

EUFORGEN/FORGER Workshop on Conservation and Monitoring of Forest Genetic Resources

Järvenpää, Finland 18-20 September 2012

Summary of the workshop

Opening of the workshop

M. Rusanen, EUFORGEN National Coordinator of Finland (Finnish Forest Research Institute (Metla)) opened the workshop and welcomed the participants to the country. She briefly introduced a new report on the state of forest genetic resources in Finland that was distributed to all workshop participants. The report was published by the Ministry of Agriculture and Forestry in 2012 and it is a summary of the country report submitted to FAO in 2011 for the State of the World's Forest Genetic Resources report. She also informed the participants that Metla had organized a field visit to a genetic conservation unit of common ash (*Fraxinus excelsior*) in Hyvinkää, near Helsinki the day before to demonstrate practical conservation work to a group of journalists. She noted that several newspapers are expected to publish articles on FGR conservation as a result of this "field press conference", which was organized in collaboration with the owner of the unit, Tornator Ltd.

T. Pehu, Counsellor (Ministry of Agriculture and Forestry) welcomed the participants on behalf of the Ministry and she then presented an overview of Finland's national programme on genetic resources. It consists of three sub-programmes focusing on agricultural crops, forest trees and farm animals. In addition to conservation and sustainable use of genetic resources, these national programmes also promote research, training and public awareness efforts and collaborate with relevant Nordic, European and global initiatives. She explained that the Ministry had established in 2003 an Advisory Board for Genetic Resources to steer the development and implementation of the national programmes. The Advisory Board also serves as a common discussion and information sharing forum for different stakeholders interested in the conservation and sustainable use of genetic resources for agriculture and forestry. She concluded her presentation by noting that she was very interested in learning more about the topics of the workshop, and in particular the development of a pan-European genetic conservation strategy for forest trees.

J. Koskela (Bioversity International) welcomed the participants on behalf of the EUFORGEN Secretariat and thanked Metla for its contributions to the practical arrangements of the workshop. Furthermore, he thanked the two EUFORGEN working groups which had prepared their draft report for further discussion during the workshop. He continued by presenting the past efforts and current status of FGR conservation in Europe. First national FGR programmes were launched in the 1980s and after the first Ministerial Conference on European forests, held in Strasbourg, France in 1990, most countries started developing these programmes. In 1994, the EUFORGEN Programme was also established to coordinate the pan-European implementation of Strasbourg Resolution 2.

J. Koskela provided a historical background to the development of the pan-European genetic conservation strategy for forest trees. He explained that the development of so called "common action plans" at pan-European level were started in early 2000s when the EUFORGEN Networks initiated the compilation of species distribution maps, listing of species-specific minimum requirements for genetic conservation units of forest trees, and collection of geo-reference data on existing conservation efforts. He then noted that the

EUFGIS project (2007-2011) was developed to support these efforts and to improve the management and documentation of the genetic conservation units. He continued by presenting the main results of the project, i.e. the EUFGIS Portal and the pan-European minimum requirements and data standards for the units. Currently, the EUFGIS database contains information on a total of 2629 units in 31 countries. These units are managed for genetic conservation of 3420 populations of nearly 100 tree species. The data on the units in the EUFGIS database is maintained by the National Focal Points. He concluded by presenting the results of a EUFGIS study which showed that there are still large gaps in genetic conservation efforts at the pan-European level.

Finally, J. Koskela noted that the workshop is an important milestone in the EUFORGEN work. Now that harmonized data on the genetic conservation units is available through the EUFGIS database, the next challenges are to define the targeted level of FGR conservation at the pan-European level and how to monitor the genetic diversity conserved within the units. At the end of his presentation, he reminded the participants on the purpose of the workshop, which is to review the approaches and options presented by the EUFORGEN working groups for developing the pan-European genetic conservation strategy for forest trees and establishing the related genetic monitoring scheme. Furthermore, he explained that the workshop is organized in collaboration with the new FORGER project and that it also serves as an expert consultation on FGR conservation and monitoring during which the participants have an opportunity to comment and provide inputs to the FORGER work. He noted that this will increase the usefulness of the project results for future EUFORGEN work on FGR conservation and monitoring.

