First meeting of the EUFORGEN Working Group on Genetic Monitoring

Maccarese (Rome), Italy, 17-19 January 2012

Summary of the meeting

Opening of the meeting

J. Koskela (EUFORGEN Coordinator) welcomed the participants to Bioversity and introduced the meeting. He also briefed the participants on the CGIAR reform process and the envisaged changes at Bioversity. He concluded by stressing that these changes would have no impact on the hosting arrangements of the EUFORGEN Secretariat.

The meeting agenda was adopted without changes. All participants then introduced themselves. F. Aravanopoulos (Greece) was elected as Leader of the Working Group, and J. Koskela and A. Pilipovic (Serbia) were nominated as rapporteurs of the meeting.

EUFORGEN update and expected outputs of the Working Group

J. Koskela briefly revisited the objectives of EUFORGEN Phase IV (2010-2014) and explained the new modus operandi, which is based on small working groups and workshops. In September 2010, the EUFORGEN Steering Committee decided to establish three working groups for 2011-2012 focusing on 1) genetic conservation strategies, 2) genetic monitoring, and 3) forest reproductive material. The members of each working group (max. 10 experts) were selected from a pool of national experts nominated by the EUFORGEN National Coordinators. Other nominated experts for Objectives 1 (use of forest genetic resources) and 2 (conservation of forest genetic resources) will have an opportunity to contribute to the work of the different working groups by email and to attend the workshops. A total of 52 and 50 experts have been nominated to Objectives 1 and 2, respectively.

J. Koskela continued by presenting the tasks of the Working Group, which is expected to prepare:

- Synthesis of existing documents
- Analyses of the EUFGIS and other databases relevant (e.g. ICP forest) for genetic monitoring purposes
- Recommendations for improving EUFGIS data standards for genetic monitoring
- Options for genetic monitoring methods, including defining time intervals for monitoring (per groups of tree species)
- Cost assessment of the options for genetic monitoring methods
- Draft report

He further informed the participants about the work schedule. The second meeting of the working group will be held in spring 2012 and that the draft report should be ready by July 2012. The results of the Working Group will be then presented for further discussion at the EUFORGEN workshop on conservation and monitoring of forest genetic resources (FGR) that will be organized in Finland on 18-20 September 2012. The EUFORGEN Steering

Committee is then expected to make decisions on further action during its next meeting in France in November 2012. He also informed the participants that EUFORGEN would organize another workshop on FGR documentation in Hungary on 8-10 May 2012.

He continued by noting that three new FGR projects have been approved recently by the European Commission (EC) under the Knowledge-Based Bio-Economy Programme (KBBE) of the seventh framework programme for research. These include PROCOGEN on conifer genomics, TREES4FUTURE on increasing the use of forest resources for wood products and services, including tree breeding, and FORGER on managing genetic resources of forest trees. The FORGER project will be implemented in collaboration with EUFORGEN. More information on these and other KBBE projects are available on the EC website (http://ec.europa.eu/research/bioeconomy/projects/index_en.htm). Furthermore, he also informed the participants that the DG Agriculture and Rural Development of the EC is expected to make decisions on the continuation of the AGRI GEN RES Programme during 2012. This programme co-financed the EUFGIS project (Establishment of a European Information System on Forest Genetic Resources, 2007-2011).

Overview of the EUFGIS Portal

J. Koskela presented the results of the EUFGIS project focusing on the pan-European minimum requirements for genetic conservation units of forest trees, data standards and the EUFGIS Portal (http://portal.eufgis.org). The minimum requirements are based on the concept of dynamic conservation of genetic diversity. The units should have a designated status as genetic conservation areas of forest trees at national level and they can be located can be located in forests managed for multiple uses, protected areas or seed stands (but not in seed orchards). He further noted that the units should have a certain minimum population size, target tree species identified for genetic conservation, and that they should be visited frequently. The database includes 26 unit-level and 18 species-level data standards for each unit. In January 2012, the Portal contained data on 2369 units, which harbour 3154 populations of nearly 100 tree species.

