WORKSHOP 5

Genetic Erosion and Pollution Assessment Methodologies

Terceira Island
Autonomous Region of the Azores
Portugal
8-11 September 2004
Workshop 5 Organisers

**Workpackage 5 Coordinators**
Sónia Dias  
Brian Ford-Lloyd

**Workshop Assistant**
Eliseu Bettencourt

**Project Coordinator**
Nigel Maxted

**Project Officer**
Shelagh Kell

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**Workshop 5 Objectives**

**Objectives relating to Workpackage 5**
- Agree on genetic erosion and pollution assessment methodologies for European wild crop relatives

**Objectives relating to Workpackage 1, 3, 4**
- Progress Reports

**Objectives relating to Workpackage 2 and 6**
- Updates on scope, plans and arrangements

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**Workshop 5 Participants**

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<tr>
<th>Dr. André Toussaint</th>
<th>Dr. Helena Korpelainen</th>
<th>Dr. Martine Mitteau</th>
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<tr>
<td>Mr. António Flor</td>
<td>Dr. Helmut Knuepffer</td>
<td>Dr. Michael T. Abberton</td>
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<td>Dr. Åsmund Asdal</td>
<td>Prof. Isaac Rashal</td>
<td>Dr. Mike Wilkinson</td>
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<td>Dr. Brian Ford-Lloyd</td>
<td>Mr. Jay Moore</td>
<td>Dr. Nigel Maxted</td>
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<td>Ms. Caroline Pollock</td>
<td>Dr. Jozef Turok</td>
<td>Ms. Sabine Roscher</td>
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<td>Mr. Dag Terje Endresen</td>
<td>Dr. Juozas Labokas</td>
<td>Ms. Shelagh Kell</td>
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<td>Mr. Damiano Avanzato</td>
<td>Dr. Kell Kristiansen</td>
<td>Ds. Silvia Strajeru</td>
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<td>Dr. Daniela Benedikova</td>
<td>Dr. László Holly</td>
<td>Ms. Sónia Dias</td>
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<td>Dr. Elena Torres</td>
<td>Ms. Lori De Hond</td>
<td>Dr. Stefano Diulgheroff</td>
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<td>Mr. Eliseu Bettencourt</td>
<td>Dr. Lothar Frese</td>
<td>Dr. Tamara Smekalova</td>
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<td>Dr. François Lefèvre</td>
<td>Dr. Malgorzata Cyrlker</td>
<td>Dr. Vojtech Holubec</td>
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<td>Dr. Hans den Nijs</td>
<td>Ms. Maria Scholten</td>
<td>Dr. Zdenek Stehno</td>
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ACKNOWLEDGMENT

The Organisation of the Workshop 5 “Genetic erosion and pollution assessment methodologies” is grateful to the support given by:

- Secretaria Regional de Agricultura e Pescas
  - Direcção Regional de Desenvolvimento Agrário
  - Serviço de Desenvolvimento Agrário da Terceira

- Secretaria Regional de Educação e Cultura

- Secretaria Regional do Ambiente
  - Direcção Regional do Ambiente
  - Direcção de Serviços de Promoção Ambiental

- Secretaria Regional de Turismo
  - Delegação de Turismo da Ilha Terceira

- Câmara Municipal de Angra do Heroísmo
  - Divisão Cultura e Promoção Municipal

- Gabinete da Zona Classificada de Angra do Heroísmo

- Universidade dos Açores
  - Departamento de Ciências Agrárias
## AGENDA

**8-11 September 2004**

Workshop 5: Genetic erosion and pollution assessment methodologies

### DAY 1: Wednesday 8 September

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<td>9.00 - 9.30</td>
<td>Host Institute welcome</td>
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<td>9.30 - 11.40</td>
<td><strong>PGR Forum progress reports</strong></td>
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<td>Chair: Eliseu Bettencourt</td>
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<tr>
<td>9.30 - 10.40</td>
<td>WP2 Update - Caroline Pollock, Kell Kristiansen 10 min</td>
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<td>WP6 Update - Josef Turok, Shelagh Kell 10 min</td>
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<td>WP1 Progress Report - Shelagh Kell, Jay Moore, Maria Scholten 50 min</td>
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<td>10.40 - 11.00</td>
<td><strong>COFFEE BREAK</strong></td>
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<td>11.00 - 11.20</td>
<td>WP4 Progress Report - Lori De Hond</td>
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<tr>
<td>11.20 - 11.40</td>
<td>Overview of objectives of workshop and focus on CWR list</td>
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<td>Brian Ford-Lloyd, Sónia Dias</td>
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<tr>
<td>11.40 - 12.10</td>
<td>Measuring and predicting genetic change in CWR species</td>
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<td>Jozef Turok</td>
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<td>12.10 - 12.30</td>
<td>WP3 Progress Report - Sabine Roscher</td>
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<td>12.30 - 14.00</td>
<td><strong>LUNCH</strong></td>
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<tr>
<td>14.00 - 18.30</td>
<td><strong>Session 1: Introductory (including time for discussion)</strong></td>
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<td>Chair: Sabine Roscher</td>
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<tr>
<td>14.00 - 14.30</td>
<td>A global overview on assessing and monitoring genetic erosion of crop</td>
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<td>wild relatives and local varieties using WIEWS</td>
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<td>Stefano Diulgheroff</td>
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<td>14.30 - 15.00</td>
<td>Political, legislative and practical aspects of in situ conservation in</td>
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<td>Germany in the context of genetic erosion</td>
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<td>Lothar Frese</td>
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<td><strong>COFFEE BREAK</strong></td>
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<td>16.00 - 17.30</td>
<td><strong>Session 1 working groups</strong></td>
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<td>Chair: Silvia Strajeru</td>
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<td></td>
<td>Working group discussions on generalities and realities: The CWR list -</td>
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<td>what is the task and how big is it?</td>
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<td></td>
<td>o Group 1-Political and legal issues - (Facilitator: Eliseu Bettencourt)</td>
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<td>o Group 2-Genetic erosion - (Facilitator: Caroline Pollock)</td>
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<td>o Group 3-Genetic pollution - (Facilitator: Mike Wilkinson)</td>
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<tr>
<td>17.30-18.30</td>
<td>Presentation of Session 1 working group results and recommendations</td>
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### DAY 2: Thursday 9 September

