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Состояние, мониторинг и задачи селекционных программ

Материалы совещания лесных селекционеров и генетиков северных стран Европы, 13-15 сентября 2005 г., Сыктывкар, Россия

Status, monitoring and targets for breeding programs

Proceedings of the Meeting of Nordic Tree Breeders and Forest Geneticists, September 13-15, 2005, Syktyvkar, Russia

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Состояние, мониторинг и задачи селекционных программ: Материалы совещания лесных селекционеров и генетиков северных стран Европы (Сыктывкар, Республика Коми, Россия, 13-15 сентября 2005 г.). – Сыктывкар, 2005. – 112 с.

Представлены материалы докладов совещания лесных селекционеров и генетиков северных стран Европы, проходившего на базе Института биологии Коми научного центра УрО РАН (13-15 сентября 2005 г.). Работы посвящены селекционной стратегии, генетической изменчивости и сохранению генофонда лесных древесных пород, а также созданию и эксплуатации лесосеменных плантаций.
Сборник предназначен для лесных селекционеров и генетиков, студентов, аспирантов и преподавателей лесных вузов.

А.Л. Федорков (отв. ред.).

Status, monitoring and targets for breeding programs: Proceedings of the Meeting of Nordic Tree Breeders and Forest Geneticists (Syktyvkar, Komi Republic, Russia, September 13-15, 2005). Syktyvkar, 2005. – 112 p.

The contributions of participants of the Meeting of Nordic Tree Breeders and Forest Geneticists are presented. The Meeting was held by the Institute of Biology, Komi Science Center, Ural Division, Russian Academy of Sciences at September 13-15, 2005. The proceedings are devoted to breeding strategy, genetic variation, gene conservation of tree species as well as seed orchards.
The proceedings are designed for tree breeders, forest geneticists, PhD students and lectures of universities.

Aleksey Fedorkov (ed.-in-chief).

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FOREWORD

In September 13-15, 2005, Institute of Biology, Komi Science Center, Russian Academy of Sciences hosted a Meeting of Nordic Tree Breeders and Forest Geneticists. The papers and abstracts that follow in this proceeding were presented at this meeting entitled «Status, monitoring and targets for breeding programs». This was the last meeting of the former Nordic Group for the Management of Genetic Resources of Trees but the first meeting this group in Russia. GENECAR (Centre for Advanced Research in Forest Genetics and Tree Breeding) will replace the former Nordic Group for the Management of Genetic Resources of Trees and will be responsible for its activities, including common Nordic meetings and initiation of research projects. Forty tree breeders and forest geneticists from 8 countries, Denmark, Estonia, Finland, Latvia, Norway, Poland, Russia and Sweden gathered in Syktyvkar, Komi Republic, Russia. Twenty – one oral presentations and seven posters presentations were made. The contributions were devoted to the breeding strategy, genetic variation, gene conservation and seed orchards.

The meeting consisted of two days of presentations and one day field excursion. The field excursion was organized to visit the Scots pine progeny/provenance field trial consisting Swedish and Russian material, Forest Museum, Kortkeros conifer provenance experiment, Scots pine seed orchard and progeny test, Siberian larch plus trees.

On behalf of all the highly satisfied participants, the organizers are grateful to the financial sponsors. The travel of participants from Scandinavian and Baltic countries to Russia was supported by Swedish Association of Tree Breeding. Russian participants were supported by Mondi Business Paper. I would like to thank the staff of Department of Forest Science for the practical arrangements of the meeting. My appreciations goes also to all colleagues, who submitted manuscripts for these proceedings.

Meeting secretary ***Aleksey Fedorkov***

ПРЕДИСЛОВИЕ

Совещание лесных селекционеров и генетиков северных стран Европы проходило на базе Института биологии Коми научного центра УрО РАН 13-15 сентября 2005 г. Тема совещания – «Состояние, мониторинг и задачи селекционных программ». Это было последнее совещание Группы по Управлению Генетическими Ресурсами Древесных Пород, но первое, которое проходило в России. В настоящее время Группа по Управлению Генетическими Ресурсами Древесных Пород реорганизуется в GENECAR (Centre for Advanced Research in Forest Genetics and Tree Breeding – Центр исследований по лесной генетике и селекции), который будет ответственным за организацию подобных совещаний и научных проектов. В совещании приняли участие 40 селекционеров и генетиков, а также лесоводов-практиков из восьми стран (Дании, Эстонии, Финляндии, Латвии, Норвегии, Польши, России и Швеции). Были представлены 21 устный и 7 стендовых докладов, которые касались селекционной стратегии, генетической изменчивости, сохранения генофонда лесных древесных пород, а также создания и эксплуатации лесосеменных плантаций.

В ходе совещания была организована полевая экскурсия, в течение которой участники ознакомились с испытательными культурами плюсовых деревьев сосны, географическими культурами сосны и ели, лесосеменной плантацией и плюсовыми деревьями лиственницы.

Организаторы выражают благодарность за финансовую поддержку Шведскую ассоциацию лесной селекции, благодаря которой многие участники из Скандинавских и Балтийских стран смогли прибыть на совещание, а также ОАО «Монди Бизнес Пейпа – Сыктывкарский ЛПК», который выделил грант для российских участников. Хотел бы также выразить признательность сотрудникам Отдела лесобиологических проблем Севера Института биологии Коми научного центра за практическую работу по организации совещания и всем участникам, представившим свои материалы в данный сборник.

Секретарь совещания ***А.Л. Федорков***

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THE ROLE OF NATURE PROTECTED AREAS SYSTEM OF THE KOMI REPUBLIC IN GENE CONSERVATION OF FOREST TREES

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The Komi Republic is situated in the north-east of European part of Russia and occupies about 416 thousands km^2. The Komi Republic borders with Archangel province in the north and north–west and Kirov and Perm provinces in the south and south-east. The Urals is the east boundary of the Komi. There are 5 orographical regions in this territory: Vychegodsko-Mezenskaya Plane, Northern Hills, Timan Ridge, Pechorskaya Plane and Western macroslope of the Urals. Largest part of the territory belongs to the Russian Plane. Climat of the Komi Republic is moderate continental and temperate cold. Northern part of the territory belongs to the area with arctic climate. Central regions which are situatied between Polar Circle and 63°N latitude belong to the zone of atlantic-arctic climate. All others belong to the zone with atlantic-continental climate. Period of temperature above +10°C is continuing from 90 to 105 days, period of temperature above 0°C is up to 195 days. Average temperature of January is -15°C. Duration of the winter is 5 month in the southern part of republic and about 7 month in the northern one. Territory is situated in the zone of surplus moisture. Total precepitations per year are 500-600 mm, most of them are felling during warm season. There are more than 3500 rivers with the lenghts above 10 km here. The main rivers are Pechora, Mezen, Vychegda, Luza. Supplying of rivers, lakes and wetlands is mainly by atmospheric precipitations.

