

GUIDELINES FOR SEED HARVESTING IN FOREST SEED STANDS

GUIDELINES

FORGER

TOWARDS THE SUSTAINABLE
MANAGEMENT OF FOREST GENETIC
RESOURCES IN EUROPE

The strategic selection of seed stands represents a cost-effective and quick method in forestry for obtaining forest reproductive material of improved quality. Hence, for more than 50 years already the EU has regulated how these seed stands are to be selected and respective regulations have been implemented in the Member States accordingly (the first EU-Directive on forest reproductive material was issued).

In general, forest stands are certified as basic material if certain requirements are fulfilled. For approval, the volume of wood production in the selected stand must normally be superior to the accepted mean under similar ecological and management conditions. In addition, good wood quality and optimal tree stem forms are desirable phenotypic traits that are taken into account in the selection of forest seed stands. Finally, seeds stands should be well adapted to their environment and free from attacks of damaging organisms, such as pathogens.



In order to make sure that these desirable traits are present in forest reproductive material originating from seed stands, the tree population to be harvested must be made up of a large number of spatially well-distributed individual trees to ensure adequate cross-pollination. Moreover, promising seed stands must be situated at a sufficient distance from poor stands of the same species to avoid unwanted genetic pollution. These legally binding requirements shall secure that progenies from seed stands are also of a superior quality.

These technical guidelines have been prepared to support forest practitioners when seeds are to be harvested in seed stands. As not all European forest trees could be considered, emphasis has been placed upon tree species of the temperate zone, such as Norway spruce (*Picea abies*), oaks (*Quercus* spp.), beech (*Fagus sylvatica*) and wild cherry (*Prunus avium*). For these species, information is provided on how many seed trees within seed stands should be harvested and what spatial arrangement they should have for seed harvests to be genetically sustainable. These recommendations may be of relevance also for other tree species that share biological similarities with the above-mentioned tree species.



Besides practical concerns such as accessibility of the trees and fructification intensity, attention should be drawn to adequate sampling in seed stands. The mode of seed harvest affects the genetic quality of seeds significantly. A bias can arise from two variables: (1) the number and spatial distribution of seed stands for a certain tree species and (2) the number and spatial arrangement of sampled seed trees within a seed stands. Seed sampling in seed orchards is not considered in these guidelines.

A genetically sustainable seed harvest should optimize the genetic diversity in the seeds obtained and minimize genetic differences between seed harvest and the seed stand, respectively. Imagine that in an extreme case the seeds were only obtained from one single seed tree. The seedlings originating from such a seed lot would be genetically all very closely related (full-sibs and half-sibs) as they all would share a common “mother tree”. The genetic variation which is so essential for forest trees to cope with environmental change would be extremely narrow compared to the offspring of a fully representative seed harvest. At the other extreme, harvesting all seed trees in a stand is not feasible economically.

Besides the number of seed trees needed, also the spatial arrangement of seed trees is relevant as harvests may occur in neighbouring trees, randomly spaced trees or trees with a certain minimum distance. Distribution of genetic diversity within stands may not be random and may depend on environmental heterogeneity, but may also be the result of a specific mating system and mode of seed and pollen dispersal. When seed stands are established from natural regeneration neighbouring trees are more genetically related than expected by chance due to more limited pollen and seed dispersal. This phenomenon is often referred to as positive ‘spatial genetic structure’. Natural clonal propagation, as found for instance in black locust (*Robinia pseudoacacia*), wild cherry (*Prunus avium*), poplar (*Populus* spp.) and wild service tree (*Sorbus torminalis*), also contributes to such a spatial genetic structure.



Subsequent mating among neighbouring (and genetically related) trees increases the levels of inbreeding, which in turn may be detrimental for survival, growth and adaptive traits of the following generations due to possible effects of inbreeding depression.

Other factors that must be kept in mind when determining a representative sample are: the immigration of genes through pollen and seeds (in cases where seeds are collected from the ground), patterns of pollen and seed dispersal, the number of seeds obtained from a single seed tree, and dominating pollen sources within the seed stands.

RESEARCH ON OPTIMAL SEED HARVESTING

Generally seed harvesting is a sampling issue. Theoretical models tackling sampling are generally pertinent but provide only a general framework because model assumptions, such as departure from a genetic equilibrium and complete genetic isolation over long periods, are not fulfilled in forest trees. Therefore, experiments, including simulations, were carried out in order to address the question of how a genetically sustainable seed harvest should be undertaken. Key questions are: how many seed trees should be selected for seed harvesting? How may the spatial arrangement of these trees affect the genetic quality of seeds obtained? (Degen et al. 2012, Blanc-Jolivet and Degen 2014).

Generally the experiments were based on genetic inventories of real forest stands using DNA-microsatellites as molecular markers. One should note that these experiments cannot examine to what extent important adaptive genetic variation is captured in the seed harvests obtained from different harvest scenarios. Nevertheless, these results provide very useful information and guidance. These studies were carried out for important European tree species, such as Norway spruce (*Picea abies*), common beech (*Fagus sylvatica*), oaks (*Quercus* spp.) and wild cherry (*Prunus avium*) so that specific characteristics of the reproductive system of different tree species, which directly or indirectly influence the results of the various seed harvesting methods applied, could be taken into account.