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<tr>
<th>Time</th>
<th>Session 2: Practical aspects of measurement, monitoring and prediction (including time for discussion)</th>
<th>Chair: Juozas Labokas</th>
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<tr>
<td>9.00-17.00</td>
<td>Session 2: Practical aspects of measurement, monitoring and prediction (including time for discussion)</td>
<td>Chair: Juozas Labokas</td>
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<tr>
<td>9.00-9.30</td>
<td>Risk assessment and gene flow</td>
<td>Mike Wilkinson</td>
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<td>9.30-10.00</td>
<td>Using ecogeography and GIS to assess genetic erosion</td>
<td>Nigel Maxted</td>
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<td>10.00-10.30</td>
<td>Red List assessments and change indices as indicators of genetic erosion</td>
<td>Caroline Pollock</td>
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<td>10.30 – 11.00</td>
<td><strong>COFFEE BREAK</strong></td>
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<td>11.00-11.30</td>
<td>Genetic erosion and pollution – genetic and conservation consequences for <em>Populus</em> and other European forest species</td>
<td>François Lefèvre</td>
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<td>11.30-12.00</td>
<td>Using populations for monitoring and prediction</td>
<td>Lori De Hond</td>
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<td>12.00-12.30</td>
<td>Realistic molecular and population genetic tools for genetic assessment</td>
<td>Brian Ford-Lloyd</td>
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<td>12.30 – 14.00</td>
<td><strong>LUNCH</strong></td>
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<td>13.30 - 13.45</td>
<td><em>In situ</em> conservation of crop wild relatives through enhanced information management and field application: an introduction to the five country GEF-funded project</td>
<td>Jozef Turok</td>
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<td>14.00-15.30</td>
<td>Session 2 working groups</td>
<td>Chair: Zdenek Stehno</td>
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<td>Working group discussions on practical aspects: developing the hierarchy of techniques</td>
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<td>o Group 1-Monitoring at the taxonomic level – (Facilitator: Shelagh Kell)</td>
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<td>o Group 2-Monitoring at and around the population level – (Facilitator: Lori De Hond)</td>
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<td>o Group 3-Monitoring at the gene level – (Facilitator: Helena Korpelainen)</td>
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<td>15.30 – 16.00</td>
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<td>16.00-17.00</td>
<td>Presentation of Session 2 working group results and recommendations</td>
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<td>17.00</td>
<td>Development of Work Package 5 products</td>
<td>Brian Ford-Lloyd</td>
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<td>17.30</td>
<td><strong>Steering Committee and Advisory Board Meeting</strong></td>
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<td>Social dinner</td>
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### DAY 3: Friday 10 September

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<tr>
<th>Time</th>
<th>Session 3: Case studies from the CWR list (including time for discussion)</th>
<th>Chair: Issak Rashal</th>
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<tr>
<td>9.00-9.30</td>
<td>Wild brassicas</td>
<td>Mike Wilkinson</td>
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<td>9.30-10.00</td>
<td>Wild forages</td>
<td>Michael Abberton</td>
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<td>10.00-10.30</td>
<td>Changes in management practices</td>
<td>Åsmund Asdal</td>
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<td>10.30-10.45</td>
<td>Genetic erosion and extinction threat of old world cottons, <em>Gossypium</em> L.</td>
<td>Vojtech Holubec</td>
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<td><strong>COFFEE BREAK</strong></td>
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<td>11.00-12.30</td>
<td>Session 3 working groups</td>
<td>Chair: Daniela Benedikova</td>
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<td>Working group discussions on prioritising the CWR list</td>
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<td>o Group 1-Agricultural – (Facilitator: Sónia Dias)</td>
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<td>o Group 2-Horticultural (including ornamentals) – (Facilitator: Kell Kristiansen)</td>
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<td>o Group 3-Forestry – (Facilitator: Francois Lefèvre)</td>
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<td><strong>LUNCH</strong></td>
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<td>Genetic erosion of fruit varieties and their recovery from Historical gardens</td>
<td>Damiano Avanzato</td>
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<td>14.00-15.00</td>
<td>Presentation of Session 3 working group results and recommendations</td>
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<td><strong>15.00-18.00</strong></td>
<td><strong>Session 4: The way forward for CWR conservation: specific proposals regarding methodologies and prospects</strong></td>
<td>Chair: Tamara Smekalova</td>
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<tr>
<td>15.00-15.30</td>
<td>Indicators for the CWR species list prioritisation</td>
<td>António Flor</td>
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<td><strong>15.30 – 16.30</strong></td>
<td><strong>Session 4 working groups</strong></td>
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<td>o Group 1-The CWR species list prioritisation – (Facilitator: Nigel Maxted)</td>
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<td>o Group 2-The hierarchy of methodologies – (Facilitator: Brian Ford-Lloyd)</td>
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<td>o Group 3-Future demands/prospects/opportunities – (Facilitator: Jozef Turok)</td>
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<td><strong>16.30 – 17.00</strong></td>
<td><strong>COFFEE BREAK</strong></td>
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<tr>
<td>17.00-18.00</td>
<td>Presentation of Session 4 working group results and recommendations</td>
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<td>18.00</td>
<td>Final reporting and recommendations</td>
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### DAY 4: Saturday 11 September

Field trip including a visit to the endemic flora park
DAY 1 – Morning (8 September)

Opening session

Welcome

Chair: Eliseu Bettencourt

Workpackage updates and progress reports

- Workpackage coordinators for WP2 and WP6 will provide an update on the scope, plans and arrangements in progress for the associated workshop. WP1 and WP4 progress reports will be presented to the forum:
  - WP2 – Caroline Pollock, Kell Kristiansen
  - WP6 – Jozef Turok, Shelagh Kell

  o WP1 Progress report- Shelagh Kell, Jay Moore, Maria Scholten
  o WP4 Progress report - Lori De Honde

Introduction to Workshop 5

Brian Ford-Lloyd and Sónia Dias will provide an overview of WS5 objectives and focus on CWR list

- **Keynote address**: “Measuring and predicting genetic change in CWR species” by Jozef Turok

- Progress report on WP3 will be presented to the forum:
  
  o WP3 - Sabine Roscher
DAY 1 – Afternoon (8 September)

1. Genetic erosion and pollution assessment methodologies
   Presentations and groups’ discussions

Objective: Agree on genetic erosion and pollution assessment methodologies for European wild crop relatives

Work description: The working groups will debate how plant genetic erosion might be predicted and assessed; how plant genetic pollution or introgression, either by GMOs or from conventionally bred crops, might be predicted and assessed. Establishing methodologies.

Workshop deliverables:
- Methodology for predicting plant genetic erosion
- Methodology for assessing plant genetic erosion
- Methodology for assessing plant genetic pollution
- Methodology for predicting plant genetic pollution
- Publication on genetic erosion and pollution assessment methodologies

Session 1

Chair: Sabine Roscher

- “A global overview on assessing and monitoring genetic erosion of wild crop relatives and local varieties using WIEWS” by Stefano Diulgheroff
- “Political, legislative and practical aspects of in situ conservation in Germany in the context of genetic erosion” by Lothar Frese
- “Introgression of GM plants and the EU monitoring guidance note” by Hans den Nijs

Chair: Silvia Strajeru

Group discussions: The purpose of group discussions is to make the best use of workshop time by establishing small working groups to discuss different subjects related to genetic erosion and pollution assessment for European CWRs. Participants should join the group for which their expertise is most appropriate.

Session 1 – Working group discussions on generalities and realities: The CWR list – what is the task and how big is it?

- Group 1: Political and legal issues
  - Facilitator: Eliseu Bettencourt
  - Discussion points:
• In the context of the CWR list, what are the political and legal issues surrounding genetic erosion and pollution

• **Group 2: Genetic erosion**
  - **Facilitator:** Caroline Pollock
  - **Discussion points:**
    - What do we mean by genetic erosion?
    - Are existing definitions appropriate for our purposes?
    - Discuss whether in a practical sense, there is any difference between genetic erosion and genetic pollution
    - Does the genetic erosion concept apply equally to all the CWR list species?
    - How much genetic erosion can be tolerated?
    - Do we need to consider genetic erosion in a global rather than just a European context?