Tundra and taiga are main vegetation zones in the Komi Republic. Southern boundary of tundra zone is situated in the head of Usa and Vorkuta river basin. The main vegetation types in this zone are shrubby-mosses tundra in the watersheds and willow’s communities along rivers. Rare forest stands (belt of pre-tundra forests) are distributing between tundra and taiga zones. Landscapes are characterized by complex of shrub communities and birch-spruce low-density stands, which are situated in the river valleys. Density of the canopy is lower than share one fifth and heights of the trees are 6-8 m. In the vegetation cover mosses and lichens are dominated. Permafrost in soil under rare stands is absent.

The largest part of territory is occupied by taiga with sub-zones of far northern, northern, middle and southern taiga. Stable primary boreal taiga communities which have been formed during long-time evolution of vegetation prevail in forest fund. Nowdays major share of virgin forests in the northern Europe are situated in the Komi Republic. There are 8 coniferous and 17 deciduous tree species, more than 50 species of shrubs and dwarf-shrubs in the forest of the Komi Republic. Among them such coniferous trees as *Pinus sylvestris, Picea obovata*, hybrid forms of *Picea abies* x *P. obovata, Abies sibirica*, *Larix sibirica*, *Juniperus communis*, *J. sibirica*, *Pinus sibirica*, *Picea abies*. Last two species have breaking up areas. Birch (*Betula pendula*, *B. pubescens*, *B. tortuosa*), alder (*Alnus incana*) and aspen (*Populus tremula*) stands are more common among the deciduous ones. There are scattered stands of elm (*Ulmus laevis*, *Ulmus scabra*) and lime (*Tilia cordata*) in the southernmost part of Komi. Coniferous stands occupy 80 % of the forest covered area. The share of mature and over-mature stands is about 70 % of forests.

Siberian spruce (*Picea obovata*) and mixed spruce and birch (*Betula pubescens*) stands with dominance of Polytrichum and Sphagnum in the moss cover are widly spread in far north taiga sub-zone. Density of the canopy is low (up 0.3 to 0.5). Average height of trees is 8-15 m. Quality of stands is very low. Spruce stands are forming not only on the glay soils, but also on the sandy soils too. Areas of wetlands are large enough, rised bogs with pools and ridges as well as peat moss bogs are prevail. In the Pechora river basin willow and birch stands and meadows are distributing. Subzone of northern taiga is characterised by predominance of forest communities and decreasing of wetlands share. Stands are forming by Siberian spruce, Silver birch, Scots pine (*Pinus sylvestris*) with admixture of Siberian fir (*Abies sibirica*), Siberian pine (*Pinus sibirica*), Siberian larch (*Larix sibirica*), European aspen (*Populus tremula*). The density of canopy varies from 0.5 to 0.7 and average height of trees is 13-15 m. In the moss cover green mosses (*Pleurozium schreberi, Hylocomium splendens*) are prevail, in ground vegetation dwarf-shrubs (*Vaccinium uliginosum, Ledum palustre*) and sedge *Carex globularis* are dominate. In watershed territories spruce forests are wide spread. Pine stands of lichen and green moss types are distributed in flood plain terraces with good drainage and sandy soils. In the depressions of relief paludification is developing. In such sites green mosses are replaced by Sphagnum species. In ground vegetation *Vaccinium uliginosum*, *Ledum palustre*, *Chamaedaphne calyculata* are abundant. The main features of the northern taiga are fragments of tundra landscspes with prevailing of *Betula nana*, which are situated in the valleys of small rivers.

Below 63°N latitude sub-zone of middle taiga is appearing. In the sites with good drainage the spruce stands with admixure of birch, aspen, pine, rare fir, larch, Siberian pine of III-IV quality classes and canopy density 0.7-0.8 have been formed. Average heights of the tree’s trunks are 18-20 m. In the ground cover green mosses and dwarf-shrubs (*Vaccinium myrtillus*, *V. vitis-idaea*) are dominated. In the central part of watershed territiries green mosses is replaced by Sphagnum species. A lot of peat moss bogs are distributed in this territory. On most of them stands are absolutly absent. The main feature of middle taiga forests is low abundance of herbs and grasses. Pine forests are distributed on sandy flood plain terraces. In the ground cover of these communities the lichens or green mosses are prevailed. Meadows are distributed in the flooding areas along rivers only. Grasslands which are forming in the watershed territiries are unstable and very rapidly replaced by forests. Territory which is occupied by southern taiga is small enough. In this area spruce and mixed spruce and fir forests prevail. Good quality birch and aspen stands have been developed in the clear felling areas. Density of the canopy is over 0.8.

In the Urals and Timan Ridge different altitude belts are represented. Before altitude 450-660 m above see level mountain’s forests are prevail. In the highest altitudes tundra and goltzy are presented.

Productivity of forest ecosystems in the Komi Republic is not high and decreasing from south to north. Average growing stand volume is 200-400 m^3/ha in southern taiga sub-zone, 120-140 m^3/ha in northern and 60-90 m^3/ha in far northern one, respectively. Total standing volume of forests is 2.8 billion m^3. Average annual growth increment is about 1 m^3/ha. Average annual growth increment is about 2.2-2.4 m^3/ha in the southern taiga and 0.4-0.6 m^3/ha in the northern taiga.

Diversity of ecological conditions, for example, plain and flood plain terraces forests along rivers Pechora, Mezen, Vychegda, etc., pre-mountain and mountain stands of the Northern and Subpolar Urals and Timan Ridge, pre-tundra forests caused unique natural diversity of the forest genetic resources. That’s why the forest genetic resources of the Komi Republic are of great value for tree breeding. Most of forest communities are characterised by not only rich genetic diversity of tree species, but high diversity of rare, protected plants and herbs, lichens, fungi.

At the same time increasing of clear cutting area, rates of the territory anthropogenic transformation and some disastrous factors, such as fires, wind-falls, lead to decreasing areas of virgin and primary forests. The most serious and often disastrous changes in the composition, productivity and sustainability of forest ecosystems take place in the impact zones of large industry and transport installations. There are regions of oil and gas-extracting enterprises, mineral resources mining, areas along pipelines and etc. Disturbed natural forests are replaced by secondary birch and aspen stands. By this reason it is necessary to take all due measures for the conservation and effective using of the boreal taiga forests genetic resources.

The most effective approach to the protection of the taiga ecosystems is creation of a system of nature protected areas (NPA). Forest genetic research take a lot of time, so inventory and conservation of the genetic forest resources of the Komi Republic seems to been an urgent and priority goal.

As a result of research, which have actively developed in the Institute of Biology (Syktyvkar) from the end of 60's the System of NPA was organised in the Komi Republic. The major principles of NPA's net creation are protection of rare and typical ecosystems, conservation of rare and threatened species by protecting their habitats, development of ecotourism and recreation conditions.

At present the NPA System of the Komi Republic includes Pechoro-Ilych Preserve (700 thousand hectares), National Park «Ugyd Va» (about 2.0 million hectares), which are situated in the western macroslope of the Urals, and 256 reserves of different types: botanical, geological, landscape, etc. (Table 1). The total area of NPA is more than 6 million hectares (about 14.6% of whole area of Komi Republic). All kinds of the human activities are prohibited in the NPA's. In most of them monitoring of environment is organised. Information about NPA's is generalised not only in books, but also at the special map (scale 1:1 200 000).

