METSÄNTUTKIMUSLAITOKSEN TIEDONANTOJA 842, 2002
FINNISH FOREST RESEARCH INSTITUTE, RESEARCH PAPERS 842, 2002

Integrating Tree Breeding and Forestry

Proceedings of the Nordic Group for Management of Genetic Resources of Trees, meeting at Mekrijärvi, Finland, March 23 – 27, 2001

Matti Haapanen & Jouni Mikola (eds.)

VANTAAN TUTKIMUSKESKUS – VANTAA RESEARCH CENTRE

METLA

INTEGRATING TREE BREEDING AND FORESTRY

Proceedings of the Nordic Group for Management of Genetic Resources of Trees

Meeting at Mekrijärvi, Finland, March 23 – 27, 2001

Editors

Matti Haapanen & Jouni Mikola

Haapanen, Matti & Mikola, Jouni (Eds.) 2002. Integrating Tree Breeding and Forestry — Proceedings of the Nordic Group for Management of Genetic Resources of Trees, Meeting at Mekrijärvi, Finland, March 23 – 27, 2001. The Finnish Forest Research Institute Research Papers 842. 112 p. ISBN 951-40-1822-2, ISSN 0358-4283

Publisher: Finnish Forest Research Institute, Vantaa Research Centre
P.O. Box 18, FIN-01301 Vantaa, Finland

Accepted by **Kari Mielikäinen**, Research Director, April 4, 2002

This publication can be purchased from the Library of the Finnish Forest Research Institute, tel. +358-9-85705580, fax. +358-9-85705717, e-mail: kirjasto@metla.fi

ISBN 951-40-1822-2
ISSN 0358-4283

Hakapaino Oy
Helsinki 2002

Foreword

The annual meeting of the Nordic Group for Management of Genetic Resources of Trees was held in Finland on March 23–27, 2001. The Finnish Forest Research Institute acted as the main host and organiser. The meeting started with a train trip from Helsinki to Joensuu, the capital city of Finland's North Carelia province. The first session was held in a conference wagon on the train trip. The rest of the indoor part of the meeting took place at Mekrijärvi Research Station of the University of Joensuu. The field excursions on March 25–26 included visits to several research institutions, experimental sites, historical and cultural attractions, small enterprises, and also gave some touristic highlights of the wild nature of North Carelia. The whole meeting period was blessed with a fresh and sunny winter weather, with temperatures around –15 °C.

The main theme of the meeting was "Integrating Tree Breeding and Forestry". The first session consisted of invited reports about the status of tree breeding and the utilisation of genetically improved reforestation material in each of the eight participating countries (Denmark, Estonia, Finland, Iceland, Lithuania, Norway, Scotland and Sweden). Other sessions included both invited and voluntary papers and poster demonstrations on related topics like breeding strategies and economics, genetic resources and biodiversity aspects etc.

The present proceedings contain papers varying in length and thoroughness, depending on the material provided to the editors. In order to get as many of the meeting presentations as possible to be included into these proceedings, the organisers did not give any exact instructions or demands for the form of the papers. The editors express their sincerest thanks to the writers and regret that the publication of these proceedings was delayed because of some unforeseen obstacles.

Vantaa, Finland, January 2002

The Organisers,
Finnish Forest Research Institute
Vantaa Research Centre

Participants

Ahtikoski, Anssi	Finland	anssi.ahtikoski@pp.inet.fi
Antola, Jukka	Finland	jukka.antola@metla.fi
Haapanen, Matti	Finland	matti.haapanen@metla.fi
Hagqvist, Risto	Finland	risto.hagqvist@metla.fi
Harju, Anni	Finland	anni.harju@metla.fi
Koski, Veikko	Finland	vekoski@saunalahti.fi
Kukkonen, Hannu	Finland	hannu.kukkonen@kttk.fi
Lepistö, Martti	Finland	martti.lepisto@metla.fi
Mikola, Jouni	Finland	jouni.mikola@metla.fi
Napola, Jaakko	Finland	jaakko.napola@metla.fi
Nikkanen, Teijo	Finland	teijo.nikkanen@metla.fi
Rusanen Mari	Finland	mari.rusanen@metla.fi
Velling, Pirkko	Finland	pirkko.velling@metla.fi
Venäläinen, Martti	Finland	martti.venalainen@metla.fi
Viherä-Aarnio, Anneli	Finland	anneli.vihera-aarnio@metla.fi
Viljakainen, Anne	Finland	anne.viljakainen@metla.fi
Yrjänä, Leena	Finland	leena.yrjana@metla.fi
Hansen, Jon Kehlet	Denmark	jkh@fsl.dk
Hansen, Ole K.	Denmark	oha@fsl.dk
Nielsen, Ulrik Bräuner	Denmark	ubn@fsl.dk
Olrik, Ditte Christina	Denmark	dco@fsl.dk
Roulund, Hans	Denmark	hro@kvl.dk
Kurm, Malle	Estonia	mkurm@eau.ee
Möls, Tõnu	Estonia	tonu@zbi.ee
Tamm, Ulo	Estonia	ytamm@eau.ee
Trei, Piret	Estonia	ptrei@eau.ee
Edvardsen, Øyvind Meland	Iceland	oyvindrsr@simnet.is
Eysteinsson, Thröstur	Iceland	throstur@simnet.is
Baliuckas, Virgilijus	Lithuania	virgis.baliuckas@takas.lt
Danusevicius, Darius	Lithuania	darius.danusevicius@takas.lt
Myking, Tor	Norway	tor.myking@nisk.no
Skrøppa, Tore	Norway	tore.skroppa@nisk.no
Lee, Steve	Scotland	steve.lee@forestry.gsi.gov.uk
Samuel, Sam	Scotland	sam.samuel@forestry.gsi.gov.uk
Andersson, Bengt	Sweden	bengt.andersson@skogforsk.se
Boije, Maria	Sweden	maria.boije@skogforsk.se
Eriksson, Gösta	Sweden	gosta.eriksson@sgen.slu.se
Kang, Kyu-Suk	Sweden	kyu-suk.kang@genfys.slu.se
Karlsson, Bo	Sweden	bo.karlsson@skogforsk.se
Lindgren, Dag	Sweden	dag.lindgren@genfys.slu.se
Martinsson, Owe	Sweden	owe.martinsson@ssko.slu.se
Rosvall, Ola	Sweden	ola.rosvall@skogforsk.se
Son, Seog-Gu	Sweden	seog.gu.son@genfys.slu.se
Ståhl, Per	Sweden	per.stahl@skogforsk.se

Contents

Country Reports

Research and Discussion Papers

Short Notes

* * *

WWW home page of the meeting at
http://www.metla.fi/tapahtumat/2001/nordicgenetics/

COUNTRY REPORTS

Genetic quality of reproductive material in forest regeneration in Finland

Country Report I – Finland

Hannu Kukkonen
Ministry of Agriculture and Forestry
(Current address: KTTK, Box 42, FIN-00501 Helsinki, Finland)

Summary

The total annual area of forest regeneration in 1975-99 has varied between 142 000 ha and 188 000 ha (Fig. 1) reflecting the fluctuation in the wood markets. Also the proportions of regeneration methods have changed. Planting, especially pine planting, has decreased since early 1980's. It has been replaced both by natural regeneration and by direct seeding. There is a steady increase in direct seeding since 1993; the annual direct seeding area was 36 000 hectares in 1999. This is mainly due the widespread automatic seeding method applied simultaneously with the soil preparation resulting good regeneration results and essential savings in regeneration costs. Seeding of birch is a relatively new innovation and, although not yet used in a large scale, probably increasing. The interest for natural regeneration, especially with spruce has diminished when diverse and often poor results with this method have been demonstrated.

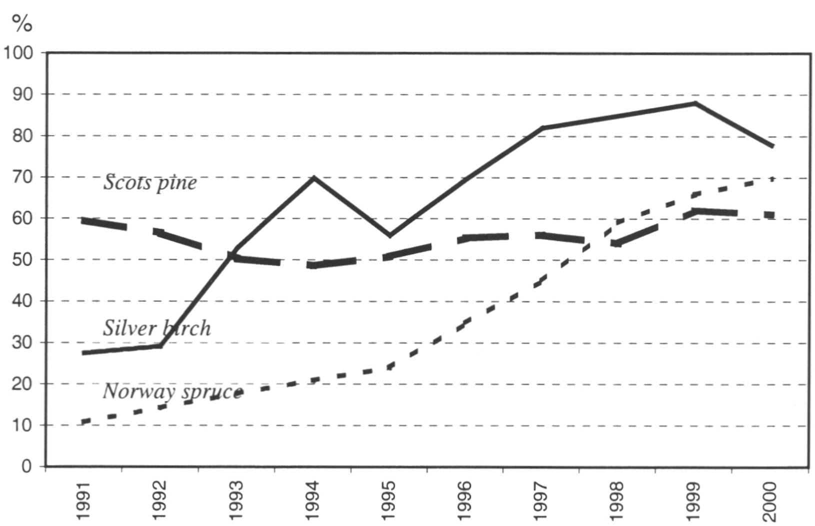


Fig. 1. Natural and artificial regeneration in Finland, 1975 – 1999.

The era of 1982–1990 was the "golden years" of seedling production, and the total amount of seedlings delivered from the nurseries reached over 250 million plants (Fig 2). The decrease in production is mainly caused by the reduction in pine planting. The year 2000 was the first year of slight recovery of seedling production. The import of seedlings has increased too, reaching now the level of more than 10 million seedlings.

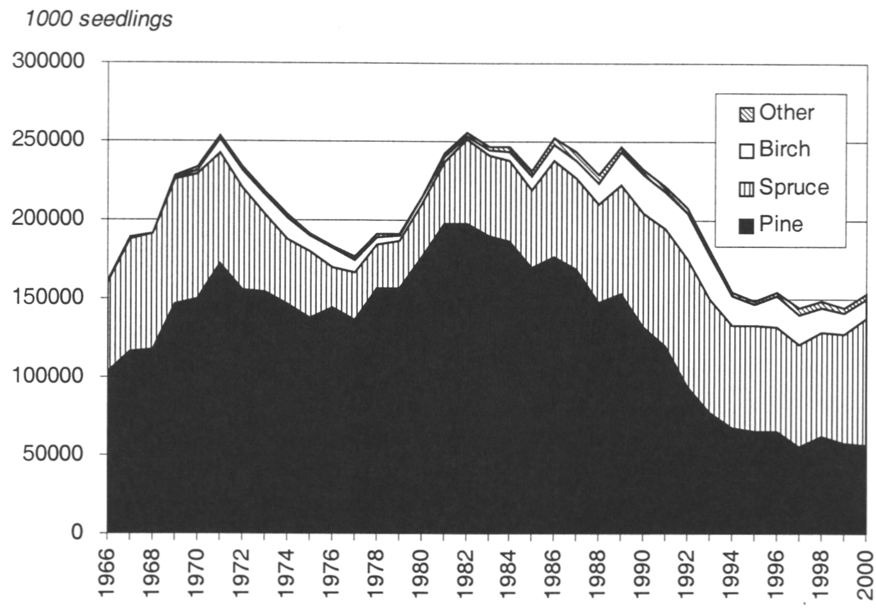


Figure 2. Number of seedlings delivered for planting, 1966 – 2000

The need to emphasise the cost savings in the nurseries (and in the forest) has led to structural changes in the nursery production. The most prominent features are the decrease in the bare root production to only 10 % of the total production, the use of smaller containers and shorter growing periods in the container production and urgent need to take a full advantage of using in nursery seeding only one seed per container. The development in the nursery practices, consequently, has forced to put much more emphasis in the seed quality.

The 200 seed orchards covering the total area of almost 3000 hectares are the main source of the seed used in the nurseries (Table 1). Genetically improved seed from the seed orchards is widely used in the nurseries, although the price of this seed is higher compared to the seed from forests (category source-identified). In addition to the better genetic quality, the better physiological properties of the orchard seed give it an advantage in the nursery production.

For the seedling production of pine, seed-orchard seed is available and used up to the line of 800 day degrees (Fig 3.). The use of seed-orchard seed has substantially increased also in direct seeding during last years. Unfortunately, there are no exact figures available. The proportion of seed orchard seed of spruce in the nursery seedings is still increasing covering now ca. 70 per cent of the total use of the seed. Corresponding figure for birch is ca. 80 per cent (Fig 3). The seedling production of other tree species is very limited and seed comes mainly from seed collection in forests.

Table 1. Seed orchards by tree species.

Species	Number of orchards	Area, ha
Pine	159	2485
Spruce	23	277
Silver birch	7	0,5[1]
Others	21	68
Total	210	2830

[1]Plastic covered seed orchards

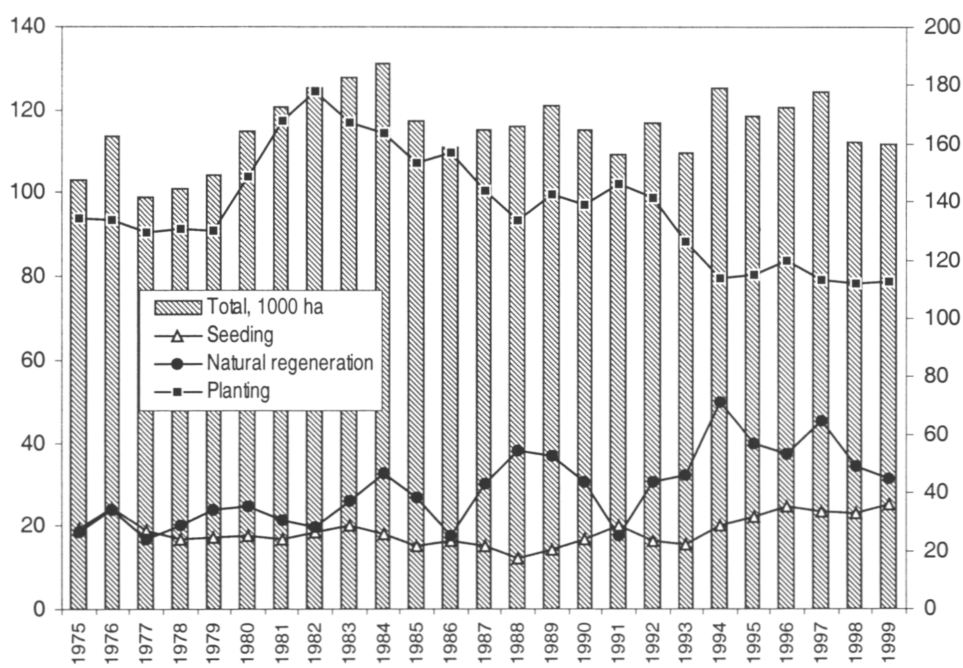


Figure 3. Proportion of seed orchard seed used in nurseries, 1991 – 2000.

Long-Term Tree Breeding Strategy in Finland: Integration of Seed Production And Breeding

Country Report II – Finland

Jouni Mikola
Finnish Forest Research Institute, Vantaa Research Centre, Box 18, FIN-01301 Vantaa, Finland

Summary

First-generation seed orchards of phenotypically selected plustrees of Scots pine and Norway spruce, established mainly between years 1965 and 1975, are now in full production in Finland. The economically productive stage of these orchards is expected to last 40-50 years. The establishment of second phase seed orchards (mainly so-called 1,5 -generation orchards) has been started, and will be carried out through the whole country within next 10-15 years.

Establishment and juvenile-stage management of seed orchards as well as long-term forest tree breeding have always been completely state funded in Finland. The latter was formerly organised as a co-operation of several forestry institutions. Since the beginning of year 2000, tree breeding at the national level has been centralised as the responsibility of the Finnish Forest Research Institute.

Finnish tree breeding strategy was reformulated in the late 1990s. The present strategy is based on the idea of open nucleus breeding system in which the breeding material in each breeding zone is organised into a main breeding population of about 300 progeny-tested plustrees, and a nucleus population of 50-70 best ranked genotypes. The new strategy is closely linked to the planning of the 1,5-generation seed orchards. Simultaneously with the selection of about 50 best-ranking mother trees for new seed orchard units, roughly the same sets of individuals are adopted as the nucleus populations of the respective species and zones. The second cycle of breeding begins with controlled crosses in the nucleus populations to produce progeny for forward selection. In the main populations, breeding is planned to be continued mainly with phenotypic selection of 2nd generation candidates in existing 10-20 years old progeny tests. Several alternatives are open for the procedures of testing and forward selection (e.g., generative or vegetative progeny, phenotypic or genotypic selection). The final choices in different species naturally depend, first of all, on the availability of economic resources for tree breeding in the coming years.

The basic principle of present Finnish tree breeding strategy is its integration to the seed orchard programme, which again is based on predicted needs of reforestation seed in practical forestry. The second cycle of breeding must be carried out in such a way that new selections are available at the right time to serve the establishment of third phase of seed orchards (mainly 2nd generation orchards). In Scots pine and Norway spruce this would require the breeding cycle to be limited to 40-50 years. In birch species the breeding cycle maybe must be adjusted to 20 years, although seed orchard rotation is only 10 years at maximum.

Establishment of third phase (mainly 2nd generation) seed orchards of Scots pine and Norway spruce is likely to become necessary in Finland within next 40 to 50 years. Of course, quite new options for the production of planting stock may be hoped and expected to show up much before that. In this respect, the present Finnish long-term tree breeding strategy may seem very slow and conservative. However, it should quite effectively serve immediate needs and new alternatives as well. The strategy should be able to offer genetically well-known individuals and families for commercial multiplication, short-term breeding operations and biotechnical manipulations almost continuously, and at least much before the end of the 40-50 years long breeding cycle.

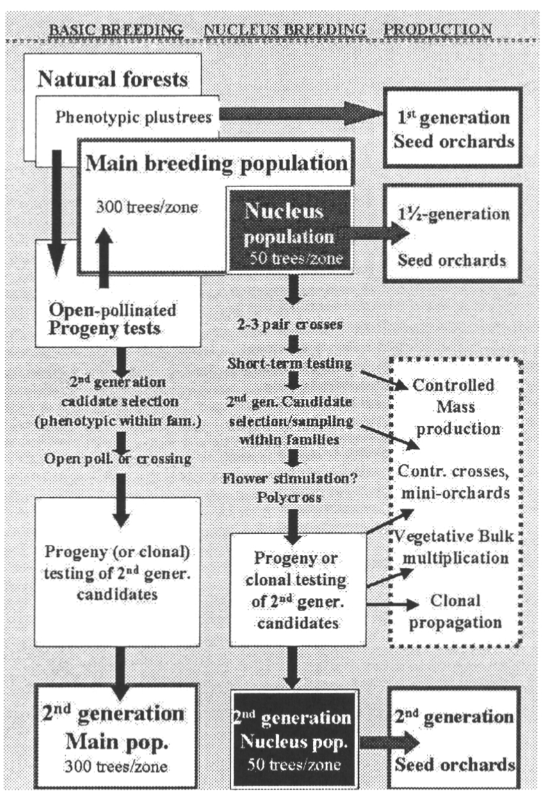


Figure 1. A schematic illustration of the Finnish tree breeding strategy

Tree Breeding in Sweden

Country Report – Sweden

Per H. Ståhl & Gunnar Jansson
Skogforsk, Uppsala Science Park, S-751 83 Uppsala, Sweden

Summary

The Swedish approach to long-term breeding is to integrate intensive breeding for general-purpose goals with gene conservation and preparedness for climatic changes. More than 80 % of the long-term breeding resources are spent on Norway spruce *(Picea abies)* and Scots pine *(Pinus sylvestris)*, the dominant forest tree species. The following will concentrate on these two species.

A multiple breeding-population system is applied to spruce and pine. Meta-populations of more than 1000 parent trees are divided into some 20 breeding populations (sub-populations) per species, each containing around 50 individuals. Each breeding population has a target area defined by photoperiod and climate. Long-term breeding is carried out in each breeding population. The selection of candidates is essentially on a within-family basis. A double-pair mating design is used and positive assortative mating is strived for. Progeny testing (for Scots pine) or clonal testing (Norway spruce) is used to increase the accuracy of the selections. Material for mass-propagation for a certain area can be selected from one or more adjacent breeding populations. The main goals of Swedish breeding are to increase the yield, adaptability and quality of the wood harvest, while safeguarding a necessary diversity in the breeding populations. The goals vary slightly from population to population

Research indicates that the breeding programmes are sustainable, robust, effective, and that the diversity losses are low. The long-term breeding is financd 50:50 by the government and the forestry sector.

SkogForsk, The Forestry Research Institute of Sweden, is responsible for all forest tree breeding in Sweden. The Institute provides interested orchard owners with orchard designs and suitable parent materials. The orchard owners then establish and manage the orchards, often with SkogForsk as their advisor.

Forest cultivation is of course a prerequisite for tree breeding. In Sweden, artificial reforestation is used on 68 % of the regeneration area. Seedling consumption in 1999 was some 304 million seedlings, of which 124 million Scots pine and 171 million Norway spruce. Direct seeding of Scots pine is gaining interest.

There are 924 ha of Scots pine seed orchards and 464 ha of Norway spruce orchards. These areas produce 80 % of the pine seed requirements and 20% of the spruce seed.

Clonal forestry has a limited use in Sweden (totally some 6000 ha) and is under strict legal control.

Among priority research topics are, in addition to classical topic: gain vs. diversity, shortening of generation interval, vegetative propagation of Scots pine, and how to handle climatic change.

Brief description of breeding methods and goals

The Swedish approach to long-term breeding is to integrate intensive breeding for general-purpose goals with gene conservation and preparedness for climatic changes.

More than 80 % of the long-term breeding resources are spent on Norway spruce *(Picea abies)* and Scots pine *(Pinus sylvestris)*, and the future presentation will be almost totally concentrated to these two species.

For Norway spruce and Scots pine a multiple breeding-population system is applied to sustainable improvement of general-purpose goals and for the conservation of alleles. For Norway spruce and Scots pine meta-populations of more than 1000 parent trees are divided into some 20 breeding populations (sub-populations) per species, each containing around 50 individuals. Each breeding population has a target area defined by photoperiod and climate. Within economical constraints, the size of meta- and sub-populations were selected to give a low probability both of rare-allele losses occurring in the meta-populations and of common-allele losses occurring in the sub-populations.

Long-term breeding is carried out in each breeding population. The selection of candidates is planned essentially on a within-family basis. A double-pair mating design is used and positive assortative mating is strived for. Progeny testing (for Scots pine) or clonal testing (Norway spruce and Silver birch (*Betula pendula*)) is used to increase the accuracy of the selections. Progeny testing of candidates is time consuming because of the problems of inducing early flowering. Clonal testing is therefore used for species where vegetative propagation methods are available (spruce and birch). Material for mass-propagation for a certain area can be selected from one or more adjacent breeding populations.

The main goals of Swedish breeding are to increase the yield, adaptability and quality or economic value of the wood harvest, while safeguarding a necessary diversity in the breeding populations. While the general target traits are the same throughout the country, important differences in e.g. climate makes it important to vary their relative importance from one area to another. In the harsh climate of northern Sweden adaptability is absolutely essential whereas in the more favourable climates of central and southern Sweden more weight can be put on quality traits.

Of the selected plus trees all are represented in progeny or clonal tests and as of December 1999 59 % of the spruce and 54 % of the pine parent trees for the next generation were selected.

A lot has been learnt about the variation in and heritability of wood properties that would make it possible to breed for these. Because of long rotations it is, however, very hard to say anything about what wood properties would be desirable in the distant future, indeed predict what wood could be used for in such a distant future. Today the effort is to make sure that the breeding programs do not lead to obviously undesirable wood property changes. For instance, no Norway spruce parent trees with a low density are selected since open plantation spacing and frequent thinning leading to rapid growth of the individual trees already lower the spruce wood density.

Research by Rosvall et al. give clear indications that the outlined breeding programmes are sustainable, robust, effective, and that the diversity losses are low.

Finally, just a few words about the other species. There is a basic breeding programme for Lodgepole pine (*Pinus contorta var. latifolia).* The programme is similar to that of Scots pine with 11 sub-populations of 50 trees each. The latest established orchards are seedling seed orchards, built on the open-pollinated offspring from 1100 in Canada selected phenotypically superior trees. – It may be of interest to you that Sweden by now has over 600000 ha of lodgepole pine stands in Sweden. Today the annual plantation area of the species is just some 3000 ha/a.

For silver birch there are 1300 selected parent trees, mainly Swedish but also Finnish, Lithuanian, Polish and German. Progeny and clonal tests exist. For this species there are two greenhouse seed orchards in Ekebo to produce seed from tested plus trees for use south of latitude 59.5°N. In Sävar, Umeå there is another greenhouse orchard for latitudes 60-62°N. It contains untested plus trees. For other species only rudimentary work is being carried out.

In addition to the traditional breeding duties, SkogForsk is also responsible for the long-term conservation of the genetic diversity of the breeding materials.

Organisation

SkogForsk, The Forestry Research Institute of Sweden, is responsible for all forest tree breeding in Sweden. The Institute provides interested orchard owners with orchard designs and suitable parent materials. The orchard owners then establish and manage the orchards, often with SkogForsk as their advisor.

The long-term breeding is financed with a 50:50 financing from the forestry sector and the government. The financing is guaranteed on a long-term basis and at a level, which is satisfactory. SkogForsk has also been quite successful in competing for national and European research grants and in obtaining sector financed R&D jobs.

Within SkogForsk the breeding and genetic research is organised into three programmes:

- Breeding for northern Sweden, located to Sävar
- Scots pine breeding for southern Sweden, Uppsala
- Breeding of Norway spruce and other species, southern Sweden, Ekebo

Program 2 is in charge of research on orchard establishment and management and co-ordinates breeding strategy work.

Vegetative propagation, an essential tool for the breeders, is co-ordinated by a fourth research programme, which as its main duties has to look into seed research and nursery operations. There are cutting programmes for Norway spruce and Scots pine and, in close co-operation with the Swedish University of Agricultural Science also with somatic embryogenesis for the same two species.

Stand establishment

Forest cultivation is of course a prerequisite for tree breeding. According to an inventory carried out by the Swedish National Forestry Board in 2000, artificial reforestation was used on 68 % of the regeneration area; 1 % was direct seeding, the rest planted. Natural regeneration, mainly through seed tree regeneration of Scots pine, was used on 26 % of the area. On the remaining 6 % of the regeneration area the landowners do nothing active to accomplish a new stand. Mechanical site preparation was used on 75 % of the inventoried area. On 16 % of the area the regeneration failed to reach the minimum requirements of the Forestry act.

The Swedish seedling consumption in 1999 was some 304 million seedlings, 124 million Scots pine, 171 million Norway spruce, 7.7 million other conifers and 1.8 million hardwood seedlings. Included in the seedlings statistics are perhaps half a million Norway spruce cuttings. More than 80% of the seedlings are containerized. The National Forestry Board estimates that some 85 % of the total number of seedlings are of Swedish sources.

There is a definite increase in the interest for direct seeding, especially of Scots pine in parts of northern and central Sweden. This could have a dramatic effect on the demand for seed. In comparison with planting of containerized seedlings, with direct seeding the increase in seed required to obtain a desirable regeneration stocking is at least 25-fold.

Orchards

The first "generation" of seed orchards was planted from the end of the 1940s up to the late 1970s. These orchards are based on phenotypically superior plus trees mainly selected in mature stands without any progeny testing. Grafting material was collected off the mature trees, and nursery produced grafts used as planting stock in the orchards. There are 574 ha of Scots pine orchards and 234 ha of Norway spruce orchards of this "generation". Seed from these orchards is typically 10 % superior to seeds collected from natural stands. This superiority is not only due to genetic quality. Swedish breeders estimate that 6 % is genetic due to selection, 2 % to outcrossing and 2 % to better seed physiology.