• **Group 3: Genetic pollution**
  - **Facilitator:** Mike Wilkinson
  - **Discussion points:**
    - What do we mean by genetic pollution – not just GM?
    - Can we specify unwanted outcomes (Hazards) from gene flow into CWR populations?
    - Are there advantages as well as disadvantages to gene flow into CWR populations?
    - Can we estimate ‘risk’ of genetic erosion by way of genetic pollution?
    - Discuss whether in a practical sense, there is any difference between genetic pollution and genetic erosion
    - Does the genetic pollution concept equally apply to all the CWR list species (trees, ornamentals, cereals...)?
    - How much genetic pollution can be tolerated?
    - Do we need to consider genetic pollution in a global rather than just a European context?
    - What is the scope for secondary ecological effects resulting from adaptive changes conferred by a transgene?

**Group presentations:** Each group will present to the forum the conclusions reached by the group, difficulties faced and recommendations for future progress.

**General discussion Session 1:** The conclusions reached by each group will be discussed. Possible answers to the problems faced by each group will also be discussed. Guidelines for future progress will also be agreed upon.

**Summing up of Day 1:**
- Sabine Roscher to briefly sum up the day’s activities and results
DAY 2 Morning (9 September)

2. Genetic erosion and pollution assessment methodologies
   Presentations and groups’ discussions

Objective: Agree on genetic erosion and pollution assessment methodologies for European wild crop relatives

Work description: Using existing techniques for measuring, monitoring and prediction as a starting point for the discussion, the working group will debate and resolve how these might be adapted to the CWR

Session 2: Practical aspects of measurement, monitoring and prediction

Chair: Juozas Labokas

- “Risk assessment and gene flow” by Mike Wilkinson
- “Using ecogeography and GIS to assess genetic erosion” by Nigel Maxted
- “Red List assessments and change indices as indicators of genetic erosion” by Caroline Pollock
- “Genetic erosion and pollution – genetic and conservation consequences for Populus and other European forest species” by François Lefèvre
- “Using populations for monitoring and prediction” by Lori De Hond
- “Realistic molecular and population genetic tools for genetic assessment” by Brian Ford-Lloyd
- “In situ conservation of crop wild relatives through enhanced information management and field application: an introduction to the five country GEF-Funded project” by Jozef Turok

DAY 2 Afternoon (9 September)

2. Genetic erosion and pollution assessment methodologies
   Presentations and groups’ discussions

Chair: Zdenek Stehno

Group discussions: The purpose of group discussions is to make the best use of workshop time by establishing small working groups to discuss different subjects related to genetic erosion and pollution assessment for European CWRs. Participants should join the group for which their expertise is most appropriate.

Session 2 – Working group discussions on practical aspects: developing the hierarchy of techniques
• **Group 1: Monitoring at the taxonomic level**
  - **Facilitator:** Shelagh Kell
  - **Discussion points:**
    - Can genetic erosion be assessed and monitored at taxonomic level?
    - Can genetic pollution be assessed and monitored at taxonomic level?
    - What are the potential methods of assessing and monitoring genetic erosion and pollution at taxonomic level? E.g.
      - Extinction:
        - Species, subspecies, varieties
        - GP1, GP2, GP3 and/or TG1, TG2, TG3, TG4, TG5
        - Local, regional, national, global
      - Hybridisation i.e. are new hybrids appearing between taxa?
        - Inter-specific, inter-generic
      - Red List change indices
    - Can the methods be practically and realistically applied?
    - Are the methods applicable to all taxa/taxon groups in the CWR list?
    - Can the methods be used to predict genetic erosion and pollution?
    - Where does taxonomic assessment fit into the hierarchy of techniques for assessing and monitoring genetic erosion and pollution?

• **Group 2: Monitoring at and around the population level**
  - **Facilitator:** Lori De Hond
  - **Discussion points:**
    - Identify the available techniques for assessing genetic erosion and genetic pollution in populations
    - Identify the available techniques for monitoring genetic erosion and genetic pollution in populations
    - Consider the ease with which assessment could be made for example of changes in population size, adaptation, effects of habitat change/destruction; can we use GIS or remote sensing?
      - How can Red Data listing help?
    - What is feasible given the number of CWR species?
    - Which technique should we start with – is there an obvious hierarchy?

• **Group 3: Monitoring at the gene level**
  - **Facilitator:** Helena Korpelainen
  - **Discussion points:**
    - Identify the available techniques for assessing genetic erosion and genetic pollution at the genetic level
    - Identify the available techniques for monitoring genetic erosion and genetic pollution at the genetic level
    - Which molecular markers?
    - Which population genetic parameters are informative for our purposes?
    - How can Red Data listing help at the gene level?
- What is feasible given the number of CWR species? Which techniques should we start with and are most important?

**Group presentations:** Each group will present to the forum the conclusions reached by the group, difficulties faced and recommendations for future progress.

**General discussion Session 2:** The conclusions reached by each group will be discussed. Possible answers to the problems faced by each group will also be discussed. Guidelines for future progress will also be agreed upon.

- “Development of Work Package 5 products” by Brian Ford-Lloyd

**Summing up of Day 2:**
- Juozas Labokas and Zdenek Stehno to briefly sum up the day's activities and results

**Steering Committee and Advisory Board Meeting**

**Social Dinner**
DAY 3 – Morning (10 Septembo)

3. Genetic erosion and pollution assessment methodologies

Presentations and groups’ discussions

Objective: Agree on genetic erosion and pollution assessment methodologies for European wild crop relatives

Work description: Case studies from CWR list. The working group will debate the prioritisation of the CWR list.

Session 3: Case studies from CWR list

Chair: Isaak Rashal

- “Wild brassicas” by Mike Wilkinson
- “Wild forages” by Michael Abberton
- “Changes in management practices” by Aasmund Asdal
- “Genetic erosion and extinction threat of old world cottons, Gossypium L.” by Vojtech Holubec

Chair: Daniela Benedikova

Group discussions: The purpose of group discussions is to make the best use of workshop time by establishing small working groups to discuss different subjects related to genetic erosion and pollution assessment for European CWRs. Participants should join the group for which their expertise is most appropriate.

Session 3 – Working group discussions on prioritising the CWR list

- **Group 1: Agricultural**
  - **Facilitator:** Sónia Dias
  - **Discussion points:**
    - Are there any differences and specific examples and methodologies to consider when considering genetic erosion and pollution in agricultural CWR?
    - Are there any special cases?
    - Are there any special needs?

- **Group 2: Horticultural (including ornamentals)**
  - **Facilitator:** Kell Kristiansen
  - **Discussion points:**
Are there any differences and specific examples and methodologies to consider when considering genetic erosion and pollution in horticultural CWR
Are there any special cases?
Are there any special needs?