He continued by noting that two case studies were developed at the end of the project, one assessing dynamic FGR conservation efforts in Europe and another one trying to quantify the impact of climate change on the dynamic conservation units. Furthermore, an additional review paper was developed based on the pan-European minimum requirements. The EUFGIS Portal is now maintained and further developed by EUFORGEN. He concluded by noting that the Portal can also be used as a platform for genetic monitoring of the units and it is thus an useful tool for the Working Group to complete its tasks. Furthermore, he invited the Working Group to provide recommendation for improving the Portal and the data standards for genetic monitoring purposes.

Genetic monitoring of tree populations

F. Aravanopoulos made a presentation based on the earlier work of the EUFORGEN Scattered Broadleaves Network, which had discussed development of a genetic monitoring system that should focus on genetic conservation units of model forest tree species during Phase III (2005-2009). He started by defining genetic monitoring as the quantification of temporal changes in population genetics and demographic characteristics, which are measured using appropriate parameters. He noted that the debate around genetic monitoring in conservation genetics started about 25 years ago and listed some of the most recent papers and proposals on the topic. He continued by discussing various parameters which have been proposed for this purpose and concluded that they are often numerous within a single scheme and difficult to assess in terms of time, expertise and financial resources.

He then proposed that genetic monitoring should focus on keystone (or model) tree species of ecological and economic importance, as well as endangered and/or rare species. He also stressed that genetic monitoring should pay attention to so called "rear-edge" populations. He pointed out that genetic monitoring efforts should be targeted to selected populations, and that the method used should be applicable to all tree species and be based on a minimum set of parameters.

Following this, F. Aravanopoulos proposed that genetic monitoring could be based on three indicators and their verifiers (in brackets):

- natural selection (age class distribution, reproductive fitness (measured by percentage of filled seeds or percentage of germination) and regeneration abundance)
- genetic drift (effective population size, allelic richness, latent genetic potential)
- gene flow (outcrossing/actual inbreeding rate)

He noted that this approach requires a much lower number of verifiers than various earlier presented schemes in which the number of verifiers ranges between 12 and 23. In this three-indicator approach, the data and sample collection can be done during a single field visit, sample sizes per unit are reasonable ($N_{indiv} \geq 30$, $N_{loci} \geq 20$, $N_{seeds} \geq 300$) and the monitoring frequency is one evaluation per decade. He estimated that the field work and seed testing would require a total of 14.5 days per population.

He concluded that the scientific community should agree on a minimum level of measurable parameters instead of relying *ad hoc* studies and monitoring approaches that are not directly comparable. More detailed discussion on the proposed approach can be found in a recently published paper (Aravanopoulos, F.A. 2011. Genetic monitoring in natural perennial plant populations. Botany 89: 75-81).

The German concept for genetic monitoring of forest trees

R. Kätzel (Germany) briefed other participants on the German approach which is based on permanent sample plots (selected ICP Level II plots) and four indicators (level of genetic variation, directional change in gene or genotypic frequencies, changes in mating system processes and gene migration between populations). The size of the monitoring plots is four ha and their inner zone (one hectare) is fenced. The fenced area then includes a core area of 50x50 m. When a monitoring plot is being established, a field inventory is carried out to map the coordinates of all adult trees and the demongraphic structure of the population. Furthermore, samples are collected from adult trees to to assess the genetic structure of the population. Subsequent annual monitoring include vitality and mortality, flowering, fructification of each adult tree and phenology of buds. Seeds are also collected for testing their quality. Additional measurements (e.g. ground layer vegetation, natural regeneration, growth and crown volume/structure) are carried out every 5-10 years.

R. Kätzel continued by presenting some results from the monitoring plots of sessile oak (*Quercus petraea*). So far, five monitoring plots have been established for sessile oak in Germany while the target is to have 10 plots. The results show considerable variation in vitality (measured as crown transparency), fructification and seed quality (germination) between years and plots. He also reported that trees with low vitality or damages produced more acorns as compared to healthy ones and questioned the impact of this to the genetic structure of the next generation. He then noted that, in terms of staff time, the establishment of two plots located nearby each other requires 14 days of field work, annual monitoring 16 days and field inventories (every 5-10 years) 8 days. These estimates do not include the laboratory work needed to analyze the samples collected from the plots.