At the beginning of the 1980s, a new set of plus trees was selected, this time mainly from 25-50 years old successful, sound-quality plantations. These trees, together with some tested plus trees from the first "generation" and selected clones from trials with Norway spruce cuttings, became the parents of a second "generation" of orchards. Nursery produced grafts were the normal planting materials in the orchards, but examples exist of field-grafted orchards and Norway spruce orchards established from cuttings. As of 1999 350 ha of Scots pine orchards and 230 ha of Norway spruce orchards of this "generation" had been established. These orchards are of varying quality, giving seed 10-20 % superior to stand seed, in a few cases up to 25 %, where tested parents were available at the orchard establishment.

The Swedish statistics on seed production are not complete, but the following should be enough to give a general impression. The total harvest of Scots pine orchard seed in the period 1979-94 was 49.2 tonnes, with a highly variable average annual harvest of 2.1 tonnes in the 1979-88 period. On average, 5,5 kg of seed per hectare were annually collected in pine seed orchards older than 15 years; if the area of orchards where no cones were collected is included, the average falls to 4 kg/ha. The best average annual production per ha was obtained in south central Swedish (Svealand) orchards with a record of 17.5 kg/ha/a during the 10-year period. On average, the highest yields, 8 kg/ha/a, were obtained in 20-25 years old orchards. The yields, for a number of reasons (trees too high, pruning and the fact that younger and genetically superior orchards come on line) tend to decline in older orchards.

The seed crop in Scots pine orchards is around 0.65 kg of seed per 100 litres of cones. The thousand-grain weight of the seed is rather constant at 6 g per 1000 filled seed, although the weight tends to fall slightly from south to north, but less markedly than for Norway spruce.

The total harvest of Norway spruce orchard seed between 1968 and 1994 was 9.7 tonnes, with an average annual harvest of 294 kg over the 1979-88 ten-year period. The variation year to year is very large. During the 1978-94 period, 70 % of the total harvest was obtained in 3 years; 1983, 1989, and 1993. On the average, in orchards where cones were actually collected, 8.1 kg/ha/a were collected in orchards over 15 years during the

1979-88 period. If the area of orchards where no seed was collect is included, the average annual yield falls to 1.6 kg/ha. In years with good crops, yields in excess of 50 kg/ha have been collected in both south and north Swedish orchards.

Seed yield and seed quality varies more in Norway spruce than in Scots pine. The yield is around 0.9 kg of seed per 100 l of cones. The thousand-grain weight is varies from up to 11 g in southern orchards to 6 g in northern ones.

SkogForsk estimates that long-term need for pine and spruce seedlings respectively, including restocking, is 170 and 240 million seedlings. To meet this there is a need of approximately 1.3 tonnes of Scots pine and 2.8 tonnes of Norway spruce seed. To this should be added some 1.5 tonnes of Scots pine seed for direct seeding.

Today, and for the near future, existing Scots pine seed orchards for all but the northernmost part of the country can supply the nursery requirements and also some seed for direct seeding. From around year 2030 a substantial shortage is foreseen, not even enough seed for the nursery production, if new orchards are not established in the near future.

The situation is worse for Norway spruce. For this species there is a substantial shortage of seed up to year 2030. The situation is especially problematic in the south where the requirement of the nurseries can only be supplied to 25 % by improved seed. At present orchard seed fulfils 70-80 % of the requirements in the rest of the country but this will also fall to only 30 % by year 2030.

Luckily enough Swedish forestry is now in the situation where there for both Scots pine and Norway spruce (as well as Lodgepole pine and Silver birch) is much better parent materials available for just about all of the country than ever before. O. Rosvall will present this information plus a description of the planed establishment of new orchards in a separate presentation.

Clonal forestry

Clonal forestry has a very limited use in Sweden. The use of clonal material of conifers is strictly controlled in the legislation. The law clearly states the number of clones which must be included in clonal mixtures and how much of a single clone can be used. At the moment SkogForsk has a project running in co-operation with the major companies of central Sweden to select clonal material suitable for that part of the country. There may in total be some 6000 ha of traditional, i.e. with tested clones, plantations of Norway spruce in Sweden.

It should be mentioned that in research on Norway spruce cutting some interesting differences between seedlings and cuttings have been found.. Frost and winter damage is less severe to cuttings than to seedlings of similar genetic constitution. This might be a result of the cuttings being physiologically older than the seedlings. More mature materials have a later bud break and earlier in-wintering than young materials.

Rooted cuttings also have a lower mortality from pine weevil damage than seedlings of a similar height. Several factors may be behind this. Rooted cuttings, in comparison to seedlings of a similar size, have a coarser bark the root collar, a higher diameter at the root collar in relationship to their height, and needles at the base of the stem. All these factors could make the cuttings less accessible to the weevils.

In spite of advantages such as these and the rapid growth of cuttings, it is not probable, mainly because of the high production cost, but also because of drawn out and costly testing, that clonal plantations will ever become wide spread in Sweden. There may be a brighter future for bulking up sexually propagated materials, e.g. in greenhouses produced controlled crossed seed of the very best trees. Here the legislation is not very restrictive in that 200 copies of each individual seedling (clone) can be used.

Future research

A major research task for Swedish breeders is to find an optimum balance between gain and diversity in the breeding populations. Shortening the generation interval is critical to increase the efficiency of forest tree breeding. One way is through finding juvenile characters strongly correlated to target traits. Another is via inducing early flowering. Both possibilities are looked into. Ways to vegetatively propagate Scots pine are also studied. This would increase the accuracy of testing and could also lead to shortened breeding generations. The study of climate changes and how the trees would adapt to these is another important research field. The development of marker-aided selection, and on a longer horizon also the use of genetically modified trees, are other coming tools to Swedish breeders.

Additional reading

Danell, Ö. 1993. Breeding programmes in Sweden - General approach. In: Progeny testing and breeding strategies. Proceedings of the Nordic Group for Tree Breeding, Edinburgh, Scotland. 6-10 October 1993. Edited by: Lee, S J. Forestry Commission (Edinburgh)

Hannerz, M., Eriksson, U., Wennström, U. & Wilhelmsson, L. 2000. Scots pine and Norway spruce seed orchards in Sweden – a description with an analysis of future seed supply (Swedish with English summary). Redogörelse nr 1, 2000. SkogForsk, Uppsala, Sweden. 40 pp.

Rosvall, O. 1999. Enhancing Gain from Long-Term Forest Tree Breeding while Conserving Genetic Diversity. Silvestria 109, SLU, Umeå.

Rosvall, O. 2001. New seed orchards give high genetic gain. Results No. 2, Forestry Research Institute of Sweden, Uppsala. 4 pp. (In press).

Forest tree breeding in Norway – status and challenges for the future

Country Report – Norway

Tore Skrøppa
Norwegian Forest Research Institute, Högskoleveien 12 N-1432 Ås, Norway

Summary

During the last 50-year period there has been drastic changes in Norwegian reforestation practices. The annual planting area has decreased from 40.000 to 20.000 ha, the total annual seed consumption from 7.500 kg to 800 kg and the number of seedlings planted from 105 to 40 million. The main emphasis in reforestation is on Norway spruce, which accounts for nearly 80% of the annual seed consumption. Of the 591kg of spruce seeds bought by forest nurseries in 2000, 60% was from source identified stand seeds, 14% was from selected stands, 25% was from seed orchards and less than 2% was imported seed.

Most breeding activities in our country has been with Norway spruce. With this species 260 hectares of grafted seed orchards have been established, of which 190 hectares are still productive. In total 8.000 kg of spruce seed have been produced in these orchards. Progenies from approximately 2.000 spruce clones have been tested in early tests or in progeny tests planted either on agriculture land or on forest sites. Some of the orchards are now being re-grafted with clones selected on the basis of preliminary progeny test information.

A new strategic plan from 1999 recommended that genetically improved plant material should be used for all artificial regeneration in the future and that such materials should be produced in seed orchards. It concluded that different breeding strategies should be followed in different parts of the country. In the productive areas the 1.5 generation seed orchard program should be continued. New orchards based on individuals selected from full-sib families should in the long-term replace these orchards. A low cost strategy has been proposed for the more marginal areas. For each breeding zone 200-300 families should be planted in progeny tests and plantations established with open-pollinated families from natural stands. One out of 3-4 test sites should be located at a site within the breeding zone favourable for seed production. The plantations, including the progeny tests, will grow successively into stands with the possibility for both timber and seed production. When preference is given to seed production, the plantations will be converted to a seedling seed orchard. Genetic thinning can be used in the trials, while phenotypic thinning has to be used in the

ordinary plantations, as long as individual identity is not being kept. One of the drawbacks with this strategy is the delayed time until seed production compared to the grafted seed orchard. An important decision, which has not been made yet, is the number of breeding zones needed.

The general Norwegian forester is not much interested in tree improvement. He wants to spend low amounts in long-term investments such as artificial regeneration. There is also a non-justified belief that natural regeneration will be sufficient for the establishment of the future production forest. Negative experiences in plantations established with Central European spruce provenances, the after-effects observed in seedlings from seed produced in orchards located in warm climates and the lack of sufficient documentation of long-term genetic gain make it sometimes difficult to convince foresters to use seed from seed orchards. These are also critical factors when support for continuous long-term breeding is needed.

Tree Breeding in Denmark

Country Report – Denmark

Ulrik Bräuner Nielsen
Danish Forest and Landscape Research Institute, Kongevej 11 2970 Hørsholm, Denmark

Present status of tree breeding

During the last decade tree breeding activities in Denmark have expanded from previously being focused on Norway spruce, Sitka spruce and Hybrid larch to include species like Oak, Noble fir and Nordmann fir. The two last-mentioned are the main species for Christmas tree and greenery production. Recently, in the fringe of tree breeding for forestry a program for genetic improved material for landscape trees and shrubs has been initiated.

Sitka spruce is now entering the 3rd breeding generation (see also Roulund 1990), Norway spruce partly the 2nd breeding generation (see also Wellendorf 1989, Wellendorf et al. 1994), and Noble fir is on the edge for 2nd generation (Nielsen 2000). Oak, Nordmann fir, landscape trees and mostly all shrubs are in the 1st breeding generation. All activities on Hybrid larch are mostly based on previous test results. Recently, a clonal propagation program for Nordmann fir based on somatic embryogenesis has been initiated.

Breeding objectives are in general focusing on health, quality and productivity, but are of course tailored to individual species and the environment in which they are intended to be used. Evaluation of older field trials continues to focus primarily on these traits.

Establishment of new trials in Norway spruce continues, because they are linked to specific seed orchards. The extensive use of open-pollinated seedling seed orchards in oak breeding combines orchard management with progeny testing and creation of the 2nd generation of the breeding population. Testing of already selected and grafted plustrees in field trials is going to proceed for Nordmann fir.

An improvement strategy involving 31 tree and shrub species for landscape use has been elaborated. The 1st breeding generation for 11 of the species is based on collection of seed from single trees, while the 1st breeding generation of the remaining species is based on collections of seed from stands. The strategy aims at providing local, adapted and genetic broad seed and plant material for landscape use, and to provide the base for a better genetic understanding and management of these species in the future. As a part of the strategy, Denmark is divided in to two zones - an Eastern and Western region. Depending on species, different concepts of improvement and testing are planned ranging from breeding seed orchards (Barnes

1995), less intensive seedling seed orchard designs and simple stand collections/establishments.

Regarding the older traditional provenance trials evaluation of growth and adaptation continues, and only a minor effort is made to establish new trials for the wood producing species. However, new Oak trials are under establishment in relation to the breeding activities and landscape use covering 89 Danish, 25 Polish and 13 Norwegian seed sources (Jensen, J.S., pers. comm. 2001). The older provenance trials are a valuable basis for evaluating timber quality and long term economics, juvenile-mature correlation, and several species have been involved in common European research projects – like beech (Hansen et al. 2000). Within the genus *Abies* a set of new provenance trials related to Christmas tree and greenery production has been established. The main goal is to evaluate provenances of new and poorly tested species for Christmas tree characteristics in relatively short term studies (10-15 years). These activities include a common Nordic project on *Abies lasiocarpa* and ssp, and further the species *Abies magnifica* and ssp., *Picea pungens*, and also *Abies balsamea*.

Some breeding and gene conservation activities are related to projects carried out by Danida Forest Seed Centre and consulting operations by private companies throughout the (sub)tropical world. Teak is one of the main species (Kjær 1998), but also other species like e.g. *Pinus merkusii* is dealt with (Theilade et al. 2000).

The proportions of genetically improved material in reforestation practise

The yearly plant consumption for broad leaves and conifers are each a little above 20 million (Jensen et al. 2001), Figure 1. The conifers include the species Nordmann fir and noble fir which are used for Christmas tree and greenery production. These two species account for a major part of the total use of conifers – maybe around 12-15 mill.

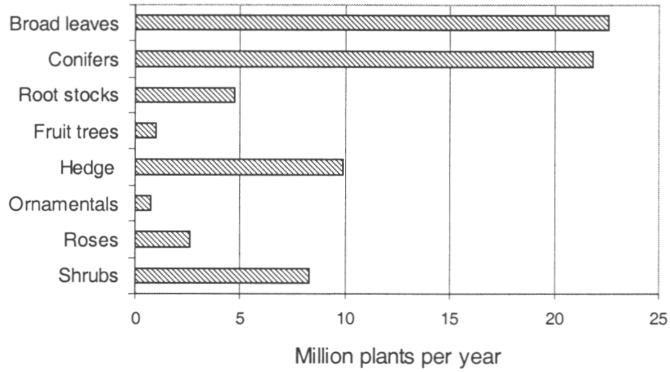


Figure 1. Consumption of plants per year (Jensen et al. 2001).

Table 1. Overview of main species involved in tree breeding activities in Denmark. cso: clonal seed orchards, sso: seedling seed orchard, DK: Denmark. Numbers in brackets are proportion of selected trees under testing in field trials).

Species	Selected plus trees in 1. Generation	Main groups	Selected plus trees 2. generation	Seed orchards [2] (ha) cso:	sso:
Noble fir[1]	180 (150)	DK unknown origin		11,0	8,0
Nordmanns fir[1]	464 (230)	DK Borshomi, Ambrolauri Pjatigorsk origin		29,3	
Sitka spruce[3]	153 selected in old stands 851 selected at nursery stage	DK Queen Charlotte Isl. Origins DK Washington origins	20 from the selection in old stands after testing 80 of the selected after testing	16,2	2,5
Norway spruce[4][*]	1000 selected in old stands 660 selected at nursery stage	DK West continental origins	100 20-year-old progenies 1300 nursery stage	29[4]	10[4]
Oak (Q. robur)[5]	150 120	DK origins Dutch origins		15,0	17[5] 7[5]
Oak (Q. petrea)[7]	140 (approx.)	DK natural stands		5,0	
Hybrid larch[6]	50 (approx.)	DK origins of Japanese larch European larch, and Imports from Poland	100 (approx.)	18,1	

References [1] Nielsen 2000, [2] Skov og Naturstyrelsen (2000), [3] Roulund (1990), [4] (Wellendorf, H. pers. comm. 2001) [5] (Wellendorf, H. pers. comm. 2001) [6] (Nielsen, C.N. pers. comm. 2001). [7] (Jensen, J. pers. comm. 2001)[*]: Only plustrees accepted and/or propagated are included.

The proportion of available improved reproductive material varies a lot depending on tree species. The Danish Tree Improvement Station and partly Hedeselskabet are the major suppliers of improved forest seed. Estimates for improved seed in 2000-2004 are as follows: Norway spruce, Hybrid larch and Noble fir approx. 40 %, Sitka spruce 20 %, Nordmanns fir 5 % and Oak 0 %. Twenty years ahead the estimates for noble fir indicate a more than hundred percent domestic supply relative to consumption based on improved seed sources, while the estimates for oaks are 25-30% and the others around 70-80%.

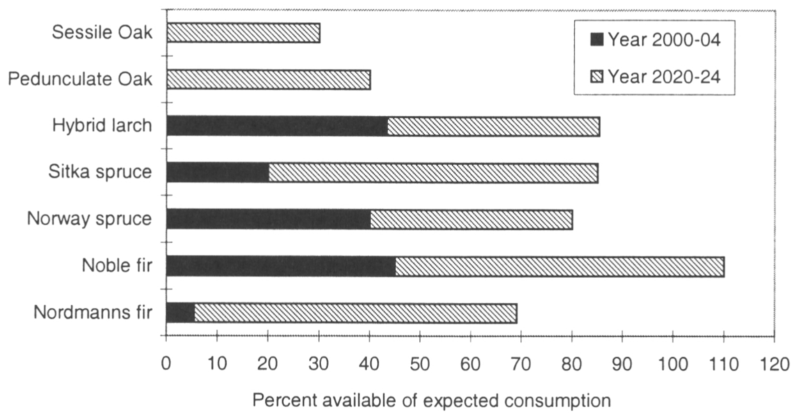


Figure 2. Available genetic improved material in year 2000-04 and year 2020-24 in percent of expected consumption. Skov & Naturstyrelsen (2000a).

Recent changes and development trends

A general trend in spruce breeding is the shift in breeding goals towards health and disease problems - and further into research on more causal and general problems like insect resistance, population genetics and QTL's. Oak breeding is, aside of the growth and stem form characteristics, focusing on health - mainly by a survey program for the selected plustrees. Resent research efforts in the breeding for Christmas trees and greenery have concentrated on adelgid resistance and post-harvest quality.

Furthermore, focus has been put on wood quality and quantitative genetic parameters have recently been estimated for traits like spiral grain and "Microfibril angles" (MfA) in Sitka spruce and Norway spruce (Costa e Silva et al. 1999, Costa e Silva 2000, Hansen 1999).

Problems and challenges

Political decisions have introduced some new restrictions to forestry - especially the Christmas tree production, but also for traditional forestry. From January 2003 all pesticides, herbicides and fertilisers are excluded in the Danish State Forest (Miljø & Energiministeriet 1999). Enhanced use of forests for protecting ground water reserves imply restrictions on application of herbicides for weed control, pest management, fertilisation etc. These restrictions lead to increased interest for resistance breeding, and frost hardiness and early growth-weed competition issues, and nutrient efficiency.

Another shift in forestry is the intention to use natural regeneration to a much wider extent and not only for beech, but also oak and the spruces. Potentially, this will have a great impact on breeding strategies and the long term use of improved material.

Needs for research and future plans for tree breeding

A future research challenge is to establish efficient breeding programs taking into account the restricted economic resources and the increased number of species. The objectives for the breeding programs are to optimise the relations between costs, genetic gains diversity and to secure the demanded supply of genetic improved plant material as fast as possible.

Further, it is a challenge to provide forestry politicians and silvicult-urists with new decision tools by looking more careful into the interaction between genetics and forest management in a sustainable forestry, including mixed forestry based on natural regeneration. Also the current policy of doubling the forest area in Denmark during the next 100 years needs high attention from a genetically point of view – essential decisions are taken by choice of seed source. This stresses the needs of updated, easy available information to foresters and politicians.

Population genetics of seed orchards based on few clones/families in relation to natural regeneration is a specific topic, which is going to be evaluated by use of molecular markers combined with traditional quanti-tative measurements. In general molecular methods will be introduced into a wide range of genetic studies. For example background pollination in seed orchards, QTL analysis of MfA and spiral grain, seed source identification etc. Further, it is necessary to pay attention to - and to promote educational aspects of forest genetics covering the range from university lectures, seminars, extension for growers, to field excursions etc.

Acknowledgements

Colleagues at the Danish Forest and Landscape Research Institute, the Arboretum and the Tree Improvement Station are gratefully thanked for comments and information for this report.

References

Costa E Silva, J. 1996: Clonal variation in wood quality, growth and growth rhythm in young sitka spruce (Picea sitchensis (Bong.) Carr.) : indirect assessment of wood density and lignin amount, estimation of quantitative genetic parameters, and index selection for improved pulpwood. Ph.D. thesis, Royal Veterinary- and Agricultural University, Copenhagen. 157 pp.

Costa E Silva, J., Borralho, N.M.G. & Wellendorf, H. 1999. Genetic parameter estimates for diameter growth, pilodyn penetration and spiral grain in Picea abies (L.) Karst. Silvae Genetica 49: 29-36.

Hansen, J.K. 1999. Genetic variation of spiral grain in Sitka spruce growing in Denmark : multiple-trait selection for improved timber quality. Ph.D. thesis, Royal Veterinary- and Agricultural University, Copenhagen.111 pp.

Hansen, J.K., Jørgensen, B.B. & Pedersen, P.S. 2001: Results from 61 to 79-year-old European beech provenance tests in Denmark: variation in economically important traits and economic returns. In Common Beech for Forestation and Diversification: Development of Forestation Techniques and Assessment of the Genetic Variation in Reproductive Material. EU-FAIR3 contract no. FAIR3-CT96-1464.

Kjær,E.D. 1998: Sustainable Use of Forest Genetic Resources. DSR Grafik, Frederiksberg.

Jensen, J.S., Lauersen, A.B. & Kjær, E.D. 2001: Forbruget af træer og buske i Danmark. Park og Landskabsserien nr. 28-2001, Forskningscentret for Skov & Landskab, Hørsholm, 201, 177pp. ill.

Miljø & Energiministeriet 1999: Natur- og Miljøpolitisk Redegørelse 1999. Miljø- og Energiministeriet 1999, 664p.

Nielsen, U.B. 2000: Forædling af nordmannsgran og nobilis – status og muligheder. Pyntegrøntserien nr. 15, Forskningscentret for Skov & Landskab, Hørsholm, 2000,54pp.

Roulund, H. 1990: "Outline to a revision of the Sitka spruce breeding plan in Denmark". Forest Tree Improvement, 23: 131-143.

Skov & Naturstyrelsen 2000a: Fremavl af skovtræer status 2000. Statsskovenes Planteavlsstation. Skov og Naturstyrelsen. Miljø og Energiministeriet, 69p.

Skov & Naturstyrelsen 2000b: Forskning, undervisning og formidling vedrørende træ som materiale. Rapport fra en arbejdsgruppe nedsat af Bevillingsudvalget for Skovbruget og Træindustrien. Miljø og Energiministeriet, 67p.

Theilade, I, Graudal, L., Kjær, E. D. & Hald, S. (editors) 2000: Conservation of genetic resources of Pinus merkusii Jungh & de Vr. in Thailand. DFSC, FAO & RFD. DFSC Series of Technical Notes TN 58. ISSN 0902-3224. Danida Forest Seed Centre, DK-3050 Humlebaek, Denmark.

Wellendorf, H. 1989: "A Danish Norway spruce breeding plan from 1972 – a retrospective review 15 years later." Proceedings of the IUFRO working party meeting, S2.02-11 in Sweden 1988: 279-316.

Wellendorf, H., Skov, E., & Kjær, E. 1994: "Suggested updating of improvement strategy for Danish-grown Norway spruce." Forest Tree Improvement, 25: 1-12.

A short review of the status of tree improvement in Iceland 2001

Country Report – Iceland

Thröstur Eysteinsson
Iceland Forest Service, Egilsstadir, IS-700 Iceland

Summary

The Althing greatly increased funding for farm afforestation in the national budget for 2001. The increase was according to the 40-year plans of 5 Regional Afforestation Projects and thereby indicates that funding will continue to be increased during the next few years assuming that those plans are followed. This increases the need for both tree improvement research and improved material. Unfortunately, funding for research has not been increased.

Native birch provenance trials are being used for research into genetic diversity using RFLP and RAPD markers. Preliminary results indicate that two populations differ significantly from the rest. Incidentally, these two populations are the tallest birch forests in Iceland and one of them is the main source of birch planting material used throughout the country. Planting of native birch has been increasing during the last 10 years and 1999 was the first year since 1951 that it was the most planted tree species in Iceland.

A potted larch seed orchard established in 1993 was moved into a new 1000 m^2 breeding hall in the spring of 2000, which should lead to increased seed yields by 2002. The first progeny tests from this orchard were planted in two locations in 1999. Improvements to a facility for freeze testing near Akureyri in north Iceland were completed this winter. The facility will vastly improve our ability to do frost tolerance research in agriculture and forestry.

Introduction

The history of organised forestry in Iceland now spans a century. During the 20th century, birch woodland remnants were protected, plantations were established and many Icelanders went abroad to study forestry. Experience was gained and knowledge increased. However, the extent of forest and woodlands did not increase appreciably, with roughly the same proportion of Iceland being wooded at the end of the century as at the beginning, or about 1%. This was due to the predominant land use (sheep grazing), low levels of funding for afforestation and the general belief for most of the 20th century that trees could not grow in Iceland. The greatest progress in forestry in

Iceland can be seen in the change in public attitude. Now, not only do people know that trees can grow in Iceland, some are worried that they grow so well that forests will "ruin the landscape" and "spoil the view".

Regional afforestation projects

Five regional afforestation projects aimed at providing grants for afforestation on farms have now been set up to cover all of Iceland. The projects provide grants covering 97% of the cost of establishing shelterbelts, woodlots of 20-100 ha and even forest plantations covering hundreds of ha. Roughly 500 farms participate in these projects with another 1000-1200 expected to join within the next 10 years (out of a total of only 2800 farms in Iceland). This considerable interest in afforestation by farmers has led to increases in funding for these projects every year, which in turn has lead to increases in planting.

Until now, increases in funding have followed the 40-year plans set up for the projects. If that continues, tree-planting will increase roughly 4-fold during the next 10 years, or up to 20 million seedlings annually. With a large part of this afforestation aimed at timber production, the need for seed and cuttings of well adapted material will increase as will the need for forest genetics and tree improvement research. Unfortunately, funding for research has not kept pace with increases in funding for afforestation.

Status of tree improvement by species

Three species; *Betula pubescens, Larix sukaczewii* and *Picea sitchensis*, together make up 75% of trees planted in Iceland (Petursson 2000). Tree improvement efforts are concentrated on these species along with the clonally propagated *Populus trichocarpa* and *Salix alaxensis*. Other important species include *Pinus contorta, Betula verrucosa, Picea engelmannii* and *Alnus sinuata*, but no active improvement work is ongoing with these species.

Native downey birch (*Betula pubescens* Ehrh.)

Native birch is now the most planted species in Iceland, comprising roughly 30% of trees planted in 1999 (Petursson 2000). Greenhouse seed production orchards for birch have been established in 3 locations to meet the increased demand for seed. The oldest birch seed orchard is privately run and produces seed from trees selected mostly for aesthetic traits under the name 'Embla'. The other two are run by the Iceland Forest Service and produce seed of specific provenances, one intended for North Iceland and higher elevations, the other for lowland areas throughout Iceland. Active tree improvement work is carried out using the material from all three orchards with progeny trials established beginning in 1993 for the 'Embla' orchard and 1997 for progeny of select trees from North and East Iceland (Tomasson

1995, Eysteinsson unpubl. data). Large progeny trials from the Forest Service orchards are planned for 2003.

Material from country-wide provenance trials of native birch planted 1998-1999 is being used in research using RFLP and RAPD markers to gage genetic diversity and chromosome studies to look at introgression between Betula pubescens and B. nana. Preliminary results indicate that for most Icelandic birch, within-population variability is greater than between population variability with two notable exceptions; the provenances Bæjarstaðaskógur in southeast Iceland and Vaglaskógur in north Iceland, which differ considerably from other populations (Thorsson et al. 2000). Incidentally, these two populations are the tallest birch forests in Iceland and the Bæjarstaðaskógur provenance (including planted seed stands and indoor seed orchards) is the main seed source for birch used throughout the country.

