservation of CWR</strong></td>
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<tr>
<td><strong>14:00 Introduction</strong> Ehsan Dulloo, 30 min.</td>
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<tr>
<td><strong>14:30</strong> &quot;Strategies and methodologies for the in situ genetic conservation of <em>Populus nigra</em>, an example of CWR in forestry&quot; François Lefèvre, 30 min.</td>
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<tr>
<td><strong>15:00</strong> &quot;Rationale for <em>in situ</em> management of wild <em>Beta</em> species&quot; Lothar Frese, 30 min.</td>
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<td><strong>15:30 Coffee Break</strong></td>
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<td><strong>Session chair:</strong> Shelagh Kell</td>
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<tr>
<td><strong>16:00 Group discussions 1: Population management methodologies</strong></td>
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<tr>
<td>Parallel sessions:</td>
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<tr>
<td>- Group A: Genetic Reserve Location and Design. Integration of PGR Conservation in Protected Area Management.</td>
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<tr>
<td><strong>17:30 Summing up of Day 1 and outline of Day 2</strong></td>
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</tbody>
</table>
Day 3 | Friday, April 23
---|---
Session chair: Martine Mitteau

09:00 | Group presentations 2.2
- Group A: autogamous crop wild relatives 15 min.
- Group B: allogamous crop wild relatives 15 min.

09:30 | General discussion 2.2

Session chair: Stelios Samaras

3. Species and habitat recovery techniques. Back-up *ex situ* strategies

10:00 | "From *ex situ* to *in situ* conservation: an assessment of the microreserve initiative" Emilio Laguna, 30 min.

10:30 | Coffee Break

11:00 | Group discussions 3: Species and habitat recovery techniques. Back-up *ex situ* strategies.

Parallel sessions:
- Group B: Habitat recovery techniques.

12:00 | Group presentations 3
- Group A 7 min.
- Group B 7 min.

12:15 | General discussion 3

12:30 | Summing up of Day 3 and outline of Day 4

12:45 | Excursion Arrangements Lori De Hond

13:00 | Lunch

14:30 | Excursion

Day 4 | Saturday, April 24
---|---
Session chair: Daniela Benedikova

09:00 | Workshop 4 final remarks and further steps

<table>
<thead>
<tr>
<th>Red List Training Workshop</th>
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| 10:00 | IUCN Red List Categories and Criteria
| 10:30 | Coffee Break
| 11:00 | IUCN Red List Categories and Criteria
| 13:00 | Lunch
| 14:30 | Regional Application Guidelines
| 15:00 | Examples of how to apply the system
| 15:30 | Working Groups – Case studies
| 16:30 | Coffee Break
| 17:30 | Group presentations
<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>18:30</td>
<td>Farewell</td>
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<td></td>
<td>- Group presentations and discussion</td>
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</tbody>
</table>
APPENDIX II. PGR Forum Participants

(See 2.2.1 for list of Workshop 4 participants.)

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APPENDIX III. Working Groups for the Development of Population Management Methodologies

Working Group 1: Identification of milestones for *in situ* conservation. Genetic reserve location and design.

1. Eliseu Bettencourt
2. Sônia Dias
3. Ehsan Dulloo - leader
4. Lothar Frese
5. José Iriondo
6. Shelagh Kell
7. Juozas Labokas - leader
8. Emilio Laguna
9. François Lefèvre
10. Nigel Maxted
11. Martine Mitteau
12. Sabine Roscher
13. Stelios Samaras
14. Tamara Smekalova
15. Silvia Strajeru
16. André Toussaint

Working Group 2: Minimum contents and basic structure of a management plan. Minimum baseline information for the development of a management plan.

1. Asmund Asdal
2. Ehsan Dulloo
3. José Iriondo
4. Shelagh Kell
5. Nigel Maxted - leader
6. Wieslaw Podyma


1. Ehsan Dulloo
2. Brian Ford-Lloyd - leader
3. José Iriondo - leader
4. Shelagh Kell
5. Helena Korpelainen
6. François Lefèvre
7. Nigel Maxted
8. Maria Pohjamo
9. Isaac Rashal

1. Damiano Avanzato
2. Daniela Benedikova
3. Eliseu Bettencourt
4. Sónia Dias
5. Ehsan Dullloo
6. Dag Terje Endresen
7. Craig Hilton-Taylor
8. José Iriondo
9. Shelagh Kell - leader
10. Kell Kristiansen
11. Juozas Labokas
12. Emilio Laguna
13. François Lefèvre
14. Nigel Maxted
15. Wieslaw Podyma - leader
16. Stelios Samaras
17. Zdenek Stehno
18. Silvia Strajeru