Further information on the German approach and its pilot testing can be found from a paper by R. Kätzel and other German colleagues (Konnert, M. et al. 2011. Genetic monitoring in forests-early warning and controlling system for ecosystemic changes. iForest 4, 77–81, http://www.sisef.it/iforest/contents/?id=ifor0571-004).

Development of genetic monitoring protocols as part of the FORGER project

J. Koskela presented the planned work on genetic monitoring that will be carried out as part of the new FORGER project, which will start in March 2012 for a period of four years. The project is coordinated by Alterra (Netherlands) and it included eight other partners (BFW (Austria), vTI (Germany), INRA (France), Metla (Finland), NymE (Hungary), Bioversity, CNR (Italy) and UKW (Poland)). The overall goal of the project is to enhance the conservation and use of forest genetic resources by making available sound and integrated information on forest genetic resources for forest managers and policymakers. The project has five objectives:

- To improve inventories on forest genetic resources in Europe by linking existing databases
- To assess the current distribution of genetic diversity and how forest genetic resources are conserved in selected tree species at pan-European level
- To assess both the future distribution of genetic diversity of selected tree species at pan-European level under climate change and the adaptation options by forest management
- To develop a common protocol for measuring and monitoring genetic diversity of tree populations at pan-European level
- To improve guidelines and recommendations for transfer of forest reproductive material and management of forest genetic resources in genetic conservation units and production forests

One of the Work Packages, titled as "Measuring and monitoring genetic diversity", includes a task to further develop at the European scale protocols for monitoring of genetic diversity in forest stands to assess the impact of climate change and forest management. As part of this work, the project will carry out a pilot study on genetic monitoring focusing on beech (*Fagus sylvatica*), Norway spruce (*Picea abies*), Scots pine (*Pinus pinaster*) and pedunculate oak (*Quercus robur*). A total of 16 plots will be selected for this purpose from the EVOLTREE Intensive Study Sites, the genetic conservation units and production forests under different management regimes. In each plot, 500 individuals will be sampled in three ontogenic stages (100 mature trees, 15 single tree progenies with size of 20 individuals, and a sample of 100 saplings). A number of genetic and demographic parameters proposed by earlier studies (cf. Namkoong et al. 2002; Schwartz et al. 2007; Aravanopoulos 2011; Konnert et al. 2011) will be then tested for improving protocols for genetic monitoring of forest trees in Europe.

J. Koskela added that another task in the same Work Package would also apply molecular tools to assess adaptive genetic diversity in these tree species. This work will select and sample 50 new tree populations and generate new molecular data (SNP arrays, high-through genotyping).

He then clarified the tasks of the FORGER project and the Working Group. The project will address genetic monitoring of forest stands to assess the impact of climate change and forest management while the task of the Working Group is to explore options specifically for monitoring of the genetic conservation units across Europe. The project will carry out field testing of different monitoring approaches whereas EUFORGEN does not have resources for that kind of work and the Working Group have to rely on the currently available information and earlier studies. The time scales are also different; the Working Group is expected to present its finding to the EUFORGEN Steering Committee in November 2012 while the project will test the earlier presented monitoring approaches during the next four years.

J. Koskela continued that there are considerable synergies between the two efforts, and that both of them can benefit from each other's work. For this purpose, an expert consultation will be held during the EUFORGEN workshop on FGR conservation and monitoring in September 2012 so that a broader group of EUFORGEN experts and the project partners can exchange ideas and views on genetic monitoring. Furthermore, he noted that he would ask relevant project partners to join the second meeting of the Working Group so that it can learn more about the project activities and consider them while finalizing its report to the Steering Committee.

Other relevant studies, projects and databases

The meeting participants exchanged information on other ongoing or past studies and projects relevant to the Working Group. National projects have been in implemented in Bulgaria (on oaks) and in Norway (for common ash). Genetic studies on beech and black poplar have also been carried out in Slovenia but these were not designed for genetic monitoring purposes. National projects on Norway spruce and wild cherry have also been done in Greece. No specific projects on genetic monitoring have been conducted in Hungary and Serbia. In Spain, the importance of genetic monitoring has been discussed by the national FGR programme which is interested in applying the European approach once it has been developed and agreed.