For the conservation of forests in the frames of NPA System 38 reserves at the total area about 48 thousand hectares have been organised. The most valuable among them are NPA's, in which natural populations of Siberian pine (*Pinus sibirica*) are protected. Populations of this species in the Komi Republic are on the western boundary of the area. From the middle of 20th century cutting of Siberian pine trees were prohibited in the region, in 1998 this species was included into the «Red Data Book of the Komi Republic». Nowdays 6 reservs («zakazniks») and 14 nature monuments for the Siberian pine stands and single trees are founded at the total area about

Table 1. Nature protected areas of the Komi Republic

Type	Number	Square, ha	Share, %
Zapovednik	1	721322	1.73
buffer zone		497500	1.19
National park	1	1891701	4.58
Zakazniks			
Landscape	31	1289259	3.09
Forest	20	47475	0.11
floristic and meadow	9	24096	0.06
Bog	95	421824	1.01
Ichthyological	14	1114100	3.14
Ornithological	1	20000	0.05
Geological	1	2230	0.01
Nature monuments			
Forest	18	604	
floristic and meadow	11	584	
Bog	18	1676	
Water	11	49814	0.12
Geological	23	56	
Total	254	6082241	14.57

20000 ha. All these territories have been investigated and system of special actions for protection, support and restoration of Siberian pine populations is function.

Forest ecosystems dominate also at the territories of landscape reserves, Pechoro-Ilych Biosphere Zapovednic and National Park. In 1996 The National Park and Pechoro-Ilych Biosphere Zapovednic were included into The UNESCO List of World Heritage and named «Virgin Forests of Komi».

In the territory protected under UNESCO umbrella forest ecosystems are covered more than half of the total area. Forests have been developed without any anthropogenic impact. *Picea obovata* dominate in most of forest lanscapes. In mountain forests of the Northern Urals Siberian fir and Siberian pine are main stand forming trees also. In northern area the share of these species is being decreasing. At the same time Siberian larch trees and stands are appearing. Up to 64°N latitude *Larix sibirica* is forming mountain forests and rare stands. Square of the Scots pine forests is not large. Stands of *Pinus sylvestris* are situated in sandy soils of moraine plain and Pechora river terraces. In the pristine stands 3-5 generations of coniferous trees with different heights are fixed. Number of coniferous seedlings is enough to support their populations. Among deceduous trees common component of pristine stands is birch. In plain and premountain hills *Betula pubescens* widwly spread. In mountains it replaced by *B. tortuosa*. In flood plains and high mountains small plots of primary birch and willow stands are spread. After fires and windthrow coniferous forests is replaced by secondary birch and aspen stands. During last 200 years self-restoration of coniferous stands takes place.

The shrub layer in protected forest ecosystems has low density. It is formed by single low shrubs of *Sorbus aucuparia* and *Juniperus communis*, sometimes – *Duschekia fruticosa* and *Betula nana* also. Species number of ground cover in watershed forests is not high. More common dwarf-shrubs for boreal zone are: *Vaccinium myrtillus*, *V. vitis-idaea*, *V. uliginosum*, *Ledum palustre*, *Empetrum hermaphroditum.* Among herbaceous plants *Avenella flexuosa*, *Carex globularis*, *Equisetum sylvaticum* are usually presented. Under canopy of plain and pre-mountain stands cover of mosses and/or lichens is developed. Green mosses are common dominants. In mountains forest where tall-herbs are abundant moss cover is supressed.

Most of specially protected virgin forests are characterised by not only rich genetic diversity of trees, but high diversity of rare, protected plants and herbs, lichens and fungi, as well as animals and birds. For example, at the territories of zapovednik and national park are 172 of 253 protected vascular plant species (68 %) are presented. Some of them are included into the «Red Date Book of Russia» (*Calypso bulbosa*, *Castillea arctica* ssp. *vorkutensis*, *Cypripedium calceolus*, *Dactylorhiza traunsteineri*, *Schiverekia podolica*) and Red Lists of IUCN (*Cypripedium calceolus*). Few species are endemics (*Anemonastrum biarmiense*, *Gypsophila uralensis*, *Linum boreale*, *Thymus talijevii*, etc.).

60 species of protected mosses (39 %) are distributed in this territory, 5 species protectes in the whole Europe (*Dicranum viride, Schistostega pennata, Neckera pennata*, *Hydrohypnum norvegicum*, *Scleropodium arellanum*). There are a lot of rare lichens in the pristin forests (total 64 species). *Sphinctrina turbinata, Pannaria conoplea, Lobaria pilmonaria* are protected not only in the Komi Republic, but also in the whole Russia. *Lobaria hallii*, *Leptogium rivulare* are very rare in the whole world. Rare lichens *Pannaria confusa, Cheiromycina flabelliformis, Phaeophyscia hyrsuta, Chaenotheca subroscihda, Chaenotecopsis vainioana, Phaeocalicium praecedens* are unknown in the different regions of Russia. Most of common lichens, which are fixed in the virgin forests of the Komi Republic (species from Calicium, Cephelium, Chaenotheca genera, *Usnea longissima, Cetrelia olivetorum, Heterodermia speciosa,* etc.) are rare in northern European countries with similar nature conditions (Finland, Sweden). 24 species of rare fingi are fixed in protected forest areas, 4 species are included to the «Red Date Book of Russia» (*Tylopilus alutarius*,

Leccinium percandidum, *Grifola frondosa*, *Hericium coralloides*). Among rare species of birds are *Haliaeetus albicilla*, *Falco rusticolus*, *Pandion haliaetus*, *Aquila chrysaetos*, *Falco perigrinus.* All these species are included into the Red Lists of IUCN.

About 37 % of the total forest area in the Komi Republic belongs to the protected forests category. Among them most considerable areas are occupied by pre-tundra forests and protected belts along the rivers.

Establishment of genetic reserves (GR) system for the conservation genetic resources of main tree species has been started. The first batch of 38 GR at the total area about 28 thousand hectares were confirmed by Government Decision in 1990. Among GR are stands with high biological productivity and standing crop, which are characterised by intensive energy of growth and valuable features. Most of them are pristin stands common for the different taiga sub-zones. Conservation of genetic resources of trees is the most important goal of forest genetics and tree breeding. There are some data about forms diversity of coniferous and deciduous trees in the forests of the Komi Republic, but intraspecific variability of main stand-forming trees is not studied yet. Investigation of genetic variation of Siberian pine, Siberian fir, Siberian larch, which are in the natural limits of their areas in Komi and also primary Scots pine, Siberian spruce and mixed forests is very important. Valuable forms, which may be found in the process of this research, will be useful not only for the forest genetics and selection, but also for ornamental purposes. It is also necessary to study biological processes connected with their flowering and cone production and to develop citoembryological, morphological and physiological, as well as caryological research. The System of NPA is good field for such kind of investigations.