J. Koskela then introduced the workshop agenda which was adopted without changes. He also explained the planned steps after the workshop. The two working groups will incorporate the comments received during the workshop into their draft reports which will be presented to the EUFORGEN Steering Committee in November 2012 for further discussion and action.

J. Koskela, M. Bozzano and E. Hermanowicz were nominated as rapporteurs of the workshop. The members of the two working groups were also asked to take specific notes to improve the draft reports. All participants then briefly introduced themselves.

Development of a pan-European genetic conservation strategy for forest trees

E. Collin (IRSTEA, France), Chair of the session, provided a brief introduction to the topic and stressed the importance of pan-European approach in conserving genetic resources of forest trees which typically occur across many countries.

S. de Vries (Centre for Genetic Resources the Netherlands) presented the draft report of the working group on genetic conservation strategies. The working group had met twice during the course of its work; first meeting was hosted by Bioversity International in Maccarese, Italy on 2-4 November 2011 and the second one by the Research Unit for Intensive Wood Production (CRA-PLF) of the Italian Agricultural Research Council in Casale Monferrato on 14-16 February 2012. Furthermore, he noted that data and other information needs for the development and implementation of the pan-European genetic conservation strategy were discussed during a workshop on FGR inventories, held in Szombathely, Hungary, 8-10 May 2012.

S. de Vries explained that the overall goal of the strategy is to conserve both adaptive and neutral genetic diversity of forest trees by creating a pan-European core network of genetic conservation units. He further explained that the purpose of the strategy is to clearly specify the targeted level of genetic conservation at the pan-European level. He then listed the steps the working group had used for preparing the draft strategy. They included 1) selection of model tree species, 2) ranking of the units for the establishment of the core network, 3) assessment of the genetic conservation status of the model tree species, and 4) identification of gaps in the conservation efforts. He continued by noting that the selection of model tree species (14 in total) was done based on their geographical distribution (wide or restricted) and ecological appearance (stand-forming or scattered). The ranking of the most valuable units for the establishment of the core network was done by first eliminating ex situ units as well as those units which had introduced genetic material. The ranking also preferred public ownership, large size (both in terms of individuals and hectares) and active management.

The working group assessed the genetic conservation status of the pilot tree species based on the data available in the EUFGIS Portal and then identified gaps in the conservation efforts. Gaps in adaptive genetic diversity were determined based on the so called “country x zone” areas, i.e. by dividing each country within the distribution range of a given species into environmental zones and then evaluating how many of the zones within the countries had conservation units. S. de Vries briefly explained the environmental zones defined by Metzger et al. (2005) and informed the participants that a new and more detailed environmental zoning at the global level will be published in early 2013 by the same research group. He reported that the working group had also considered gaps in neutral genetic diversity based on “area of interest” approach (i.e. migration routes, refugia areas and contact zones) using the available information from earlier genetic studies. He then presented a summary table of countries, environmental zones and the “country x zone” areas for each model species and showed detailed maps for selected species.

S. de Vries concluded his presentation by noting that the implementation of the pan-European strategy, including the selection of additional units to the core networks and identification of gaps, is a continuous process. Furthermore, he pointed out that the units selected and the gaps identified should be considered as tentative ones. The report will be finalized after the Steering Committee has commented it. The working group also plans to use the forthcoming environmental zoning for preparing the final report. Once finalized, the idea is that the strategy will be revised, as needed, and that the progress made in implementing it will be monitored regularly. He also noted that the working group urges all countries to continue their FGR inventories and to provide data on their conservation units to the EUFGIS Portal.

Some participants commented that the environmental zoning by Metzger et al. (2005) has some inconsistencies in their countries. S. de Vries clarified that the working group is aware of this issue and that it is expected that the new zoning by Metzger et al. (2013) will solve most, if not all, inconsistencies of the previous zoning. Other participants asked whether different approaches for environmental zoning should be considered for solving the inconsistencies. S. de Vries noted that the working group had also tested other zoning approaches and that every zoning approach has its strengths and weaknesses. He explained that the zoning by Metzger et al. was found to be the most workable approach for the purpose.