- **Group 3: Forestry**
  - **Facilitator:** F. Lefèvre
  - **Discussion points:**
    - Are there any differences and specific examples and methodologies to consider when considering genetic erosion and pollution in forestry CWR
    - Are there any special cases?
    - Are there any special needs?

**DAY 3 – Afternoon (10 September)**

### 3. Genetic erosion and pollution assessment methodologies

#### Presentations and groups’ discussions

- “Genetic erosion of fruit varieties and their recovery from Historical gardens” by Damiano Avanzato

**Group presentations:** Each group will present to the forum the conclusions reached by the group, difficulties faced and recommendations for future progress.

**General discussion Session 3:** The conclusions reached by each group will be discussed. Possible answers to the problems faced by each group will also be discussed. Guidelines for future progress will also be agreed upon.

**Session 4: The way forward for CWR conservation: specific proposals regarding methodologies and prospects**

**Chair:** Tamara Smekalova

- “Indicators for CWR species list prioritisation” by António Flor

**Group discussions:** The purpose of group discussions is to make the best use of workshop time by establishing small working groups to discuss different subjects related to genetic erosion and pollution assessment for European CWRs. Participants should join the group for which their expertise is most appropriate.
Session 4 – Working group discussions on the CWR list – the way forward

• Group 1: The CWR species list prioritisation
  o Facilitator: Nigel Maxted
  o Discussion points:
    ▪ Priority given to species on the basis of degree of threat (in other words not based on current conservation status, socio-economic value (use), genetic distinctiveness, biological importance, cultural importance, cost, feasibility and sustainability, legislation, and ethical and aesthetic considerations)
    ▪ Identification of threats from genetic erosion and pollution
    ▪ Genetic erosion
      • Species with a restricted geographical and ecological range
      • Species growing in natural habitats subject to destruction, degradation and fragmentation
      • Species poorly adapted to their niche and easily displaced by competition from aggressive or alien species
      • Species found in anthropogenic or disturbed habitats
      • Species growing in marginal or very localised anthropogenic environments that are vulnerable to changes in agricultural practices or land use
      • Species growing in environments subject to regular natural or human-directed disasters.
      • Species subject to wild harvesting, over-exploitation and incidental take
    ▪ Genetic pollution
      • Species closely related to the polluting species
      • Species closely related to the polluting species and found sympatric with the polluter
      • Out-breeders (?)
    ▪ How to assess these threats on individual CWR species, are some threats worse than others
    ▪ Recommendations for the prioritisation of the CWR list in relation to genetic erosion and genetic pollution
    ▪ Would it be possible to develop further the comparative ranking system suggested by Guarino (1995)


• Group 2: The hierarchy of methodologies
  o Facilitator: Brian Ford-Lloyd
  o Discussion points:
    ▪ Recommend methodologies for each group of CWR (agricultural, horticultural and forestry)
- Recommend the hierarchy of the methodologies identified for each group of CWR (agricultural, horticultural and forestry)

- **Group 3: Future demands/prospects/opportunities**
  - **Facilitator:** Jozef Turok
  - **Discussion points:**
    - Recommendations for the CWR list and genetic erosion and genetic pollution in relation to future demands/prospects/opportunities
    - Consider political, technical and conservation issues

**Group presentations:** Each group will present to the forum the conclusions reached by the group, difficulties faced and recommendations for future progress.

**General discussion Session 3:** The conclusions reached by each group will be discussed. Possible answers to the problems faced by each group will also be discussed. Guidelines for future progress will also be agreed upon.

**Summing up of Day 3 and outline of Day 4:**
- Martine Mitteau and Tamara Smekalova to briefly sum up the day's activities and results
- Eliseu Bettencourt to outline for Day 4 and further logistic information

**Workshop 5 final reporting and recommendations**

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**DAY 4**

**4. Field trip including a visit to the endemic flora park**
Workshop 5: Genetic erosion and pollution assessment methodologies - Overview

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1. Objective: agree genetic erosion and pollution assessment methodologies for CWR

- How to assess and predict genetic erosion? Examine existing methodologies
- How to assess and predict genetic pollution (transgenic crops, conventional crops and introduced exotic species or aliens)? Few existing methodologies?

2. Assessing taxa on the CWR list

- There are currently around 20,000 species on the list. It will be impossible to assess all of them in terms of erosion/pollution. Also it will not be necessary.
- Prioritisation for erosion/pollution assessment is therefore necessary
- Simple methodologies, and in some cases, molecular profiling, are required
- A hierarchy? We need to be realistic and not identify assessment methodologies that cannot address the need to genetically assess all species on the CWR list
- Workshop 2 will cover: Assessment of threat of plant diversity loss and conservation status for European wild crop relatives. “...plant diversity loss...” is in effect genetic erosion. Workshops 2 and 5 are closely interlinked. The outcomes of WS 5 should directly/indirectly inform the work of WS 2, namely the “...potential threat category for each of the CWR taxa...”
- Prioritisation - which taxa do we assess in detail?
- Completion of WS 2 would actually highlight the taxa where more detailed assessment of genetic erosion/pollution and subsequent monitoring were needed. The Red List threat category could be a determining factor in choosing the level of assessment of genetic erosion/pollution.
- Simple assessments of genetic diversity?
- When we have determined taxa of greatest importance and threat: can we use ecogeography? Red listing? Indicators? ... (2010)? Taxonomy? Population biology/breeding systems?

3. Session 1 presentations and discussions:

- Political and legal issues
- Genetic erosion: what do we mean by it? Can we tolerate it? etc.
- Genetic pollution: what is it? Are there advantages? etc.

4. Session 2:
• Monitoring at the taxonomic level: simple methods? Red data listing? Place in hierarchy?
• Monitoring at the population level: simple techniques? Habitat enforced changes in population size? GIS? Red data listing? Reproductive biology?
• Monitoring at the gene level: Techniques? Red data listing? What is feasible?

5. Session 3 Case studies:
• Agricultural crops
• Horticultural crops
• Forestry

6. Session 4: the way forward
• The CWR species list prioritisation: how to prioritise the CWR list in relation to erosion and pollution? Recommendations?
• The hierarchy of methodologies: what are the methodologies? Are they hierarchical?
• The future: demands, prospects, opportunities? .... 2010? ...

7. 2010 Biodiversity Target - Focal Areas
• “Reducing the rate of loss of the components of biodiversity, including: biomes, habitats and ecosystems, species and populations, genetic diversity”
• “Loss” is genetic erosion
• PGR forum can contribute to the 2010 CBD goals (2 & 3)
Political, legislative and practical aspects of in situ conservation in Germany in the context of genetic erosion

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Political aspects
The Convention on Biological Diversity (CBD) became national law of the Federal Republic of Germany on 30th of August 1993. Germany has ratified the International Treaty on Plant Genetic Resources for Food and Agriculture on 31st of March 2004. The CBD as well as the Treaty must be considered as very important political documents which have strengthened already ongoing activities in the field of nature protection and conservation of genetic resources. The CBD negotiation was let by the Ministry for the Environment, Nature Conservation and Nuclear Safety (BMU) while the responsibility for the negotiations of the Treaty rested with the Ministry of Consumer Protection, Food and Agriculture (BMVEL). The leading Ministries received support from additional Ministries amongst which were the Ministry of Education and Research (BMBF) and the Ministry of Economic Co-operation and Development (BMZ). Owing to this complex negotiation and mutual consultation process today there is no longer a controversy on the need for nature protection but a debate on how the competence can best be shared between the responsible Ministries.