RESEARCH FINDINGS

- Theoretical models suggest that no fewer than 15 trees should be sampled (Brown and Harder 2000), provided that seed samples per tree are large, and the species are characterized by random mating. Small numbers of seeds sampled per tree and departure from random mating require increasing the number of sampled trees.
- The genetic diversity captured in the seed harvest is dependent on the spatial genetic structure and the reproductive system of forest trees.
- Forest trees are characterized by intensive gene flow. Although this may increase the genetic diversity per se, it becomes more difficult to minimize genetic differences between the genotype of adults in the seed stand and their seed harvest, when the number of seed trees is increased. The proportion of successful external pollen depends on the relation between the amount of local pollen production versus the amount of external pollen. Large seed stands with a high number of reproductive trees produce a lot of local pollen.
- The number of genotypes represented in the seed harvested is dependent on the number of seed trees harvested.
- Positive spatial genetic structure increases in natural-regenerated stands. This pattern is most pronounced in Norway spruce, followed by beech, oaks and wild cherry.
- Generally, directly neighbouring trees contribute strongly their genetic information to the seed tree, with a declining effect from more distant tree individuals. In insect-pollinated tree species this phenomenon is especially pronounced. But even in Norway spruce, which is a wind-pollinated tree species, relative mating success decreases rapidly with increasing distance from the seed tree.
- Due to limited pollen dispersal within stands, neighbouring trees (unless they have distinct flower phenologies) tend to have similar pollen clouds fertilizing their ovules. This similarity decreases with increasing distance between mother trees.
- Sampling over time a variable number of seeds from the same tree individuals reduces the effective number of trees contributing to the seed harvest, decreasing the genetic diversity of seed lots.

GENERAL RECOMMENDATIONS

- Seed harvesting should preferably be carried out in years of intense flowering and heavy seed crops, thereby maximizing the numbers of individuals participating in mating.
- Trees harvested for seed should be distributed uniformly throughout the seed stand.
- Harvesting seeds from trees growing at the edge of forest stands should be avoided, because a considerable proportion of the seeds they produce result from fertilization with immigrant pollen.
- The number of seeds harvested from every tree should be uniform.
- Whenever possible the selection of large seed stands (more than 10 ha) with many reproductive individuals (N more than 300) is recommended because this ensures a high proportion of the pollen is locally produced and minimises the risk of pollen contamination from outside.

SPECIES-SPECIFIC RECOMMENDATIONS

- Generally any seed harvest of directly neighbouring trees should be avoided. It appears that this is especially important for heavy-fruited tree species, such as **oaks** and **beech**. In small seed stands of oak and beech (less than 10 ha) a minimum distance of 20 m is recommended; in large seed stands (more than 10 ha) this distance should be increased to 30 m. If crowns overlap significantly, these distances should be increased.
- The minimum number of seed trees to be harvested in an **oak** seed stands should be 30 individuals. If seed stands are genetically well isolated (more than 5 km from the next reproductive stand of the same species) this number can probably decrease to 25.

Although for **beech** a much smaller experimental data set than in **oak** species is available, it seems justified to use the above-mentioned number as guidance. In insect-pollinated tree species, such as **wild cherry**, a minimum of 25 seed trees are recommended.

- The available data from field experiments or simulations in wind-pollinated **conifers** are very limited and it is very difficult to recommend an ideal seed-harvesting mode. Gene flow from distant sources is generally high in **conifers**, although directly neighbouring trees disproportionately contribute their pollen to the seed tree. The number of seeds collected from each seed tree is generally high. Therefore a minimum of 20 seed trees for **Norway spruce** is recommended.



Selected references

Blanc-Jolivet, C. and Degen, B. 2014. Using simulations to optimize genetic diversity in *Prunus avium* seed harvests. *Tree Genetics & Genomes* 10: 503-512.

Burczyk, J., Lewandowski, A. and Chalupka, W. 2004. Local pollen dispersal and distant gene flow in Norway spruce (*Picea abies* [L.] Karst.). *Forest Ecology and Management* 197: 39-48.

Brown, AHD and Hardner, C.M. 2000. Sampling the gene pools of forest trees for ex situ conservation. In: A.Young, D. Boshier and T. Boyles (eds.) *Forest Conservation Genetics* CSIRO Publishing. Pp. 185-196.

Degen B., Jolivet C., Rogge M., Fussi B., Konnert M., Eva Cremer E., Becker F., Ralf Kätzel. 2012. Etablierung einer Standardmethode zur genetisch nachhaltigen Ernte von forstlichem Vermehrungsgut in zugelassenen Saatgutbeständen, Endbericht eines Verbund- Modell- und Demonstrationsvorhabens des BMEL.
http://www.ble.de/SharedDocs/Downloads/03_Forschungsfoerderung/05_MuD-Vorhaben/Endfassung_ProjektberichtSaatgut.pdf?__blob=publicationFile

These guidelines present recommendations that are based on the findings from the FORGER project.

Reference to the document:
Guidelines for seed harvesting in forest seed stands

Authors: Thomas Geburek (BFW), Jarek Burczyk (UKW) and Bernd Degen (VTI) FORGER Guidelines 2016

Photos credits:
© Bioversity International; © VTI

www.fp7-forger.eu

For more information on FORGER:

Dr. Koen Kramer, Project Coordinator
Alterra, Wageningen, The Netherlands
E-mail: koen.kramer@wur.nl
Tel.: +31-317-485873



The FORGER project is financially supported by the European Commission under the 7th Framework Programme