The goals of the strategy and its links to the monitoring efforts were also questioned by several workshop participants. The working group members explained that the ultimate goal of the strategy is to improve the management and geographical coverage of the pan-

European network of the units. They also noted there are indeed many linkages to the genetic monitoring efforts and that these will be further discussed during the workshop once the other working group has presented its draft report. It was proposed that the minimum requirements for the genetic conservation units could be explained in more detail in the report. In addition, the workshop participants provided several editorial comments to the draft report.

Forest genetic diversity in forest monitoring & management

Genetic monitoring in forests: lessons from the German system and new pilot studies in Europe

B. Degen (vTI, Germany) presented the background and some results of the work on genetic monitoring of forest trees that has been done in Germany during the past decade. A national working group developed the German system between 2003 and 2006, the first monitoring plots were established in 2005-2008 for beech (*Fagus sylvatica*) (4 plots) and wild cherry (*Prunus avium*) (5 plots). These efforts were financed by the German Federal Ministry for Agriculture, Food and Consumer Protection (BMELV). In 2008, the results of the pilot studies were used to prepare a manual on genetic monitoring and after that, the work has been continued by collecting additional data and establishing some additional monitoring plots. 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, the position, diameter and height of all adult trees are recorded. Data is also collected on the number and position of saplings, flowering phenology, seed quality (seed weight, vitality, germination), the social ranking class of the trees (KRAFT class), stand history and the level of isolation of the studied stand.

B. Degen mentioned that the monitoring system is based on four indicators (level of genetic variation, directional change in gene or genotypic frequencies, changes in mating system processes and gene migration between populations). He continued by explaining the genetic inventories and their results in detail.

He then moved on and briefed the participants on further pilot studies on genetic monitoring that will be carried out as part of the FORGER project (2012-2016). These studies will focus on four tree species (*Fagus sylvatica*, *Quercus robur*, *Picea abies* and *Pinus pinaster*). The project will establish a total of 16 plots (four per each species) to 1) monitor changes in genetic composition caused by genetic drift, mating system, gene flow and selection based on the screened genetic and demographic parameters, and 2) to develop ecological alternatives for the rapid and economic monitoring of genetic diversity. The monitoring sites will be selected among the Intensive Study Sites (ISS) of the EVOLTREE Network, the genetic conservation units and forests managed with different intensities across Europe. In each plot, the sample will consist of 100 mature trees, 15 single tree progenies with a size of 20 individuals each, and 100 saplings. In total, 500 individuals will be sampled in each plot. He then explained that 8-20 nSSRs markers will be used for studying neutral genetic diversity and 200 SNPs for assessing adaptive genes. He explained that overall goal of this work is to improve various protocols for genetic monitoring of forest trees at the European scale. These protocols include criteria for selecting the monitoring plots, sampling design, criteria for gene markers selection, descriptions for screening of genetic and demographic parameters, establishment

of reference values for genetic and demographic parameters, and description of cost-effective ecological alternatives for genetic monitoring.

He concluded his presentation by noting that there are still several open questions related to genetic monitoring. They are related to design of the monitoring plots (e.g. fixed plot size or fixed number of adult trees), definition of critical thresholds, the link between demographic data and genetic selection, and monitoring of the dynamics of genealogy in the plots. Furthermore, he noted that there are also additional challenges, i.e. how to deal with the rapid development of new markers and how to standardize analyses among different laboratories.

Introduction to the FORGER project

K. Kramer (Alterra, Netherlands) provided the participants with an introduction to the new FORGER project (Towards the Sustainable Management of Forest Genetic Resources in Europe), which is also funded by the EC (FP7-KBBE Programme). The project started in March 2012 and it will end in February 2016. The is coordinated by Alterra (Netherlands) and it has a total of 9 partners. The project aims at integrating and extending existing knowledge to provide science-based recommendations on the management and sustainable use of FGR for the EC, policy makers, forest managers, and managers of protected areas. FORGER has five objectives, namely 1) improve and analyze FGR inventories in Europe, 2) develop a common protocol for measuring and monitoring genetic diversity, 3) analyze past, current and future use and management of FGR, 4) provide improved tools, guidelines and recommendations, and 5) disseminate and communicate the results to stakeholders.