SIBERIAN LARCH FAMILY FIELD TRIAL: SURVIVAL AND HEIGHT GROWTH THREE GROWING SEASON AFTER PLANTING IN SWEDEN

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Abstract

Larch (*Larix sp.* Mill.) is a natural element of the boreal forest. Different species of *Larix* dominates the boreal forests of Eurasia. Larch also had a natural distribution in Scandinavia nine thousand years ago but disappeared for unknown reasons in prehistoric time. It was reintroduced by man in the 18th century and has for a long time attracted interest from forestry in Scandinavia. One major obstacle for reintroduction of Siberian larch in Scandinavia has been availability of seed sources for establishing test plantations. A co-operation between three Russian research institutes on one side and two organisations in Scandinavia on the other started in 1996. Seed was collected from 1005 individual trees distributed over 17 regions and 45 larch stands from Kamchatka in the east to Onega in the west. Seedlings were produced in 2002 and family field tests of 1005 families were established on three sites in Sweden. According to this report the best adaptation and productivity of Siberian larch growing in Sweden were found in larch provenances originating from western Russia with the exception that material of too northern origin do not perform well. Also the very fast growth and vitality of the eastern provenances are interesting. The long term vitality and growth of these provenances should be followed up carefully before any recommendations can be done.

Test plantations of this material were also established in Norway, Iceland, Finland, northwest Russia (Komi and Archangelsk), China, Japan, Alaska, Saskatchewan, Minnesota and Quebec.

Introduction

Larch (*Larix sp.* Mill.) is a natural element of the boreal forest. Different species of *Larix* dominates the boreal forests of Eurasia (Milyutin & Vishnevetskaya 1995, Putenikhin & Martinsson 1995, Abaimov et al. 1998). Larch also had a natural distribution in Scandinavia nine thousand years ago but disappeared for unknown reasons in prehistoric time (Kullman 1998). It was reintroduced by man in the 18th century and has for a long time attracted interest from forestry in Scandinavia (Martinsson 1992). One major obstacle has been availability of seed sources for establishing test plantations. A co-operation between four Russian research institutes on one side and two organisations in Scandinavia one in Japan and one in the USA on the other started in 1996 (Table 1).

Material

In phase 1 of the project seed was collected in 17 regions and 1005 individual trees from Kamchatka in the east to Onega in the west (Figure 1). A detailed report on the seed collection was published in 2002 (Abaimov et al. 2002). Material for the Swedish and Norwegian field experiments were brought up in 2002 in Alstahaug nursery in central Norway. In addition to this, seed of the same

Table 1. Participating organisations of phase 1 of the Russian-Scandinavian Larch Project – Seed Collection 1996-2001

Organisations	Countries
Swedish University of Agricultural Sciences, Umee	Sweden
Helegland Forest Society	Norway
V N Sukachev Institute of Forest, Krasnoyarsk	Russia
Arkhangelsk State Enginering University	Russia
Institute of Northern Biological Problems, Magadan	Russia
Bashkirian Botanical Garden Institute, Ufa	Russia
Akita Prefectural University, Noshiro	Japan
The University of Minnesota, Minneapolis	USA

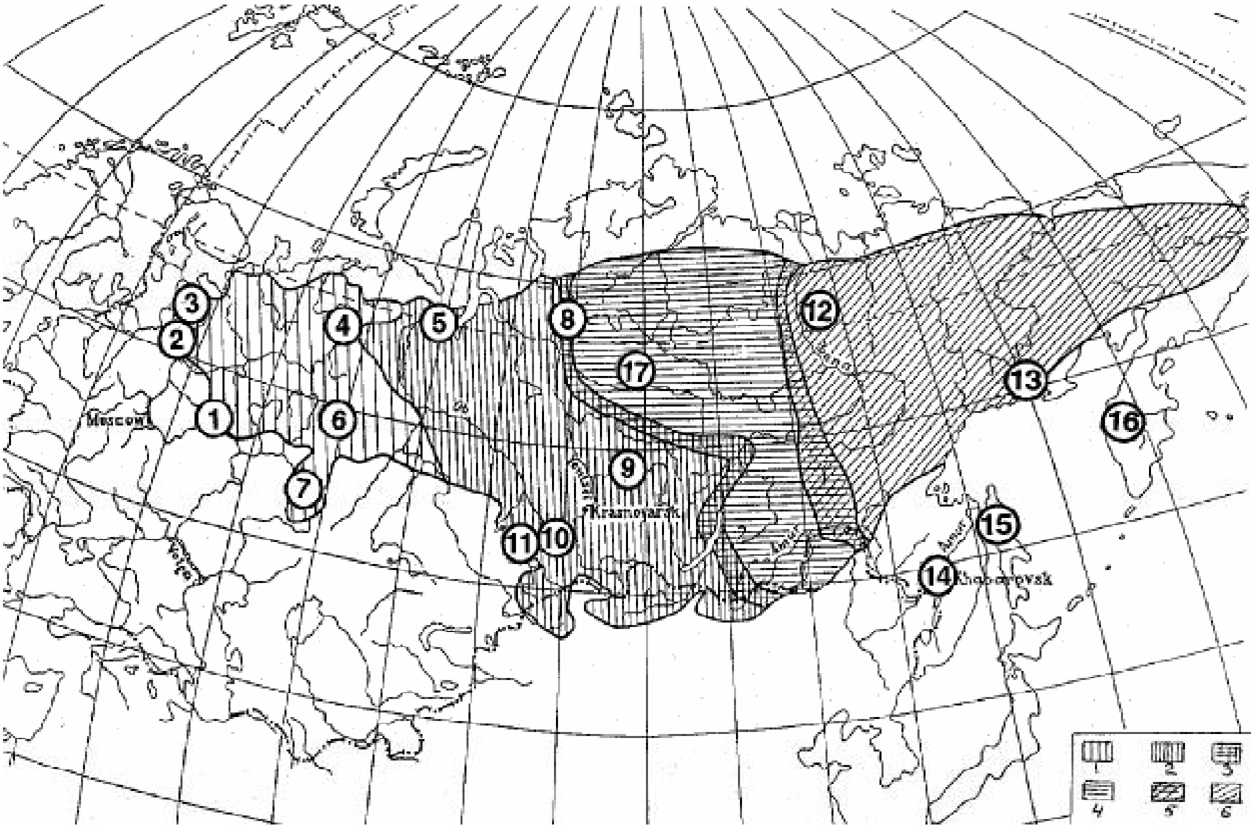

Figure 1. 17 seed collection regions in Russia. The six different patterns are indicating larch species and their hybridisation zones 1= *Larix sukaczewii* Dyl., 2=*Larix sibirica* Ledeb., 3=*Larix czekanowskii*, 4= *Larix gmelinii* Rupr., 5=*Larix gmelinii x Larix cajanderii*, 6= *Larix cajanderii* Mayr.

material was distributed to 11 more participants resulting in a circumpolar participation of this progeny series of Eurasian larch species (Table 2).