Larch (Larix sukaczewii Dylis and L. Sibirica Ledeb)

Siberian larch comprised 29% of seedlings planted in Iceland in 1999 (Petursson 2000) Most of the seed used comes from Finnish seed orchards. The greenhouse seed orchard established in 1993 was moved to a 1000 m^2 breeding hall in the spring of 2000 and is expected to supply about half of the current seed need within the next few years. The first progeny tests from this orchard were planted in two locations in 1999.

Seedlings from a total of 16 larch seed sources were available in Icelandic nurseries in 1999. These included 6 Icelandic stands of various origin, 5 Russian sources, 3 Finnish seed orchards, one Swedish seed orchard and the Icelandic greenhouse orchard. A provenance trial was planted.

Sitka spruce (*Picea sitchensis* (Bong.) Carr.)

Sitka spruce comprised 16% of seedlings planted in 1999 (Petursson 2000) and is increasing in importance. Icelandic plantations 30 years old and older regularly produce seed crops and the majority of seed used since 1995 has been of domestic origin. A seed stand in West Iceland of the provenance Cordova has been identified and thinned.

A large proportion of the Sitka spruce provenances in Icelandic provenance trials of material collected in Alaska in 1987-88 was freeze-tested in both spring and fall of 1996. The results show a great deal more within-provenance variability in frost hardiness than between-provenances, indicating that selection of individual trees within provenances rather than provenance selection could lead to greater gains with respect to this trait (Skúlason et al. 2001). Recent improvements in a freeze testing facility in north Iceland will improve our ability to do frost tolerance studies in the future (Edvardsen et al. 2000).

Black cottonwood (*Populus trichocarpa* Torr. & Gray) and felt-leaved willow (*Salix alaxensis* (Anderss.) Cov.).

Together, these clonally propagated species made up about 5% of trees planted in 1999 (Petursson 2000) and their importance is increasing both for use in shelterbelts and in mixtures with conifers in plantations. Extensive clonal trials of both species have been planted since 1992. Newly identified well adapted clones are being put into production and poorly adapted clones are being identified and taken out of production with the aim of improving these species by clonal selection while maintaining a reasonably broad genetic base. About 12 black cottonwood clones and 6 felt-leaved willow clones are now in general use.

References

Edvardsen, Ø. M., Guðleifsson, B.E. & Skúlason, B. 2000. Kalstofan á Möðruvöllum (The low temperature laboratory at Möðruvellir). IFRS Report no. 2/2000: 1-15.

Petursson, J.G. 2000. Skogræktarstarfid 1999: Tölulegar upplýsingar (Forestry in 1999: statistical information). Icelandic Forestry; Journal of the Icelandic Forestry Association 2000 vol. 2: 119-121. (In Icelandic).

Skúlason, B., Sigurgeirsson, A., Guðleifsson, B.E. & Edvardsen, Ø.M. 2001. Frost tolerance among provenances and families from the *Picea* complex in Alaska. Icelandic Forestry: Journal of the Icelandic Forestry Association 2001 vol.1: 188-190.

Thorsson, Æ.Th., Sigurgeirsson, A., Jóhannsson, M. , Tomasson, Th. & Anamthawat-Jónsson, K. 2000. Genecology of birch in Iceland. Paper presented at the Forestry Beyond the Timberlins workshop, Akureyri, Iceland, June 27-30, 2000.

Tomasson, Th. 1995. Embla – Kynbætt birki fyrir íslenska trjárækt (Embla – improved birch for Icelandic tree growers). Icelandic Forestry; Journal of the Icelandic Forestry Association 1995: 77-94. (In Icelandic with English summary.)

Integrating tree breeding and forestry in Estonia

Country Report – Estonia

Ülo Tamm & Malle Kurm
Forest Research Institute of Estonian Agricultural University,
Fr. R. Kreutzwaldi Str. 5, 51014 Tartu Estonia

Review of Estonian forest resources

According to the latest official land balance (in 1993) the area of woodland in the Republic of Estonia is 2.015.500 ha (Viilup, 2000), 1.942.500 ha (96.4%) of which is occupied by managed forest land, 885.700 ha (45.6%) of the managed forest land has been taken into account while characterizing state forests and 160.900 ha (8.3% of the managed forest land) has been taken into account while characterizing private forests.

As a result of sustainable forest management and increased afforestation of previous agricultural and drained land, the forest area increased by 2.248.071 ha between 1940 and 2000 (Fig. 1).

At the present time forest land makes up about 49.7% of the whole territory (Viilup, 2000). Dominant tree species in the Estonian forests are pine, birch and spruce. There are two species of birches in Estonian forests: the silver birch (*Betula pendula* Roth.) and the downy birch (*B. pubescens* Ehrh.). Until now no difference has been made between the species of birches in our forest inventory. According to their size birch stands are on the second place after the Scots pine among the main tree species. The composition of stands (by tree species) differs greatly in private and state forests (Fig. 2).

Figure 1. Area of forest land (1000 ha) in 1940, 1958, 1975 and 2000

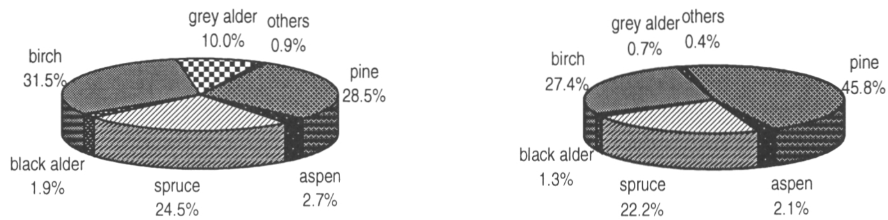


Figure 2. Distribution of forest land in state forest (left) and in private forest. Source: Estonian Forest Survey Centre

It is primarily the result of the different origin of the stands: the management of state forests was conducted more or less consistently and systematically and hewn forests have predominantly been reafforested by equivalent tree species, while most of the private forests have emerged naturally on former agricultural land.

Stands with prevailing coniferous trees constitute 67.8% of the total area of stands and 67.5% of the growing stock in state forests, in private forests the figures are 53.8% and 59.8% respectively.

There is a significant difference between the amount of pine forests and grey alder forests: while pine forests constitute the majority (45.8%) of the area of stands and grey alder forests grow on 0.7% of the area in state forests, then in the private sector the area of birch forests is larger (31.5%) than that of both pine (28.5%) and spruce (24.5%) forests, and grey alder forests occupy 10.0% of the area of stands.

Conservation of forest genetic resources

Protected forest areas

In Estonia, the problems of forest protection have an important role. For the protection of valuable forest ecosystems and biotopes, the habitats of rare species have been identified and recorded. Special attention will be given to the forests in ecologically sensitive areas, to the areas with natural or virgin forests, to the forests with high spatial and structural variety and with an abundance of species. There are different calculations to estimate the area of protected forests in Estonia.

Establishment of the Estonian Forest Conservation Area Network (in 1996) was an important step in the protection of biological and genetical diversity of forests (Viilma et al., 2000).

In the recent years, several political documents have been drawn up in Estonia to bring the organization of environmental protection into a better conformity with international requirements.

Forests, which grow on various protected territories, fulfill complex functions of protecting the environment. National parks, nature reserves, protected landscapes (nature parks) and nature sanctuaries are the most important types of protected territories.

Thus, nearly 100 000 ha of the Estonian forests can also be regarded as genetic reserves in addition to their nature conservation purposes. The areas have different protection regimes starting from restricted cuttings to the complete protection including prohibited visiting.

Restitution of independence has increased the importance of forests as economic entities again and, therefore, more attention needs to be paid also to the protection of them (Örd, 2000).

In the recent years, several political documents have been drawn up in Estonia to bring the organization of environmental and biodiversity protection into better conformity with international requirements. The documents described below are of particular importance for the development of the network of forest conservation areas.

Genetic reserve forest areas

Although the conservation activity of nature objects has quite long traditions in Estonia the classical nature conservation was created only in the 19th century. In 1910 the first nature reserve (Kumari, 1973) was founded on the islands of West Estonia, after 1923 some more new nature reserves were formed among them the nature conservation compartment at Järvselja (Kasesalu, 1997). The first Estonian nature conservation law was passed in 1935 (Viiding, 1986).

Decree of Minister of Forestry and Nature Conservation nr. 183 from December 20, 1985. 10 conservation areas with the total area of 3 540 ha or 0.2% of the forest land were established to protect the genetic resources of forest trees (Kurm, Tamm, 1997). Four of the areas, mainly pine stands make up 1987 ha or 56%, five stands are dominated by spruce – 1136 ha or 32% and one of them is dominated by birch which is 417 ha or 12% of the genetical forest reservations.

The following activities are forbidden in genetic reserves: clear cutting, resin tapping, disturbances of the soil, afforestation with the seeds coming from outside the reserve and any kind of economic activities that could endanger the maintenance of the gene pool and worsen the growing conditions of the trees. The only exception is cutting to improve the sanitary conditions of the forest stands or cuttings to protect the stands.

At the present time genetic reserves are being confronted with management problems resulting from the damage caused by bark beetles and the elk. Natural regeneration of Scots pine is often troublesome.

Plus trees and clonal archives

In Estonia the work in the field of forest selection started more than 40 years ago already. It was started by prof. E. Pihelgas in 1959 when he compiled his instructions for the selection of plus trees of the Scots pine. 4 years later it was followed by an instruction for the selection of plus trees of the Norway spruce by prof. I. Etverk. In 1966 both authors cooperated in writing the instruction for the selection of plus trees of both tree species mentioned above.

The ideas of selection have become an essential part of forest management practice in the course of various operations and activities: the selection and evaluation of plus trees, the collecting of scions and grafting of coniferous trees and establishment of seed orchards.

The establishment of seed orchards with all related activities has been most labour-consuming operation and promoted the co-operation between forest researchers and practicing foresters.

To date, 443 plus trees of pine, 135 spruce, 13 larch and 23 silver birch trees have been selected in Estonia. The selection of plus-trees has activated a little bit, so has the collection of seeds. The inventory of plus trees was conducted by the Centre of Forest Protection and Silviculture (Fig. 3). Most of these trees have been propagated and are now represented in clonal archives, seed, orchards and progeny trials. First clonal seed orchards of coniferous trees were established in 1965. All the existing seed orchards were established in the years 1965–1986. At present there are 180 ha of pine and 32 ha of spruce seed orchards. Altogether 503 clones of pine and 178 clones of spruce are included in the seed orchards (Kurm, 1996, Kurm et al., 1996).

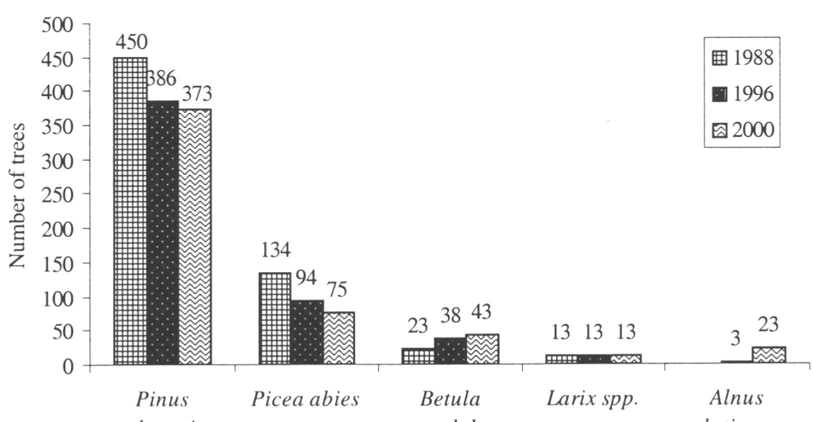


Figure 3. State of selected plus trees in Estonia in 1988, 1996 and 2000

At the present time the situation requires complementing the existing seed orchards with the grafts from tested clones and also the foundation of new 1.5 generation seed orchards.

In the years from 1999 to 2000 22.1 ha 1.5 generation seed orchards of pine (altogether about 55 clones) were established and 0.7 ha of spruce (17 clones). A year ago was started the establishment of the seed orchards of silver birch.

Results of forest breeding in last years

Analysis of progeny trials

The progeny trials of the Scots pine founded in Järvselja Training and Experimental Forest District in 1965, 1966 and 1968 by E. Pihelgas were analyzed to estimate the heritability of height and diameter characteristics, and also the dependence of progeny properties on the mother tree phenotype (Kurm, Tamm, Möls, 1998, Kurm et al., 2000).

From the results of statistical analysis conducted by new SAS/STAT software, one can see that the mother tree habitat has a significant effect on progeny ($P=0.002$). This effect is realized, probably, through the mother tree depending on the habitat. Among the phenotypical properties of the mother trees, the weight of seeds had the most significant influence on the progeny. Considering the mother tree phenotypic characteristics, the height, height deviation, and BHD were significantly ($p<0.005$) correlated with the progeny BHD while the progeny height was probably correlated only with the mother tree height deviance ($p=0.007$). Comparing the low BHD heritability with the high correlation between the progeny BHD and mother tree phenotype, it is conjectured that besides the genetic heritability some other (epigenetic) channels of transmitting parents' properties to the progeny can also be found.

Cultivation of hybrid aspen

As we know the crossing of Populus tremula and P. tremuloides has had a successful result in Finland and Sweden. The hybrid aspen plantations in Estonia have been established since 1999 using the planting material micro propagated in Finland. The introduction of alien species has caused some resistance and protest by green movements. The area of hybrid aspen plantations has been as follows: 1999: 130 ha; 2000: 280 ha; 2001: 50 ha.

Needs for research

The number of research workers decreased significantly in September 1996 after the Estonian Forest Research Institute was closed. Also, compared to the earlier period there has been considerably less interest in forest tree breeding in Estonia. Therefore, our main attention has been turned to the analysis of the experiments of forest tree breeding, started 30 years ago.

Still, it is good we have had a chance to collaborate with some scientists from neighboring countries e.g. Finland, Byelorussia etc. We have conducted some laboratory analyses together with our foreign colleagues, for example DNA analyses of genetic reserves.

We are lucky to have excellent cooperation with the Centre of Forest Protection and Silviculture in Estonia in more practical tasks. Needs to make better research: 1) to involve young researchers in forest tree breeding; 2) to increase the funding.

References

Kasesalu, H. 1997. Järvselja läbi aegade. Tartu, 19 lk. Zusammenfassung: Järvselja im Laufe der Zeiten.

Kumari, E. 1973. Looduskaitse areng Eestis. Looduskaitse. Tallinn, 100–108. Summary: Nature Conservation.

Kurm, M. 1996. Scots pine (Pinus sylvestris L.). Forest Tree Breeding in Estonia. Tartu. 7–11.

Kurm, M., Tamm, Ü. 1997. Conservation of forest genetic resources in Estonia. Forestry Studies XXVII. Tartu, 36–45.

Kurm, M., Tamm, Ü. & Siimon, V. 1996. Vegetatiivsed seemlad männi genofondi säilitajana. – Metsanduslikud uurimused XXVII. Tartu, 47–61. Summary: Vegetative seed orchards as the Retainers of the Gene Pool of Scots Pine.

Örd, A. 2000. Kaitsemetsad ja nende majandamine Eestis. Tartu, 234 lk.

Viiding, 1986. Eluta looduse kaitse ajaloost Eestis. – Teaduse Ajaloo Lehekülgi Eestis, VI kogumik. Tallinn, 5–23. Summary: On the History of Protection of Inanimate Nature in Estonia.

Viilma, K., Öövel, J., Tamm, U., Tomson, P., Amos, T., Ostonen J., Sørenson P. & Kuuba, R. 2001. Estonian Forest Conservation Area Network. Final Report of the Estonian Forest Conservation Area Network Project. Tartu, 95 p. + 306 p.

Viilup, Ü. 2000. Forest resources. Yearbook Forest 2000. Tartu, 1–38 (in Estonian).

Forest Tree Breeding in Lithuania

Country Report - Lithuania

Virgilijus Baliuckas
Lithuanian Forest Research Institute, Girionys 1, LT-4312 Kaunas reg., Lithuania

Present status of tree breeding

At present the activity in forest tree breeding in Lithuania covers selection of new plus trees, gene reserves and seed stands, and establishment of populational testing trials with open pollinated half-sib families. Most of experimental field trials established, general scientific scope and interest in the past were concentrated on coniferous species. Now situation is changing and more and more main forest tree species are being investigated in Lithuania.

The basis for tree breeding is shown in table 1 and the locations of different objects - in Figure 1. Strategies of forest tree breeding for single tree species mainly follows the line presented in scheme in Figure 2.

Figure 1. Progeny test plantations of all forest tree species in Lithuania.

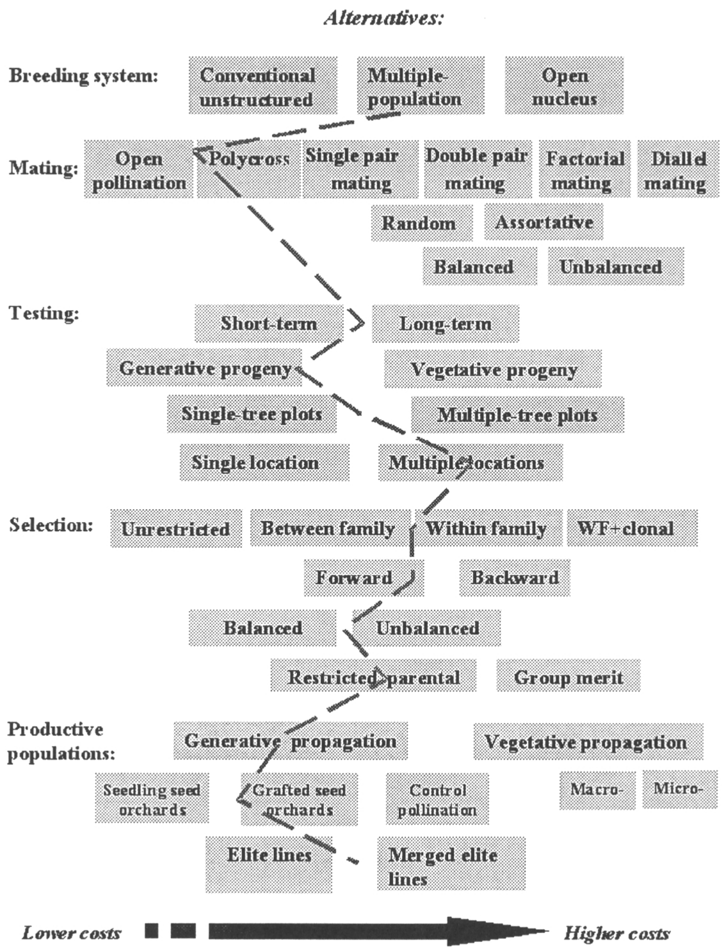


Figure 2. The schematic illustration of different alternatives of breeding strategy, where the dashed yellow line is the base of breeding strategy planned for main Lithuanian forest tree species (after Pliura 2000).

Table 1. The prospective change of the area (ha) of seed orchards by species planned for the period 1995-2015 in Lithuania. The planned ones to establish is shown in bold, while the area of newly established seed orchards go after slash.

Seed orchards	*Pinus sylvestris*	*Picea abies*	*Larix decidua*	*Quercus robur*	*Fraxinus excelsior*	*Alnus glutinosa*	*Betula pendula*	*Populus tremula*
Populational	23/10,9	39/6,0	-	18/-	13/-	5/3,2	2/1,3	2/-
Second generation	170/90,0	130/-	-	-	-	-	-	-
Hybrid	40/-	-	30/-	-	-	-	-	6/-

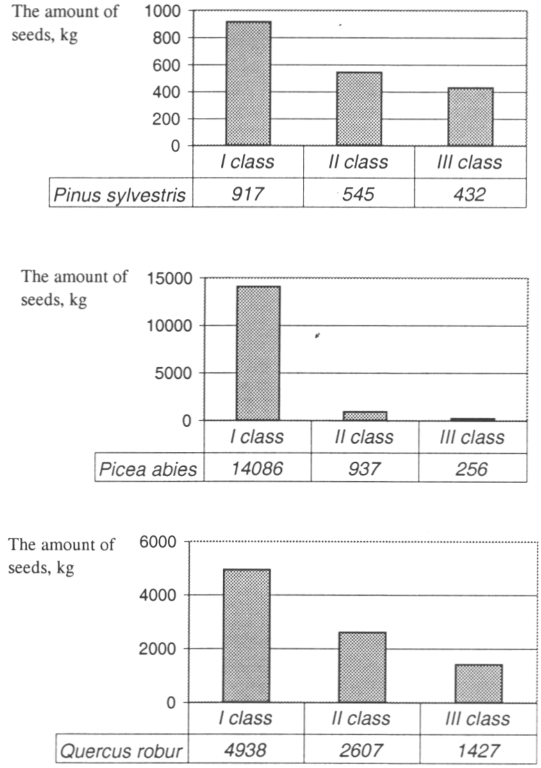
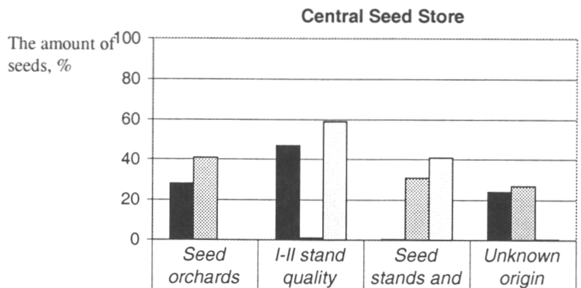


Figure 3. The amount of seeds of some forest tree species in Central Seed Storage by seed germinative capacity classes at year 2001.

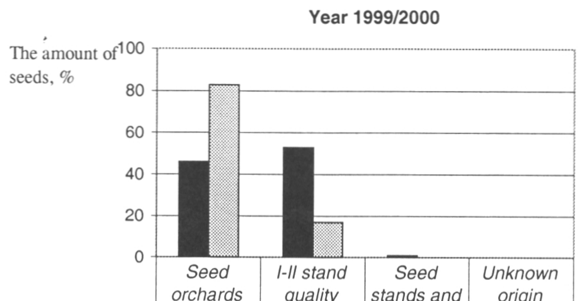
The proportions of genetically improved material in reforestation practise

Recent years the proportions of seed gathering of the main coniferous species from the seed orchards increased 1,5-2 times and no seeds of unknown origin for planting in forest sites are permitted. Forest tree seed resources available in 2001 are presented in Figure 3. The present situation and kind of last years dynamics of forest tree seed categories stored in Central Seed Store is given in Figure 4. The usage of seeds of two main coniferous species in Lithuania in 2000 is shown in Figure 5.

Recently prepared, but not yet approved, program on gene conservation and breeding development of coniferous in Lithuania deals with the proportions of 70% from seed orchards to 30% from approbated seed stands for artificial reforestation. Gene conservation objects and activity will be joint with tree breeding in a way of use of the same objects and will be based on dynamic multiple population breeding system (MPBS).

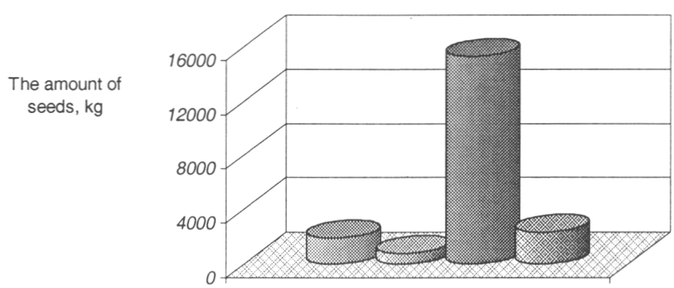


	Seed orchards	I-II stand quality	Seed stands and	Unknown origin
■ *Pinus sylvestris*	28	47	0	24
▨ *Picea abies*	41	1	31	27
□ *Quercus robur*	0	59	41	0



	Seed orchards	I-II stand quality	Seed stands and	Unknown origin
■ *Pinus sylvestris*	46	53	1	0
▨ *Picea abies*	83	17	0	0

Figure 4. The amount of forest tree species seeds by seed origin. The lower graph illustrates the last year's dynamics as regards seed categories.



Pinus sylvestris	***1893***
Sown in 2000	***778***
Picea abies	***15280***
Sown in 2000	***2313***

Figure 5. The usage of seeds of two main coniferous species in Lithuania year 2000.

Recent changes and development trends

Breeding zones are being delineated for *Pinus sylvestris*, *Picea abies* and *Quercus robur*. The seed database was created and documentation system was built adequate to that of the latest OECD rules.

Problems and challenges

The problem is becoming the control of reforestation and plant material used in private forest areas. In the nearest future there will be, roughly counting, 50% of private forests in Lithuania. 65% of the forest owners have less or near 3 ha and only 6% more than 10 ha. Due to deficiency in funds and awareness of forest owners the usage of bred material for regeneration is very limited. The common problem is also an awareness of decision makers.

Needs for research and future plans for tree breeding

There is a lack of field-testing results and selected genotypes of the domestic material of forest tree species to continue the establishment of the second generation of seed orchards. The second circle of testing and breeding of coniferous half-sib families will start soon, while *Betula pendula*, *Quercus robur*, *Alnus glutinosa* test plantations of the first circle of testing and breeding are still at juvenile age. The strategy for forest tree breeding is under consideration. Program on gene conservation and breeding development of broadleaves in Lithuania is under preparation. There are plans to start tree breeding on *Fraxinus excelsior*, *Acer platanoides* and *Ulmus laevis*, and some introducents as *Pseudotsuga menziesii*.

On the integration of improved material into forestry

Country Report – Scotland

Sam Samuel
Northern Research Station, Roslin, Midlothian, EH25 9SY, United Kingdom

Introduction

Tree improvement programmes were started in the UK in 1948. For the first 15 years effort was concentrated on developing appropriate techniques across a varied range of species. Work since the mid-1960s concentrated on the main production conifers: Sitka spruce, Scots pine, Corsican pine, hybrid larch and, during its time as an important species, lodgepole pine. Full progeny testing programmes were completed for all original selections in Sitka spruce, Scots and Corsican pine between 1967 and 1993 and tested clonal seed orchards have been established for these species. Testing in larch has been lees complete but a number of 2-species clonal orchards have been set up. Seedling orchards were used in lodgepole pine.

Improved Sitka spruce is also produced by the mass vegetative propagation of small quantities of improved seed using cuttings. Typical seed mixtures involve 20 superior half-sib families and each stock plant may yield over 1000 cuttings through summer and winter re-propagation cycles together with some hedgeing. This method allows greater flexibility in the manipulation of gains in specific selection characters.

There has been a revival of interest in Douglas fir over the last 10 years and a testing programme is now under way. Improvement of broadleaved species has also received recent attention. Initial work has concentrated on provenance evaluation but a cooperative initiative between public and private sector interests has started breeding programmes in six major broadleaved species, ash, oak, birch, cherry, walnut and sweet chestnut.

Major changes in the organisation of tree breeding within Forest Research (the research agency of the Forestry Commission (FC)) have taken place over the last 5 years. Breeding programmes are now customer-led by forestry policy-makers. This has inevitably involved a more short-term view of breeding work with agreed annual outputs and some funding constraints. All future work will now concentrate on Sitka spruce with any work on other species aimed to maintain current production capacities for improved material and to consolidate breeding archives for future reference.

Sitka spruce – the largest and most advanced programme in this species

The following table summarises details of the work and achievements in Sitka spruce.