K. Kramer then explained the tasks of the different work packages and their leaders:

- WP1: Inventories of FGR (Metla)
- WP2: Measuring and monitoring genetic diversity (vTI)
- WP3: Use and management of FGR (BFW)
- WP4: Tools, guidelines and recommendations on the conservation of genetic diversity (BFW)
- WP5: Communication, dissemination and knowledge transfer (Bioversity)

Furthermore, there are two additional work packages (led by Alterra) dealing with project management. He noted that many activities of the project are of direct relevance to the EUFORGEN work. In addition to the further testing of genetic monitoring methods, he pointed out the project will extend FGR inventories in Europe by linking the GD² and EUFGIS databases. This enables characterization of the genetic diversity conserved within the genetic conservation units or found nearby the units.

K. Kremer concluded by highlighting that the key target groups for communication, dissemination and knowledge transfer include the National Focal Points of EUFGIS as well as the EUFORGEN Steering Committee, working groups and experts. In addition, the EUFORGEN Steering Committee has selected two representatives to the three-member External Advisory Board of the project. The member of the Board is representing the European Environment Agency. He mentioned that the FORGER project also plans to collaborate closely with other relevant European projects, such as the TREES4FUTURE project. Further information is available on the FORGER website (www.fp7-forger.eu).

Development of a genetic monitoring system for dynamic conservation units of forest trees in Europe

L. Graudal (Forest and Landscape, University of Copenhagen), Chair of the session, introduced the topic and highlighted the importance of the EUFGIS database for developing both the pan-European genetic conservation strategy and the genetic monitoring system for the units.

F. Aravanopoulos (Aristotle University of Thessaloniki, Greece) presented the draft report of the working group on genetic monitoring. He started by explaining different definitions for genetic monitoring and noted that the debate on this topic started 25 years ago in the context of fishery management. He then clarified the purpose of genetic monitoring and related terminology (e.g. indicators and verifiers). He also listed the earlier studies on genetic monitoring in forest trees and discussed the number indicators and verifiers these studies had proposed. He explained that the working group had selected the gene-ecological approach as the conceptual framework for developing the genetic monitoring system. The working group recognized natural selection and genetic drift as the major forces of evolution that are mediated by gene flow. Subsequently, the working group proposed that a pan-European genetic monitoring approach could be based on only two indicators (selection and genetic variation & mating system) and 10 verifiers.

F. Aravanopoulos continued by explaining the two approaches the working group had investigated for identifying potential monitoring regions, i.e. a systematic sampling approach (e.g. various grid options) and an expert-based approach. He noted that the uneven distribution of genetic conservation units within and among tree species makes any systematic approach by definition impractical due to large gaps and scale differences. Therefore, the working group decided to use the expert-based approach as a basis for identifying the potential monitoring regions. He then provided further details on the selection of model species and genetic monitoring units. He explained that genetic monitoring efforts should focus on keystone tree species of ecological and economic importance and endangered and/or rare tree species. For a proof-of-principle exercise, the working group had selected 13 keystone species and one endangered species.

The expert-based approach for identifying the genetic monitoring regions includes the following steps. Firstly, monitoring regions are tentatively identified based on the distribution map of a tree species. In the second step, the distribution map is overlaid with genetic conservation units characterized by environmental zones to identify additional monitoring regions and potential monitoring units. In the third step, layers of available genetic information (marker data or adaptive traits from provenance trials) are added to locate potential refugia and migration routes to identify additional areas for monitoring. The final number of monitoring areas and monitoring units, as well as their location, are then fine-tuned. The minimum number of monitoring units needed depends on the number of environmental zones within the distribution range of a given species. The maximum number of monitoring units is determined by the number of “country x zones” areas within the distribution range. The working group set the final number of monitoring units close to the minimum number needed in the model species tested in the report. F. Aravanopoulos demonstrated the expert-based approach in detail by showing how the step-wise process

was done for one of the model species. In addition, he showed maps with potential monitoring regions for several other model species.

