Common ash

Fraxinus excelsior

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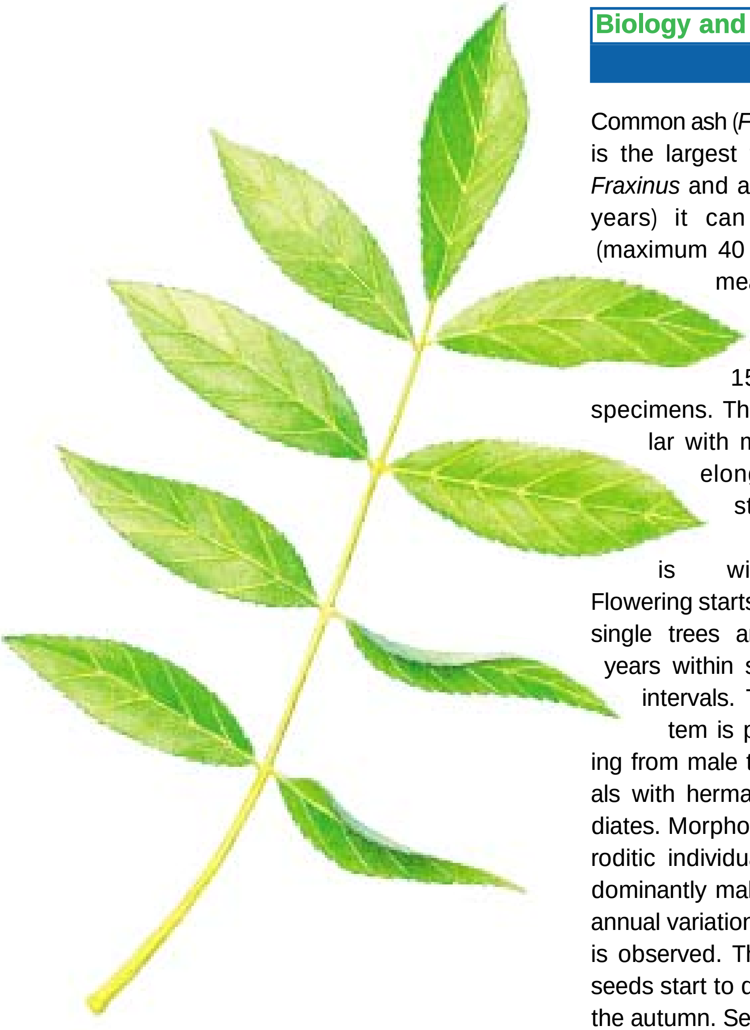
These Technical Guidelines are intended to assist those who cherish the valuable ash genepool and its inheritance, through conserving valuable seed sources or use in practical forestry. The focus is on conserving the genetic diversity of the species at the European scale. The recommendations provided in this module should be regarded as a commonly agreed basis to be complemented and further developed in local, national or regional conditions. The Guidelines are based on the available knowledge of the species and on widely accepted methods for the conservation of forest genetic resources.



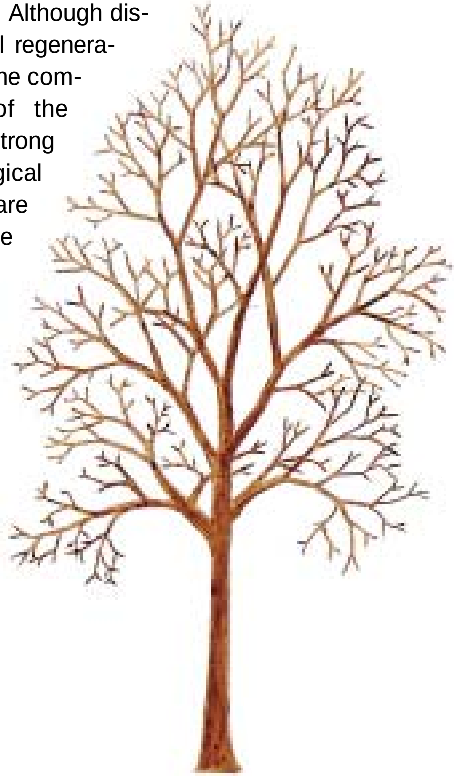
Biology and ecology

Common ash (*Fraxinus excelsior* L.) is the largest tree in the genus *Fraxinus* and at maturity (90-120 years) it can reach 20-35 m (maximum 40 m) in height. The mean stem diameter varies from 30-70 cm (maximum 150 cm) in adult specimens. The crown is irregular with massive branches, elongated in forest stands.