<table>
<tr><td>Base population</td><td>2700 plus trees selected</td></tr>
<tr><td>Progeny testing</td><td>392 progeny trials (more than 300 hectares)

First generation half-sib testing (open-pollinated and polycrosses) now completed with 90% of original selections in test</td></tr>
<tr><td>Breeding populations</td><td>240 clones already re-selected

Up to 400 clones anticipated when screening is completed

Two further populations based on southern and northern types – 120 re-selections in each</td></tr>
<tr><td>Production populations</td><td>9 Clonal seed orchards (35 hectares)

Regular (annual) family mixtures compounded for mass vegetative propagation

Production units (orchards or mixtures) normally based on 40 individuals

3 populations in use, general, high density, high straightness</td></tr>
<tr><td>Genetic gains</td><td><table>
<tr><th>Production Population</th><th>Diameter</th><th>Density</th><th>Straightness</th></tr>
<tr><td>General</td><td>22</td><td>0</td><td>16</td></tr>
<tr><td>High density</td><td>15</td><td>9</td><td>13</td></tr>
<tr><td>High</td><td>16</td><td>-2</td><td>24</td></tr>
</table></td></tr>
<tr><td>Second generation</td><td>Will be selected from full sib crosses made on assortative mating basis within up to 6 sub-lines in the breeding population. Crosses for some sub-lines completed and the first already planted.</td></tr>
</table>

Seed orchards

A large number of clonal orchards was created in a range of species in the early years of the programme. These were based on untested parents. As progeny testing proceeded, new orchards based on tested clones were set up to replace these. A regular programme of orchard planting ceased in 1988. All orchards were originally planted and managed by Forest Research but during the 1990s the management of the active orchards was passed to the Forest Enterprise (FE), the agency of the FC responsible for the management of the state forests. Clearly, new independent initiatives with adequate funding are now needed before FR can consider the production of component material and the establishment of new orchards. There has been some recent interest.

The seed orchard establishment programme has unfortunately not been well-synchronised with the testing programme. Because methods of timber density evaluation were developed later and could not be carried out until progeny trials were around 15 years old, the clonal orchards planted for Sitka spruce were based on growth rate and straightness only. Breeding values for timber density are now known to be below average. Various solutions to this problem are now being considered. These include selective seed collection from clones with higher density, selective use of this material on sites in which it is safe to reduce spacing or even abandoning the use of these sources of improved material.

Promotion of improved material and its uptake by the forest industry

Improved cuttings from vegetative propagation of family mixtures were available before commercial production of seed began in orchards; promotion of improved material therefore centred on this source. Specific publicity meetings were arranged in the early 1990s to coincide with this. Subsequently, tree breeders have appeared at a range of professional gatherings in the forest industry and several articles in the more popular trade press have also stimulated uptake. One major marketing strength of all types of improved material is seen as reduced establishment costs through the use of a more vigorous plant. In practice, fewer herbicide applications are needed in the early years of establishment. Production based on family mixtures also offers the user greater flexibility in the balance of gain among the selection traits and brings the latest superior clones found in the testing programme into more immediate use. The vegetative propagation system does, however, involve high investment costs and so far there has only been a small number of large producers. There is also found to be some resistance to planting stock which costs more than twice the price of normal seedling material

The supply of improved material, however, only goes some way towards meeting the total demand in Sitka spruce. The following table summarises the situation but it must be emphasised that the figures given may be no more than fairly accurate conjecture, since there are no systems for recording the source of planting stock in the UK.

Source	Millions of plants	
Forest Enterprise (State forests)	VP Orchards Unimproved	6.5 3.0 12.0
Private sector	VP Orchards Unimproved	1.5 2.0 15.0
Total		40.0

These figures suggest that improved material in Sitka spruce accounts for around 33% of current planting with cuttings from improved family mixtures around 20% and orchard seed 13%

In Scots pine, flowering is much more predictable and orchard production has been sufficient to fulfil most of the needs for commercial planting stock for some years. In the other commercial conifers in which breeding has been pursued, orchards make some contribution to the supply of planting stock. It must, however, be emphasised that climatic conditions in the UK are not ideal for flowering and that good seed production is very irregular.

Among the broadleaved species, birch is the only one in which improved seed has been produced. The use of a polythene house to produce seed on potted grafts of untested clones met with considerable success and the methods will be used to develop regional production populations.

As already indicated, advanced generation breeding is currently only assured in Sitka spruce and the use of molecular markers to assist future selection work is being investigated. First generation gains made in other commercial conifers will be maintained and initiative on the improvement of broadleaved species may gather momentum over the next few years.

RESEARCH & DISCUSSION PAPERS

Decay resistance of Scots pine wood

Harju, Anni & Venäläinen, Martti
Finnish Forest Research Institute, Punkaharju Research Station, Finlandiantie 18, FI-58451 Punkaharju, Finland

Introduction

Decay of wood is a phenomenon that belongs to nature, but is not wished to exist in built environment. Decay of wooden structures can be prevented by using proper construction techniques or chemical impregnation of wood. However, impregnation may have harmful effects on the environment and human health.

The heartwood of old-growth Scots pine (*Pinus sylvestris* L.) has been traditionally used in structures exposed to a risk of decay (e.g. Löyttyniemi 1986). Present-day timber from managed forests comes from younger trees having a relatively low proportion of heartwood. For evaluating the possibilities to increase the quality and the proportion of heartwood by the methods of tree breeding, knowledge of genetic parameters is needed.

Material and methods

We estimated genetic parameters for the decay resistance of Scots pine sapwood and juvenile heartwood. The wood material of standing trees was obtained from two about 30-year-old half-sib progeny tests and from a clone archive. The 30-year-old progeny tests located at Kerimäki (61°50'N, 29°23'E, on 90 m elevation) and Korpilahti (62°48'N, 29°20'E, on 85 m elevation), and the clone archive of the same age located at Punkaharju (61°50'N, 29°23'E, on 90 m elevation). From Kerimäki 25 half-sib families, 10 sibs per family, and from Korpilahti 26 half-sib families, 16 sibs per family, were sampled. From Punkaharju clone archive 20 clones, 2 grafts per clone, were sampled. The clones sampled were mothers for 20 of the half-sib families growing in Korpilahti progeny test. Increment core specimen were decayed for 6 weeks *in vitro* using a brown-rot fungus *Coniophora puteana* as the test organism (a modification of a standardised EN 113 method) (see e.g. Viitanen *et al.* 1998, Venäläinen *et al.* 2001, Harju *et al.* 2001). The weight loss of the wood samples (mg/cm^3) was used as an inverse measure of the decay resistance. Estimation of genetic parameters was based on the simplified genetic model (Jacquard 1983, Ericsson 1997).

Results and discussion

The most marked feature describing the weight loss distribution was the considerably wider phenotypic variation in the heartwood samples compared to the sapwood (Fig. 1).

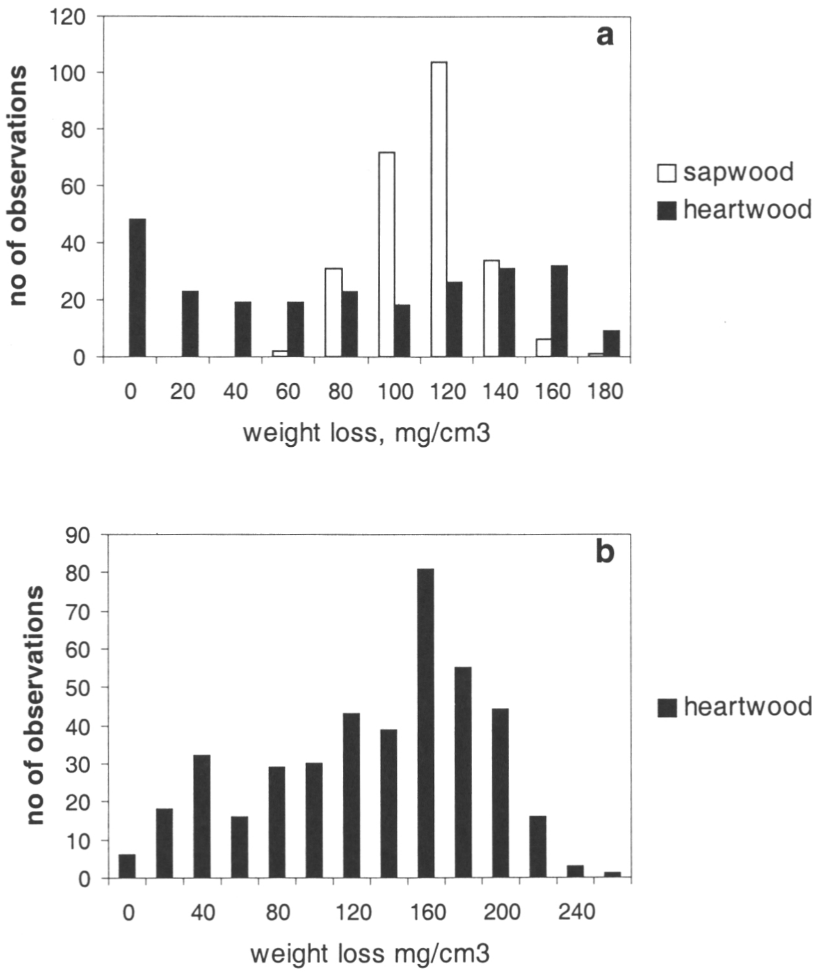


Figure 1. Weight loss distribution of Scots pine wood caused by *Coniophora puteana* in an *in vitro* decay test. Samples originated from Kerimäki (a) (Harju et al. 2001) and Korpilahti (b) half sib progeny tests.

The proportions of the variance components differed greatly between the two progeny tests (Table 1). At the Kerimäki progeny test, the additive genetic component for the weight loss of sapwood and heartwood was small compared to the total phenotypic variance, which resulted in negligible narrow-sense heritabilities (Harju et al. 2001). At the Korpilahti progeny test, where heartwood only was sampled, the narrow-sense heritability and the coefficient of additive genetic variation indicated that it would be possible to improve the decay resistance of Scots pine heartwood by direct selection (Harju and Venäläinen, submitted manuscript). Offspring-parent regression showed a moderate genetic determination of the heartwood decay resistance (Harju and Venäläinen, submitted manuscript).

Table 1. Weight loss of Scots pine wood caused by Coniophora puteana in an in vitro decay test. Mean weight loss, the range of weight loss, narrow-sense heritability or offspring-parent regression (h^2), and the coefficient of genetic variation (CV_A) are given. (Harju et al. 2001, Harju and Venäläinen, submitted manuscript).

Population	Sample	Mean (mg/cm³)	Range (mg/cm³)	h^2	CV_A (%)
Kerimäki	sw[a]	114	72	0.04	2
	hw[b]	80	199	0.07	19
Korpilahti	hw	123	250	0.37	28
Punkaharju,	hw	80	190	0.29[c]	

sw[a] = sample from sapwood
hw[b] = sample from heartwood
[c] = heritability based on offspring-parent regression

However, decay resistance as such is a complicated combination of traits that are poorly known. In order to carry out the phenotypic selection successfully, and especially to manage the stands to produce durable wood, the role of environmental factors in the mechanisms associated with the passive decay resistance of heartwood should be elucidated.

Acknowledgements

We are grateful to Heikki Kinnunen, Eija Matikainen, Heikki Paajanen, Tarja Salminen, and Jussi Tiainen for sampling and measuring the increment cores. Liisa Seppänen carried out the decay test in the laboratory of VTT Building Technology. We thank Pirkko Velling and Hannu Viitanen, VTT, for co-operation during the study. The study belongs to the Finnish Forest Cluster Research Programme WOOD WISDOM, and was mainly financed by the Academy of Finland (Project no. 43140).

References

Ericsson, T. 1997. Enhanced heritabilities and best linear unbiased predictors through approriate blocking of progeny trial. Can. J. For. Res. 27: 2097–2101.

Harju, A.M., Venäläinen, M., Beuker, E., Velling, P., & Viitanen, H. Genetic variation in the decay resistance of Scots pine wood against brown rot fungus. (accepted to Can. J. For. Res. 3/2001).

Jacquard, A. 1983. Heritability: One word, three concepts. Biometrics 39: 465–477.

Löyttyniemi, K. 1986. Männyn sydänpuu – Luonnon kestopuuta: Männyn sydänpuun luontaisen lahon- ja hyönteistuhonkestävyyden hyväksikäytöstä. Summary: On natural durability of pine heartwood. Metsäntutkimuslaitoksen tiedonantoja 231: 50. ISBN 951-40-0877-4.

Venäläinen, M., Harju, A., Nikkanen, T., Paajanen, L., Velling, P., & Viitanen, H. 2001. Genetic variation in the decay resistance of Siberian larch (Larix sibirica Ledeb.) wood. Holzforschung 55(1): 1-6.

Viitanen, H., Paajanen, L., Nikkanen, T. & Velling, P. 1998. Decay resistance of Siberian larch wood against brown rot fungi. Part 2. The effect of genetic variation. The International Research Group on Wood Preservation, Stockholm. IRG Doc. No: IRG/WP 98-10287. 6 p.

Heritability studies in open-pollinated *Pinus sylvestris* populations in Estonia

Malle Kurm[1], Tõnu Möls[2], Ülo Tamm[1]
1 The Forestry Research Institute of the Estonian Agricultural University, 5 Kreutzwaldi, EE-51014 Tartu, Estonia
2 The Biometrics Group of the Institute of Zoology and Botany, The Estonian Agricultural University, Riia 181, EE-51014 Tartu, Estonia

Introduction

Estimation of heritability of economically important merits in trees is a difficult problem due to (1) long generation period, (2) mostly unknown pollination type and (3) poorly controlled growth conditions for progeny. In Estonia the tree progeny tests were launched many decades ago but were not enough well designed, tracked and documented. Nevertheless, the trials initiated by E. Pihelgas in the former arable land on compartments of Järvselja Training and Experimental Forest District in 1966 and 1968 continue to be a valuable source of information about genetic properties of the Scots pine.

In the present study we revisit P. sylvestris data of E. Pihelgas trials, updating them with a set of earlier measurements. We focus on the heritability of tree height and diameter, and also test how progeny properties depend on mother tree phenotype.

Data

Overview of the used data is in Table 1. All the main characteristics of 65 mother trees from 22 habitats (age, height (H), the diameter at breast height (BHD), deviance of the height (the difference of the height of a mother tree from the average height of the trees of the same age) and BHD from the corresponding expected values; seed weight, cone measures: weight, length, diameter, and volume; mean length of the roots of 100 seedlings', etc. were considered. Seedlings from each mother tree were grown in different compartments and plots within compartments. The dataset is not balanced.

Data transformation

Residual distribution of tree height (H) and the BHD in progeny was rather normal. Nevertheless, for the following statistical analysis a logarithmic transformation of H and BHD was carried out. This followed two purposes: (1) to make the variance less dependent on mean, and (2) to make the variance components free of scale. Histograms of residual distributions are shown on Figures 1 and 2 where a moderate asymmetry can be seen.

Table 1. Data overview. N: number of groups of seedlings (about 6 - 50 seedlings in a group), H: height (m), BHD: brest-height diameter (cm).

Child-tree age (years)													
	1		2		3		4		6		28-30		
Compart-ment	N	Mean H	N	Mean H	N	Mean H	N	Mean H	N	Mean H	N	Mean H	Mean BHD
312	28	0.3	28	0.5	.	.	26	0.9	.	.	30	14.3	15.5
313	11	0.2	10	0.4	1	0.5	11	1.0	.	.	22	14.6	15.9
315	.	.	.	.	.	.	.	.	.	.	27	16.2	15.1
316	.	.	21	0.6	21	1.0	12	1.5	13	2.6	.	.	.
330	10	0.3	10	0.5	.	.	9	1.0	.	.	.	.	.
All	49	0.3	69	0.5	22	0.9	58	1.1	13	2.6	79	15.0	15.5

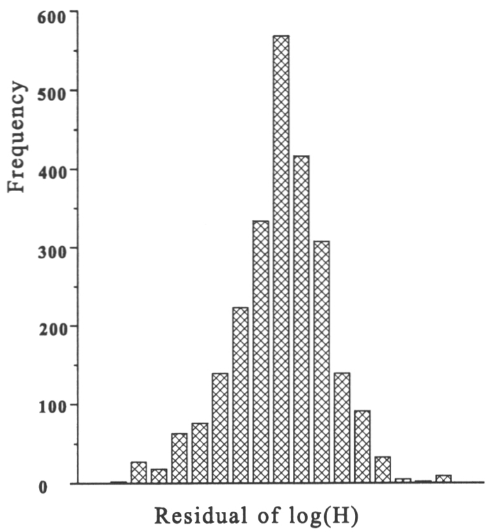


Figure 1. Residual distribution of log-transformed tree height in progeny.

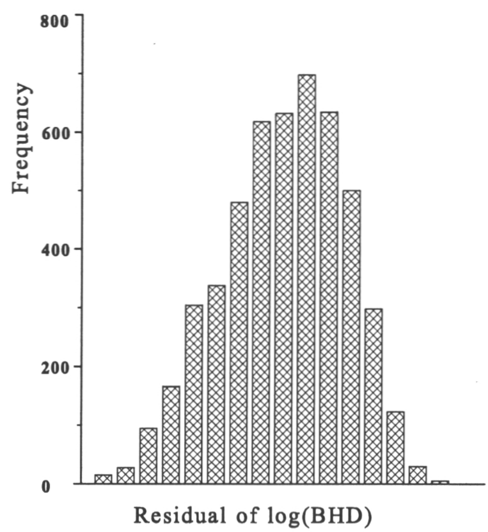


Figure 2. Residual distribution of log-transformed BHD in progeny.

Statistical analysis of heritability

The main statistical toolkit in the analysis was SAS/STAT software, Release 8.1 (SAS Institute Inc. 1997), especially the MIXED procedure. For estimating mother tree effect on the distribution of logarithmic tree height (LH) in progeny, the following MIXED model was used:

```
proc mixed data = progeny covtest;
  class mother compartment plot;
     model LH = age|age|age|age;
    random age(compartment plot) age(mother);
  weight weight;
run;
```

The growth curve for LH is presented here by a fourth-order polynomial which is assumed fixed (standard) for all the progeny. Mother-tree and plot effects are simply random fluctuations of the linear part of this standard curve. The weight variable takes into account that the available H values were in fact the means. The program used default REML estimation method.

For logarithmic BHD (denoted here LBHD) the analogous model was

```
proc mixed data = progeny covtest;
  class mother compartment plot;
     model LBHD = age / noint;
    random age(compartment plot) age(mother);
  weight weight;
run;
```

Here only a linear growth curve, forced through the zero at age 0, was fitted because BHD was measured in 28 - 30 years old trees only.

Results for heritability

Table 2 summarises the results for the covariance parameters. Parameters for the Age are variances for random fluctuations in progeny growth curve slope, assuming H and BHD are log-transformed. These parameters characterize the mother-tree effect.

Table 2. Results of the Covariance Analysis of logarithmic height and BHD in progeny. Square root of a parameter estimate the part of standard deviation of the measured (logarithmic) progeny variable that can be related to variability in factor levels. P-values are approximate

	Covariance parameter	Square root of parameter estimate	Factor effect in %	P-value
log(H)	Age(Compartment*Plot)	0.0377	3.84	0.0226
	Age(Mother)	0.0027	0.27	0.0002
	Residual	0.2741	31.53	<.0001
log(BHD)	Age(Compartment*Plot)	0.0057	0.58	0.0398
	Age(Mother)	0.0026	0.26	<.0001
	Residual	0.2746	31.60	<.0001

The slope of the tree growth curve (in the age of 1 to 30 years) has a mean mother effect of 0.26% ! 0.27% on both of child-tree height and BHD. This new approach to heritability is scale-free (because it works in percentile-scale) and the parameter Age(Mother) can be taken as a characteristic of the heritability of corresponding variable. Dependence of progeny H and BHD on mother tree characteristics. For calculation correlations, only progeny trees of age 28 - 30 years can be used. The related correlations are given in Table 3. A significant negative correlation between the seed weight and progeny height is illustrated in Figure 3.

Table 3. Correlations between the mother tree and its progeny averaged traits. Notations: n - number of mother trees, r - Pearson correlation, P - p-value

	Mean BHD of the progeny			Mean height of progeny		
Mother tree measure	n	r	P	n	r	P
Age	60	0,247	0,0573	59	-0,051	0,7013
Height	46	0,505	0,0003	45	0,186	0,2220
Height deviance	46	0,410	0,0046	45	0,395	0,0072
BHD	46	0,444	0,0020	45	0,094	0,5392
Seed weight	72	-0,203	0,0877	71	-0,241	0,0425
Cone weight	64	-0,257	0,0400	64	-0,085	0,5061
Cone length	62	-0,304	0,0163	62	-0,204	0,1122
Cone diameter	61	-0,241	0,0610	61	0,006	0,9648
Cone volume	61	-0,252	0,0503	61	-0,045	0,7322
Mean lenght of 100 seedlings roots	60	0,276	0,0331	59	-0,052	0,6948

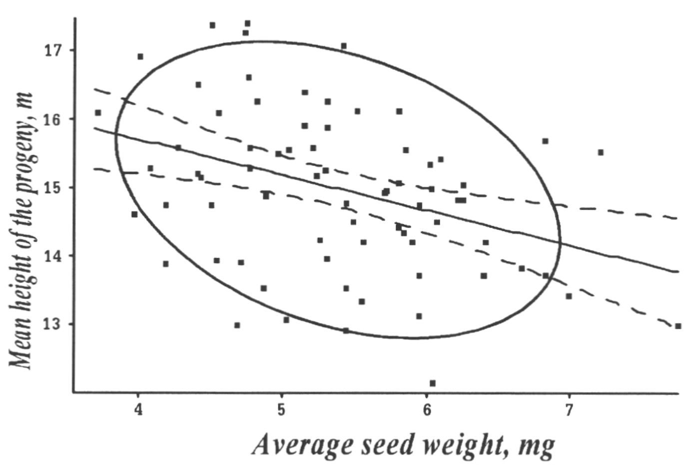


Figure 3. Trees, grown from lighter seeds are taller on an average. The 80% confidence ellipse for individual trees and 95% confidence limits for the regression line (Kurm et al. 2000) are shown.

Discussion

Using logarithmic method for estimating heritability has certain plusses. Probably more studies are needed to see all preferences and drawbacks of this approach. The mother-induced variability in progeny has caused by at least three main sources: (1) 1/2 of mother DNA, (2) mother epigenetic information, (3) 1/2 father-tree DNA. If we are interested in breeding value variability of the mother-trees, we have to separate these components what is somewhat problematic. Using controlled pollination, one can eliminate fathers' influence, and if additionally assume that epigenetic effects do not exist, the variance of the breeding value of mother tree is about 4H(observed mother-caused variance component). If the father is unknown, we have to replace the multiplier 4 by some other coefficient from 1 to 4, depending on pollination type. This is shortly discussed by Kurm et al. (Kurm et al 2000).

A negative correlation between the seed weight (and also cone measures) and progeny height remains unclear. This dependence was observed also in our earlier work (Kurm et al. 1998) based on other data. It can be hypothesised that some mother-tree epigenetic properties may change with the age of the tree (see Table 3), and the seed weight might be negatively correlated with the tree age.

References

Sas Institute Inc. 1997. SAS/STAT Software: Changes and Enhancements through Release 6.12. Cary, NC, USA: SAS Institute Inc.

Kurm, M., Tamm, Y. & Möls, T. 1998. Mother tree influence on progeny in Scots pine. Proceedings from the meeting of the Nordic Group for the Management of Genetic Resources of Trees. Forest Tree Improvement, 26, 38 - 46.

Kurm, M., Möls, T., Tamm, Ü. & Jõepere, E. 2000. Heritability of stem height and BHD in Pinus sylvestris L. Metsanduslikud uurimused XXXII, 32 - 42.

Tree Breeding Tools (TBT)

Dag Lindgren
Department of Forest Genetics and Plant Physiology,
Swedish University of Agricultural Sciences, SE-90183 Umeå, Sweden

Introduction

The web site "Tree Breeding Tools" is a service to make programs and other tools available for free downloading. Most "tools" are related to Forest Tree Improvement and Forest Tree Seed Orchards, and in particular applications in quantitative genetic theory for tactic and strategic decisions. Collaborators or me (or both) have constructed most of the programs offered. It is my hope that this service will improve forest tree improvement and result in improved future forests, which hopefully will contribute to a better future World!

The programs together address key problems in forest tree breeding: how to combine information on environment, breeding value, genetic parameters, gene diversity, time, cost and technique into efficient tactic and strategic breeding decisions. TBT and its concepts have been developed with different collaborators and students, this interaction has – among other things – resulted in five recent PhD thesis (Andersson 1999, Bila 2000, Kang 2001, Olsson 2001 and Rosvall 1999).

Technicalities

The web structure can currently (2001) be found via
`http://www.genfys.slu.se/staff/dagl`

Tree Breeding Tools is the most important part of this structure, which can be approached more directly at
`http://www.genfys.slu.se/staff/dagl/Breed_Home_Page/`

Some programs are subject for further development. A recently created file is rather likely to be the object for improvement and a new version may appear later. Old programs are less likely to change or be severely wrong, even if warnings appear within them. If a program is downloaded and used at a later occasion for an important purpose, it may be worth to check if a new version has appeared. Often older versions of programs are kept available, as a service for those who have not access to recently updated computer systems. They old versions may also be simpler as they offer fewer options. Currently the philosophy is to remove programs from 1997 and earlier, if there is a more recent which does the same thing. Usually the last edit of sheets and programs is noted in them. Currently (1997-2001) I use

MS. Files edited after 01-03-16 use a computer upgraded to the latest versions available early 2001. Since 2001 I use FrontPage 2000 for managing the site.

The user of TBT is allowed copying, using, developing, changing or extracting from the files and programs placed on TBT, if I have the copyright. For the case I do not own the copyright, it seems anyway likely this should be permissible. If results are used in documents, the author(s) may find it fair to make a citation.

Mistakes occur, some formulas or interpretations may be erroneous. Sometimes mistakes are corrected in later versions. Please, focus my attention if any mistake is suspected. Off course I do not accept any formal or legal responsibility for anything, which may happen if you import the files or programs found on the websites or use them or let the suggested values or information lead decisions.

Browser and computer peculiarities

Much of what occurs on screen is related to the browser and other features in your own computer or server, and thus not controlled by TBT. Warnings may occur against loading files from a non trusted source. Advertisements rubbish may bloom. How the texts appear on screen may depend on local computer settings. Often the fonts and background colours are your own default. Non-Latin characters (e.g. Swedish letters and many symbols) may either vanish or appear odd. Features like an equation editor may not work. That may result in unfilled boxes (although some unfilled boxes may be made visible just by clicking on them). Screen size, screen setting and magnification influence appearance. Old computers had 640 pixels wide screen, now few do not have 800 and codes developed 2001 usually heads for 1024 or up to 1280. Programs written for old narrow screens may not fill modern screens.

Some programs (like many EXCEL workbooks) can be run from the website. Sometimes it can overcome a compatibility problem to run the program from the web site. But usually it is not wise to run programs from the web more than for getting an impression of what they do, and it is sometimes impossible to run a program without downloading it. E.g. some programs create or change files, which an outside user is not allowed to do on our server. Some programs require support files to run, so be attentive to instructions and see that needed support files are downloaded in the same directory. Sometimes example files are supplied, which much facilitate the understanding.

It may be more or less easy to load files depending on your browser or your local IT-managers. The files themselves may not be interpretable in the intended way in your computer with its current settings. It is quite likely the programs themselves work fine, even if some of the "pedagogical" output does not work.