How tasks can be shared is described in an expert program for PGRFA. The National Expert Program for the Maintenance and Sustainable Use of Plant Genetic Resources of Agricultural and Horticultural Crops launched by the BMVEL in August 2002 was jointly elaborated by federal and state offices, research centres, universities, and associations representing the public and commercial sector. It is the second of five expert programs to be developed within the framework of a master plan for genetic resources published by BMVEL in 1998. Chapter 5.1 "In situ maintenance, monitoring and development (incl. on farm management) of the expert program for PGRFA“ describes the current status of in situ maintenance in Germany and the measures required to improve the status.

Legislative aspects
There is no national law for plant genetic resources for food and agriculture protection neither at the federal nor state level. Hence, a wide interpretation of the CBD, which often uses the phrase “as far as possible and as appropriate”, is possible. The Agenda 2000 of the EU and derived national regulations play a certain role in the in situ maintenance of PGRFA. More important however are the Flora Fauna Habitat guideline (FFH) and Federal Nature Protection Law (BNatSchG) amended in 1998. That year a significant new protection category, the biosphere reserve, was introduced. The Federal Government however has a guiding competence only. When practical actions need to be undertaken each individual member state stresses its responsibility according to our basic law Art. 75 GG. The state Lower Saxony regulates the biotope mapping in § 28 NNatG of the state's nature protection law. Art. 75 GG in theory allows allocation of competence where the problems can best be solved but in practice also makes cooperation between the states and between the states and the federal level more complicated.

Practical aspects
The divided political and legislative responsibilities stringently call for co-ordination at the federal level. The BMVEL has established a Consultation and Co-ordination Committee
charged with controlling the implementation of the National Expert Program for PGRFA. This Committee is currently assisted by two experts groups, one for in situ and on farm management aspects and the second for ECP/GR matters. One of first actions taken by the Consultation and Co-ordination Committee consisted in the development of a priority list of the large number of measures described in the Expert Program for PGRFA. Currently no extra funds are available for the implementation of the Expert Program for PGRFA. The major part of work will therefore be carried out by those institutions which contributed to the elaboration of the program from their core funding. High priority received the development of an inventory of PGRFA species either naturally occurring in Germany or used in Germany. The PGRFA list, version 8th of September 2003, contains 1770 taxa. This list will serve to discuss and agree on sharing of responsibility for in situ management of crop wild relatives between the Ministry of Environment, Nature Conservation and Nuclear Safety (BMU) and the Ministry of Consumer Protection, Food and Agriculture (BMBF). For illustration of the task: the flora list of Lower Saxony published in 2004 encompasses 2022 taxa of which about 16% falling into one of the red list threat categories also occur on the PGRFA list. In view of this high amount of taxa, active in situ management of all in the state Lower Saxony is beyond our facilities and capabilities. We plan therefore investigating landscape planning approaches allowing the general protection of plant species and will suggest specific active management measures where possible and appropriate.
Introgression of GM plants into wild relatives, the EU Guidance note for Monitoring, and the need for base line data

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According to EC Directive 2001/18/EC and its Appendix VII and EC Regulation 1829/2003, there will be mandatory monitoring of genetically modified organisms (GMO) placed on the market to 1) trace and identify eventual effects of the placing on the market of GMO on environment and health, and to 2) give feed back to the risk assessment procedure. A short overview is given of the accompanying guidance note for monitoring that recently has been implemented, including current opinions of the EFSA (European Food & Safety Authority). Although following the EU prescribed monitoring framework, this contribution will be restricted to genetic interactions between GM plants and their wild relatives, which - following initial hybridization- eventually may lead to introgression of transgenes into wild type genomes. Introgression of transgenes in a wild relative can be through GMP pollen siring hybrids directly, and indirectly through initial dispersal of the whole GMP (as seed or vegetative diasporo), and subsequent hybridization.

According to the EU, the monitoring must have two focuses: (1) the possible effects of the GM crop (if any), identified in the formal Risk Assessment (RA) procedure, and (2) unforeseen effects. Where there is scientifically valid evidence of a potential adverse effect linked to the genetic modification, then (alone) in this first part, “case-specific monitoring” should be carried out after commercialization in order to confirm the assumptions of RA. Any evaluation of the potential consequence of that effect should be science-based and compared with baseline information. In the second part of the monitoring, unanticipated effects of the environmental release are subject to a “general surveillance” program that should be implemented independently of whether the RA found an indication of harmful effects or not. The guidance note explicitly suggests that this latter part may well be long term monitoring, given the fact that unexpected effects can be of delayed and long-term type. It is emphasized that basic to the monitoring and the consecutive evaluation is the availability of baseline data which give reference values for weighing of the GMP effects. Baseline data comprise a full array of sets of information on, among many others, biology, reproduction, relatedness, and compatibility of the pertaining species, as well as on the effects of current agricultural practices on the environment. Some of the former aspects are elaborated in this contribution, and an example of the assessment of introgression and predictive modelling of its effects are presented. It is acknowledged that there is as yet a large demand for such data sets. Further to this, it is the quality of the GMP traits that counts, since a large amount of gene flow from GMP with environmentally neutral traits is less concerning than minimal gene flow of traits that enhance fitness.

In any case, in order to be able to record and monitor the consequences of transgene introgression, identification of GMP’s is a prerequisite. Therefore, cost-effective and unambiguous markers should be placed in the GMP’s, like PCR-able eventually non-coding
sequences in the constructs. There is one more complication in that the Directive places the full responsibility for the establishment of the entire monitoring plan and the data report (to the competent state authorities) with the consent holder, which are or will be in many cases private companies. Since particularly for General Surveillance, existing public monitoring systems are foreseen to contribute, the latter point may prove impractical, therefore, it is suggested that part of the general surveillance, as well as additional monitoring elements outside the regulatory requirements should be placed under public responsibility.
Genetic exchange between crops and their wild relatives by introgressive hybridisation has been a reality ever since the birth of agriculture. The significance of such gene flow has received little interest, however, until the advent of molecular biotechnology and the emergence of GM crops. In principle, the scope for transfer of certain, completely novel transgenes from GM crops into wild relatives means that there is an increased capacity rapid jumps in the adaptation profile of the recipient. This carries risks for the genetic integrity and evolutionary survival of the wild species, and of the survival of other species with which it coexists. In evaluating such potential problems, one must first define the unwanted endpoints (hazards) as clearly as possible and then measure the likelihood of their occurrence (exposure) so that an assessment of risk can be compiled (Risk=hazard x exposure). In measuring risks in this way, it is important to consider the management of the crop, the ecology, demography and population genetics of the wild species, the number, nature and location of the transgene(s) and the extent of introgression within the natural setting. Crucially, these assessments should be made against comparable risks posed by non-GM cultivars of the same crop (i.e. baseline data) so that judgements can be made over the significance of any change envisaged.
Red List assessments and change indices as indicators of genetic erosion

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The IUCN Red List is widely recognised as the most authoritative and objective system for classifying taxa in terms of their extinction risk. It uses a range of categories and quantitative criteria to list species according to their degree of threat. Since the criteria often reflect actual or potential loss of reproductive individuals, the IUCN Red List can be used to highlight taxa where genetic erosion may be occurring.