It was also discussed what lessons can be learnt from various biodiversity monitoring efforts in Europe, such as the Natura 2000 network. Several participants pointed out that the biodiversity assessments can also support genetic monitoring efforts. However, the problem is that these monitoring efforts have so far only focused on assessing species. It was noted that genetic level will soon probably be also introduced to the biodiversity assessments and this offers opportunities for collaborating with these efforts, especially in those cases when the genetic conservation units of forest trees are located within a protected area.

Case studies carried out as part of the EUFGIS project

J. Koskela presented preliminary results of two case studies, which were carried out at the end of the EUFGIS project. The first one focused on assessing dynamic conservation of forest genetic resources in Europe and the second one on quantifying the impact of climate change on the conservation units of forest trees in Europe. He pointed out that the first case study in particular is very useful for this working group as it demonstrates how the units for genetic monitoring efforts can be selected.

He started by showing an example of how ecosystem-based conservation gap analysis has been applied to conservation of plant genetic resources. He then explained that the first case study identified gaps in genetic conservation efforts within tree species' distribution range using different geographical scales. The scales included 1) country borders, 2) environmental zones, 3) environmental strata, and 4) country x zone, i.e. each country divided into zones. The environmental zones and strata were obtained from an earlier study, which developed an environmental stratification for Europe (see Metzger et al. 2005, Global Ecology and Biogeography 14: 549-563, http://onlinelibrary.wiley.com/doi/10.1111/j.1466-822X.2005.00190.x/full). He concluded that there are genetic conservation units in all major environmental zones at pan-European level. However, when the gap analysis is done focusing on the distribution ranges of individual tree species and applying the different geographical scales, considerable gaps can be observed in the conservation efforts for most tree species. Furthermore, the results show that the geographical distribution of the units is often rather clustered and not covering all environmental zones within countries. This suggests that certain environmental zones are favoured, for different reasons, when the units are being established.

He continued by presenting the second cases study which aimed at 1) characterizing the current climate conditions of the conservation units and 2) analyzing how the climate envelopes of selected tree species are expected to shift as a result of climate change to identify most threatened units. He then showed the how well the genetic conservation units represent the climatic conditions of selected tree species at range-wide level, and how the climatic envelopes are expected to shift as a result of climate change. He noted that this approach helps to identify those units which are at risks and which could be selected for genetic monitoring efforts.

Recommendations for improving the EUFGIS data standards

The meeting participants decided to postpone the discussion on this topic to the second meeting when are the potential monitoring options would have been better clarified. Once the options are further developed, the needs for new data standards can then be identified in a more efficient manner.

Identification of most feasible options for genetic monitoring

The meeting participants continued discussing various options and methods for genetic monitoring of the conservation units (including criteria for selecting species and populations). J. Koskela also briefed them on the discussions of the first meeting of the EUFORGEN Working Group on genetic conservation strategies. The other Working Group had decided that the targeted level of genetic conservation should be at the country x zone level. This means that within the distribution range of a species, there is at least one conservation unit in each zone within a country. Moreover, the other Working Group decided to establish a core network of the conservation units by selecting the most valuable units at pan-European level. The core conservation network is also targeting to cover all country x zones “niches” across the distribution area of selected tree species.

While discussing the monitoring options and methods, it was agreed that the reasons why we need genetic monitoring should be explained clearly to policymakers and managers in the report of the Working Group. It was also decided that various approaches for genetic monitoring, and especially their indicators, verifiers and frequency of application, should be reviewed in the report.