F. Aravanopoulos then presented estimated costs of the monitoring efforts. The working group had calculated that average labour costs (per decade and per 10 tree populations) would be approximately eight person-months. Related genetic analyses would cost \$34,500 and \$8,000 for nSSR and SNPs, respectively (for 10 populations, 30 individuals, 300 seeds and 20 loci). He concluded by noting that genetic monitoring is an invaluable tool for the management of forest genetic resources and that the development of the monitoring system is a long-term investment. Furthermore, he pointed out that monitoring actually starts only when the data is collected for the second time. He also noted that the proposed pan-European genetic monitoring system is a unique one and of global importance.

The workshop participants made several general comments and questions following the presentation. Some clarifications were requested on the identification of the potential monitoring regions and their demarcation in the maps presented. F. Aravanopoulos provided further explanations on the process and noted that the demarcation of the regions should be considered indicative, i.e. the borders of the regions were defined based on expert knowledge and available information on the distribution of genetic diversity and climatic conditions. Several participants highlighted the importance of coordination at the pan-European level in defining the monitoring regions and selecting the actual monitoring units. Many participants appreciated that countries can have the final say in the selection of the monitoring units. It was also pointed out that it needs to be clarified how the establishment and maintenance of the genetic monitoring system will be funded. F. Aravanopoulos clarified that the working group is aware of the fact that it cannot be established without specific funding but he also emphasized that some preparatory work could be started both at the national and European levels while exploring funding opportunities. It was concluded that the scale of monitoring efforts ultimately depends on the financial resources available. Considering this, it was proposed that the monitoring system could involve less tree species so that the number of monitoring units could be increased.

Working session 1 on the pan-European genetic conservation strategy

The workshop participants discussed and reviewed the draft report of the working group chapter by chapter during the morning session on 19 September and provided many detailed comments and suggestions to improve the text. Recommendations for the implementation of the strategy were also discussed.

It was proposed that the management aspects of the pan-European minimum requirements for the genetic conservation units could be better explained in the introduction chapter of the report. Furthermore, it was noted that a brief description of the data on units in the EUFGIS database could be added. It was recommended that the underlying concept, i.e. that genetic resources are conserved for present or future use, could be also emphasized in the introduction chapter. Furthermore, several participants noted that the distinction between “conservation units” and “monitoring units” should be better explained. It was agreed that no acronyms should be used in the report when referring to different types of the units (and especially not “GMU”). It was also agreed that term “model species” will be replaced with “pilot species” throughout the report.

Concerning the chapter on the objectives, some clarifications were proposed to the text describing different environmental or vegetation classification systems in Europe. It was further agreed that the paragraph of this chapter should be moved to the chapter on methods. The workshop participants then spent considerable amount of time in discussing the targeted level of genetic conservation at the pan-European level. Some of them were concerned that the systematic application of the country x zones approach leads to rather high conservation targets for most tree species. It was also pointed out that, in case on most species, the conservation targets still include many “false gaps”, i.e. irrelevant country x zones within species’ distribution ranges, and that these should be excluded so that the conservation targets for different species at the pan-European level become more realistic. The members of the working group clarified that they are aware of this and that the problem of “false gaps” is due to the fact that the spatial accuracy of the species distribution maps and the environmental zoning of Europe (Metzger et al. 2005) is different. Furthermore, they noted that a new climatic zoning at the global level will be soon published (Metzger et al. 2013) and that the working group is planning to test its applicability before the strategy is finalized.

In case of the methods chapter, most comments and discussion were related to the ranking of the units for the establishment of the core network. It was suggested to indicate later in the report how many *ex situ* and other units were excluded before the ranking was done. Considering the ranking, many participants wanted to clarify how the criteria (i.e. ownership, number of reproducing trees, management and area) were applied in the process.

While discussing the results chapter, the participants recommended that the list of species in Table 1 and 2 should be organized per groups of pilot species instead of the alphabetical order. Furthermore, different types of gaps were discussed in detail and it was emphasized that not all gaps are equally important. Regarding Table 5, it was noted that the total number of countries within species distribution range also includes countries outside Europe and that these countries should be excluded from the gap analysis. It was agreed that it should be explained in the report that “Europe” is defined based on the geographical definition.