In the spring of 2003 1-year-old container-seedlings were planted on three main sites and ten small sites in Sweden. This report is describing the rate of survival in the three main sites after two growing seasons, i.e. October 2004.

The three main sites for field experiments in Sweden are located in Цsterbymo, Sдrna and Jдrvtrдsk. The properties of the three sites are explained in Table 3.

Each experimental locality was established as 60 sub-plots of 30Ч40 m on each site. 300 seedlings, representing one region, were planted in each subplot with spacing 2Ч2 m. One family (progeny of one selected tree) was represented by 3 or 4 seedlings. All regions were replicated

Table 2. Participants of the International Progeny test of Eurasian Larch Species

Country/province	Organisation	Contact person
Norway	Helgeland Forest Society, Mosjцen	Jaap Buitink, Gisle Skaaret
Sweden	SLU; Umee	Owe Martinsson
Arkhangelsk	NFRI, Arkhangelsk	Natalia Demidova, Vladimir Barzut
Komi	Komi Science Centre, Syktyvkar	Aleksey Fedorkov
Japan	Kyushu University	Katsuhiko Takata
China	Beijing University, Beijing	Shen Xi Huan
Alaska	U S Forest Service, Alaska, Fairbanks	John Alden
Saskachewan	Agriculture and Agri-Food Canada, Indian Head	Bill Schroeder
Minnesota	University of Minnesota	Andrew David
Quebec	Ministry of Forest	Martin Perron
Iceland	Iceland Forest Service	Thrцstur Eysteinsson
France	INRA,Orleans	Luc Рвques

Table 3. Localities and site properties of the three main test sites in Sweden

Locality	Latitude, N	Longitude	Altitude, m	Topography	Soil
Цsterbymo	57є47’	15є37’	250	Slight southern slope	Gravelly morain
Sдrna	61є31’	13є00’	540	Slight western slope	Stony morain
Jдrvtrдsk	65є11’	19є31’	410	Steep eastern slope	Sandy morain

three times in three sub-plots. Three commercial Swedish and Finnish seed sources and two Russian collections (No 18-22) were included as standards in the experiments. All seed sources and their origins are explained in Table 4.

Results and discussion

In October 2005, i. e. three growing seasons after planting in the field, survival rate and tree heights were recorded of all trees in the three sites (Table 5).

Survival

The average survival rate three growing seasons after plantation was between 65 and 80 %. The overall survival was best in the northernmost site Jдrvtrдsk, 80 %. The lowest survival was in Sдrna, 65 %. In the southern site Цsterbymo several of the most northern and most continental provenances have very low survival rate. The opposite situation does not seem to occur in Jдrvtrдsk, where the southern provenances do not suffer so much from the very great moving to the north. Even the hybrid larch Maglehem and the provenance from Irkutsk can survive in Jдrvtrдsk. However, the period is still too short for this estimation, only three growing seasons after plantation.

Height growth

Цsterbymo

The most fast growing larch trees are to be found in Цsterbymo. The highest individual tree here is a hybrid larch from Maglehem, 285 cm. However, the hybrid larch from Maglehem do not have the tallest mean height. The tallest five mean heights are: 14 Chabarovsk, 15 Sachalin, 21 Maglehem, 1 Nishnij Novgorod and 7 Ufa. The most maladapted here are 12 Yakutia and 11 Altai.

Table 4. Seed sources and their origins in the three Swedish main test sites, Цsterbymo, Sдrna and Jдrvtrдsk

Number of region	Name of region	Site	Nearest village	Latitude, N	Longitude, E	Elevation, m	Number of selected seed trees	Species of larch
1	Nizhnij Novgorod	A	Vetluga	57є30'	45є10'	-	7	*Larix sukaczewii*
		B	"	57є30'	45є10'		29	*Larix sukaczewii*
		C	"	57є30'	45є10'		17	*Larix sukaczewii*
		D	"	57є30'	45є10'		13	*Larix sukaczewii*
2	Plesetsk	A	Emtsa	63є05'	40є21'	100	20	*Larix sukaczewii*
		B	Korasi	63є00'	40є25'	120	25	*Larix sukaczewii*
		C	Shelekса	62є09'	40є19'	120	18	*Larix sukaczewii*
3	Onega	A	Leskhoz Onezhskii	64є01'	38є15'	110	7	*Larix sukaczewii*
4	Petchora	A	Usinsk	66є00'	57є48'		64	*Larix sukaczewii*
5	Salechard	A	Beloyarsk	63є41'	66є44'	60	20	*Larix sukaczewii*
		B	Kharp	66є56'	65є45'	130	20	*Larix sukaczewii*
		C	Labytnangi	66є28'	66є39'	40	20	*Larix sukaczewii*
6	Perm'	A	Okhansk, Yugo-Kamsky	57є18'	55є27'	160	20	*Larix sukaczewii*
		B	Nyazepetrovsk, Uzaim	56є09'	59є32'	460	20	*Larix sukaczewii*
		C	Kyshtym	55є43'	60є27'	480	20	*Larix sukaczewii*
		D	Nizhnij Tagil	57є30'	59є48'	350	12	*Larix sukaczewii*
		E	Sotrino	59є27'	60є59'	110	Mix of 30 trees	*Larix sukaczewii*
7	Ufa	A	Maginsk	55є45'	56є58'	370	20 + mix of 10	*Larix sukaczewii*
		B	Miass	54є58'	60є07'	380	20 + mix of 10	*Larix sukaczewii*
		C	Zlatoust	55є07'	59є30'	600	20	*Larix sukaczewii*
		D	Ziliar	52є13'	57є25'	550	Mix of 10 trees	*Larix sukaczewii*
		E	Bolshoy Iremel	54є33'	58є57'	1200	10	*Larix sukaczewii*
8	Norilsk (vacant)							*Larix sibirica*
9	Boguchany	A	Boguchany	58є39'	97є30'	158	27	*Larix sibirica*
		B	Karabula	"	"	96	25	*Larix sibirica*
		C		"	"	--	23	*Larix sibirica*
10	Novokuznetsk	A		53є48'	88є00'	mountain	20	*Larix sibirica*
		B		54є12'	88є42'	"	20	*Larix sibirica*
		C		52є48'	87є24'		20	*Larix sibirica*