The content on levels closer to the root (below) /DAGL and dagl/Breed_Home_Page/ may be set to be invisible. The files are currently available on a server Picea in the domain Skogum/Webum at "Skogis", Umeå, Sweden.

In end of 1999 TBT got around 5 visits per day average. Since that, the web-site was reorganised as a part of our departmental web and made more complex. Now it seems to get around 1/4 of the total number of visits to the departmental web structures and around half of the visits to the pages allocated to individuals at the department (75 persons). TBT is not very visible on the world wide web, and does not get a high score by most webcrawlers. But some search machines searching for "tree breeding" regards it as the second ranked web site (replications and irrelevant hits not counted). At 1997 files and directories connected to TBT were at the servers Mendel and Linne. In the end of 1999 they were moved to Picea. Mendel and Linne do not exist any more.

Viruses and bugs

Viruses; bugs; worms; Trojan horses or other creep may spread via a site for file and program distribution. If download or execution or open macros derived from TBT, probably the browser or another system component will issue a warning or even forbid the operation. If the macros are disabled it is unlikely the programs will work!!! TBT is now (2001) hosted by the web-server of "Skogis, Umeå" (that server is supporting 350 employees) and is claimed to be frequently searched for viruses with late search programs. Old files ought to be safe, while those done the previous weeks could suffer from some yet undetected infection. A word about macros. The EXCEL workbooks and some other programs will not work if the macros do not work. When loading the programs the macros may become disabled. If so you may see the message "NAME?" in EXCEL on places where macros (e.g. functions) should work. You may be tempted to disable macros when loading from the net or as you computer is set for a high security, but if you do that, it will probably not work! Nowadays the safety on your computer may be set so it seems impossible to download as TBT is not trusted. It ought to be possible to instruct your computer to regard TBT (or genfys.slu.se) as a "trusted source", information on such procedures is available on TBT.

EXCEL workbook programs

EXCEL is often used on TBT. EXCEL is available on many computers all over the world and most forest tree breeders and forest geneticists have access to it. EXCEL can host lots of explanation close to the actual operations, thus the operations can be made rather transparent. As little of is hidden the user can reconstruct the operations in detail. Many formulas are given explicitly, thus the sheets can be used directly as formula collections, and sometimes the sheets may have other information embedded. The sheets are open and can be further developed by the user to fit better for the special application in mind. EXCEL functions (like "SOLVER") can be run. The results of a series of runs can be written directly and more or less automatically in the workbook. Experimentation with rewriting the workbooks is encouraged. It is true that their function can be destroyed, but it is easy to download a new fresh version instead of the damaged one.

Your machine may not be compatible with modern EXCEL versions or does not work with the TBT files for some other reason. Do not give up understanding too soon! Is all explaining text read? Maybe you are in the wrong sheet in the workbook? Clicking at the bottom menu changes sheets! Or you may not have looked at the right place of the sheet (sometimes the curser is left on the net so one enters it on an unintended spot); you may be able to see only a part of the sheet, in particular if you have a small screen or a high magnification setting. The magnification can be changed, try to look at the sheet in a sufficiently small scale so all of it can be seen. Something important may be missed, if the whole sheet is not searched. One useful question when a result appear, which does not seem appealing, is if the problem was properly addressed. A common mistake in science is to get the right answer on the wrong question! There may be more information elsewhere, so try some trial and error before quitting!

Changing cells meant for output (usually indicated by blue colour) destroys the function of the workbook. Usually nothing prevents from inserting "impossible" entries. This is a common reason for odd; not interpretable; or absence; of results. You can insert big values or get output with many digits, that often results in confusing symbols on the screen in spite of that everything actually works. A remedy may be to widen the columns where the problem appears. Language settings may cause problems; e.g. EXCEL in Swedish setting may appear "too stupid" to recognise "." in new entries as decimal separators. This can be remedied by definitions (from the Windows operating system by regional settings in the control panel), but still my impression is that program developers often do not comprehend all type of problems met by different flavours of non-Americans.

The EXCEL (.XLS) files were developed as workbooks for Windows. The sheets often also contains insertions, e.g. from MS Word or MS Equation, these are not essential for the function, but may be relevant for the understanding. E.g. MS Equation editor may not be installed into the host computer, and when empty boxes may appear, which contain useful information for others. A Mac may add to these transcription problems. Old versions are sometimes kept on the site for some time. Even when I use a modern program, it often initially was developed into an earlier version, and the memory of that may remain in some code.

I guess the files can be helpful if you adapt them to own problems, even in the case you can not use the worksheets as they are organised. If you understand how the worksheets work, you may extend or fine-tune them to your own problem; they may serve as useful templates for further development. They are also intended to serve a pedagogical purpose; they offer a way to understand concepts I feel important. They may even serve as collections of relevant formulas.

Genetic particulars

In the genetic programs usually only a single character on a single site is considered. This "character" can, however, be an index considering several characters, sites and tests. Thus, the limitation to a single character is not as severe constraint, as it may appear at first sight.

The programs contains many explanation and efforts to make it clear why the relationships appear in the way they do, but the purpose of the workbook is still more often to carry out calculations than proving the theory behind. Thus there is sometime necessary to go back to the original papers to get a full understanding. Usually references are given.

The programs use input, of course the programs cannot be better than the input, thus unreliable or unknown inputs cannot be compensated by sophisticated calculations. However, varying the input can test robustness against assumptions. The programs can be used to make predictions. Very often in forest tree breeding forecasts cannot be made based on reliable experiments. Experiments are too time-consuming and too costly; environments and silvicultural methods changes. Thus decisions has to be made.

Major programs and some comments

Describing environment

Temperature and day length are key elements in environments. The Swedish breeding program uses temperature and day length (=latitude) as a basis for sharing the breeding population in subpopulations (e.g. Ståhl in this volume). Numeric values for these factors can be calculated as a function of coordinates of the site and the time.

TEMPRED.EXE

The expected temperature and the expected accumulated temperature sum are obtained as a function of latitude, elevation, country and (for temp sum) threshold temperature. A library file is needed to run the program; it should exist on your computer installation, but is available for downloading. The calculations are based on regressions of latitude and altitude calculated form official weather statistics from meteorological stations of forestland in Sweden and Finland during 1961 to 1990. The material, calculations and algorithms used are tabulated and documented in Lindgren (1994).

Lindgren (1994) deals much with the problem at what date an accumulated heat sum is attained. These documentations may also be downloaded. There is also an essay about the temperature at the Sävar experimental station, giving correction factors, so the temperature at Sävar can be derived from the temperature at Umeå airport.

DagL.exe
The length of light and dark period of the day is given as a function of date and latitude (and some other factors). Some relationships can be expressed as tables on file. The algorithm was described in and appendix to Lindgren (1993).

Sites, Range, Adaptation and Number
Regeneration materials are tested and used over a range. On TBT are some tools connected to problems like: genotype by environment interaction; response surfaces; adaptation patterns; range over which materials can be used; number of test sites; number of test plants, these tools may be helpful when genetics over a range of environments is considered.
sites.xls

In setting up genetic tests, number of test plants and number of test sites are chosen, this program suggest suitable values. The program assumes (like a breeder) that the objective of the test is to maximize the breeding value of entries selected based on test data. The smaller the interaction between entries and test sites is, the fewer tests sites are needed. The cheaper it is to distribute test plants over many test sites, the more sites will be used. The optimal number of test plants per site does not depend on the resources available. Thus the optimal allocation of resources is to spend all extra resources on increasing the number of test sites; none of the extra resources should be spent on increasing the number of test plants per site! (Lindgren 1985).

ADAPTATION.XLS
A genetic material used where it is not perfectly adapted causes a loss. This workbook evaluates the size of this loss on a site and over a range. Such considerations are helpful to evaluate the suitable range of seed zones. Seed orchards are composite genetic material, where plus-trees have been recruited from an area rather than a spot, and thus have adaptation patterns, which differ from that of a natural provenance. Thus they have a wider range of adaptation but are not perfectly adapted for a particular site. They represent a genetic gain, and will thus be superior to the local provenance within a range of sites. (Lindgren & Cheng, 2000).

Selection in normal distributions
To predict the effects of selection, it is helpful to study what effect selection has in a standardised normal distribution ("the ideal case"). For "genetic

gain" predictions, the "selection intensity" is essential. The program SELEINT2.EXE calculates selection intensity for values derived from a normal distribution. Selection intensity when the j top ranking out of n normal distributed values are selected can be derived. The program can generate normal order statistics ("rankits") on file (the expected values of the j: th highest ranking value out of n); these can be seen as "selection intensity" (used in breeding value prediction) for an individual selection. These values are useful as "typical" values to use for illustrating the likely outcome when an algorithm is applied to real data. More about algorithms and typical output is available in Lindgren and Nilsson (1985) and Lindgren and Bondesson (1987).

The program SELENOR3.EXE calculates optimal contributions (= linear deployment, see below) and characteristics of that, when values for genotypes are distributed as a normal distribution. Another useful statistics for predicting genetic gain is additive genetic variance, this is reduced by selection, and the program predicts how much. Some output from SELENOR.EXE and more information about what it does are available in Lindgren and Bondesson (1990) and Lindgren (1991).

Concepts group coancestry, status number, effective clone number, gene diversity, group merit selection and group merit progress

Gene diversity is a buzzword, but breeders have difficulties to deal with the concept. As far as the type of gene diversity, which is connected to the increasing relatedness and the associated chance that genes are identical by descent, is concerned, TBT offers options and concepts to manage gene diversity. Some central concepts are mentioned here. Group coancestry of a population is the chance that two genes taken at random (with replacement) from the population are identical by decent. Group coancestry can be viewed as "latent inbreeding". Diversity means that things are different and gene diversity means that genes are different. Gene diversity is here defined as the probability that genes taken from a population are not identical by descent (thus diverse). Concepts referring to relatedness (like inbreeding) are relative and need a reference. For forest tree breeding the wild forest, from which plus trees were selected, often constitutes a relevant reference. The major interest is how forest tree breeding is influencing this "initial" genetic diversity. Group coancestry is the fraction of gene diversity lost since the initiation of forest tree breeding. Status number is a way of expressing group coancestry as an effective number. A review of the concept has been made by Lindgren and Kang (1997). Status number is the half the inverse of group coancestry. An attractive property of the status number is that it is the same as the census number for a population of unrelated, non-inbred individuals. Status number is an intuitively appealing way of presenting group coancestry, as it connects to the familiar concept of number (population size). Status number has similarities with "effective number" in the classical sense as it predicts inbreeding following random mating. We can talk about "effective number of clones" in a seed orchard when clones are represented with different ramet number (cf. Kang et al 2001). It is the status number of the clones for unrelated and non-inbred clones where each ramet is given the same importance. Group merit is the weighted average of breeding value and gene diversity for a population. Group Merit Selection is selection, which aims for maximising group merit (this maximisation is mathematically difficult and I believe no method which can generally find the maximum in a reasonable amount of time is possible, the methods suggested in TBT are just approximates. The goal of breeding may be set as maximising Group Merit Progress per time at given cost (Wei and Lindgren 2001). TBT has different tutorials, (texts, demonstrational programs, slide shows) to clarify these concepts and even to make numerical calculations of the values for some cases.

Gene drop analyses

EXCEL workbook "retention2000.xls" aims to perform gene drop analysis. Leopoldo Sanchez- Rodriguez constructed it. Gene dropping refers the destiny of copies of individual founder genes when dropped through a genealogy, not only the risk of loosing founder genes, but also how likely it is that they appear in different number of copies.

Linear deployment

Linear deployment means that clones are deployed to a clonal seed orchard with a ramet number (as a prediction of reproductive success), which is linearly related to the breeding value of the clone (as long as this gives a positive number of ramets) (Lindgren and Matheson 1986). The idea that it may not be optimal to have the same representation of all clones in seed orchards, was initially presented by Lindgren (1974). It is possible to generalise linear deployment, but this is not done on TBT. This procedure optimises the expected relation between genetic gain and "effective number of clones" in an orchard at establishment or genetic thinning. Effective number of clones is a relevant measure to predict selfing and gene diversity of the orchard crop. I do recommend linear deployment where breeding values of clones are available. It boosts the gain about 5% at the same effective clone number compared to the conventional truncation selection and in the same time extend the lists of represented clones. Linear deployment is also worthwhile for genetic thinning of seed orchards, when an upper constraint can be applied (number of ramets before thinning) (Bondesson and Lindgren 1993) and for deployment of clones to clonal forestry (Lindgren, Bondesson and Libby 1989).

LINEAR_DEPLOYMENT.XLS is an EXCEL workbook made 1997 with linear deployment algorithms. It has the dual purpose to explain the algorithms and to facilitate for others to use the algorithms for their material by supplying worksheets. Actually every linear deployment is in a sense an optimum under some circumstances, the method of the worksheet may be formulated as identifying the problem, which corresponds to the solution, and when - by trial and error (iteration) - identify the right problem. In

LINEAR_DEPLOYMENT_2000.XLS the worksheet for establishment of seed orchards is improved and minor changes been made in other sheets, the improvements are mainly cosmetic. It may be of interest to look at the consequences of linear deployment on normal distributions (Lindgren 1991 and 1993). SELENOR3.EXE does that.

Status.exe

A program for calculation the status number (and thus also group coancestry) was developed on New Zealand by Gea, Jefferson and Weaver (Gea 1997). The input is a text file with genotypes and their pedigree back to the founders.

Group merit selection

Group merit selection was developed for forest tree breeding by Lindgren and Mullin (1997) (although they initially called it "population merit selection"). The idea is to consider both gain and gene diversity (relatedness) when selections are done. The input is the breeding value of the candidates, the coancestry among the candidates and the desired weighting of gene diversity versus breeding value. The group merit selection principle was used by Thuy Olsson (assisted by Peter Lidström) to construct a program with a user-friendly interface named “Selection Tool”. The program also has an option to consider only cross coancestry, thus the average coancestry excluding self-coancestry can be weighted against breeding value. Some applications are found in Olsson (2001). Selection tool has been used to suggest the best choice of clones to orchards, where candidates are related, by balancing the inbreeding occurring after selections of relatives to the higher gain achievable if some relatedness and subsequent inbreeding is tolerated in the seed orchard. The program is somewhat simplified compared to the algorithm used by Lindgren and Mullin (1997), it runs only a single iteration and does not certainly consider arbitrary relatedness, but it is likely to find the optimum for all situations of practical tree breeding interest.

Seed orchard manager

This is an EXCEL workbook (ORCHARD MANAGEMENT.XLS) concerned with number of clones in clonal seed orchard and how this and other interacting factors influence the seed crop. This program calculates gain (breeding value) and status effective clone number (=group coancestry; gene diversity) depending on the number of plus tree clones used as seed parents and as pollen parents (they may be different or partly overlapping). Male and female fertility (reproductive success) may be correlated. Pollen contamination is considered (both amount and genetic value). The clones may vary in fertility and the magnitude of variance may be different for seeds and for pollen.

Thoughts resulting in the program were presented by Lindgren (1974) and Lindgren and El-Kassaby (1989). I wrote a simpler version 1997. Kyu-Suk Kang and I have developed the program further and taken new features into account till 2001. The workbook is organised so that there are three progressively more advanced worksheets as well as one mainly for domestic Swedish use about selective harvest. The theoretical foundation for gene diversity of seed orchard crops were developed by Lindgren and Mullin (1998). This and other background for the program is developed and described by Kang (2001) in his PhD thesis. One of the studies is focusing on the structure and results obtained by this program (Kang, Lindgren and Mullin 2001). There are a number of exercises constructed specifically to train to use this tool; they can also be found in the workbook itself.

Gainpredictor

GAINPRED is tool to evaluate tree improvement practices regarding breeding value, gene diversity, genetic parameters, between and within family selection, breeding strategy (technique), cost, time (progress of genetic gain and group merit over time) and relatedness. GAINPRED evaluates suggestions of production population (seed orchards, clonal forestry). You can yourself search for something appealing or which constitutes a reasonable use of resources or check how the current strategy works. "Gainpred" focus on short term breeding heading for a forest generation material within a limited time, typically starting with plus tree selection and ending with a seed orchard. For questions focusing on long term breeding, "breeding cycler" is a better choice of program. There is a simple and old version GAINPRED.xls and a more advanced version. GAINPRED is actually more a deterministic breeding simulator than just a gain predictor (the name has hanged on while more aspects were given to the program). There are some examples, which may help you to better understand GAINPRED. The genetic gain of different breeding alternatives are compared based mainly on calculations by Lindgren and Werner (1989). Cost features are exemplified by Lindgren, Wei and Lee (1997). Group merit progress per year is a new feature, which was introduced by Wei and Lindgren (2001).

Breeding cycler

The answer for the best selection strategy as regards genetic gain, gene diversity cost and time can be found by experimenting with BREEDING_CYCLE2001.XLS. It is a deterministic simulator aiming to compare strategies for evaluation and selection to the next generation of the breeding population in a long time cyclic breeding program. The simulator evaluates one full breeding cycle from mating of the breeding population till mating of the next breeding population. The simulator can handle (1) phenotypic selection, (2) clonal test and (3) progeny test. The simulator compares simultaneously gain, gene diversity, cost and time for given parameters, like genetic variance components, cost components, time components and selection strategy. Thus it is possible to search for a strategy, which combines highest annual group merit progress with a fixed annual budget. That is actually my formulation of a tree breeding specialists major job. By a combination of trial and error, common sense and optimisations for part of the problem long term breeding strategies can be suggested or evaluated. BREEDING_CYCLE2001_2STAGES....XLS considers also selection

Tutorials

Many of the programs contain much tutorial material themselves within the individual programs. There is tutorial material on TBT, like a minicourse in "quantitative genetics", a PowerPoint presentation of TBT (this paper is based on that lecture!) and different collections with examples (e.g. EXCEL files with coancestry matrixes). There are tutorial examples and programs in the site (sometimes within the programs) to help understanding and learning the programs and concepts at TBT.

Acknowledgements

Support from Carl Trygger Foundation for arranging this WEB-site and some of its content is gratefully acknowledged. Especially the Kempe-foundation has supported projects, which resulted in programs on this web-site. Some visitors more or less paid by foreign countries or the Swedish Institute has contributed. Many persons have helped me in different ways.

References and other literature

Andersson, E.W. 1999. Gain and Diversity in Multi-Generation Breeding Programs. Acta Universitatis Agriculturae Sueciae. Silvestria 95 42pp+4 chapters.

Bila, A.D. 2000. Fertility variation and its effects on gene diversity in forest tree populations. Acta Universitatis Agriculturae Sueciae. Silvestria 166. 31pp+4 chapters

Bondesson, L. and Lindgren, D. 1993. Optimal utilization of clones and genetic thinning of seed orchards. Silvae Genet. 42:157-163.

Gea, L. 1997. Genetic diversity and gain – the concept of status number. PhD thesis, University of Canterbury.

Kang, K.S. 2001. Genetic gain and gene diversity of seed orchard crops. Acta Universitatis Agriculturae Sueciae. Silvestria 187 75pp+ 11 chapters.

Kang, K., Harju, A., Lindgren, D., Nikkanen, T., Almqvist, C. & Suh, G. 2001. Variation of ramet number and effective number of clones in seed orchards. New Forests, 21(1): 17-33.

Kang, K., Lindgren., D and Mullin, T. 2001. Prediction of genetic gain and gene diversity in seed orchard crops under alternative management strategies. TAG in press.

Lindgren, D. 1974. Aspects on suitable number of clones in a seed orchard. In: Population and Ecological Genetics, Breeding Theory and Progeny testing, Proc. Joint IUFRO Meeting, Stockholm, Sweden, pp.293-305.

Lindgren, D. 1985. Cost-efficient number of test sites for field trials. Biometrics, 41:887-893.
Lindgren, D. & Nilsson J-E, 1985, Calculations concerning selection intensity. SLU, Dept of Forest Genetics and Plant Physiology. Departmental report 4.
Lindgren, D. and Matheson, A.C. 1986. An algorithm for increasing the genetic quality of seed from seed orchards by using the better clones in higher proportions. Silvae Genet. 35:173-177.
Lindgren, D. & Bondesson, L. 1987. Calculation of selection intensity and rankits. SLU, Dept of Forest Genetics and Plant Physiology. Arbetsrapport 23. ISSN 0280-7988.
Lindgren, D. and Werner M. 1989. Gain generating efficiency of different Norway spruce seed orchard designs. In Stener L-G and Werner M (editors) Norway spruce: provenances, breeding and genetic conservation. Institutet for skogsförbättring. Rapport 11:189-206.
Lindgren, D., Libby W. & Bondesson, F. 1989. Deployment to plantations of numbers and proportions of clones with special emphasis on maximizing gain at a constant diversity. Theoretical and Applied Genetics 77(6):825-831.
Lindgren, D. & El-Kassaby, Y. 1989. Genetic consequencies by combining selective cone harvesting and genetic thinning in clonal seed orchards. Silvae Genetica 38:65-70
Lindgren, D. 1991. Optimal utilization of genetic resources. Forest Tree Improvement nr 23. s. 49-67.
Lindgren, D. & Bondesson, L. 1990. Optimal utilization: Normal approximation and the case of an upper bound on the utilization. SLU, Inst. f. skoglig genetik och växtfysiologi. Arbetsrapport 39. ISSN 0280-7988.
Lindgren, D. 1993. Quantitative comparison between truncation selection and a better procedure. Hereditas 118:289-292.
Lindgren, Dag 1994. When do temperature events take place in Sweden and Finland? Sveriges lantbruksuniversitet. Institutionen för skoglig genetik och växtfysiologi. Arbetsrapport 51. ISSN 0280-7998.
Lindgren, D. 1993. Accelerated adaptation of trees at tree limits by selective breeding. In: Alden, J., Mastrantonio, J. & Odum, S. (editors) "Forest development in cold climates". Plenum Press, New York. pp 299-320.
Lindgren, D., Wei, R. & Lee, S. 1997. Optimum family number in the first cycle of a breeding program. For. Sci. 43(2):206-212.
Lindgren, D. & Kang, K. 1997. Status number - a useful tool for tree breeding Research Report of the Forest Genetic Research Institute of Korea 33:154-165.
Lindgren, D. & Mullin,T. 1997. Balancing gain and relatedness in selection. Silvae Genetica. 46:124-129.
Lindgren, D. & Mullin, T. 1998. Relatedness and status number in seed orchard crops. Canadian Journal of Forest Research, 28:276-283.
Lindgren, D. & Cheng, Y. 2000. A model integrating seed source adaptation and seed use. New Forest 20: 87-104
Olsson, T. 2001. Parameters, relationship and selections in pines. Acta Universitatis Agriculturae Sueciae. Silvestria 192: 27p. +4 chapters.
Rosvall, O. 1999. Enhancing Gain from Long-Term Forest Tree Breeding while Conserving Genetic Diversity. Acta Universitatis Agriculturae Sueciae. Silvestria 109: 65p. +4 chapters.
Wei, R.-P. & Lindgren, D. 2001. Optimum breeding generation interval considering build-up of relatedness. Canadian Journal of Forest Research. 31: 722-729

Predicted genetic gain from existing and future seed orchards and clone mixes in Sweden

Ola Rosvall[1], Gunnar Jansson[2], Bengt Andersson[1], Tore Ericsson[1], Bo Karlsson[2], Johan Sonesson[2], & Lars-Göran Stener[3]
[1]*Skogforsk, Box 3, S-918 21 Sävar, Sweden, Sweden*
[2]*Skogforsk, Uppsala Science Park, S-751 83 Uppsala, Sweden*
[3]*Skogforsk, Ekebo 2250, S-268 90 Svalöv, Sweden*

Abstract

Genetic gain in production per hectare was predicted to support decisions on the establishment of third-round seed orchards of *Pinus sylvestris*, *Pinus contorta*, *Picea abies* and *Betula pendula* in Sweden. Initially, genetic gain was calculated for existing seed orchards and clone mixes for vegetative propagation, together with the additional improvement possible by genetic thinning. Thereafter, calculations were made of the potential additional gain for the two coming rounds of seed orchards and clone mixes, and the time at which the gain could be realized for each seed zone. The predictions were based on genetic parameters summarized from hundreds of genetic field tests throughout Sweden.

The gain refers to the genetic level of the unimproved base populations and assumes ideal functioning of seed orchards and clone mixes, eg, no background pollination. As a simplification, gain is presented for only one character per hectare of production, although, in reality, an index of many traits is used, including, eg, survival and stem quality. The gain in survival was also predicted for Scots pine orchards intended for localities with a harsh climate. All gain predictions took sufficient genetic variability in the production populations into account.

In general, the genetic gain of current seed orchards is 10–25%, and can reach 20–25% in all new third-round orchards. The feasible gain from thinning is 2–3%, which is half of the theoretical level, and can be attained only in the most closely spaced orchards. The next step of improvement will achieve a gain of 35% for orchards established in 2015–2020, or as early as 2010 in some cases. Clone mix gains are of the same magnitude as for seed orchards, but can be realized sooner in commercial planting stock.

Introduction

Tree breeding of Scots pine, lodgepole pine, Norway spruce and silver birch is carried out under a multiple population strategy with breeding populations covering the whole of Sweden (Danell, 1993a, b). Breeding activities have proceeded to different points of the breeding cycle depending on species and region (SkogForsk 1995a, b). As a simplification, 1980 can be chosen as a milestone year for three major activities. First, in the early 1980s, the results of numerous field tests started to become available from the very first large set of plus trees selected during the 1950s and 1960s. These trees make up the first round of seed orchards, which still produce most of the seed used today. The test results confirmed that tree breeding worked in reality as forecast, and formed the basis for more accurate gain predictions (Danell 1991a). Secondly, in around 1980, a second round of seed orchards was initiated. These were needed to secure future seed supplies, ie, to replace old orchards and to accomplish full geographical coverage of improved seed for all tree species. Thirdly, the base population was greatly extended to make possible long-term sustainable breeding as well as a high, short-term gain. Thousands of new plus trees and tens of thousands of new juvenile spruce clones were selected in forest stands and nurseries (Werner et al. 1982, Danell 1991b, SkogForsk 1995a). After progeny and clone testing of all these trees, a great increase in gain can now be realized either by means of a new, third round of seed orchards or by some other form of mass propagation.

To support decisions concerning investments for mass propagation of genetically improved planting stock, genetic gain was predicted for all existing seed orchards and clone mixes, and for the two coming rounds of orchards and clone mixes, at the times when great advances in gain will be reached in the breeding populations. Predictions were made for seed orchards of Scots pine, lodgepole pine, Norway spruce and silver birch, for clone mixes of Norway spruce, and for each seed utilization zone of Sweden. This presentation is summarized from Rosvall et al. (2001).

Material and methods

Total gain from a seed orchard is made up of a number of effects: genetic response to provenance selection, phenotypic plus-tree selection, selection among plus trees based on genetic testing, and nongenetic effects, eg, due to improved seed quality or other *C* effects in planting stock from seed orchards and clone mixes. Here, genetic gain refers to the difference between improved and unimproved stands of the base population. Generally the base populations are of superior provenance, an effect which is not included in the predicted gain, but should be added to determine the total gain in comparison to unimproved stands of local origin.

A simplified testing and selection scheme for a single breeding population is shown in Figure 1. Under this scheme, genetic gain was predicted for each existing second-round seed orchard of the four principal commercial tree species and their seed zones in Sweden. To facilitate comparability, the genetic gain was generally predicted for only one character—per hectare production over the rotation. For Scots pine in harsh areas in the north of the country, gain in survival was also predicted at the reference level of 50% survival.