The discussion then moved to the report chapter on the implementation of the genetic conservation strategy. It was suggested that the role of the EUFORGEN Steering Committee in making the final selection of the units for the core conservation networks should be explained more clearly in this chapter. Several editorial changes were also proposed to the chapters on implementation and recommendations to improve the text.

Working session 2 on genetic monitoring

During the afternoon session of 19 September, the workshop participants focused on the draft report on genetic monitoring. The session started by general comments to this working group to harmonize the abbreviations used in the report with the other report on the genetic conservation strategy. In addition, it was noted that some references were missing from the list of publications and that all references used in the text and the list should be cross-checked. It was also suggested that it might be better to use the word “plot” instead of “genetic monitoring unit” as the monitoring efforts would only focus on a small part of the whole unit in most cases. It was agreed to keep “units” as the sampling scheme and other details of the genetic monitoring system have not yet been decided.

Some of the definitions explained at the beginning of the chapter on state-of-the-art were clarified, especially “criterion”, “genetic conservation units” and “genetic monitoring units”. It was noted that the reference to the CBD “headline indicator” may cause some confusion and it was suggested to be moved to the next chapter where different types of indicators are discussed. It was agreed that it is useful to explain and make a reference to the headline indicator in the report to show that the genetic monitoring system also has a linkages to the CBD and not only to the FOREST EUROPE process. It was also recommended to include “genetic monitoring plot” and “genetic monitoring regions” to the list of definitions, or explain them better later in the report. After some discussion on different types of indicators, it was concluded that this sub-chapter could be expanded and explain bit more about the indicators developed by the CBD and those ones that are used for the monitoring sustainable forest management. Regarding threats to forest genetic resources, it was suggested that more text could be developed on topics such as introduced species and hybridization, for example.

It was then discussed whether any additional databases relevant for genetic monitoring of forest trees should be added to the report. It was noted that databases of botanical gardens may be useful for identifying the genetic monitoring regions but it was not clear how well they could be used for genetic monitoring.

The participants exchanged again different views on the use of “genetic monitoring units” and “genetic monitoring plots” while discussing the design of these units/plots. It was concluded that this issue can be solved later when a more detailed sampling protocol will be developed based on the German system and the results of the FORGER project.

Considering the proposed indicators and verifiers, it was suggested to combine verifiers on reproductive fitness and fructification into one verifier. It was further noted that fructification should be assessed annually and that the frequency of mast years could be recorded separately. Additionally, a verifier on mortality at the plot level could be added as all mature trees will be marked and recorded in any case. It was also pointed out that the table on the proposed indicators and verifiers seems to include several options for genetic monitoring and that they should be presented more clearly. This would also make it easier to compare the proposed indicators and verifiers with the costs assessment in the report. The working group members agreed that it is important to explain the options and their costs more clearly to the readers and especially to the Steering Committee. The options could be tagged as “ambitious” and “light version”, for example.

While discussing the criteria for selecting the genetic monitoring units, many participants emphasized that the monitoring units should be selected, as much as possible, from the core

networks of the conservation units. This should be also explained more clearly in the report. Regarding the size of a monitoring unit, it was commented that the dual requirement, i.e. minimum size of 4 hectares in terms of area and the population size of 50 reproducing trees, can be difficult to meet in case of scattered tree species. It was concluded that the population size of 50 trees should be followed in case of scattered tree species while in case of stand-forming species, a 4-ha plot typically includes more than 50 mature trees. Considering the identification of the genetic monitoring regions, it was agreed that the process should be more clearly explained by adding an annex to the report based on the guidelines that were earlier developed by the EUFORGEN Secretariat.

Several changes were also suggested to the chapter on costs of genetic monitoring. Firstly, it was recommended that the cost assessments need to be developed for the different monitoring options (e.g. ambitious and light versions). Secondly, the costs should also be indicated per year and per monitoring circle, and also separated between field and laboratory work. Thirdly, the costs of storing of sample and data should be estimated. Finally, the participants discussed the conclusions and recommendations of the draft report. It was agreed that the chapter needs to be improved and better structured based on the different options that will be presented to the Steering Committee. It was also suggested that a sort of priority list could be presented, i.e. which activities and tasks can be started now or during the next year, and which ones need to wait additional funding before they can be started.