11	Altai	A	Kosh-Agash Tenedu	50є16'	87є54'	1630	26	*Larix sibirica*
		B	Kosh-Agash Karnagalu	50є12'	87є47'	1580	26	*Larix sibirica*
		C	Kosh-Agash, Turgune	50є14,5'	87є3'	1630	26	*Larix sibirica*
12	Yakutiya	A	Zhigansk	66є45,5'	123є22'	70	20	*Larix cajanderi*
		B	Zhigansk	66є51'	123є21'	80	20	*Larix cajanderi*
		C	Zhigansk	66є45'	123є22'	90	20	*Larix cajanderi*
13	Magadan	A		59є30'	150є15'	60	25	*Larix cajanderi*
		B		59є20'	152є30'	100	25	*Larix cajanderi*
		C		59є30'	148є30'	80	25	*Larix cajanderi*
14	Khabarovsk	A	Vaninskyi	49є08'	149є00'	90	20	*Larix gmelinii var. olgensis*
		B	Vaninskyi	49є09'	149є00'	100	20	*Larix gmelinii var. olgensis*
		C	Vaninskyi	49є12'	149є00'	125	20	*Larix gmelinii var. olgensis*
15	Sachalin (missing data)						60	*Larix gmelinii var. japonica*
16	Kamchatka (missing data)						60	*Larix gmelinii var. kamchatica*
17	Evenkiya	A	Tura	64є19'	100є13'	285	25	*Larix gmelinii*
		B	Tura	64 є19'	100є14'	310	25	*Larix gmelinii*
		C	Tura	64 є17'	100є16'	270	25	*Larix gmelinii*
18	Lassnmaa		Seed orchard (Fi)					*Larix sukaczewii*
19	Ivanov		Seed stand (Ru)					*Larix sukaczewii*
20	Irkutsk		Seed stand (Ru)					*Larix sibirica*
21	Maglehem		Seed orchard (S)	55 є46'	14є10'	20		*Larix eurolepis*
22	Oesteg		Seed orchard (S)	63 є48'	20є16'	10		*Larix sukaczewii*

Table 5. Initially planted seedlings, survival and mean tree height three growing seasons after planting

Provenance	Цsterbymo			Jдrvtrдsk			Sдrna		
	N of seedlings	Survival %	Mean height, cm	N of seedlings	Survival %	Mean height, cm	N of seedlings	Survival %	Mean height, cm
1 Nishnij Novgorod	900	94,4	119	900	81,7	46	900	60,7	52
2 Plesetsk	900	95,7	80	900	81,9	51	900	75,2	48
3 Onega	524	89,1	66	524	85,3	53	524	79,6	44
4 Petchora	900	51,7	31	900	81,1	42	900	79,6	32
5 Salechard	900	26,9	36	900	83,8	41	900	71,7	26
6 Perm	900	95,9	96	900	76,6	44	900	66,8	53
7 Ufa	900	94,8	117	900	84	46	900	69,1	49
9 Boguchany	900	60,9	78	900	82,4	50	900	73,3	46
10 Novokuznetsk	900	80,7	81	900	84,7	53	900	68,2	46
11 Altai	900	9,6	47	900	81,7	36	900	68,3	38
12 Yakutiya	900	0	0	900	62,7	40	900	36,6	22
13 Magadan	900	91,1	90	900	86,2	58	900	66,6	42
14 Chabarovsk	900	94,1	147	900	77,3	66	900	37,4	49
15 Sachalin	900	94,9	141	900	79,7	61	900	67,7	59
16 Kamchatcka	900	90,6	76	900	80,2	44	900	75,4	43
17 Evenkia	-	-	-	-	-	-	473	49,3	29
18 Lassinmaa	900	91,7	75	885	84,6	54	900	87,6	52
19 Ivanov	823	96,1	112	900	85,7	54	900	73,6	50
20 Irkutsk	900	59,0	70	448	81,9	46	450	50,2	50
21 Maglehem	900	82,4	138	448	61,8	41	450	23,8	47
22 Цstteg	900	85,7	71	900	81,2	51	900	61,9	43
	17547	73,8	96	16705	80,6	49	17197	65,3	44

S∂rna

The over all mean height in Sдrna three growing season after planting is 44 cm. The four best growing provenances in Sдrna are Nishnij Novgorod, 6 Perm, 15 Sachalin and 18 Lassinmaa.

The very northern provenances 12 Yakutia, 5 Salechard demonstrate the lowest mean height.

J∂rvtr∂sk

Here the over all result is the most even. Most provenances seem to have a relatively good growth and survival here, also the most southern origins. The five fastest growing provenances are: 14 Chabarovsk, 15 Sachalin, 13 Magadan, 18 Lassinmaa and 19 Ivanov. The most maladapted are: 11 Altai, 12 Yakutia and 21 Maglehem.

Conclusion

Only three growing seasons is a too short period for estimation of survival, growth rate and adaptation to the three sites. The survival rate is so far very good in the most southern and the most northern sites. In Sдrna the survival is not acceptable and one of the reasons is the plantation which was rather often done outside the site preparation. Another reason may be the grazing cattle since the fence around the area was not complete until autumn 2005.

Larch from 12 Yakutiya and 17 Evenkia are adapted to a more continental climate than anywhere in Sweden and show bad adaptation in Sweden. The very fast growth and vitality of the eastern provenances are interesting. The long term vitality and fast growth of these provenances should be followed up carefully before any recommendations can be done.

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SCOTS PINE BREEDING IN POLAND

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Abstract

The aim of this paper is to present data from all provenances and progeny experiments with Polish origins of Scots pine with emphasis to evaluation. It was considered that last data (both these published and not published yet), should be provided by researchers taking care on particular plots. For data from each experimental plot it was calculated average and their standard deviation. The value for provenance was expressed as deviation from average value in standard deviation unit. The proveniences are grouped under the regions of provenances. Results were calculated first for the provenance and then for the region of provenance. The calculations were performed for Polish provenances only, skipping foreign origins represented on some experimental plots.

In this comparison, 27 experimental plots with 76 proveniences from 41 regions were tested (including 21 maternal regions designated for pine). Provenance regions (maternal for pine) nos. 105, 107, 302 and 403 were not represented in investigations. The best origins of pine under the quantity traits grow in western Poland. From this part of the country only provenance from Bystrzyca Kłodzka representing seed region no 702 is growing worse. The proveniences from the south-eastern part of Poland regions nos. 605, 606 and 661 also are growing worse than the average. Much better are growing pine trees from Wyszkow (seed region 402) and Parciaki (region 451). Results above the average belong to pine trees from regions 305, 356 and 157. Results of Pine from region 205, Tabyrz (106) and Mazurian (206) are close to the average or somewhat below. Pine trees from Supraњl (207) show results above average. On the other hand, pine from mountain-foot region (Grybow and Nowy Targ) performs the worst in all experimental plots.

The selection in Poland based on choice of whole populations for reproduction assures larger genetic variability and assures also good economic effects.

Introduction

Scots pine is the most important forest tree species in Poland. It is forming stands both on dry and moist soils. Scots pine grows also on very poor and on more fertile soils. It results in large areas of lowlands occupied by Scots pine (accounting for 69.3% of forest area when considered along with larch).

The pine is valuable also in terms of wood quality. Large possibilities of Scots pine selection exist because of high population diversity. Many experiments were established to recognize the genetic value of different population of pine and to select the best for forest practice.

So far results of these experiments are an object of many publications concerning mainly single experimental plots. These experiments contain different sets of the population. Measurements concern different features and they are being made in the different age. So the overall assessment of results is very difficult and every result has a different value depending on quantity of experimental plots and traits it concerns.

Overall provenance comparison experiments with the Scots pine in Poland were done by Giertych (1996). These results are more and more reliable because they are coming from more and more old plots and they are including more origins which were included in newly established experiments. The aim of this paper is to evaluate the data from all experimental plots with the Scots pine in Poland.