The Working Group then concluded that it is important that genetic monitoring efforts focus on both neutral and adaptive genetic diversity, and that a stratification approach can be used as a proxy for considering the adaptive diversity of forest trees conserved in Europe. It was also recognized the genetic monitoring efforts should be based on the range-wide approach and that it is not feasible to monitor all units in the EUFGIS database for this purpose. Subsequently, the Working Group decided to further investigate various ways of selecting units for genetic monitoring based on different geographical scales. These scale options were identified as follows:

- Distribution area x zone
- Distribution area x country x zone
- Distribution area x regular grids (either 50x50 km or 100x100km)

It was noted that the stratum level of the European environmental stratification is probably too detailed for the purpose but it was agreed that this option should be also investigated as part of the distribution area x country x zone option. This option is similar to the one used by the other Working Group for selecting units for the core genetic conservation network. It was agreed that the option of selecting units for genetic monitoring from the core network would also be further discussed during the second meeting.

The Working Group continued by discussing the need to select model tree species to facilitate its investigations on the monitoring options. The group first considered the list of model tree species identified by the other Working Group on genetic conservation strategies. It was decided to use this list as a basis and add a few species. One species (*Populus tremula*) was removed from the earlier list. Furthermore, it was concluded that it would be better to group the selected model species into two categories, 1) keystone species and 2) endangered species at pan-European level. The list of the model species for this Working Group is as follows:

Keystone species	Endangered species at pan-European level
*Abies alba** *Castanea sativa** *Fagus sylvatica** *Fraxinus excelsior** *Picea abies** *Pinus brutia* *Pinus cembra** *Pinus halepensis* *Pinus nigra** *Pinus pinaster* *Pinus sylvestris** *Prunus avium* *Quercus petraea** *Quercus robur* *Sorbus torminalis**	*Populus nigra** *Ulmus glabra* *Ulmus laevis*

* model species of both Working Groups

It was also concluded that once the work has reached the phase when genetic conservation units will be selected for genetic monitoring, the group should consider giving priority to multi-species units instead of single-species ones as this would make the future monitoring efforts more cost efficient. Finally, it was agreed that the issue of time interval for genetic monitoring would be discussed during the second meeting.

Cost assessment of the options

The Working Group decided to postpone the cost assessment of different monitoring options to the second meeting. It can be carried out only once the final options have been identified.

Report of the Working Group

Based on the above-mentioned discussions and decisions, the Working Group developed a tentative outline of the report (see Annex 1). Lead contributor(s) were also identified for each chapter of the report.

It was agreed that all contributions should be send to the Working Group Leader (F. Aravanopoulos) by 19 March 2012 with carbon copy to all members of the Working Group. F. Aravanopoulos will then compile the first draft of the report by 16 April 2012 and circulate it to all members who should then provide their comments to him by 23 April 2012. F. Aravanopoulos will incorporate the comments received and circulate the revised draft of the report to all experts (Working Group members and email contributors) by 30 April 2012.

The draft report and comments received from the email contributors will be then discussed during the second meeting of the Working Group. An improved draft will presented by the Working Group Leader at the EUFORGEN workshop on FGR conservation and monitoring in September 2012 for further discussion.

Wrap-up session

The Working Group members agreed to continue the work by email and to prepare the first draft of the report for further discussion at the next meeting. A. Soto de Viana kindly offered to host the next meeting of the Working Group in Madrid. As a second option, P. Zhelev and M.M. Tollefsrud offered to host the meeting in Sofia and Oslo, respectively.

The week of 21-25 May 2012 was tentatively identified as suitable dates for the second meeting. The exact meeting dates will be confirmed later. The Working Group members considered the length of the first meeting (2.5 days) ideal and recommended that the next meeting should have the same length.

Closure of the meeting

F. Aravanopoulos thanked all participants for their inputs to the discussions and the Secretariat for organizing the meeting. With no other business, he then closed the meeting.

Annex 1. Outline of the Working Group report and lead authors for different chapters.