Common ash is wind pollinated. Flowering starts at 15-20 years on single trees and at around 30 years within stands at irregular intervals. The breeding system is polygamous, ranging from male to female individuals with hermaphroditic intermediates. Morphologically hermaphroditic individuals are often predominantly male or female. Interannual variation in sex expression is observed. The fully developed seeds start to disperse by wind in the autumn. Seed dormancy usually lasts for two winters but can last for up to six. Stored seed requires combined warm-cold stratification to germinate.

Common ash requires a rich soil and tolerates a pH as low as 4.5, but prefers soil above 5.5. It is highly tolerant of seasonal water-logging and favours flood-plain forests. It is also a typical species of slopes and ravines, growing in association with other characteristic species such as maple, lime and elm. Although dormant trees are very cold hardy, the young shoots are sensitive to frost.

Common ash exhibits intermediate properties between a pioneer species and a permanent forest component. Although dispersal and natural regeneration are efficient, the competition ability of the species is only strong when the ecological requirements are met. Vegetative regeneration is strong after coppicing.



Distribution

The natural range of common ash covers most of Europe from the shores of the Atlantic Ocean in the West to the Volga River in the East, with the exclusion of the most northern and southern parts. The northern limit of the natural range is about 64° North in Norway, the southern margin reaching 37° North in Iran. In mountainous areas, common ash is found in the Pyrenees at 1750-1800 m above sea level and in the Swiss Alps at 1630 m. In Asia (Iran), it can be found at much higher elevations of up to 2200 m.

Importance and use

Of the four different ash species growing naturally in Europe, common ash is the most important commercially. Despite the high demand for this quality timber, only a few European countries have gene conservation or tree breeding programmes in place for this species.

Common ash timber is hard, elastic and withstands pressure, shock and splintering. It is used mainly for tool handles, and for sports equipment such as hockey sticks, oars and hurdles. It has a straight grain and there is little distinction between sapwood and hardwood, making it very valuable for furniture, veneer and flooring. The formation of “black heart”, a dark stain of the hardwood, can occur in mature trees. This varies within and between individual trees and different sites and reduces the economic value. Ash bark and leaves are astringent and the leaves are used in modern herbal medicine for their laxative properties.

Genetic knowledge

The genetic variation of a species, both within and between populations, is influenced by many factors. The mating system, pollen and seed dispersal, role and successional stage in forest ecosystems, site conditions and historical influences such as colonisation patterns after the glacial periods of the Quaternary are particularly important. Two types of genetic variation can be distinguished: (i) adaptive variation (i.e. enabling adaptability) and (ii) *a priori* neutral variation (i.e. not affected by natural selection).

Adaptive variation, expressed in the phenotype in response to natural selection, has been investigated through provenance and progeny trials. These studies revealed that variation between families within provenances/ populations was generally as high as variation between provenances/populations.

Phenological traits, including the date of bud burst and set, displayed geographic patterns on a large spatial scale, whereas growth and form, which are influenced by soil and competition conditions, varied at the local level. The existence of different ecotypes, (i.e. floodplain, hillside, slope and limestone ecotypes), has never been proven by progeny studies.

Chloroplast DNA data used to investigate neutral variation suggests ice age refuges in the Iberian Peninsula, the Alps and/or in Italy and in the Balkan Peninsula. This result is in agreement with fossil pollen data and the postglacial re-colonisation of Europe from these refuges. Nuclear DNA markers reveal levels of intra-population differentiation similar to other Noble Hardwoods such as chestnut, elm and walnut, but higher than is found in oak and beech. High differentiation was particularly observed between populations in southeastern Europe and in northern central Europe, indicating the high conservation value of ash genetic resources from these areas.

Threats to genetic diversity

On the European scale, common ash is not an endangered species. However, the natural range and area of ash forests has decreased during the last 4000 years as the area of agricultural lands has increased. Silvicultural methods have promoted common ash in the last 30-40 years due to the high economic value, supporting natural regeneration, planting and thinning.