In the evening of 19 September, the members of the working group on genetic resources met separately and developed a list of action points for revising the draft report based on the feedback received. Furthermore, they also developed a template for the cost analysis and agreed deadlines for finalizing the draft report for the Steering Committee.

Working session 3 on linkages and synergies

During this session, the participants discussed two types of linkages and synergies, i.e. 1) those between the development of the core network of the conservation units and the genetic monitoring system, and 2) those between the EUFORGEN activities and the FORGER and other relevant projects in Europe.

It was noted that somewhat different criteria was used by the two working groups in selecting units for the core network and for genetic monitoring. Many participants emphasized that it is important the tentative selection of units for both purposes should be send together to the National Coordinators so that they can consider various aspects before confirming the selected units or proposing changes, if needed. It was pointed out that practical considerations influence much more the selection of units for genetic monitoring (selected units should be easily accessible, for example) as compared to the selection for the core network. Most participants pointed out that the monitoring units should be selected from the core network but some noted that this may not be possible in all cases. After some discussion, it was agreed that, as much as possible, the monitoring units should be selected from the core network and that other units can also be selected for genetic monitoring if there are specific reasons for that. These additional units should also qualify for the core network and they should be added to the core network once they have been selected for monitoring,

The participants then discussed an additional selection criterion which was not yet considered by the working groups, i.e. that it is necessary that seed collection within the units is allowed. Several potential units are located within protected areas and in many countries legislation prohibits the collection of seed and other material from these areas. Such units are unsuitable for genetic monitoring and their suitability for the core network is also questionable as conservation of genetic resources is done for present or future uses. It was agreed that the importance of seed collection should be emphasized in both reports, and that National Coordinators should check that seed collection from all selected units is possible before they confirm their selection.

Regarding the synergies between the EUFORGEN work and the FORGER and other projects, many participants commented that there are many ongoing European projects on forest genetic resources and that they would all benefit from increased exchange of information and results. This would also benefit the EUFORGEN work and facilitate the use of the project results in practical conservation of forest genetic resources. It was recommended that the projects should make their databases and other results widely available (i.e. beyond project partners) as soon as the projects have ended.

Concerning the linkages and synergies between EUFORGEN and FORGER, several participants noted that these are obvious and that many of the FORGER activities build on the earlier work by EUFORGEN. The FORGER work on FGR inventories and genetic monitoring will directly benefit the implementation and future revision of the pan-European genetic conservation strategy. Furthermore, field-testing of genetic monitoring protocols would not have been possible with the current EUFORGEN resources. The FORGER results on genetic monitoring are also very useful for finalizing many technical details of the planned pan-European genetic monitoring scheme and making the whole scheme more feasible to implement in practice.

Workshop recommendations

The participants discussed additional recommendations to the working groups and the EUFORGEN Steering Committee. They agreed the following recommendations;

1. The working group approach as the new *modus operandi* of EUFORGEN has been useful and efficient in addressing important issues of the pan-European work on the conservation of forest genetic resources.
2. The composition of the working groups, including the e-mail contributors, has ensured adequate and active representation of the member countries to ensure broad inclusiveness and ownership. It has also made possible to address the variety of problems faced by different countries and to benefit from the experiences and knowledge of experts throughout Europe.
3. The interaction between the two working groups during the workshop had been very useful – and necessary – for the development of the pan-European genetic conservation strategy for forest trees, including the establishment of the core network of the units, and the genetic monitoring scheme for selected units. It was noted that it would have been useful to also interact with the third working group focusing on forest reproductive material.
4. It was recommended that EYFORGEN should continue to carry out its activities through the working group approach and to facilitate interaction between relevant working groups as needed.

Wrap-up of the workshop

J. Koskela thanked Chairs of the two working group, S. de Vries and F. Aravanopoulos for their efforts in leading the development of two very important initiatives. He also expressed his gratitude and appreciation to all other working group members and workshop participants for their inputs and contributions.

F. Aravanopoulos, Chair of the session, thanked the local organizers for the meeting arrangements and the Secretariat for its work. With no other business, he then closed the workshop.