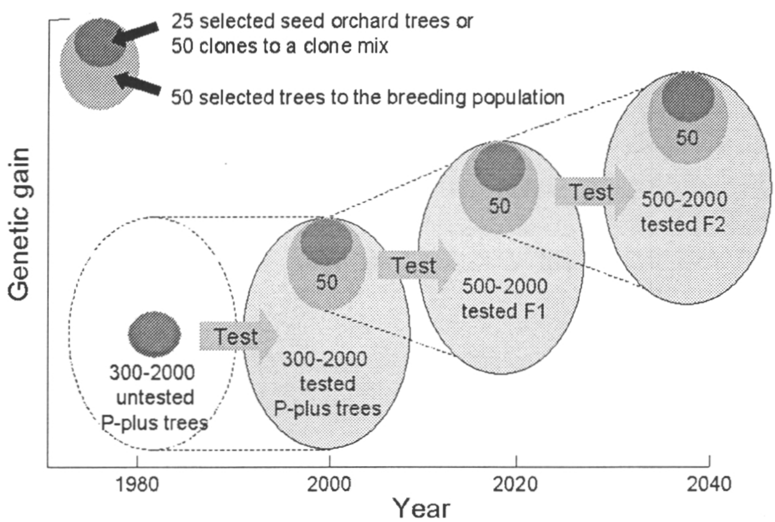


Figure 1. After many founder plus trees (P) have been tested, the best 50 are selected to breed a new generation of trees (F1) for testing before a new set of 50 is selected to generate additional generations (F2, F3, and so on). After each round of testing, new seed orchards and clone mixes can be established with the very best trees (25 clones in a seed orchard and 50 clones in a clone mix). In reality, the development is more gradual than indicated in the figure.

Following Danell (Appendix 2 in Lindgren and Werner, 1989), we predicted the percentage genetic selection response for the mature trait (*m*) for additive effects (R_{Am}) for mass propagation by seed and genotypic effects (R_{Gm}) realized by vegetative propagation of clones.

$$R_{A_m} = i\, r_{A_j I}\, r_{jm}\, \mathrm{CV}_{A_m} \qquad [1]$$

where i is selection intensity (selection differential in units of standard deviation), r_{AjI} is the correlation between an index for measured (I) and true additive value (A_j) for the measured traits at juvenile age (j) (test accuracy for A_j) of tree height and survival; r_{jm} is the correlation between the measured trait at juvenile age and the target trait at the rotation end; CV_{Am} is the additive coefficient of variation for the mature target trait, ie, dry-matter production per hectare over the rotation and seed utilization zone [adjusted for genotype x environment interaction (GxE) according to Dickerson (1962)]. When A_j at juvenile age is the target trait itself, as for field survival, r_{jm} is 1.0. The product of r_{AjI} and r_{jm} *is* r_{TI}, which is the correlation between measured index and true breeding value for the target trait (T). We assumed no maternal or paternal effects, but C effects were considered when mature birch plus trees were cloned.

To estimate selection response for vegetative mass propagation (R_{Gm}) [1] was modified to:

$$R_{G_m} = i\, r_{G_j I}\, r_{jm}\, \mathrm{CV}_{G_m} \qquad [2]$$

where r_{GjI} is the correlation between an index for measured (I) and true genotypic value (G_j) for the measured trait at juvenile age, and CV_{Gm} is the genotypic coefficient of variation for the mature target trait adjusted for GxE.

Genetic parameters were compiled from hundreds of genetic field tests throughout Sweden (Table 1). Empirical CV_{Am} for per hectare production was estimated by Jansson et al. (1998) for Scots pine, and was used here for all coniferous species. For silver birch, only a few empirical values exist as a basis for the educated guesses given in Table 1 (Danell and Werner 1991).

Twenty-five trees were selected (Figure 1) for the establishment of a seed orchard, and trees with higher breeding values were allowed to contribute more ramets per clone than trees with lower breeding values. With a graft proportion of 3:2:1 for each third of the plus trees classified by breeding value, the same selection intensity and gain are achieved as if 15 trees were selected and propagated with an equal number of grafts. Swedish legislation stipulates that no single clone should make up more than 2.5% of a commercial clone mix, ie, a mix not containing fewer than 40 clones, and the clones should come from at least five unrelated full-sib families. To ensure that the minimum target would not be exceeded in practice, 50 clones were selected and assumed to be used in equal proportion. We have assumed mass propagation to be ideal, ie, an equal gene contribution from each seed-orchard clone and no pollen contamination.

We have presupposed that phenotypic selection of coniferous plus trees in forest stands (no genetic testing) results in a 10% seed-orchard gain in production per hectare (Wilhelmsson et al. 1993). Phenotypic plus-tree selection in birch stands is less efficient, since the stands are small and uneven, and we therefore assumed a 5% gain here. These figures include the genetic response to phenotypic plus-tree selection, a seed-orchard effect resulting from the breaking-up of inbreeding depression by outcrossing among unrelated plus trees in seed orchards and controlled crosses, and, in conifers, the effect of physiologically improved seed from seed orchards. We assigned an assumed value (2%) to the magnitude of the seed effect, so that we could calculate the basal gain of juvenile seedlings from conifer plus-tree full-sib progeny selected for clonal testing (in which there can be no lasting seed effect), and obtained a total gain of 8%. For plus-tree half-sib progeny, the clone selection gain was half that of full sibs, and for simplicity the same effect of outcrossing was used, resulting in a total 5% gain. We also assumed that there was no effect from phenotypic selection among siblings. It was assumed that depressed trees due to selfing in seed orchards would be purged naturally (Lesica and Allendorf 1992) or removed by artificial selection with no loss in gain. No seed or cutting effect or any other C effects were included for birch seed orchards and vegetatively propagated clones of Norway spruce.

Results

Genetic gain in the second and third rounds of seed orchards

The genetic gain (expressed as a percentage increase in production per hectare) of existing second-round seed orchards and the gain that can be reached with new third-round orchards are shown on sketch maps of Sweden (Fig 2). The predicted genetic gain for existing seed orchards varies from 10 to 25% as a result of differences among tree species, and the differing numbers of tested plus trees being available for selection at the time of orchard establishment. At the low end of the scale, an approximate gain of 10% indicates orchard trees from phenotypic selection in unimproved stands and no genetic testing. At the high end of the scale, gain close to 25% indicates a large number of tested plus trees available for selection. In most cases, the gain from third-round seed orchards will increase by 10–15% and reach 25%, or even 27% in some cases (this includes the initial phenotypic plus-tree selection response and the "seed-orchard effects").

The genetic gain in survival for Scots-pine seed orchards in harsh climates varies between 5 and 13% (Fig. 2). For seed orchard T9, which is the most recent seed orchard, having been established in 2000 (centre of Fig. 2), the gain is 22% for production and 13% for survival. Here, the difference between the potential gain of 25% in production given for a new seed orchard (if only one character, ie, growth, is considered) and the realized gain of 22% indicates the loss in growth that would have to occur to achieve a 13% increase in survival.

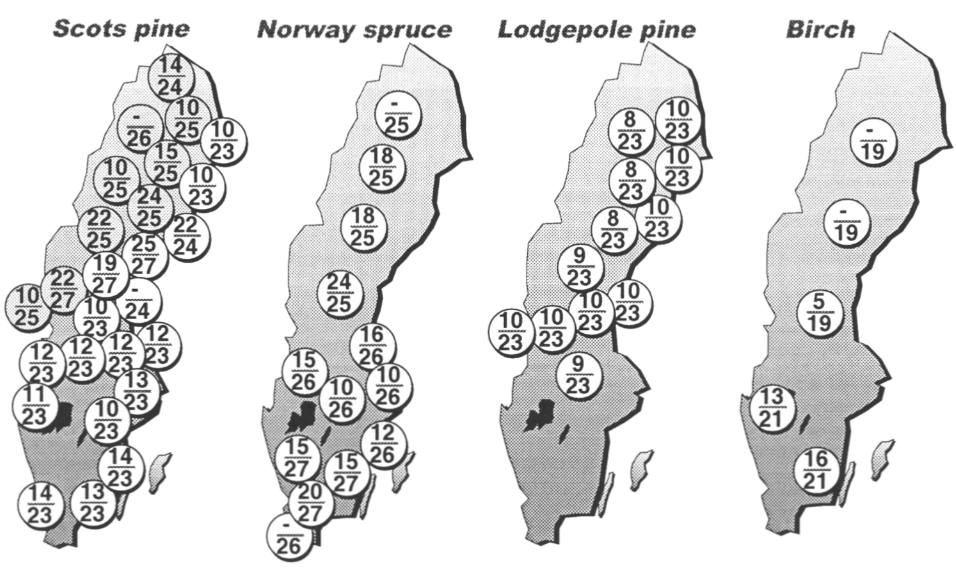


Figure 2. Genetic gain in production per hectare for existing second-round and potential third-round seed orchards (Existing/Potential) of Scots pine, lodgepole pine, Norway spruce and silver birch. Genetic gain in survival for northern and high-elevation Scots-pine seed orchards is indicated by a darker greyish colour . The gain raises the standard 50% survival level to 55–63%.

Table 1. Genetic parameters adjusted for G xE interaction compiled from reports of breeding values up to the end of 2000 and from unpublished results in Rosvall et al. (2001).

	Pinus sylvestris	Picea abies	Pinus contorta	Betula pendula[1)]
Production per hectare (full rotation)				
CV_{Am}[2)]	0.125	0.125	0.125	0.12
CV_{Gm}		0.14		0.14
Tree height (age 6–15)				
Number of test sites	123	119	18	—
CV_{Aj}	0.08	0.09	0.10	0.12
h^2	0.13	0.11	0.17	0.20
r_{AjI} (progeny testing)	0.80	0.70, 0.80[3)]	0.80	0.80
CV_{Gj}[4)]	0.09	0.11	0.11	0.15
H^2 [4)]	0.16	0.14	0.21	0.3
r_{GjI} (clonal testing)		0.8		
CV_{Cm}				0.06
V_D/V_A	0.25	0.25	0.25	0.50
r_{jm} age 10–15	0.7	0.7	0.7	0.8
r_{jm} age 6		0.5–0.6		
r_{jm} age 2		0.1		
Field survival (age 10)				
CV_{Am} (standard level = 50%)	0.20			
H^2	0.20			
r_{AmI} (progeny testing)	0.8			
r_{jm}	1.0			
Freeze test survival (age 1)				
r_{AjI} (progeny testing)	0.8			
r_{jm}	0.7			

1) Educated guesses. C effects and maternal and paternal effects expressed in units of phenotypic variance were originally assumed to be 0.1, 0.05 and 0.05, respectively (Danell och Werner 1991).

2) Jansson et al. (1998).

3) r_{AjI} For clone testing and progeny testing when selection is to a seed orchard.

4) Contrived value based on $V_D/V_A = 0.25$.

With a few exceptions, establishment of new third-round seed orchards can be started immediately, since genetic testing has now been completed for most species and test projects (data not shown—see Rosvall et al., 2001). A few more years of tree growth are necessary in a few remaining test series before they can be deemed suitable for evaluation.

Large recruitment populations for third-round seed orchards generate a greater gain for Scots-pine seed orchards in the north than in the south , and in Norway spruce than in Scots pine, since very similar genetic parameters were used for all species in the calculations (Table 1). A huge number of tested juvenile clones of Norway spruce initially intended for clonal forestry are now also available for seed-orchard selection. Lodgepole pine seedling seed orchards were initially established with unselected, untested seedling individuals from open pollinated progeny (half-sibs) of phenotypically selected plus trees with a predicted gain of 7%. After testing and operational roguing already carried out among half-sib families, the gain increased but not always up to the level of 10% predicted for untested plus-tree, clonal-seed orchards (Ericsson and Danell 1994). For the northern lodgepole-pine seed orchards, the emphasis was on survival rather than growth. The lower gain in silver-birch seed orchards than in orchards of other species is primarily due to the assumption of lower gain from phenotypic plus-tree selection and no seed effects in birch-seed orchards.

Large recruitment populations for third-round seed orchards generate a greater gain for Scots-pine seed orchards in the north than in the south , and in Norway spruce than in Scots pine, since very similar genetic parameters were used for all species in the calculations (Table 1). A huge number of tested juvenile clones of Norway spruce initially intended for clonal forestry are now also available for seed-orchard selection. Lodgepole pine seedling seed orchards were initially established with unselected, untested seedling individuals from open pollinated progeny (half-sibs) of phenotypically selected plus trees with a predicted gain of 7%. After testing and operational roguing already carried out among half-sib families, the gain increased but not always up to the level of 10% predicted for untested plus-tree, clonal-seed orchards (Ericsson and Danell 1994). For the northern lodgepole-pine seed orchards, the emphasis was on survival rather than growth. The lower gain in silver-birch seed orchards than in orchards of other species is primarily due to the assumption of lower gain from phenotypic plus-tree selection and no seed effects in birch-seed orchards.

Hedges to produce cuttings for the rooting of tested Norway-spruce clones exist for northern and central Sweden (Table 2). These hedges are rapidly ageing but for some time can still be used for small-scale commercial plantations or large-scale experimental plantations. Since clonal testing is the regular way of testing in the long-term Norway-spruce breeding programme, a great number of new tested clones are produced for each breeding generation. If testing is reduced to six years, hedges can be planted and used to produce cuttings for commercial planting stock for a limited time span. The potential extra gain from a clone mix over a seed orchard is 3–4%, as a result of exploitation of both additive and nonadditive effects. Because of Swedish regulations, the selection intensity is somewhat lower for a clone mix than for a seed orchard, but less-inhibiting restrictions on relatedness allow for selection of five unrelated full-sib crosses, resulting in a similar total selection intensity. This potential advantage, however, is diminished by shorter and, hence, less accurate testing to maintain juvenility in the propagation stock. What's more, it is assumed that a clone mix does not have any effects like the seed-orchard seed effect, which, in our calculation, adds to the superiority of a seed orchard and reduces the difference between the methods.

Table 2. Predicted percentage genetic gain in production per hectare (Prod.) for existing clone mixes in Sweden and the gain that can be reached with new clone mixes for each seed zone as per Fig. 2. The gain refers to unimproved stock of a suitable provenance and includes the effect of initial plus-tree selection: 3 and 6%, respectively, for half-sibs and full-sibs and an assumed outcrossing effect of 2%. Any provenance effects have to be added. The field-test duration for the F1 generation is 6 years. If this were extended to the same as for seed orchard selection, the gain would be increased by 2%.

	Genetic gain						
Seed zone[1)]	Present situation 2000		New clone mix from generation				
				P		F1	
	No of clones	Prod. %	No of clones	Year[2)]	Prod. %	Year[2]	Prod. %
G1	50	15	50	2002	19	2018	35
G2	50	15	50	2002	19	2018	35
G3	50	18	50	2002	22	2018	35
G4	50	18	50	2002	22	2016	36
G5	100	23	50	2006	27	2015	36
G6	100	23	50	2006	27	2015	36
G7			50			2010	37
G8			50			2010	36
G9			50			2010	36

1) Seed zones according to Figure 2.
2) Year of clone test measurement + 1.

Genetic thinning

Some second-round orchards were planted to facilitate genetic thinning after the genetic field testing had been completed. This can now be fulfilled. If the best 50% of all orchard clones are retained, there will be an additional genetic gain of about 5%. To maintain a reasonably regular spacing and to give priority to good seed-producing trees, the gain will be halved to 2–3%. Trees in young seed orchards can still be transplanted mechanically and, if this is done, a 5% gain can still be attained without any diminishing of the high regularity of trees in the rows. This action is urgent, since orchard trees will soon become too large for lifting and replanting.

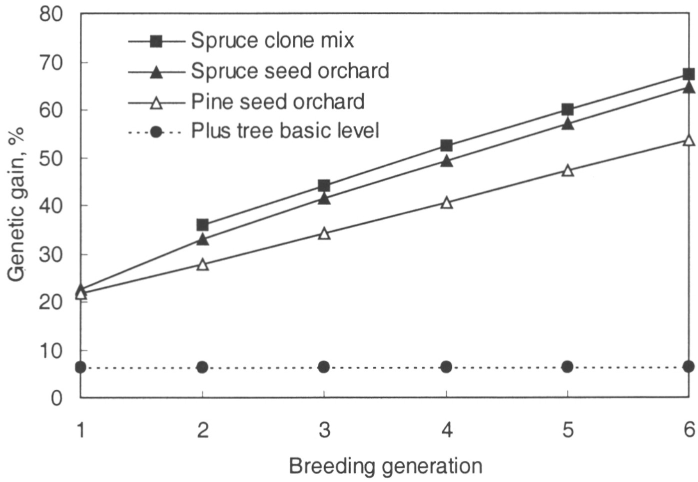


Figure 3. The development over generations of genetic selection gain in a Swedish Norway-spruce and Scots-pine seed orchard, and in a Norway-spruce clone mix. The simulations (Mullin and Park 1995) were based on 300 founder trees, 50 trees in the breeding population, 15 trees in the seed orchard and 50 in the clone mix. The population was regenerated by double-pair mating. For spruce, 40 clones per full-sib cross and 10 ramets per clone were tested and for pine 20 trees per full-sib cross and 30 progeny per tree. The genetic parameters shown in Table 1 were used.

The fourth round of seed orchards

The long-term rate of increase in gain based on results of simulation is shown in Fig. 3. In general, testing and selection are most efficient for Norway spruce and silver birch, since clonal testing is used instead of progeny testing. In addition, clonal testing can be initiated almost immediately after creating a new breeding generation, because the new generation of seedlings can be vegetatively propagated and field planted. For progeny testing of the two pine species, the new-generation seedlings first have to develop into trees, to flower and to produce seed, which reduces the rate of the generation turnover.

It will take another 15–20 years before the next set of progeny or clone tests of F1 (and F2) generation trees can be completed and the fourth round of seed orchards can be established. At that time, production per hectare is predicted to increase a further 10%, giving a total gain of 35%. This will happen in 2015–2020, but in 2010 at the earliest for Norway-spruce.

Discussion

Predicted gain

This investigation reveals that the time has come when it is possible to establish the third round of seed orchards for all species and most seed zones in Sweden. The genetic gain is predicted to increase by 10–15% compared to most existing seed orchards and to reach about 25% higher production per hectare compared with the unimproved base population. Seed orchards established now will replace existing orchards at the appropriate time. The timing will also coincide nicely with the next important 10%-enhancement of the genetic level of the breeding population in 15–20 years' time, and the fourth round of seed orchards that it will be possible to establish then.

Based on our assumptions, the clone mixes possible for Norway spruce have roughly the same genetic gain as does a seed-orchard seed crop. Thus, the main advantages of a clone mix are the reduction in the unproductive waiting time from breeding to commercial planting stock, and the greater freedom to compose and modify the clone mixes as new clones become available or the demand changes

Genetic thinning of existing densely planted seed orchards is urgently required so that regular spacing can be reestablished by mechanical replanting after thinning and before the trees grow too big. However, most seed orchards are open-spaced and genetic thinning may decrease the genetic gain by reducing the internal pollen production and increasing the background pollination. Reduced seed production from thinning also decreases the land area that can be regenerated with improved planting stock or seed for direct seeding.

Additions and reductions to the gain

Index of traits

To facilitate comparison, for the most part we have predicted the response to selection for one single trait; however, in reality, selection is done using an index of multiple characters, such as tree height, diameter, survival, various forms of damage, straightness, branch, stem and wood quality, etc., which are weighted together to maximize the total value of the gain. The value and importance of these individual breeding goals vary with species and seed zones, and these variations are taken into account in real selection. With many uncorrelated traits in the selection index, the gain for each target trait will be lower, but the total value higher, than the gains presented here. However, there is also a risk in real index selection that the gain will be valued differently at the time of harvest, ie, the economic weighting may shift in the future, along with changes in the general economy. Therefore, the ultimate value of the gain may be lower than predicted even under real conditions.

Pollen contamination

The estimated level of pollen contamination in a conventional seed orchard is usually 50%. Such a level will reduce the realized gain by 25% if the background pollination is neutral, ie, emanating from the same base population as the plus trees. If seed orchards are located outside the base population, the loss in gain can be greater still. Pollen contamination will not affect the beneficial seed-orchard effects of outcrossing and higher seed vigour. For example, neutral pollen contamination of 50% will reduce the total gain from 25 to about 20% in absolute terms (21% selection response x 0.75 = 15.75 + 4 (seed-orchard effect) = 19.75%).

Greenhouse seed orchards, which are generally used for silver birch and are being tested for use with Norway spruce, controlled pollination for vegetative mass propagation with cuttings (bulk propagation) and clonal forestry preclude any pollen contamination.

Self-pollination

Self-pollination occurs in both seed orchards and natural stands. The resulting inbreeding depression gives rise to empty seed, weak seedlings and the gradual removal of inbred trees from the stand by natural selection (Koski 1973, Lesica & Allendorf 1992). It is estimated that self-pollination causes a one per cent reduction in growth. Using the number of seed-orchard clones as assumed here, we expect the loss of gain from seed orchards to be the same as that from natural stands. However, with controlled pollination and vegetative propagation there is no loss at all due to selfing.

Intermixing of natural trees

Since some of the trees in planted stands will be the result of natural regeneration, the realized gain will be reduced somewhat, depending on the level of competition in the stand, silvicultural activites, etc. Because the scale of the reduction in gain varies widely and any estimates have to be adjusted to the real situation, we have not dealt with it here.

Provenance effects

If plus trees are of suitable provenance, which they generally are, an effect of provenance should be added if the gain is to be compared with the local stand seed. These effects vary among species and seed zone, and cannot always be determined accurately and are therefore not given for each seed orchard. The choice of suitable provenance can increase survival by 20–25% in absolute terms for Scots pine in the harsh-climate areas in the north of Sweden (standard level of survival 50%), where appropriately moved seed always constitutes the base population, but at the expense of individual tree growth. Norway-spruce seed of southern or southeastern provenances generally increase growth by 5–10%. However, it is uncertain whether the two selection effects (of plus trees and provenance) can simply be added together. Because selected plus trees have a growth rhythm resembling that of a southern provenance, we assume that the response to being moved differs from the known natural stand seed-movement patterns (Rosvall et al. 1998, Westin et al. 2000a,b). However, a seed orchard with phenotypically selected plus trees of best provenance can sometimes double the gain from 10 to 20% compared with the unimproved local provenance.

Intensified selection

In the gain calculations we have assumed that selection for a seed orchard or clone mix takes place in a single breeding population, whereas, in reality, trees can also be selected from adjacent populations. The scope for this varies among species and parts of the country, but, in general, an additional gain of 3% is possible.

Accuracy

Genetic parameters

In genetic testing, tree height, diameter, straightness, damage to branch whorls and vigour are measured in young test plantations, whereas the objective is to predict other traits for the whole rotation, eg, dry matter production per hectare and final timber quality. It is evident that the reported figures include errors and that all gain may not be realized in commercial forestry. Nevertheless, the magnitude of the predicted gain should be reasonable. Our parameters are within the range of those found in other species (Cornelius 1994) and we have fairly good estimates, for a half rotation at least, of the correlation between tree height at young age and production per hectare for Scots pine (Jansson et al. 1998); we also have good indications for the rest of the rotation (Marklund 1981). By adjusting the results to take into account reductions due to the *G*x*E* interaction, we obtain averages for the entire seed zone. Realized genetic gain of similar magnitude is also achieved under faster growing conditions (Lambeth, 2000, Matziris, 2000, Li et al. 1999). The weakest point in the calculations is the additive genetic variation in production per hectare, where empirical data for Scots pine were used for all species. Another source of uncertainty is the assumed proportion of dominance variation exploited by clonal forestry. In the near future, parameters based on empirical data for silver birch will replace the educated guesses used here.

Phenotypic selection, seed orchard and rooted cutting effects

There is a strong body of evidence to suggest that there is a total gain of about 10% in production per hectare for coniferous seed orchards containing untested plus trees. There is also a strong theoretical belief that all this does not come from phenotypic selection only, but that there is also a contribution from the increased vitality resulting from the outcrossing of inbreeding depression and the increased vigour in seed-orchard seed (Wilhelmson et al. 1993). The uncertainty in the magnitude of these three separate effects causes problems when comparisons are to be made with the gain possible from a clone mix when the seed effect cannot be reproduced. In general, *C* effects, together with maternal and paternal effects, may have a large influence on the results, but whether they really exist and, if so, what their magnitude is, is unknown. All these calculation problems can only be resolved through more empirical field research, which is a priority for SkogForsk.

Genetic variability

Compared with 15 plus trees in equal proportion in a seed orchard, gene diversity measured by status number (Lindgren et al 1997) increases from 15 to 22 if 25 trees are used in a proportion of 3:2:1, depending on the breeding value. The status number for a clone mix is 9–50, depending on the relatedness among clones and the breeding generation. In general, the status number after two rounds of selection is 13–18.

Time loss

A conventional seed orchard starts to produce seed after about 15 years and approaches full production in 20 years (Hannerz et al., 2000). During this time, a new breeding generation is tested, resulting in the option to start a new seed orchard capable of producing a 10% higher gain at the same time as the existing orchard begins to yield seed. In Sweden, we have now reached exactly that situation for the existing second-round orchards and the now attainable third-round orchards. Many seed-orchard owners are about to harvest seed that will give a genetic gain of 10–15% , while a new seed orchard giving a 25% gain can be planted. There are various ways to shorten the unprofitable, unproductive waiting time between breeding progress and large-scale mass propagation of regeneration stock:

Densely planted seed orchards: The orchard will close faster, which decreases the time required to reach extensive seed yield and acceptable internal pollen production.
Rolling seed orchards: Planting new orchard trees or entire seed orchards in or adjacent to old ones with good pollen production enables the first seed crop to be harvested sooner.
Greenhouse orchards: Small amounts of seed can be produced in a short time without any pollen contamination. For birch, all the seed required in Sweden can be provided in this way.
Vegetative bulk propagation: Improved seedlings from greenhouse orchards, conventional seed orchards or clonal archives can be bulked up by vegetative mass propagation.
Clonal forestry: The main advantage of clonal forestry is the gain in time from breeding process to commercial planting stock. The Swedish spruce-breeding programme tested the yield from clones that can be used for establishing hedges for the production of cuttings for mass propagation. The limitations come from the ageing of the hedges, resulting in low rooting capacity and poor growth in rooted cuttings.

Somatic embryogenesis: A breakthrough for somatic embryogenesis, whereby manufactured seed renders conventional seed orchards redundant and reduces the lead time between breeding and commercial application to a minimum.

Acknowledgements

Anders Fries compiled data for judging the phenotypic selection effect in *Pinus contorta*. Dag Lindgren kindly improved his computer tool "Gainpred Advanced 2001" (accessible on: http://www.genfys.slu.se/staff/dagl/) and gave valuable comments on both the manuscript and the calculations. Many more people contributed to the parameter compilation. We acknowledge all the assistance given and thank all those concerned.

References

Cornelius, J. 1994. Heritabilities and additive genetic coefficients of variation in forest trees. Can. J. For. Res. 24: 372–379.

Danell, Ö. 1991a. Possible gains in initial stages of a national tree improvement programme using different techniques (Proceedings from the Nordic tree breeders meeting, Sept. 1990, Hørsholm, Denmark). Forest Tree Improvement 23: 11–30.

Danell, Ö. 1991b. Survey of past, current and future Swedish forest tree breeding. Silva Fennica 25: 241–247.