Common ash genetic resources are threatened by deforestation, loss of suitable habitats, unsustainable exploitation and improper management (i.e. uncontrolled transfer of reproductive material), natural climatic changes, global warming, air pollution, competition with other species, pests and game damage. These pressures could lead to population extinction. Despite the high regeneration potential, the reproduction of some valuable autochthonous populations is not ensured, and the health status of mature stands in some countries has deteriorated significantly in recent years. Therefore, common ash is considered to be threatened at the population level by most countries.

Guidelines for genetic conservation and use

Genetic conservation aims at ensuring continuous survival and adaptability of the target species. These objectives are met when the Multiple Population Breeding System (MPBS) is applied. Ideally in MPBS, a breeding population is subdivided into subpopulations which are then grown over a wide range of site conditions.

In each country where common ash is found, an inventory should be undertaken to define the geographical distribution of the species, conservation status, threats and potential use patterns. Ecogeographic zones (provenance regions) should be delimited according to climatic variation, topography, soil and vegetation. Trees are generally best adapted to the ecological conditions of the region where they evolved. Therefore, local material should be used for plantations wherever possible, unless otherwise recommended as the result of data from provenance trials.

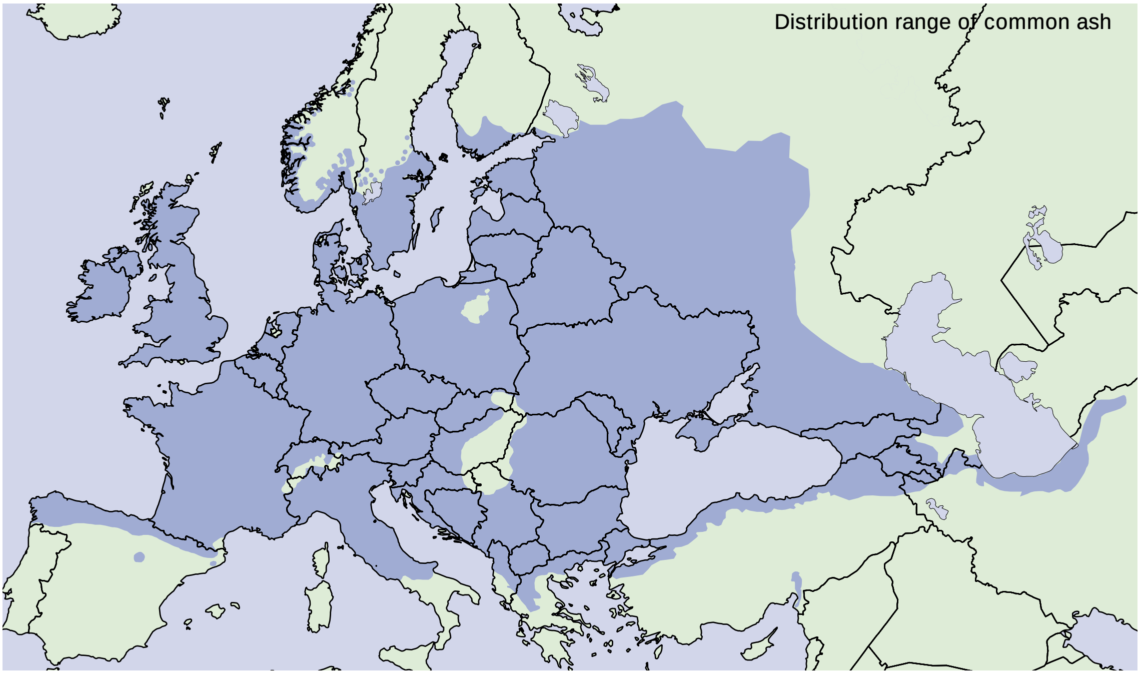
To ensure the adaptive potential of *Fraxinus excelsior* in Europe, it is recommended that two complementary gene conservation networks of populations are established, specifically: (1) a network of 20-30 *in situ* populations throughout provenance regions; and (2) a network of *ex situ* populations (progeny trials, provenance trials, collections). Whenever possible, *in situ* conservation activities should be undertaken jointly for other Noble Hardwoods.