Annex 1. Agenda of the workshop

Tue 18 Sep		
08:00-09:00	Registration to the workshop (Venue: Scandic Hotel Järvenpää)	Address: Asema-aukio (Station Square), 04400 Järvenpää
09:00	<p>Opening of the workshop (Chair: Mari Mari Rusanen, Finnish Forest Research Institute)</p> <ul style="list-style-type: none"> • Welcome and introduction to the Finnish Genetic Resources Programme (Tuula Pehu, Counsellor, Ministry of Agriculture and Forestry) • Welcome by the EUFORGEN National Coordinator (Mari Rusanen) • FGR conservation in Europe: past efforts, current status and introduction to the workshop (Jarkko Koskela, Bioversity International) 	
10:30	Coffee/tea break	
11:00	<p>Development of a pan-European genetic conservation strategy for forest trees and establishment of a core network of dynamic conservation units (Chair: Eric Collin, IRSTEA, France)</p> <ul style="list-style-type: none"> • Presentation of the draft report of the EUFORGEN Working Group on genetic conservation strategies (Sven de Vries, Centre for Genetic Resources the Netherlands) • Questions, comments & discussion 	
12:30	Lunch	Scandic Hotel Järvenpää
14:00	<p>Forest genetic diversity in forest monitoring & management (Chair: Jarkko Koskela, Bioversity International)</p> <ul style="list-style-type: none"> • Genetic monitoring in forests: lessons from the German system and new pilot studies in Europe (Bernd Degen, Thünen Institute of Forest Genetics, Germany) • Introduction to the FORGER project (Koen Kramer, Alterra, Netherlands) • Questions, comments & discussion 	
15:30	Coffee/tea break	
16:00	<p>Development of a genetic monitoring system for dynamic conservation units of forest trees in Europe (Chair: Lars Graudal, Forest & Landscape Denmark)</p> <ul style="list-style-type: none"> • Presentation of the draft report of the EUFORGEN Working Group on genetic monitoring (Filippos Aravanopoulos, Aristotle University of Thessaloniki) • Questions, comments & discussion 	
17:30-18:00	Wrap-up of the day	
Wed 19 Sep		
09:00	Working session 1: Development of the pan-European genetic conservation strategy – in-depth questions/debate and detailed comments to the draft report (Chair: Sven de Vries)	Scandic Hotel Järvenpää

	<ul style="list-style-type: none"> • Objectives (review of the targeted level of genetic conservation and the selected approach) • Results from testing the proposed approach with the model species • Implementation of the strategy / action plan 	
11:00	Working session 1: continued <ul style="list-style-type: none"> • Discussion 	
12:30	Lunch	Scandic Hotel Järvenpää
14:00	Working session 2: Options for genetic monitoring of the dynamic conservation units at pan-European level – in-depth questions/debate and detailed comments to the draft report (Chair: Filippos Aravanopoulos) <ul style="list-style-type: none"> • Purpose and objectives • Proposed indicators and verifiers • Principles and criteria for identifying genetic monitoring regions, units and species • Implementation of a pan-European genetic monitoring system (cost assessment, resources needed, etc.) 	
16:00-17:30	Working session 2: continued <ul style="list-style-type: none"> • Discussion 	
17:30-18:00	Wrap-up of the day	
19:30	Social dinner	Restaurant Ateljeeri (Krapu Estate, Tuusula)

Thu 20 Sep		
09:00	Working session 3: Linkages and synergies (Chair: Jarkko Koskela, Bioversity International) <ul style="list-style-type: none"> • Core network of dynamic conservation units vs pan-European genetic monitoring system • EUFORGEN activities vs FORGER and other relevant European projects 	Scandic Hotel Järvenpää
11:00	Workshop recommendations to the EUFORGEN Working Groups and the Steering Committee (Chair: Sven de Vries, Centre for Genetic Resources the Netherlands) <ul style="list-style-type: none"> • Discussion 	
12:30	Lunch	Scandic Hotel Järvenpää
14:00	Wrap-up of the workshop (Chair: Filippos Aravanopoulos, Aristotle University of Thessaloniki) <ul style="list-style-type: none"> • Final comments to the draft reports of the Working Groups • Closure of the workshop 	

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