Material and method

Accessible results from experimental plots are an input. I considered latest data both the ones published as well as not published still but made available by researchers taking care to the experiments. Data sources are passed in notes to Table 1. For each experimental plot an average and a standard deviation were estimated. Value of the traits for the provenance was expressed as deviation from the average in standard deviation units. Standardized, comparable data are presented in Table 1. Provenances are grouped in terms of regions of the provenances, in agreement with the directive of Environmental Ministry on March 9, 2004 (DZ.U. No. 67, 621). Results were averaged at first for the provenance, and then for the region of the provenance. Average result for the region of the provenance is shown on Figure 1. The calculations were made only for Polish origins foreign provenances represented on some experimental plots were not analyzed.

Results

The grow traits data from all experimental plots with Scots pine in Poland are presented in Table 1. It comes from 27 experimental plots with 76 provenience tested, from 41 provenance regions, including 21 maternal regions for pine. Maternal seed regions (105, 107, 302 and 403) were not represented in investigations. The some well-known from literature proveniences were sampled back several times so they are represented more then in one experiment. Mean value for the all regions of provenance in the Figure 1 is marked with solid line and that means that diagrams directed in up means positive values, and directed in bottom negative. The averaged results for all investigated regions of provenances show that the best origins of pine in terms of grow are located in western Poland. From this part of the country only provenance from Bystrzyca Kłodzka representing seed region no 702 is worse then general mean. The provenances from the south-eastern part of Poland (regions 605, 606 and 661) also grow worse than the average, but the results comes mainly from the plots located in different provenance regions. Only one experimental plot (Janyw Lubelski) is located in this region of the country. Pine from Wyszkow (seed region 402) and Parciaki (region 451) grow well. Above the average are also pine from regions 305, 356 and 157. Pine trees from region 205, Tabyrz (106) and Mazurian (206) reach results close to the average or somewhat below. From the north-east Polish proveniences good growing pine from Supraњl (207). Pine from mountain-foot region (Grybow and from Nowy Targ) performs worst at all experimental plots.

The detail data concerned growth of the particular provenances can be found in table 1. Analyzing the growth of pine from Rychtal it can be concluded, that similar to Giertych (1996) paper it result almost everywhere with better growth. Only in experiment IBL 1987 on plot in Wyszkow and Murowana Goњlina as well as on experiment of ID-PAN in Lubien it performs slightly worse than general mean value. Pine from Bolewice is growing well in almost all studied locations except of few plots only. Pine from Taborz in this comparison falls out similarly to recapitulation made by Giertych (1996). It achieves result about the average, except of few negative one.

Table 1. Data concerning growth traits from Polish Scots pine experimental plots in standard deviation units (for data source see remarks)

Experimental plots localization		Average	Number of provenances	Provenance mean	Jabłonna	Jabłonna	Sękocin	Bliżyn	Siemianice	Gryfyw	Lipce R.	Bliżyn	Miłomłyn	Wyszkyw	Kyrnik	Czapury	P. Niepołom.	Supraśl	Rogyw	Wyszkyw	Murowana G.	Mielki	Chrosno	Lubień	Kyrnik	Kyrnik	Janyw Lub.	Stepnica	Supraśl	Kyrnik	Zielonka
Experiment no					1	2	3	3	3	3	3	4	4	5	5	5	5	5	5	6	6	7	7	8	9	10	10	10	10	11	12
Trait					M	M	PP	M	M	D	D	D	D	PP	H	H	H	PP	H	M	PP	D	D	M	M	PP	PP	PP	PP	D	M
Age					40	40	37	37	30	39	38	19	19	20	13	5	8	15	16	15	15	10	10	69	35	34	34	34	34	26	25
Author					1	1	1	1	2	14	18	3	3	1	6	8	9	10	2	1	12	1	1	7	6	4	4	4	4	1	11
Reg	Provenance	M	N	P	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
101	Goleniyw	0,33	6	0,28																0,71	-0,16										
	Stepnica			0,35																						0,45	-0,65	0,69	0,71		
104	Smolarz	0,81	2	0,81																0,49	1,13										
106	Kudypy	-0,27	32	-0,91																		-0,76	-1,05								
	Miłomłyn			-0,47										0,15	-0,88	-0,50	-1,32	0,79	-1,68												
	Miłomłyn											-0,02	-0,04																		
	Miłomłyn																					-0,38	-1,05								
	Stara Jab.			-0,88																		-0,86	-1,02								
	Tabyrz			0,02			0,81	-0,63	0,27	-0,14	-0,39																				
	Tabyrz					-1,30																									
	Tabyrz																			0,17	0,56										
	Tabyrz																					0,11	-0,44								
	Tabyrz																									-0,12	1,46	-0,76	1,46		
	Tabyrz																														-0,83
	Tarda			-0,12																		-0,21	-0,03								
152	Smołdzino	-0,79	4	-0,79																						-2,29	-0,22	-0,41	-0,26		
153	Karsko	0,94	5	0,94			0,46		0,60	1,68	0,92																				
	Karsko																														0,69
167	Stary Dzie.	0,28	6	0,20																		-0,09	0,48								
	Susz			1,30																		1,32	1,29								
	Jeziorno			-0,65																		-0,55	-0,78								
204	Głęboki B.	-0,52	11	-0,88	-0,86																										
	Rozpuda			-0,71			-0,57	-0,75	-0,28	0,13	-1,19																				
	Rozpuda				-1,59																										
	Serwy			-0,16																						-0,37	-0,32	-0,42	0,49		

Continuation of Table 1.

Reg	Provenance	M	N	P	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
205	Dłużek	-0,08	17	-0,21			-0,08	0,11	-0,18	0,79	0,16																				
	Dłużek				-0,12																										
	Dłużek					0,04																									
	Dłużek																									-0,77	-0,69	-1,44	-1,14		
	Dłużek																														0,80
	Jagiełek			1,69																		1,81	1,77								
	Nowe Ram.			-0,76																		-0,76									
	Olsztynek			-0,84																		-1,55	-0,14								
206	Krutyń	0,02	23	0,47																						1,19	-0,70	-0,27	1,65		
	Ruciane			0,20			0,32	-0,44	-0,49	1,78	-0,80																				
	Ruciane																			1,11	-0,61										
	Ruciane											-0,12	-0,08																		
	Ruciane																									1,19	0,51	0,80	0,82		
	Ruciane																							-0,99							
	Spychowo			-1,85										-1,85																	
	Wilcze Bag.			-0,56																						-0,41	-1,20	-0,72	0,06		
207	Supraśl	0,26	16	0,26			0,53	0,82	0,50	0,21	-0,38																				
	Supraśl													-0,88	0,78	-0,39	1,45	0,96	0,13												
	Supraśl											-0,14	-0,08																		
	Supraśl																									-0,39	0,18	0,15	-0,03		
	Supraśl																														1,22
208	Białowieża	-0,25	12	-0,28																										-0,26	
	Hajnówka			-0,58																-0,76	-0,68										
	Hajnówka																													-0,30	
	Starzyna			-0,67			-0,62	-1,28	-0,17	-0,47	-0,39																				
	Zwierzyniec Białowieski			0,63																						0,20		0,61	1,17		
303	Radawnica	0,43	7	0,49	-0,45																										
	Radawnica																									-0,40	0,11	1,05	1,42		
303	Radawnica																														1,23
	Złotów			0,03																					0,03						
305	Bartel W.	0,36	17	1,17	1,29																										
	Bartel W.																														1,04
	Czersk			-0,22																						-1,65	-0,01	1,40	-0,63		
	Lipowa			0,40			0,25	0,49	0,25	0,69	0,40																				

Continuation of Table 1.