There are nine IUCN Red List categories: Extinct (EX), Extinct in the Wild (EW), Critically Endangered (CR), Endangered (EN), Vulnerable (VU), Near Threatened (NT), Data Deficient (DD), Least Concern (LC) and Not Evaluated (NE). As taxa move up towards the Extinct category, extinction risk increases and there is reason for increasing cause for concern over genetic erosion. However, the lower categories do not highlight where population declines are occurring at levels insufficient to qualify the taxon for one of the threatened categories. As a result, the Red List categories can only act as a course-resolution indicator of genetic erosion.

Taxa at greatest risk of extinction in the wild are assigned one of the three threatened categories (CR, EN or VU) based on a range of quantitative criteria. Each criterion focuses on a different issue related to extinction risk: rate of population decline, restricted range and ongoing decline, small population size and ongoing decline, etc. Within the criteria there are four instances where there is direct indication that mature individuals are being lost, therefore genetic erosion may be a problem and further investigation of these taxa at population and genetic level may be required:

- **Criterion A:** taxa assessed under criterion A have shown a reduction in population size, or are expected to undergo population declines, of at least 30%.
- **Criterion B:** taxa assessed under criterion B1b(v) or B2b(v) have a restricted range and are showing continuing decline (or potential decline) in population size.
- **Criterion C:** taxa assessed under criterion C have a population size of fewer than 10,000 and the population is continuing to decline (or continuing decline is expected).
- **Criterion E:** taxa assessed under criterion E have enough quantitative data to statistically show a relatively high probability of extinction in the wild in the near future.

The two remaining instances highlight taxa that may be susceptible to rapid genetic erosion and further investigation at population and genetic level may be required:

- **Criterion B:** taxa assessed under criterion B (other than B1b(v) or B2b(v)) have a restricted range and are showing continuing decline (or potential decline) in range, habitat or number of locations or subpopulations.
- **Criterion D:** taxa assessed under criterion D have a very small or restricted population.
In addition to the Red List highlighting where genetic erosion may be a serious problem, the Red List can also be used to monitor trends in overall threat status over time within a taxonomic group. In light of the CBD target of achieving a significant reduction in the rate of loss of biodiversity by 2010, the Red List Consortium has developed a methodology for producing Red List Indices that chart the overall threat status (projected relative extinction risk) of species. These indices are based on the number of species in each Red List category, and the number changing categories between assessments as a result of genuine improvement or deterioration in status. The indices can be applied to any set of species that have been fully assessed at least twice. So far, the Red List Index has been applied to birds and amphibians, and the index for both groups clearly shows that their overall threat status has continued to deteriorate over the last twenty years. Disaggregated indices show that deteriorations have occurred worldwide and in all major ecosystems.

Red List Indices complement indicators based on species population trends and habitat extent for quantifying global trends in the status of biodiversity. Their main weaknesses are that the resolution of status changes is fairly coarse and that delays may occur before status changes are detected. Their greatest strength is that they are based on information from all species in a taxonomic group worldwide, rather than a potentially biased subset. At present, suitable data are only available for birds and amphibians, but indices for other taxonomic groups are in development, as is a sampled index based on a stratified sample from all major taxonomic groups.

A paper outlining the Red List Indices for birds is currently in preparation by BirdLife International and will be published in the Public Library of Science (PloS) electronic journal, *PloS Biology*, before November 2004 (see [http://www.plos.org/](http://www.plos.org/)). For further information on the Red List Indices and their application to bird data, please contact Stuart Butchart at BirdLife International (e-mail: stuart.butchart@birdlife.org).
Forest tree species cover a broad range of biological situations. Moreover, several evolutionary processes shape the genetic diversity within local populations and interact in a complex way with human activities. Therefore it is difficult to propose a general conservation strategy that would fit all possible situations at once. However, we can try to do better than a simple case-by-case approach and define a unified frame to guide further reflexion on each particular situation. First, the main concepts and processes behind "genetic erosion" and "pollution" will be briefly reviewed in a simple way (mainly effective population size, hybridisation and introgression). Then, specific features characteristic of trees will be stressed in that respect (diversity, local adaptation, demo-genetic processes...). Finally consequences for the conservation of forest genetic resources will be drawn
Population monitoring is mainly used for the assessment of population viability, which essentially depends on the balance between births and deaths, and population size. The estimation of births, deaths and population size is easily carried out through population monitoring. The values of these variables are, nevertheless, the result of a complex interaction between genetic and environmental factors, among them, those related to the breeding system and the reproductive biology of the target species in a particular location. Therefore, genetic and environmental factors, breeding system and reproductive biology, and demography are all very much inter-related.

With this idea in mind, and taking into account that genetic reserves should be subject to periodic demographic monitoring of the target populations (just to find out what we have), the question is whether the data we gather visiting the population can provide relevant information with regard to the genetic diversity of the population and whether the population is experiencing genetic erosion at present or in a foreseeable future. We think that this information can be obtained from three sources: demographic monitoring, knowledge of the breeding system and reproductive biology, and characterisation of environmental heterogeneity in the population. The information that can be obtained from demographic data derives from two theoretical assumptions: a) a decline in population size may lead to a reduction in genetic diversity; and b) low-sized populations are likely to experience genetic drift and, thus, genetic erosion. The use of demographic models can be very helpful to provide estimations of population declines in a near future, to estimate probabilities of quasi-extinction and minimum viable populations from a demographic perspective, and to carry out sensitivity analysis about alternative management prescriptions and possible environmental changes.

Knowledge on the breeding system is essential for an accurate interpretation of demographic data from a genetic perspective. Outcrossers are able to sustain genetically diverse populations. This genetic diversity is susceptible to significant declines in population size. Similarly, low-sized populations of outcrossers are likely to experience genetic drift. On the other hand, selfers do not have genetically diverse populations to start with and, therefore, are less likely to suffer genetic erosion from declines in population size or genetic drift in low-sized populations. The availability of adequate pollinators may influence the crossing behaviour of plants with mixed-mating systems. This may in turn affect the evolution of genetic diversity in the population. Environmental heterogeneity in the habitat of natural populations may be a valid indicator of genetic diversity in the population. Thus, the occurrence of genetic differentiation processes within populations as a result of environmental heterogeneity has been reported for several species. This may lead to the existence of a spatial genetic structure in the population. The occupation of different microhabitats by a population can be accurately characterised through the use of GIS techniques.
In addition to this, population monitoring also provides the opportunity of characterising the phenotypic diversity of a population. Genetic erosion can then also be assessed by monitoring phenotypic diversity through time.
Realistic population and molecular genetic tools for genetic assessment

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Definitions?