Working title: Development of genetic monitoring methods for genetic conservation units of forest trees

Preface (J. Koskela)

Introduction (F. Aravanopoulos, J. Koskela, R. Kätzel)
    Definition and importance of genetic monitoring

Synthesis/review (F. Aravanopoulos, R. Kätzel, A. Soto de Viana, M.M. Tollefsrud, L. Graudal)
    Genetic monitoring: purpose, objectives, approaches etc
    Terminology (criteria, indicators, verifiers (cf Boyle 2000)

Databases relevant for genetic monitoring (P. Zhelev, J. Koskela)
    EUFGIS to be used as the basis for identifying units for genetic monitoring
    Recommendations for improving the EUFGIS data standards (to be discussed later)

Options for pan-European genetic monitoring methods (2-3)
    Indicators and verifiers (F. Aravanopoulos, R. Kätzel, A. Soto de Viana, M.M. Tollefsrud, L. Graudal)
    Approaches for identifying "potential monitoring regions" (L. Nagy, A. Pilipovic, M. Bozzano, J. Koskela)
        Distribution x zone (L. Nagy)
        Distribution x country x zone x stratum (A. Pilipovic)
        Distribution x grid option (M.M. Tollefsrud)
    Principles for selecting the monitoring unit(s) within the monitoring regions, including existing genetic knowledge (cf WG on genetic conservation strategies) (F. Aravanopoulos, L. Nagy, A. Soto de Viana)
    Species selection for exploring monitoring options (P. Zhelev, A. Pilipovic)
    Cost assessment (to be discussed later)

Conclusions and recommendations

References (all to contribute)

Annexes (as needed, maps, tables etc)

Annex 2. Agenda of the meeting

Mon 16 January		
	Arrival to Fiumicino Airport and train to the hotel	Hotel Express by Holiday Inn (via Assisi 53)
	Dinner on your own	

Tue 17 January		
09:00	Opening of the meeting ● Welcome to Bioversity and introduction to the meeting (J. Koskela) ● Adoption of the agenda ● Selection of WG Leader and nomination of rapporteurs	Bioversity International Scylla meeting room (Stretto building)
09:15	EUFORGEN update and expected outputs of the WG (J. Koskela) ● Discussion	
09:45	Overview of the EUFGIS Portal, including the minimum requirements for genetic conservation units and the data standards (J. Koskela) ● Discussion	
10:30	Coffee/tea break	Stretto coffee room
11:00	Genetic monitoring of tree populations (F. Aravanopoulos) ● Discussion	
11:45	The German concept for genetic monitoring of forest trees (R. Kätzel, to be confirmed) ● Discussion	
12:30	Lunch	
14:00	Further development of genetic monitoring protocols at the European scale as part of the new FORGER project (to be confirmed) ● Discussion	
14:45	Other relevant studies, projects and databases ● Discussion	
15:30	Coffee/tea break	Stretto coffee room
16:00-17:30	Synthesis of publications and projects on genetic monitoring, including approaches already applied in practice ● Discussion	
20:00	Social dinner	

Wed 18 January		
09:00	Case studies carried out as part of the EUFGIS project (J. Koskela) ● Assessment of FGR conservation in Europe ● Impact of climate change on genetic conservation units ● Discussion	Bioversity International Scylla meeting room (Stretto building)
09:45	Recommendations for improving the EUFGIS data standards for genetic monitoring ● Discussion	
10:30	Coffee/tea break	Stretto coffee room
11:00	Identification of most feasible options (2-3) to be presented in the report in more detail ● Methods and protocols, what to monitor (i.e. all units or a core network of units), time interval, etc. ● Discussion	
12:30	Lunch	
14:00	Cost assessment of the genetic monitoring options ● Approaches for conducting the cost assessment, including various cost items of genetic monitoring (lab work, field work, etc) ● Discussion	
15:30	Coffee/tea break	Stretto coffee room
16:00- 17:30	Report of the Working Group ● Development of the table of contents ● Discussion	

Thu 19 January		
09:00	Report of the Working Group (continued) ● Compilation of existing information, data, publications etc. ● Discussion	Bioversity International Scylla meeting room (Stretto building)
10:30	Coffee/tea break	Stretto coffee room
11:00	Next steps before the second WG meeting ● Tasks and deadlines	
12:15	Wrap-up session ● Any other business ● Date and place of next meeting	
12:30	Lunch	Stretto coffee room
13:00-	Transport to Fiumicino Airport, as needed	

Annex 3. List of participants

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