Where common ash occurs in large populations in a country, *in situ* conservation is sufficient, with the selection of up to three gene conservation populations/ gene reserves of 5-15 ha in size, with at least 100 flowering trees in each provenance. A high density of *in situ* gene conservation populations should be established in Southeast Europe, especially in Romania and Bulgaria, which have been colonised by populations from different ice age refuges. In these regions, neutral genetic markers show high differentiation among populations, suggesting that they may have different potentials to cope with future climatic conditions. Specific conservation efforts are also recommended in northern central Europe, due to the high level of differentiation between populations in southern Sweden, although the historical origin of this differentiation still needs to be verified.

In situ gene conservation populations need to be managed to increase their adaptive potential by ensuring the natural regeneration of the target species, creating multi-age structure and habitat diversity, and increasing generation turnover.

To conserve an even-aged mature stand *in situ*, parts of the population should be opened (thinned or cut in narrow strips of 15-30 m width) to create conditions for natural regeneration. Preferably, this should be undertaken in the year following the mast, when maximum seed is produced by the stand. An area adjacent to the gene reserve could be set aside for natural regeneration, and could later be incorporated as part of the reserve.

To promote regeneration in clear-cut strips, randomly selected, abundantly flowering seed trees should be left. If the population consists of some stands or groups of trees of different ages but there is no regeneration, the oldest stands or groups should be cut as soon as the mast years have produced sufficient seed yield or regeneration under the canopy or in areas set aside. Increasing the number of stands or demes (groups of trees) of different ages in the population enhances intra-population genetic variation as the portion of trees involved in regeneration increases. Regeneration can also be stimulated by site scarification and weed control. If these regeneration support measures are not successful, it is recommended that material originating from the population is planted: seeds



should be collected from at least 50 trees per population, preferably from central parts of the gene reserve. To prevent gene flow from outside the gene reserve, a buffer zone of 100-150 m should be created by gradually removing mature flowering ash trees within this zone.

To secure the sustainability of each population, careful tending is required. Effective treatment including adequate silvicultural measures, protection against disease or insect outbreaks, fire or other factors must be undertaken promptly. Thinning should be undertaken from below, removing suppressed and injured trees, thus simulating and stimulating the natural selection processes in the forest, and stand regeneration. Each gene conservation population must be constantly monitored, including the health status and regeneration success.

For populations that are marginal, isolated, endangered, growing under special ecological conditions or carrying rare features, *in situ* conservation should be complemented by *ex situ* measures. The most effective form is through progeny trials, which permits joint gene conservation and breeding. On a national scale, 1-3 progeny plantations for conservation/breeding (each of 2-4 ha in size) should be established in each provenance region with entries sampled from single trees randomly chosen from 10-20 stands within the region and from marginal populations if applicable. As soon as reproductive age is reached, open pollination of the best individuals selected within each family should ensure the next generation. About 50 optimally adapted individuals should be the founders of each new gene conservation/ breeding sub-population.

EUFORGEN

These Technical Guidelines were produced by members of the EUFORGEN Noble Hardwoods Network. The objective of the Network is to identify minimum genetic conservation requirements in the long term in Europe, in order to reduce the overall conservation cost and to improve the quality of standards in each country.

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Selected bibliography

Baliuckas V., T. Lagerström, and G. Eriksson. 2000. Within and among population variation in juvenile growth rhythm and growth in *Fraxinus excelsior* and *Prunus avium*. Forest Genetics 7 (3): 193-202.

Bugala, W. (ed). 1995. Our forest trees: Popular scientific monograph, Volume 17: 569 European ash - *Fraxinus excelsior* L. [in Polish]. Institute of Dendrology, Poland.

Heuertz, M. 2003. Population genetic structure in common ash: a focus on southeastern European genetic resources. PhD thesis, Free University of Brussels, Belgium, and the Public Research Centre – Gabriel Lippmann, Luxembourg.

Kleinschmit, J., J. Svolba, V. Enescu, A. Franke, H.M. Rau and W Ruetz. 1996. First results of provenance trials of *Fraxinus excelsior* established in 1982 [In German]. Forstarchiv 67: 114-122.

Wallander, E. 2001. Evolution of wind-pollination in *Fraxinus* (Oleaceae) – an ecophylogenetic approach. PhD thesis, Botanical Institute, Göteborg University, Sweden.

Weiser, F. 1995. Studies into the existence of ecotypes of ash (*Fraxinus excelsior*) [in German]. Forstarchiv 66: 251-257.

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