• Genetic erosion
  – a permanent reduction in richness or evenness of common localized alleles
  – or the loss of combinations of alleles over time in a defined area (after Guarino)

• Genetic pollution
  – gene flow from transgenic crops to natural populations

Some relevant facts about sampling variation, drift, effective population size, MVP

• the examples of Papaver dubium and Dipterocarpaceae in relation to in situ conservation
What is important information at the gene level?

- Effective population size, Change in allele frequency, Genetic diversity, Allele richness, Level of heterozygosity, Inbreeding, Gene flow,
- Genetic drift
  - genetic erosion
- Natural selection
  - erosion and pollution
- Migration
  - pollution (erosion) or replenishment

Molecular markers/DNA profiling required:

- Arbitrarily primed markers (RAPD/ISSR) -? AFLPs -? SNPs/DNA sequence -? EST based markers -? isozymes/allozymes
- SSRs (microsatellites)
  - Yes because they are co-dominant, but...

.... Are there primers available for species on the CWR list?

- Out of 160 random CWR taxa (genera) surveyed, 29% had SSR primers available in the published literature

A Reminder:

- The CWR list has around 20,000 species. In theory we could undertake detailed genetic assessment of genetic erosion/pollution on over 6000 taxa using SSRs (If we wanted to, and had the resources). Also for each taxon: How many plants to sample? How many populations? How many time points?
  - need for re-sampling to determine change?

The task is a big one! So the key issues might be:

- How can we assess the majority of our CWR species which is simpler and easier?
  - The aim being still to minimise genetic erosion/pollution and to maximise genetic diversity in \textit{in situ} conservation
- How do we prioritise the taxa on which we should consider molecular population genetic intensive study?

What might be simpler and easier guides?

- Information on breeding system: approx 80% of diversity is within populations of outbreeders, but most diversity is among populations of inbreeders

Further simple guides:

- effective and actual population sizes are not the same: effective population size is nearly always smaller that actual, but actual population size is a rough guide, and will give us an idea about erosion if actual population is getting smaller.

Resampling?

- If populations are staying the same size, then population molecular genetic analysis may be needed only once. If population size is decreasing, then we may need resampling - when? how often?

Other simple guides might be:

- Taxonomic diversity
  assuming diversity is spread across taxa, ensuring that subspecific taxa are conserved should ensure that diversity is conserved
• Ecogeographic diversity: populations that have different adaptive norms will be genetically diverse
• Red data listing: there may be important genetic information

**Genetic pollution?**
• “It is clear that spontaneous hybridisation and introgression of genes from domesticated plants into wild relatives is a common characteristic of domesticated plants”
• The Gene Pool Concept will provide an indicator of the CWR species that are vulnerable, but 22 out of 25 of the World’s most important crops have evidence of natural hybridisation with one or more wild relative. This could extrapolate to over 18,000 (90%) of our CWR species

**Can genetic pollution affect genetic diversity?**
• gene flow can cause change in genetic diversity: in 12 different studies, diversity in introgressed populations was greater
• can gene flow cause extinction? - more data are needed it is ‘speculated’ that hybridisation may have caused extinction of CWR of Capsicum, date palm, hemp, maize, sweet pea

**Can we operate by way of a hierarchy of methodologies?**
• Other prioritisations first, then -
  • are any subspecific taxa seriously threatened?
  • are any major habitats/regions threatened?
  • are most populations’ sizes declining (outbreeding species) ?
  • are some populations’ sizes declining (inbreeding species) ?
  • do sample populations contain significant genetic diversity?
    – if yes, then only re-sample if change in population size

**Monitoring genetic pollution?**
• Measure gene flow: need F<sub>ST</sub> and molecular markers
• Could assess: occurrence of hybrids and hybrid derivatives (morphological), fitness of hybrids/hybrid derivatives, spread of hybrids/hybrid derivatives
• Must be over large timescale, large geographical area, large sample size

**When to do molecular population genetics?**
• if **most** populations’ sizes are declining (outbreeding species) ?
• if **some** populations’ sizes are declining (inbreeding species) ?
  – and/or because any one major habitat/region is threatened
  – and/or because any subspecific taxon is seriously threatened
• then sample and do molpopgen to establish whether populations in protected areas are adequate, or which populations to protect

**CBD 2010 targets?**
• By addressing genetic erosion and genetic pollution assessment methodologies, and considering those in relation to the CWR list, PGR forum will be defining possible indicators of change required by the CBD!
Globally, there is approximately 3M ha of Genetically modified (GM) Oilseed rape (Brassica napus) grown annually and is one of the three GM crops in the UK that have been subjected to large-scale field trials. Of the seventeen wild species present in the UK with which this crop is capable of forming hybrids, only Brassica rapa is known to form spontaneous hybrids in the wild. Broad estimates of the annual numbers of hybrids forming between these species amount to tens of thousands. This means that containment is highly problematic in this case and so attention now focus on the likelihood of stable introgression and of the scope for transgenes to cause unwanted change to natural populations of the wild relative. A key part of this process is identifying which traits are most likely to influence fitness and survival of B. rapa. This, in turn, depends on context and on the ecotype of B. rapa being considered. In this paper, the risk profiles presented by weedy B. rapa and wild B. rapa growing on riverbanks are compared in relation to the probability of stable transgene recruitment and the types of transgenes with greatest scope for incurring unwanted change to the recipients’ ecology or genetic makeup.
Genetic erosion and genetic ‘pollution’ in forage species and their wild relatives

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Forage species such as white clover (Trifolium repens L.) and perennial ryegrass (Lolium perenne) are often long-lived out-breeders that are widespread in both agricultural and semi-natural situations. They typically persist for many years under grazing by sheep or cattle and spread mainly by vegetative means with little recruitment into mature swards.

Erosion of genetic diversity within, for instance, white clover represents a significant threat to future germplasm improvement, with loss of habitat and changes in management practices being the main factors. Material collected in regions undergoing such changes (e.g. Poland in 1990) has been used successfully in breeding programmes targeted at the evolution of systems resembling those potentially subject to erosion. However, loss of diversity is counterbalanced to some extent by the high degree of heterozygosity found in all populations, the extent of phenotypic plasticity and the relatively short breeding history of this species and forages generally.

Wild relatives are important in widening the genetic diversity available to forage breeders but the extent and effects of hybridisation are likely to be limited. A small number of wild relatives are of high priority with respect to in situ conservation but other species may have the potential to make a significant contribution to agriculture in their own right.