Danell, Ö. 1993a. Breeding programmes in Sweden: 1. General approach. I: Lee, S.J. (red.), Progeny testing and breeding strategies, Proc. from a meeting with the Nordic group for tree breeding, October 1993, 128i–128v. Edinburgh: Forestry Commission.

Danell, Ö. 1993b. Tree breeding strategy: Are we too concerned conservationists but inefficient breeders? I: Lee, S.J. (red.), Progeny testing and breeding strategies, Proc. from a meeting with the Nordic group for tree breeding, October 1993, 80–94. Edinburgh: Forestry Commission.

Danell, Ö. & Werner, M. 1991. Svensk björkförädling - förväntade framsteg under första generationen. (Rapport nr 22, Institutet för skogsförbättring),18 s. Uppsala.

Dickerson, G.E. 1962. Implications of genetic-environmental interaction in animal breeding. Animal production 4: 47–63.

Ericsson, T. & Danell, Ö. 1995. Genetic evaluation, multiple-trait selection criteria, and genetic thinning of *Pinus contorta* var. *latifolia* seed orchards in Sweden. Scand. J. For. Res. 10: 313–325.

Ericsson, T., Danell, Ö. & Andersson, B. 1994. Genetic variation in *Pinus contorta* var. *latifolia* breeding material in Sweden. Can. J. For Res. 24: 723–729.

Hannerz, M., Eriksson, U., Wennström, U. och Wilhelmsson, L. 2000. Tall- och granfröplantager i Sverige – en beskrivning med analys av framtida fröförsörjning (Redogörelse nr 1 2000, SkogForsk), 40 s.Uppsala.

Jansson, G., Danell, Ö. & Stener, L.-G. 1998. Correspondence between single-tree and multiple-tree plot genetic test for production traits in *Pinus sylvestris*. Can. J. For. Res. 28: 450–458.

Koski, V. 1973. On self-pollination, genetic load, and subsequent inbreeding in some coniferous. Comm. Inst. For. Fenn. 78. 42 pp.
Lesica, P., & Allendorf, F. W. 1992. Are small populations of plants worth preserving? Conserv. Biol. 6: 135–139.
Lambeth, C. 2000. Realized genetic gains for first generation improved loblolly pine in 45 test in coastal North Carolina. South J. Appl. For. 24(3): 140–144.
Li, B., McKeand, S. & Weir, R. Tree improvement and sustainable forestry - impact of two rounds of loblolly pine breeding in the U.S.A. Forest Genetics 6:229–234.
Lindgren, D., & Werner, M. 1989 Gain generating efficiency of different Norway spruce seed orchard designs. I: Stener, L.-G. och Werner, M. (red.), Norway spruce; provenances, breeding and genetic conservation, Proceedings of the IUFRO working party meeting, S2.02-11, in Sweden 1988 (Report no. 11, Institute for Forest Improvement), 189–206. Uppsala.
Lindgren, D., Gea, L.D. & Jefferson, P.A. 1997: Status number for measuring genetic diversity. Forest Genetics 4: 69–76.
Marklund, E. 1981. Äldre tallproveniensförsök ger underlag för produktionsprognoser. Sveriges Skogsvårdsförbunds tidskrift 5/1981: 9–14.
Matziris, D.I. 2000. Genetic variation and realized genetic gain from Aleppo pine tree improvement. Silvae Genetica 49: 5–10.
Mullin, T. J., & Park, Y.S. 1995. Stochastic simulation of population management strategies for tree breeding: a new decision support tool for personal computers. Silvae Genet. 44: 132–141.
Rosvall, O. 1982. Fröförsörjning och fröplantageprogram för Pinus contorta i Sverige. Sveriges Skogsvårdsförbunds Tidskrift 1-2/-82: 105–108.
Rosvall, O., Anderson, B. & Ericsson, T. 1998. Beslutsunderlag för val av skogsodlingsmaterial i norra Sverige med trädslagsvisa guider (Redogörelse nr 1 1998, SkogForsk), 66 s. Uppsala.
Rosvall, O., Jansson, G., Andersson, B., Ericsson, T., Karlsson, B., Sonesson, J. & Stener, L.-G. 2001. Genetiska vinster i nuvarande och framtida fröplantager och klonblandningar [Genetic gain from present and future seed orchards and clone mixes] (Redogörelse nr 1 2001, SkogForsk).
SkogForsk 1995a. Breeding programmes in Sweden. Corrected reprint from: Lee, S.J. (ed.) 1993. Progeny testing and breeding strategies, Proceedings from a meeting with the Nordic group for tree breeding, October 1993, 184+pp.Edinburgh: Forestry Commission (SkogForsk Arbetsrapport nr 302), 25 s. Uppsala.
SkogForsk 1995b. Strategi för framtida skogsträdsförädling och framställning av förädlat skogsodlingsmaterial i Sverige ("Förädlingsutredningen"). (Utredning 95-06-20. Red. Urban Eriksson. SkogForsk), 259 s + bilagor. Uppsala.
Werner, M., Hadders, G. & Rosvall, O. Förädlingsprogram för tall, gran och contortatall. I: Årsbok 1981 (Föreningen Skogsträdsförädling, Institutet för skogsförbättring), 90–158. Uppsala.
Westin, J., Sundblad, L.-G., Strand, M. & Hällgren, J.-E. 2000a. Phenotypic differences between natural and selected populations of *Picea abies* I. Frost hardiness. Scand. J. For. Res. 15:489–499.
Westin, J., Sundblad, L.-G., Strand, M. & Hällgren, J.-E. 2000b. Phenotypic differences between natural and selected populations of *Picea abies* II. Apical mitotic activity and growth related parameters. Scand. J. For. Res. 15: 500–509.
Wilhelmsson, L., Eriksson, U., & Danell, Ö. 1993. Produktion av förädlat frö. SkogForsk Redogörelse nr 3. 52 s. Uppsala.

Clonal selection and deployment in seed orchards considering both seed production and breeding value

Seog-Gu Son[1,2], Kyu-Suk Kang[1,3] and Dag Lindgren[1]
[1] *Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, SE-90183 Umeå, Sweden*
[2] *Permanent affiliation: Korea Forest Research Institute, Cheongryangri 2-207, Dongdaemun, Seoul, Korea*
[3] *Tree Breeding Department, Korea Forest Research Institute, 44-3 Omokchun, Kwonsun, Suwon, Kyonggi 441-350, Korea*

Abstract

The goal of seed orchard is achieved by high breeding value and seed production of orchard clones. Breeding value and seed production are in conflict even when they are not correlated, as high breeding value clones may have low seed production and low breeding value clones may have high seed production. As a result, it can be advantageous to give some weight to seed productivity because of the clonal variation in seed production.

The seed orchard crop from a seed orchard can be characterised by "Orchard Benefit", which is a numeric expression of how good the orchard seeds would be, considering both breeding value and seed productivity. Data on breeding value and seed production were obtained from genetic testing and relative flowering assessment, respectively. The concept of benefit was applied for a hypothetical *Pinus sylvestris* seed orchard. Four different clonal deployments were invented and compared. A higher "orchard benefit" could be obtained when seed productivity and breeding value were considered together.

Introduction

In most breeding programs, breeding values of candidates for the next cycle or for seed orchards are estimated by means of progeny testing. One trait of the easily assessed characteristics is the relative abundance of flowers and subsequently seed production in seed orchards. Since a major objective of any seed orchards is maximum seed production at minimum cost, there is an obvious attraction towards working with clones of high seed yield capacity. Large clonal differences in fertility have been reported (Kjaer 1996, Bila 2000, Kang 2001). Fertility difference causes to the different contribution of each clone to the orchard crop, which will result in the accumulated relatedness and potential inbreeding to the offspring (Lindgren and El-Kassaby 1989, Kang and Lindgren 1999, Kang 2001).

When seed orchards or breeding populations are established or thinned, it is common that the breeding value of candidate clones is regarded as a most important factor. To what extent is reduction of the total seed production likely as a result of clonal selection on a breeding value basis? This could be a good criterion when the genetic thinning is planning or when a new seed orchard is established.

In seed orchards, the breeding value is generally considered more important factor than flowering character (Owens and Blake 1985, Sorensen and Webber 1997). Seed orchards are thus rogued on the basis of the clonal breeding value rather than their seed productivity (Nikkanen and Velling 1987). On the other hand, if there is the absence of genetic information from progeny testing, record on seed production may be used as a basis of clone selection in a seed orchard programme (Danbury 1971).

The aims of present study are to express "orchard benefit (i.e., how good the seed orchard would be)", considering both seed production and breeding value, and to investigate this benefit under four clonal deployments in a hypothetical *Pinus sylvestris* seed orchard.

Material and methods

Material

The data from 41 clones in a *Pinus sylvestris* seed orchard were obtained from the Forestry Research Institute of Sweden (Almqvist et al. 1995, Sonesson 1995) and used. The data contains relative seed productivity and six characters; height, diameter, branch angle, number of branch, straightness, and density of branch, which were considered in the calculation of breeding value.

Considered situation

Breeding value of candidate clones is regarded as 100 on average. To compare the "Orchard Benefit", the benefit of candidates is also set to 100%. Benefit of selected clones is thus calculated as a percentage from this basis. A new seed orchard is formed with selected clones based on the deployment that could maximise the orchard benefit.

Theoretical background

If orchard clones with high breeding values do not produce any seed or if bad clones produce many seeds, high genetic gain from the seed orchard crop could not be obtained (Sprague and Zobel 1979). Therefore, it is necessary to give some weight to seed productivity for calculating an adequate genetic value of seed (Griffin 1982). It is commonly believed that first-generation seed orchards are established with plus trees selected from a reference population of unrelated and non-inbred individuals. The seed productivity of individual clones is estimated on the basis of seed production that is measured by female (or sometimes male) strobilus scores (Gomöry et al. 1999). In the present study, seed productivity and breeding value of candidate clones are known.

Orchard benefits are calculated and compared in four different clonal deployments. The orchard benefits of all deployments are compared under the same level of gene diversity. Orchard benefit is a numeric expression of how favourable the seed orchard would be, considering gene diversity (measured by status number) and both genetic gain. Gene diversity (status number; Ns) can be estimated according to the contribution of the selected clones (cf. Lindgren and Mullin 1998, Kang et al. 2001) as (abbreviations below):

$$N_s = \frac{\left(\sum_{i=1}^{N} s_i \cdot f_i\right)^2}{\sum_{i=1}^{N} (s_i \cdot f_i)^2} \qquad [1]$$

Benefit calculation

Different criteria were used for calculations of clonal proportions, and the orchard benefits were estimated according to equation [2]. In the present study, four clonal deployments are compared with the following variables

V_i	–	Breeding value of the clone *i*
s_i	–	Seed productivity of the clone *i*
S	–	Total seed production
B	–	Orchard Benefit
f_i	–	Contribution of clone *i*
p_i	–	Proportion of clone *i*
a	–	Seed price intercept
b	–	Seed price addition per genetic quality unit
c	–	Truncation intercept
u	–	Average breeding value of all clones

Table 1. Calculation for the number of corresponding clones based on different criteria according to deployments

Deployment	Criteria for the selection of corresponding clones (N)
1	$V_i - c > 0$
2	$S_i - c > 0$
3	$(V_i - u)S_i - c > 0$
4	$[a + b(V_i - u)]S_i - c > 0$

In the deployment 1, the status number was calculated based on the clonal breeding value only. In deployment 2, the criterion considered seed productivity only. While only one factor was used in deployments 1 and 2, respectively, both seed productivity and breeding value were used in deployments 3 and 4. In addition, two constants were used in deployment 4 to give weight on seed productivity. One is seed price intercept (a) and the other is additional seed price per genetic quality unit (b).
These constraints were used to estimate the benefit as

$$B = S \left\{ a + b\left[\left(\sum_{i=1}^{N} V_i \cdot S_i \cdot f_i \right) / S - u \right] \right\} \quad [2]$$

In the study, a and b were set to be 100 and 10, respectively. (a) represents the price for seeds of candidate clones, which correspondence with the average breeding value of candidate clones. (b) is value-added price of seed for one unit of breeding value, thus per percent-increase in breeding value. b= 10 means that one percent improvement of the breeding value increases seed price 10%. For example, seeds with 10% improved breeding value could be sold twice high price compared to seeds harvested from candidate clones.

Results and Discussion

Comparing with candidates', the benefits in deployments 1, 2, 3 and 4were 169%, 190%, 213% and 225% respectively (Fig. 1). As shown in the deployment 3 and 4, when both genetic value and seed productivity were considered together, benefits were higher than being only one factor in this study.

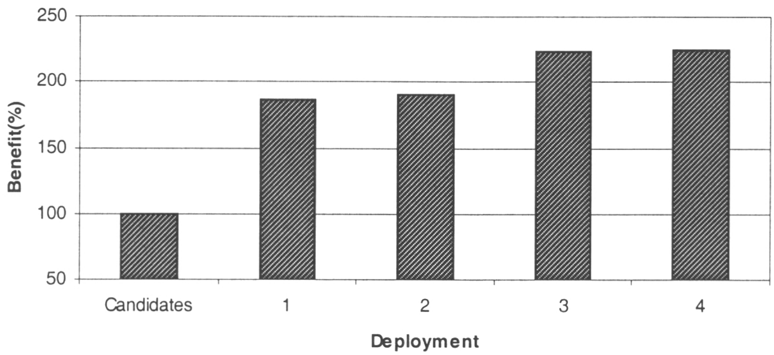


Figure 1. Benefits according to the four deployments.

Choosing clone and ramet numbers is the main concern for not only high orchard gain but also orchard efficiency that is "orchard benefit". If only the gain is concerned, the clonal genetic value could be regarded as the first factor in choosing clones. When only the breeding value is considered like in the deployment 1, the sum of breeding value is much higher than the deployment 2 with only the seed productivity (Table 2). However, since the aim of seed orchard is to produce genetically improved seeds as much as possible, the seed productivity is so important as the genetic value. When two factors are considered together in deployments 3 and 4, the sum of breeding value is higher than in deployments 1 and 2. Therefore, calculation of the seed orchard benefit must be done with integrated factors. From this point of view, keeping records of flowering (or seed production) is helpful to choose clones (Sorensen and Webber 1997).

Deployment 2 gives lowest gain, but the orchard benefit is higher than deployment 1, because the weight on seed production increased the improved seed value. Therefore, if there is needed a demand for higher seed prices, the value of improved seeds would be getting higher benefits.

Genetic gain, gene diversity, management cost, irregular seed production and pollen contamination are the major considerations in seed orchards. To some extent, these factors might be corrected by proper establishment and management practices (Owens and Blake 1985). As seed orchards are advanced, an adequate method becomes the most important strategy to reduce management cost and to increase seed orchard benefit (Li et al. 1999). The benefit of the seed orchard is a function of seed production, breeding value, and gene diversity. Griffin (1982) reported that general combining ability (GCA) for relative volume production should be weighted to female and male flowering for high genetic gain.

Table 2. Comparison of the sum of breeding value, status number and orchard benefit among four deployments

Deployment	1	2	3	4
Sum of breeding values (S·[ΣVi · pi])	766	134	1027	1043
Status number (Ns)	10.4	10.6	10.6	10.4
Benefit (%)	169	190	213	225

If there is positive correlation between genetic value and seed production, the high benefit could come from deployments 1 and 2. While, if there is negative or no correlation, deployments 3 and 4 could be good options and selective seed harvest could be applied in existing seed orchards. In this study, there was no correlation (R2=0.023) between genetic value and seed production, which gave higher orchard benefit when both seed productivity and breeding value were considered. The orchard benefit of deployment 4 is 12% higher than deployment 3. Hence, two constraints, seed price intercept (a) and additional seed price per genetic quality unit (b), can increase the benefit.

Table 3. Comparison of the orchard benefit according to a and b

Deployment		1	2	3	4
Benefit (%)	a = 100, b = 5	146	195	188	209
	a = 50, b = 5	169	190	213	360
	a = 50, b = 1	129	198	171	327

However, a and b are changeable constraints according to situation of seed demand and seed production, and thus the benefit of seed orchard would also be altered (Table 3). Under the same condition, if b would be changed to 5 then deployment 3 had higher benefit than deployment 2. Also, the other case (a = 50, b = 5 or 1) showed that the adequate deployment could be changed in accordance with a and b. Therefore, finding out the suitable values of a, b and deployment is important task for management of seed orchard.

Acknowledgement

This work was financially supported by the postdoctoral fellowship program for the first author from Korea Science & Engineering Foundation (KOSEF), by Korea Forest Research Institute and by the "Föreningen Skogsträdsförädling" in Sweden.

References

Almqvist, C., Eriksson, U. & Yazdani, R. 1995. Arbetsrapport. Nr .307. Forestry Research Institute of Sweden.

Bila, A. 2000. Fertility variation and its effects on gene diversity in forest tree populations. Ph.D Thesis. Swedish University of Agricultural Science, Umea, Sweden. Acta Universitatis Agriculturae Sueciae, Silvestria 166.

Danbury, D.J. 1971. Economic implications of selection for seed production in Radiata pine seed orchards. Aust. For. Res. 5(4): 37-44.

Gomöry, D., Rudolf, B. & Ladislav, P. 1999. Effective population number estimation of three Scots pine (Pinus sylvestris L.) seed orchards based on an integrated assessment of flowering, floral phenology, and seed orchard design. For. Genet. 7(1): 65-75.

Falconer, D.S. & Mackay, T.F.C. 1996. Introduction to quantitative genetics. 4th edn. Longman. Malaysia. p. 1-64.

Giertych, M. 1987. Seed orchard in crisis. For. Ecol. Manage. 19: 1-7.

Griffin, A.R. 1982. Clonal variation in Radiata pine seed orchards. I. Some flowering, cone and seed production traits. Aust. For. Res. 12: 295-302.

Kang, K.S. 2001. Genetic gain and gene diversity of seed orchard crops. Ph.D Thesis. Swedish University of Agricultural Science, Umea, Sweden. Acta Universitatis Agriculturae Sueciae, Silvestria 187. 75pp+11 chapters.

Kang, K.S & Lindgren, D. 1999. Fertility variation among clones of Korean pine (Pinus koraiensis S. et Z.) and its implications on seed orchard management. For. Genet. 6: 191-200.

Kjaer, E.D. 1996. Estimation of effective population number in a Picea abies (Karst) seed orchard based on flower assessment. Scan. J. For. Res. 11: 111-121.

Li, B., McKeand, S. & Weir, R. 1999. Tree improvement and sustainable forestry – impact of two cycles of Loblolly pine breeding in the U.S.A. For. Genet. 6(4): 229-234.

Lindgren, D., Fries, A. & Nilsson, J.E. 1989. Genetic improvement of forest trees at high latitudes with particular reference to lodgepole pine. Gen. Tech. Rep. PNW-GTR-247. USDA Forest Service, Pacific Northwest Research Station. p. 68-73.

Lindgren, D. & El-Kassaby, Y.A. 1989. Genetic consequences by combining selective cone harvesting and genetic thinning in clonal seed orchards. Silvae Genet. 38: 65-70.

Lindgren, D. & Matheson, A.C. 1986. An algorithm for increasing the genetic quality of seed from seed orchards by using the better clones in higher proportions. Silvae Genet. 35: 173-177.

Lindgren, D. & Mullin, T.J. 1998. Relatedness and status number in seed orchard crops. Can. J. For. Res. 28: 276-283.

Nikkanen, T. & Velling, P. 1987. Correlations between flowering and some vegetative characteristics of grafts of Pinus sylvestris. For. Ecol. Manage. 19: 35-40.
Owens, J.N. & Blake, M.D. 1985. Forest tree seed production. Canadian Forest Service, Information Report PI-X-53. Victoria, BC.161p.
Sonesson, J. 1995. Avelsvärden. Nr. 20. Forestry Research Institute of Sweden.
Sorensen, F.C. & Webber, J.E. 1997. On the relationship between pollen capture and seed set in conifers. Can. J. For. Res. 27: 63-68.
Sprague, J., Jett, J.B. & Zobel, B. 1979. The management of southern pine seed orchards to increase seed production. In: Proceedings of a symposium on flowering and seed development in trees. Southern Forest Experiment Station, Starkville, Miss. p.145-162.

How to integrate forestry to the management of gene resources

Veikko Koski
Esankuja 8, FIN-01400 Vantaa, Finland

Introduction

Tree breeders and forest geneticists would like to see genetic improvement and genetic aspects in general be integrated to silviculture and forest management. It may be, however, purposeful to turn the matter upside down and to discuss how well silviculture and forest management are taken into consideration by geneticists and breeders.

Spokesmen of advanced tree breeding and gene conservation often proudly introduce latest achievements of molecular biology and biotechnology, and complex statistical models for powerful computers. The explanation is that reports published in scientific journals have been the most valued criteria even in applied activities. I do not by any means object scientific approach and theoretical basis, but in order to develop and flourish tree breeding must be tightly linked with forest management, because the demand for genetically improved reforestation material is the only driving force of tree breeding.

During the "golden era" of tree breeding our main partners in forestry used to be well off forest companies and the stable state forest service. The true decision makers were foresters who personally knew the breeders, and the contacts were kept on local level. Repeated fusions of forest companies have resulted in faceless international giants, where the local managers follow the orders of the central administration. All actions must be profitable in short time. In many countries the state forests are now subject to the same requirement of economic profitability. Earlier the biological and ecological factors guided silvicultural measures and most of the work was done manually. Now, the minimising of expenses guides the measures and big machines do the work.

I sometimes wonder whether tree breeders have realised the impacts of all those changes. If the reality of forestry does not penetrate the circle of tree breeding, it may be difficult to speak the language that forest managers understand and to produce desirable articles to the market. There are numerous topics to discuss in this context, but on this occasion I deal with two issues: 1) experimental plantations, and 2) continuity of conservation populations.

Experimental cultivation

The purpose of progeny testing is to rank the entries for recurrent selection, and to provide data for estimating of various genetic parameters. As the genetic factors are in the focal point, the noise or error factor caused by environmental variation ought to be eliminated. Old field trials display the harmful effects of site micro variation, stochastic calamities, weed competition etc. Testing of families in more homogenous and intensive conditions with sophisticated experimental design reduces the environmental variation and thus magnifies the relative value of the genetic component. Nevertheless, the result is often that heritability of commercially important traits is rather low, and the G x E interaction is significant. Has anybody investigated what kind of effect silviculture might have? Especially when thinking of the anticipated genetic gain the non-genetic factors and methods to control them would deserve more interest.

One feature is that each test is planted once in a certain year, but in forestry the same material is used during many years. The weather conditions vary from year to year, technology changes and differs between organisations. Breeders seldom can afford replication of tests in several successive years. Breeders deal with numerous entries and small plots, forestry with hundreds of hectares and millions of seedlings every year. Specific field trials with large plots are nowadays probably out of reach of tree breeders. However, growth and yield studies need at least some sample plots where the behaviour of "cultivars" as a stand can be observed. Verification of realised genetic gain on stand level is the best advertisement of tree breeding. Another difference is in the time scale. Breeders want to obtain the results soon in order to enhance rapid progress of breeding cycles. Therefore, the measurements are carried out at sapling stage. In commercial forestry the yield with higher economic profit is available at the end of the rotation, i.e. after 40 – 80 years.

Collaboration with big forest owners is necessary; I mean in the way that breeders go to field and **see** how trees behave in normal forest.

Continuity of conservation populations

Gene conservation, including the maintenance of long term breeding populations differs fundamentally from strict nature protection. Forests within protected areas, such as nature parks and national parks, are unmanaged and their regeneration must take place by nature method. The older the trees the more valuable they are considered in terms of biodiversity.

As regards gene conservation the current tree generation is only a tool to transfer the gene pool to future tree generations. Thus, it is not enough to establish a conservation population and to imagine it perpetuates by itself. Even the existence and vigour of the trees need active and regular maintenance.

Regeneration is the most crucial event. *In situ* reserves should in strict sense regenerate from natural seeding. The ideal image of nature reserves is reflected in many *in situ* reserves so that the stands are very old and dense. There are hardly any seedlings or saplings. As dead trees do not carry over any genes, actions must be undertaken as long as the trees are fertile. The mode of regeneration is to be adopted from the local foresters. It is not just cutting down the old stand and replacing it with seedlings. Breeders must learn how to apply sound silvicultural methods and how to work cost efficiently.

I take the opportunity advertise the Finnish gene reserve forests as an example of successful combination of management and *in situ* conservation. One reason for the minimum target area of a gene reserve forest was to allow an age class distribution of even aged stands in each gene reserve. Working on hectare basis with normal methods and machines keeps the expenses reasonable and gives the owner the net income of commercial thinning and regeneration cutting. As a consequence of such guidelines most of our gene reserve forests consist of several age classes. Figure 1 shows 4 examples out of the currently registered 40 units. The total area is 7 155 ha in March 2001, which has slightly changed from last year (see Yrjänä et al 2000).

As regards long term breeding populations and other *ex situ* reserves regular maintenance is necessary. Based on more than 40 year's experience I must say that stands mature from sapling stage surprisingly fast to maturity. If e.g. thinning is disregarded, irreversible damage occurs. As regards *ex situ* gene reserves, the word "regeneration" may give a wrong impression of rejuvenation. The genetic composition of the succeeding generation is deliberately manipulated by means of controlled selection and/or crossing. The existing stand cannot be simply cut down and be replaced with a new one, but the generations must overlap. In other words, additional areas are needed. Let us think of the first generation clonal seed orchards. Besides seed production they are a kind of clonal banks and primers of breeding populations. Advanced generation seed orchards and proper breeding populations will probably diverge even physically. The currently existing seed orchards may still remain. An array of overlapping generations should be thoroughly planned in the field. It is fairly easy to design sophisticated schemes of crossings and selection, but taking management and implementation into account might favour simplicity. Fertility variation among genotypes is substantial and flowering capricious at least at spruce.

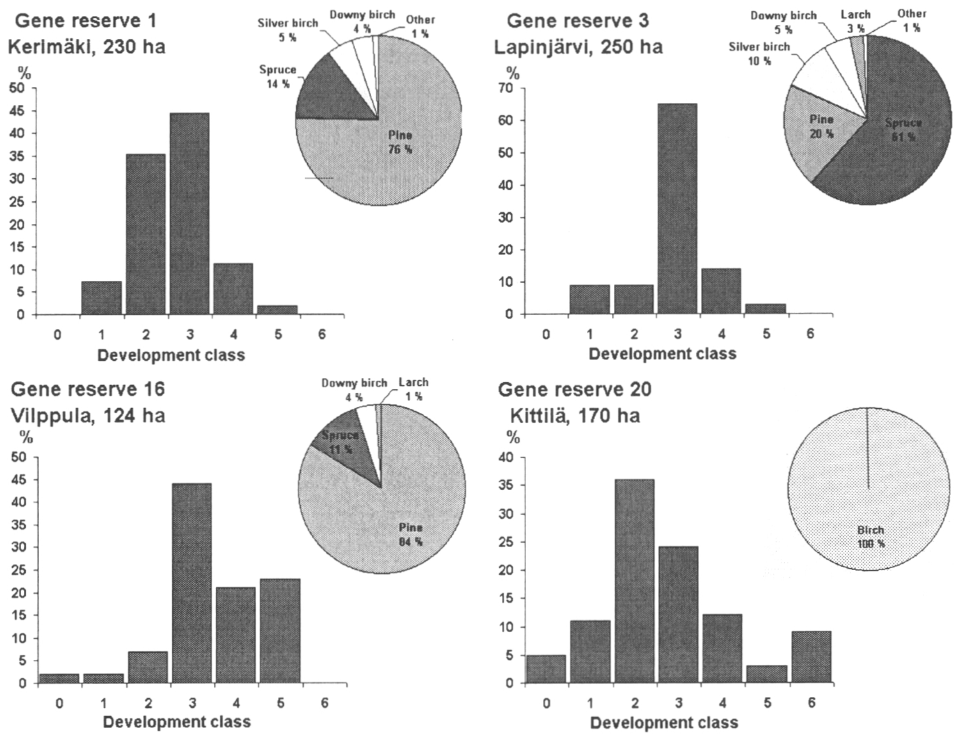


Figure 1. Patterns of development classes and tree species composition of four gene reserve forests, managed by Finnish Forest Research Institute. The developmental classes are: 0 = open regeneration area; 1 = seedling-sapling stand; 2 = advanced sapling stand; 3 = young thinning stand; 4 = advanced thinning stand; 5 = mature stand; 6 = all aged stand. Note: this classification differs from that used in the Finnish Statistical Yearbook of Forestry. Do not ask me why.