Studies of genetic ‘pollution’ in forages are few. A comparison of genetic variation within and between species showed that Agrostis curtisii, a species with a limited distribution in the UK showed a negative correlation between genetic and geographical distance but this was not the case for perennial ryegrass. Rather, this species showed clearly the ‘footprint’ of introduced varieties, but with no major ecological effect discernible. It seems likely that the major impacts of introducing new varieties are likely to be firstly, the management changes accompanying them, and secondly the introduction of genetic variation per se, resulting from sexual reproduction in variety construction. In the absence of information on the effects of genetic exchange on semi-natural populations or wild relatives of forage species it is difficult to conclude that concerns regarding genetic ‘pollution’ are warranted.
Effects of changes in grassland management on plant diversity

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The Norwegian flora consists of about 2500 vascular plants, among these 6-700 species are found in permanent grasslands as pastures and extensively managed meadows. About 350 species are exclusive to such biotopes. Quite a few of these are crop species or crop related species of socio economic value. Species and genotypes of fodder plants, such as grasses and legumes, are most important to Norwegian agriculture. The use of natural grasslands for grazing is dramatically decreasing in Norway. This is the case also regarding mowing of permanent grasslands for fodder production, causing serious concerns about the destiny of species and the genetic variation within species. Norwegians started keeping livestock about 6000 years ago. The impact of grazing and mowing on genetic development and selection has been going on for a very long time, and the in situ gene pool comprises adaptation to a broad diversity of management practices as well as climatic and edaphic growing conditions. The Genetic diversity of fodder plants has not been fully investigated, but collection missions have been carried out and seed samples from agricultural and semi wild populations of the economically most important crops are stored in the Nordic Gene Bank. In addition to traditional fodder crops there are other species with current or potential socio economic importance in these fields. This includes crop related species, medicinal and aromatic plants and other under utilized species. Their maintenance in situ depends on continuous agricultural practice. Studies have shown that once the grasslands are abandoned and other species have invaded and replaced the traditional meadow species, it is impossible to restore them. Composition of plant species in a meadow grazed by animals differs significantly from fields mowed by farmers. Grazed fields have more grasses and mowed fields have more broad-leaved species. Early flowering herbs dominate mowed meadows, while grazed pastures in general have scarce blooming, usually occurring later in the summer. To prevent extinction of the species or their genetic diversity throughout the broad diversity of growing conditions and habitats the Norwegian Programme for Plant Genetic Resources have decided to encourage further use of selected grasslands. A pilot face includes mapping of interesting fields, documentation of botanical data and management practices and considerations of possible means to encourage continued traditional farming of endangered meadows and pastures.
Wild species of old world cottons, *Gossypium* L. are confined to Africa and Arabian Peninsula. Investigation and revision of specimens in 11 world herbaria revealed that 12 wild and 4 cultivated species occur in the region. The wild species are confined to the semidesert areas of the tropical belt between latitudes 20°N and 25°S with hiatus in Zaire and the north Zambezian basins. Some species are widely distributed, but most of them are restricted and threatened. Based on herbarium and floristic data and other literature sources, distribution maps were plotted. The distribution of the wild species was compared with the vegetation map of Africa (White, 1983), and remarkable agreement was found between the areas of the distribution and several phytochoria or mapping units. This comparison suggests to estimate possible wider distribution of these species than currently recorded. The regions where the species are endangered by desertification, grazing, agriculture, or other activities or the areas where the species are very limited in distribution and endemic to them, were designated as the first priority places for collecting. These are mainly: Air Mts, Niger (and the northern Sahel throughout); coastal strip and adjacent mountains Yemen; central Somalia, and the frontier region of Somalia, Ethiopia, and Kenya; Meshra el Zerav, Sudan; Nondwa and Ruaha National Park, Tanzania; and Santo Antão, Cape Verde Islands. Civilization pressures, especially overgrazing and depleting of vegetation for agricultural purposes together with climatic changes could cause complete extinction of those valuable species and genetic resources. Examination of germplasm collections of USDA (USA), IRCT (France), Zimbabwe, and the Israel Gene Bank, revealed that African and Arabian cotton germplasm is very poorly represented, and it is likely that a similar situation exists in other collections. World research and conservation community should be aware of this fact and rescue the last *Gossypium* fragments if it is not already late.
Genetic erosion of fruit varieties and their recovery from historic gardens

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Background. The analysis of several nursery catalogues of the last 100 years shows that, year by year, a lot of varieties disappeared from the nursery cycle production. For example, some almond varieties (Buccia dura, Principessa, Mostruosa, etc.), mentioned in the nursery catalogue of the year 1900, resulted missed 10 years later and replaced by other update new varieties. After that, probably lost forever. This phenomenon occurred also when the propagation techniques didn’t allow to clone the individual tree by rooting or grafting technique. But if some accession disappeared fast from the nursery, in few cases, some genotypes survived in the historic gardens duet to the care and the specific experience of some gardeners, which saved several plants, considered missed. Consequentially, the historic gardens in several cases can be considered as genetic font of fruit abandoned by the nurseryman and kept alive for private use.

The ISF of Rome began the recovery of fruit varieties from historic gardens of Lazio region 10 years ago and a specific methodology have been developed as follow: Site prospection, Plant identification, Plant site mapping, Plant multiplication, Establish of Germplasm collection.

Site Prospection. This phase consisted of a preliminary analysis of literature from Botany Department of University of Rome to provide the list of Historic gardens and then followed by the local prospection of each site to verify the real status of fruit accessions. Fruit accessions were considered plant producing fruit or plant potentially interesting for other agricultural purposes.

Plant Identification. The identification was done in different season by making an accurate botanical exam to compile files recording vegetative and reproductive habitus, and some agronomic traits were described. Thirty sites have been visited, and in 3 of them (Gardens of Ninfa, Castelgandolfo and Valvisciolo) several old fruit genotypes have been identified.

Plant Site Mapping. The description of each single genotype included the local coordinates to identify the planting position. The “coordinates” were indicated during the propagation step and reported in the germplasm collection. The above procedure will allow the further replacement of the specific tree in the garden, after plant died. In few words: mapping = umbilical cordon between historic garden and germplasm collection.

Plant Multiplication. This step isn’t simple because pruning technique of plants growing in the historic is performed to favourite the ornamental function (especial flowering). Consequentially the plants often don’t produce enough vegetative material needed for the propagation. Beside that, shoot removing can’t be done “freely” to avoid esthetical damage of the plant shape.

Establish of Germplasm Collection. The monitor of the plants growing in the historic gardens allowed the recovery of several fruit genotypes considered lost because they were not multiplied in the nurseries, but introducing them in the ISF national germplasm collection, these accessions are saved from the risk of genetic erosion. The clones are available for eventual restore in the original sites and used for agronomical valorisation.
INDICATORS FOR THE CWR SPECIES’ LIST PRIORITISATION
(European Crop Wild Relative Criteria for Conservation)

Flor, António¹; Bettencourt, E.²; Arriegas, Pedro Ivo³; Dias, Sónia R.²

Due to the lack of a comprehensive European red list of vascular plants, until now we have been just theorizing with the “IUCN threat categories”. However we felt that a criteria of such type was needed to assess and predict genetic erosion and pollution that affects the European CWR species. It can be somewhat different, but must be commonly accepted.

The proposed criteria and methodology are a base to start from and an attempt to fill the identified gap in the establishment of standardised criteria and methodology for the European CWR species list.

The authors propose, for discussion and feedback, criteria and a methodology which application aims to prioritise a list of European crop wild relatives, for the development of appropriate assessment and prediction of genetic erosion and pollution, and conservation methodologies.

Criteria where grouped in five groups (see Table below), each one with several indicators and their valuation.

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