Provenance trials have had a “come back” due to the potential threat of the global change. As provenance trials were some years ago considered relicts from the primitive period of forest genetics, less attention was paid to the tending of the old plantations and rather few new ones have been established. Many trials are growing over aged in the near future. How to continue? Firstly we have the problem of seed sources. The trials have been subject to selection and competition, and the seed crop produced after open pollination is a real cocktail of origins. The original seed sources have perhaps vanished. New plantations will be more provenance collections than experiments, which prefers large plots and considerable areas. Management and planning are needed in order to meet this challenge.

Conclusions

Forest genetics and tree breeding have to compete for resources in order to maintain the current level of activities. For the time being biological diversity and close to nature handling of forest are more popular than intensive plantation forestry. If the currently common mode of silviculture continued over a longer period of time, it would obviously result in shortage of soft wood (Nabuurs 2001). The future demand for timber and tree biomass certainly requires increasing yield from managed forests. Without doubt forestry needs to utilise all the achievements of tree breeding to cope the increasing demand of wood. The penetration of genetic improvement requires active role of tree breeders. A feed-back system might be a smart solution. When breeders take forestry issues widely into account, they learn to know the constraints and perspectives. This kind of knowledge is certainly useful when marketing genetic improvement and when finding resources to tree breeding.

References

Nabuurs, G-J. 2001. European forests in the 21th century: impacts of nature-oriented management assessed with large-scale scenario model. Alterra Scientific Contributions 2.

Yrjänä, L., Karvinen, K. & Napola, J. 2000. General Statistics on Forest Tree Breeding in Finland 2000. Finnish Forest Research Institute, Research Papers 783.

SHORT NOTES

Threshold values for profitable tree breeding in Finland: Society's, private forest owner's and seed producer's viewpoints

Anssi Ahtikoski
Finnish Forest Research Institute, Muhos Research Station, FIN-91500 Muhos, Finland

The profitability of Scots pine (*Pinus sylvestris* L.) and Silver birch (*Betula pendula* Roth) breeding was evaluated for three *a priori* chosen agents, namely the government (here the same as society), seed producer and private forest owner. The main purpose of the study was to determine the threshold values for profitability, and further, to examine these values with respect to prevailing biological and economic conditions of each agent. Both the present and next-generation seed orchards were included in the assessment. Further, so-called differential approach was applied. In this approach, *differential* benefits and costs of tree breeding were obtained by comparing the benefits and costs of tree breeding to the corresponding of stand seed acquisition. Differential benefits were evaluated, for example, by incorporating genetic gains (based on the latest progeny test results) into widely-used growth and yield models. Both economic (a cost-benefit analysis with a specific shadow pricing procedure) and financial analyses were applied, and the net present value (NPV) was chosen as the investment criterium.

The results indicated that, in general, it is possible to attain the threshold values for profitability with respect to each agent. For example, an analysis using 8% genetic gain from the present Scots pine seed orchards, the discount rate of 3% (in real terms) and an annual regeneration area corresponding to the past 15-year-average, resulted in a positive NPV for society. Furthermore, with 20% genetic gain from the next-generation Silver birch seed orchards in southern Finland and a 14% genetic gain in central Finland, the discount rate of 5 % and an annual regeneration area of the past 20-year-average, resulted a positive NPV for society. For a private forest owner in southern Finland it was profitable to sow with improved seed from Scots pine seed orchards (rather than with *un*improved stand seed) even using as high as 5% discount rate, and with genetic gain as low as 3% . However, some caution should be exercised when interpreting some of the results. For instance, the profitability for Scots pine seed producer was very sensitive to changes in annual seed crop (kg/hectare). The profitability of Scots pine seed orchards with northern clones was dependent on labour costs. As expected, all the results (regardless of the agent) distinctively

indicated that the most critical factors to the profitability are: 1) the demand for seed orchard seed (in the form of the annual regeneration area) and 2) the attainable genetic gains. To summarise, without a sufficient demand for orchard seed the achievements of tree breeding activities cannot be converted into economic benefits.

Managing a model population in order to market the potential of breeding

Bengt Andersson,
SkogForsk, Box 3, SE-918 21 Sävar, Sweden

Tree-breeding programmes, as opposed to breeding programmes for other crops, generally suffer from long intervals between generations. Consequently, the genetic gain per unit time is often low, although this is not necessarily a major setback, because the gain can still be high enough to cover the costs. An often more important problem is that the return from a breeding investment does not materialize until many years later, which tends to damp enthusiasm and to make investments risky and less appealing. Realizing the gain from breeding sooner would be very attractive, even though it might involve higher costs. A lot of research and development effort has gone into techniques for shortening the generation turnover of a breeding cycle, including early testing and early maturation/flowering. Despite this, there are few examples where these techniques have been employed in operational breeding programmes.

We have now established a model population of operational size for Scots pine (*Pinus sylvestris* L.), i.e., 800 candidate trees from 20 top ranking full-sib families. The model population is being managed in parallel with one of the 13 operational breeding populations in northern Sweden. The goal is to shorten the generation time of the model population to approximately a third of the normal time, through intensive management and without decreasing the gain or jeopardizing either testing accuracy or genetic diversity. Apart from demonstrating the potential of breeding, we also hope to gain information on key questions for the development and implementation of new techniques for applied breeding. The principal aspects of the model system are:

Elimination of the time lag arising from sexual maturation based on vegetative propagation and clonal testing rather than on progeny testing

Early test performance as the basis for selection and crossing (a two-stage selection strategy that includes field performance is also possible)

Topworking and/or accelerated growth for early flowering and crossings for generating advanced breeding populations.

The strength of the model system is that each activity has the potential to yield benefits independently of the others, and thus may improve the breeding programme even if some of the activities fail. The weak points of the model are the risk of negative correlated response from culling in the candidate population, owing to a failure in vegetative propagation or early flowering, and that selection decisions rely entirely on early evaluations. An integrated strategy, in which early evaluation for primary selection is combined with field evaluation for final selection, enables the inherent selection insecurity to be overcome. Examples of different breeding strategies are illustrated in Fig. 1.

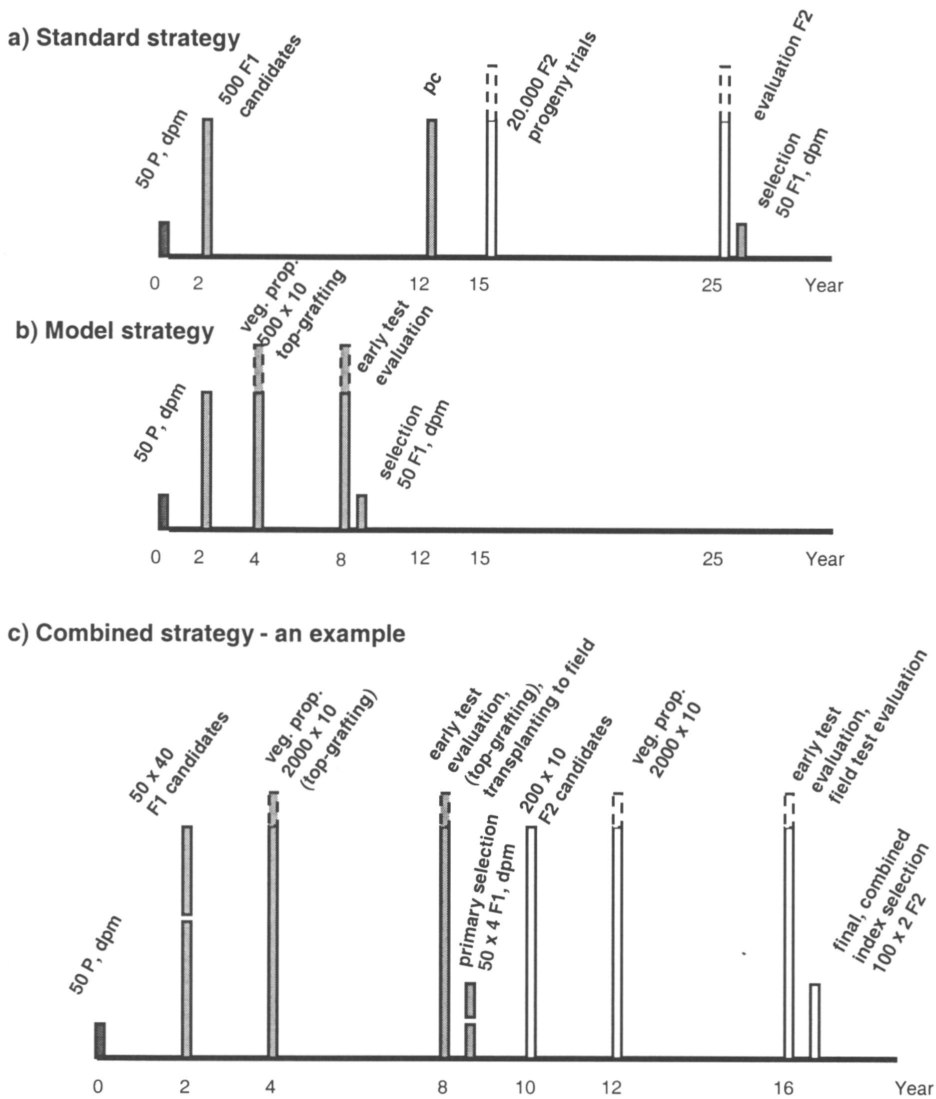


Figure 1. Brief outline of a) standard, b) model, and c) combined breeding strategies, where P is the parent generation, F1 and F2 are 1st and 2nd progeny generations, dpm is double-pair mating, and pc is polycross mating.

The clonal testing strategy – the highway for long-term breeding of Norway spruce?

Application of a simulator for long-term breeding

Darius Danusevicius[1] and Dag Lindgren[2]
[1]*Lithuanian Forest Research Institute, Dept. of Forest Genetics and Reforestation*
[2]*Swedish University of Agricultural Sciences, Dept. of Forest Genetics and Plant Physiology*

The overall goal for long-term tree breeding was formulated as maximizing annual progress in group merit (GMG/Y) at a given annual budget. Group merit is a weighted average of breeding value and gene diversity. A deterministic simulator "BREEDING CYCLER" was used to optimize breeding strategies based on testing of phenotypes, clones or progeny for selection of parents for subsequent breeding cycle as regards testing time and test-entry size. (BREEDING CYCLER is primarily aimed at evaluation of long-term breeding strategies and is available on the WEB at *http://www.genfys.slu.se/staff/dagl/Breed_Home_Page/*). The long term breeding was assumed to be based on cycling and balanced within-family selection (like the current Swedish breeding program). Dependence of GMG/Y on genetic parameters, cost and time components was investigated. The simulation scenarios were chosen with long-term breeding of Norway spruce in mind.

The clone strategy was the best over the whole range of considered cases, except for the scenarios with unrealistically high narrow-sense heritability. For the scenario which is most realistic for Norway spruce, GMG/Y from clonal strategy was for 80% greater than GMG/Y from phenotype and progeny strategies, i.e. clonal strategy can provide 80% higher annual genetic improvement at a given annual budget. The optimal time from establishment to evaluation of the clonal selection test was around 20 years. Benefit from the clone strategy was slightly reduced at a high dominance variance.

Testing of phenotypes was the second best strategy in most of the cases, except for the scenarios with low narrow-sense heritability and high budget. However, superiority of the phenotype strategy over the progeny strategy was minor. The progeny test strategy may be a better alternative to the phenotype strategy in case of shortening the time to reproductive maturity of the tested parents below around 11 years. The breeding cycle simulator used for this study is suggested to be a helpful tool for planning long-term breeding.

The Low Temperature Laboratory at Möðruvellir; Presentation of laboratory premises and research.

Øyvind Meland Edvardsen[1], Bjarni E. Guðleifsson[2] & Brynjar Skúlason[3]
[1]*Icelandic Forest Research,* [2]*Icelandic Agricultural Research Institute*
[3]*Iceland Forest Service*

Research on winter damage in herbage plants has been carried out at Möðruvellir Experimental Station since 1972. The first equipment for controlled low temperature research was purchased in 1984 and moved to the renewed current building in 1987. The agricultural research has concentrated on freezing tolerance and ice encasement damage in different grass species, white clover and winter cereals. In addition research has focused on respiration processes of plants encased in ice at low temperatures. During the last decade forestry researchers have utilized the equipment for controlled freezing tests of different tree species, provenances, families and clones, and also to test the impact of short day treatment and fertilizer on frost hardiness. The equipment have also been used in studies of insects i.a. to test the freezing tolerance of Green spruce aphid populations. In year 2000 new equipment were installed, wich makes accurate tests of frost tolerance in plants, plant parts, organs and cell cultures feasible. It is also possible to cultivate plants under controlled light and temperature conditions. Management of the laboratory is a cooperation between Rala – Agricultural Research Institute – and Mógilsá – Icelandic Forestry Research.

Balancing gene diversity (status number) and seed production

Kuy-Suk Kang[1], Erik D. Kjær[2] & Dag Lindgren[1]
[1] *Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, SE-90183 Umeå, Sweden*
[2]*The Forest and Landscape Research Institute (Denmark)*

In practical cone collections, the distribution of cones will not be a well-known variable. Even in the same seed orchards or stands, the distribution of cones would probably look very different in different orchards and years. Tools for general situations are needed as in a practical situation rather than rough guessing of fertility distribution. In the study, therefore, theory on the balancing between gene diversity (measured by status number) and seed collection was developed and applied into Danish *Corylus avelana* populations.

Keeping parental contribution equally by collecting or mixing seeds in equal proportions has often suggested in many studies. However, complete equal contribution will require substantial amount of seeds to be discarded, because least fertile trees will set the standard of constrain. Complete equal female contribution is thus not a feasible option in many practical situations. Harvesting trees with few cones may be expensive and contribute little to fertility variation. To constrain the number of seed from trees bearing many cones may increase gene diversity in the seed crop, but may also reduce the total seed harvest. Thus, the final mix of progenies will in general be a trade off between equalizing parental fertility and obtaining seed production.

By controlling female fertility based on power function ($F(x)= x^a$), a trade off between equalizing parental contribution and obtaining an acceptable amount of seed was achieved, and gene diversity during the initial phase of mobilizing the natural gene pool could be monitored. Constrains on seed production could be made on the parental proportion as both low bound (minimum contribution) and upper bound (contribution limit; fertility balancing). Two options for constrains on the cone harvest were investigated. The first option was not to harvest seed from the trees with the lowest number of seeds (low bound). These trees may be seen as too expensive to harvest. The second option was not to harvest more than a given number of seeds from each tree (contribution limit); i.e., only a fixed number was harvested from the trees bearing the high number of seed. Thus, no harvest was done from the lowest fraction of trees. On the other hand, an equal seed harvest was made on the highest fraction of trees to avoid over-representation of the most fertile individuals.

For a case of the collection of hazel nuts (*Corylus avelana*), the status number was estimated to 149 if all nuts were collected from 264 individuals. Higher status numbers could be obtained by balancing the number of nuts collected per tree. But, this high status number was connected to loss of nut production. If it was decided to truncate the progeny size at 50 nuts (the upper bound was 0.86; an individual contribution was restricted as less than 0.74%), this increased the status number from 149 to 201, while 85% of all nuts were collected.

Seeds are normally mixed from different trees during seed collection. However, as fertility variation is substantial, it is recommendable for the trade off between status number and seed production that seeds are collected separately by genotypes and the records are kept from collection through planting, as input to *ex situ* conservation or for establishment seed sources. By doing this, female fertility variation can be quantified and some extend controlled by reducing the contribution of most or least fertile trees. This can be an effective measure, which is cheap to impose as long as seeds are mixed prior to seed processing or seedling production.

The Russian-Scandinavian Larch Project

Owe Martinsson
Department of Silviculture, The Swedish University of Agricultural Sciences
S-901 83 Umeå, Sweden

Larch (*Larix* Mill.) is one of the most important elements of the boreal forests. The widest distribution of larch in the world is to be found in Russia. The wide genetic variation of larch species in Russia has, to a great extent, not earlier been available for forest research in western Europe. The objective of the Russian-Scandinavian Larch Project is to study the genetics of the four main larch species within Russia, *Larix sukaczewii* Dyl., *L. sibirica* Ledeb., *L. gmelinii* Rupr., and *L. cajanderi* Mayr., and to make future research on genotype-environment interaction in other parts of the northern hemisphere possible. The project started in 1994 and the first step, collection of seed and wood cores, was finished in 2000. The project was initiated and co-ordinated from Sweden. However, it is a result of co-operation between four different Russian research organisations, two partners in Scandinavia, one in Japan and one in the USA. Up to the end of 2000 seed and wood cores were collected from 941 larch trees distributed over 15 regions and 44 stands (Fig. 1). In addition to that larch seed has been bulk collected from 8 stands. Collected seed from 802 open-pollinated families were tested for germination in the summer of 2000. The average germination of the seed was 25 %, but with great variation between larch stands and regions. Chemical analysis of wood samples and DNA analysis of needles from all families have started.

The project and the results up to present time will be presented in the Eurasian Journal of Forest Research (Abaimov et al. 2001)

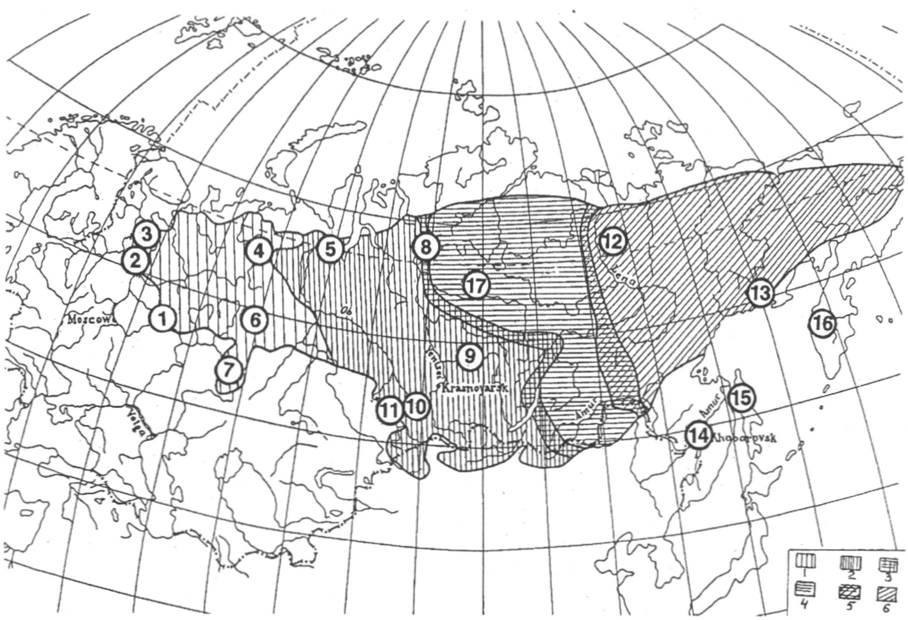


Figure 1. Distribution areas of the main larch species in Russia and the localities of the 17 seed collection regions of the project according to Table 1. 1=*Larix sukaczewii*, 2=*Larix sibirica*, 3=*Larix czekanowskii*, 4=*Larix gmelinii*, 5=*Larix gmelinii* x *L. cajanderi*, 6=*Larix cajanderi*.

Acknowledgement

The project is a result of co-operation between the nine authors and their home institutes. The project was sponsored by the Norwegian Barents Council, the Norwegian State Bank of Agriculture, the Swedish Tree Breeding Association, the Royal Swedish Academy of Science, The Nissan Science Foundation and the University of Minnesota.

References

Abaimov, A.P., Barzut, V.M., Berkutenko, A.N., Buitink, J., Martinsson, O., Milyutin, L.I., Polezhaev, A., Putenikhin, V.P.,Takata, K. 2001: The Russian-Scandinavian Larch Project- Seed collection and seed quality, Eurasian Journal of Forest Research (submitted).

Frost tolerance among provenances and families from the *Picea* complex in Alaska

Brynjar Skúlason[1], Aðalsteinn Sigurgeirsson[2], Bjarni E. Guðleifsson[3] and Øyvind Meland Edvardsen[2]
[1]*Iceland Forest Service,* [2]*Icelandic Forest Research,*
[3]*Icelandic Agricultural Research Institute*

Sitka spruce (*Picea sitchensis* (Bong.) Carr.) is the most promising tree species for production forestry in the cool, oceanic regions of southern and western Iceland. Experience suggests, however, that the species may be susceptible to frost damage during late spring and early autumn. To reduce this risk it was necessary to examine the genetic variation in growth rhythm and frost hardiness in spring and autumn among those provenances of Sitka spruce that can be successfully cultivated under Icelandic conditions. Freeze testing under controlled conditions was used on a total of 8000 Sitka spruce and Lutz spruce (*Picea x lützii*) seedlings, from among 10 families from each of 20 provenances. Differences in frost tolerance during spring and autumn were significantly different among provenances and among families within provenances. Provenances of white spruce (*Picea glauca* ((Moench) Voss) and Lutz spruce were more susceptible to damage from spring frosts than those of Sitka spruce. The converse was however true for autumn frost damage, where damage was greatest in Sitka spruce. Correlations between frost tolerance and latitude, longitude and elevation at origin, as well as seedling height were insignificant. There was however a strong and significant relationship between damage observed among provenances and families in the nursery one year earlier, attributed to autumn frosts, and damages observed after controlled freezing conditions in the following autumn. These results suggest the opportunity for using freeze testing for early selection for frost hardiness in the nursery and in the field.

Realized genetic gains from the selection of first-generation Scots pine plus trees in southern Finland

Leena Yrjänä & Matti Haapanen
Finnish Forest Research Institute, Vantaa Research Centre, Box 18, FIN-01301 Vantaa, Finland

Measurements of cumulative tree height and visual assessments of stem quality from 28 (7 for quality) carefully chosen progeny trials at ages between 10 and 30 years, were analysed in order to evaluate realized genetic gains from the selection of first-generation Scots pine plus trees. The sample of plus trees included in these field trials represented nearly the fifth of all the Scots pine plus trees selected in the southern part of Finland.

The plus tree families in the trials were first grouped by breeding method (open-pollinated vs. cross-pollinated families) and the genetic level of the plus tree parent (the plus trees found superior on the basis of progeny tests vs. all the plus trees). Differences between the four groups of families and the standard check-lots were verified using Dunnett's post-hoc test of significance. The gains in the mean annual height growth were highest (8–10%) for the CP families of the (best) plus trees. The performance of the OP families of plus trees was not statistically significantly different from that of the standard check–lots. In stem quality, the realized gains were evaluated as about 4% and 8% for the OP families of all the plus-trees and the OP families of the best plus trees, respectively.

The present results may be used for drawing conclusions of genetic gains attainable from present clonal seed orchards with various degree of pollen contamination, and with different genetic make-up (1st vs.1,5 generation seed orchards).

Moose (*Alces alces*) browsing on different origins of silver birch (*Betula pendula*)

Anneli Viherä-Aarnio & Risto Heikkilä
Finnish Forest Reseach Institute, Vantaa Research Centre, Box 18, FIN-01301 Vantaa, Finland

Moose is an important damage agent in young plantations of silver birch in Finland. It can damage the trees by breaking the stem or by browsing leaves and branches. Moose damage may, depending on its severity, reduce the growth or lower the stem and timber quality of injured trees.

Browsing by moose was measured in a provenance experiment of silver birch situated at Loppi, southern Finland. The experiment includes stand seed origins from Finland, Sweden, Estonia, Scotland and Russia, between latitudes 53° and 67°. The trial was established on a typical southern Finnish clear-cut area on moist upland forest site and protected against moose by fencing. After the break-down of the fence the experiment, at the age of 5 - 11 years, was frequently visited by moose. The effects of browsing were measured in early spring 2001 when the trees were 11 years old.

There were statistically highly significant differences between different origins in the frequency of trees browsed by the moose. The origins imported to Finland from more southern latitudes (Estonia, Scania, Scotland, Russia) were more frequently and more severely browsed than the native ones. The origin from Hammarland, Åland was also more browsed compared to the other Finnish origins.

There was a significant negative correlation between the latitude of seed origin and frequency of trees browsed by the moose. Furthermore, the frequencies of severely browsed as well as repeatedly damaged trees correlated negatively with latitude.

The reason for the variation in damage frequency may lie in phenological differences. At the time of browsing, the southern origins probably had a different physiological status compared to the native ones due to later growth cessation or insufficient winter hardening.

Baltic origins of silver birch (*Betula pendula*) in Finland

Anneli Viherä-Aarnio & Pirkko Velling
Finnish Forest Research Institute, Vantaa Research Centre

In a study, which is under way in FFRI, silver birch origins from the Baltic countries are compared with the native Finnish ones as regards growth, yield, stem quality (defects) and wood quality in 22-year-old field trials. Preliminary results are reported here on the growth, yield and stem quality.

The material of the study consists of a provenance experiment, which is situated at Tuusula, near the south coast of Finland. The experiment includes stand seed origins from Latvia, Estonia, Finland and Novosibirsk, Russia. In addition, one single tree progeny from Lithuania as well as two progenies from open-pollination and two progenies from controlled-pollination of southern Finnish plus trees are included.

There was a wide variation in the average height, dbh, average tree volume and volume/ha among different origins. Differences between the different origins were statistically significant. The average estimated volume/ha varied from 76 to 197 m^3/ha. The highest volume/ha was produced by origins from northern Latvia (Aluksne, Liepa) and Estonia (Viljandi) as well as by the southern Finnish plus tree progenies. A long seed transfer either from the south or from the north resulted in low production. The origins from Pielavesi, central Finland and Maslyanino, Novosibirsk area had the lowest volume/ha. There was wide variation within both the Finnish and the Latvian group.

The relative frequency of trees with a vertical branch or a forked stem varied from 34% (Sulkava) to 78 % (Maslyanino, Novosibirsk area). Differences between the different origins were statistically significant. A long transfer from the south seemed to increase the frequency of trees with stem defects. The Finnish plus tree progenies had somewhat higher frequency of defected trees compared to the stand origins.

The higher production and, on the other hand, the higher frequency of trees with stem defects in the Baltic material is propably due to their longer growth period, later growth cessation and poor winter hardening. Earlier it has been shown, within a very similar material from southern Latvia to southern Finland, that there is a significant negative correlation between the latitude and the seedling height in the nursery. The more southern the origin the later is the leaf yellowing in the fall and the lower the survival in the field.

More information concerning long distance transfers of the Baltic silver birch origins will be obtained as soon as the measurements at the parallel trial at Viitasaari (63°11'N) have been completed. Analysis of the wood quality of the origins in this study are also under way.

ISBN 951-40-1822-2
ISSN 0358-4283
Hakapaino Oy 2002