Reg	Provenance	M	N	P	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
305	Lipowa				1,31																										
	Lipowa																			-0,29	0,69										
	Lipowa																														-0,18
	Woziwoda			0,54	0,11																										
	Woziwoda																														0,97
306	Bolewice	0,44	19	0,44			0,58	1,10	0,55	-0,83	2,41																				
	Bolewice													0,58			-0,11	-0,87	0,85												
	Bolewice					0,71																									
	Bolewice																				1,36										
	Bolewice											0,07	0,13																		
	Bolewice																													0,57	
	Bolewice																									0,71	0,30	0,34	-0,66		
	Bolewice																								0,36						
307	Gubin	0,28	10	0,28			0,68	0,18	0,78	-1,88	0,41																				
	Gubin					1,51																									
	Gubin																			0,82	0,43										
	Gubin											0,00	0,13																		
353	Lubniewice	0,97	4	0,97																						2,04	0,64	1,88	-0,87		
356	Brodnica	0,10	2	0,10																1,16	-0,95										
354	Karczma B.	0,93	2	1,23																										1,23	
	Kyrnik			0,64																						0,64					
401	Myszyniec	-0,07	4	-0,07																						0,22	0,60	0,11	-1,22		
402	Jegiel	0,62	8	0,36			-0,08	1,04	0,25	0,09	0,48																				
	Wyszków			1,06										0,70																	
	Wyszków																			2,22	0,27										
404	Parczew	0,22	5	0,22																						0,87	0,53	0,19	0,86		
	Parczew																														-1,34
406	Kam. PN	0,32	4	0,32																						1,20	-0,30	-0,02	0,41		
451	Parciaki	0,20	2	0,20																0,32	0,08										
453	Głuchów	-0,67	4	-0,72				-1,62			0,08																				
	Łąck			-0,82																-1,13	-0,10										
454	Jabłonna	-0,68	4	-0,16	0,33																										
	Jabłonna					-0,65																									
	Zielonka			-1,20																	-0,94										

Continuation of Table 1.

Reg	Provenance	M	N	P	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
454	Zielonka																														-1,47
456	Łomża	-0,15	9	-0,37																						-0,80	-0,60	0,11	-0,21		
	Nurzec			0,02																						-0,17	0,31	-0,12	0,80		
	Nurzec																								-0,22						
501	Rychtal	0,54	20	0,54			1,05	1,01	1,83	0,77	0,48																				
	Rychtal													0,44	0,93	1,49	-0,27	0,37	0,04												
	Rychtal																			-0,28	-0,18										
	Rychtal											0,30	0,11																		
	Rychtal																													0,45	
	Rychtal																								0,53						
	Rychtal																							-0,02							
	Rychtal																					0,77	0,98								
502	Wołczyn	1,07	1	1,07																					1,07						
503	Prószków	1,08	7	1,08																0,21	0,46										
	Prószków																									1,41	1,36	1,62	1,88		
	Prószków																								0,69						
504	Brody	0,46	7	0,67																						0,82	1,40	1,34	-0,20		
	Brody																							1,01							
	Węgliniec			-0,56																-0,50	-0,65										
553	Milicz	1,04	8	1,06																0,30	1,65										
	Kubryk			1,02																						0,86	1,80	0,57	0,70		
601	Łęczno	-0,21	21	-0,79																					-0,79						
	Maszcze			-0,81																											-0,81
	Spała			-0,13			0,47	0,81	-0,08	-0,90	0,26																				
601	Spała													0,86	-1,05	-0,80	0,25	-1,26	0,67												
	Spała					-0,31																									
	Spała											0,03	-0,02																		
	Spała																									-0,40	-0,22	-0,42	0,05		
	Spała																														-0,95
602	Pionki	0,38	4	0,38																						0,74	1,20	0,55	-0,95		
604	Ratajе	-0,60	6	-0,68																						-0,62	0,32	-0,60	-1,88		
	Suchedniów			-0,32																-0,07	-0,66										
605	Zwierzyniec Lubelski	-1,18	4	-1,18																						-1,80	-0,81	-0,73	-1,64		

End of Table 1.

Reg	Provenance	M	N	P	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
606	Janów Lub.	-0,51	15	-0,51			-0,70	0,65	-1,08	-0,64	-0,18																				
	Janów Lub.											-0,11	-0,11																		
	Janów Lub.																									-0,79	-0,39	-0,58	-1,02		
	Janów Lub.																								-1,97						
	Janów Lub.																														-0,56
	Józefów			-0,24																-0,62	0,34										
607	Niepołomice	-0,62	2	-0,62																-1,67	0,64										
681	Oleszyce	-0,55	4	-0,55																						-0,57	-0,31	-0,41	-0,93		
702	Bystrzyca Kłodzka	-0,71	6	-0,71																0,27	-0,03										
	Bystrzyca Kłodzka																									-0,76	-1,66	-1,19	-0,69		
803	Pienińki PN	-1,52	4	-2,11																						-0,26	-2,92	-3,11			
	Piwniczna			0,22						0,22																					
805	Nowy Targ	-1,85	6	-1,85			-3,10	-1,80	-2,60	1,09	-2,23																				
	Nowy Targ																			-2,05	-3,05										
	Nowy Targ																													-1,67	
Number of provenances					5	6	15	15	15	16	16	8	8	7	4	4	5	5	5	20	22	12	11	3	8	31	29	30	28	8	13

Remarks to table 1.

Standardized data from Scots pine experimental plots the last measurements of growing traits. Experiments names coding: 1 – IBL 1962, 2- IBL 1964, 3- IBL 1966, 4 – IBL 1977, 5 – IUFRO 1982, 6- IBL 1987, 7 – IBL 1994, 8 – IUFRO 1938, 9 – ID PAN 1963, 10 - ID PAN 1967, 11 - ID PAN 1977, 12 – AR Poznań 1960. Traits: M – volume m^3/ha, PP – DBH cross sections area m^2/ha, D – DBH , W- height. Source of data: 1 – (Kowalczyk 2004), 2 – (Kowalczyk et al. 2000), 3 – (Korczyk 2002), 4 – (Rożkowski 2005), 5 – (Rożkowski 1999), 6 – (Oleksyn et al. 1999), 7- (Chmura 2000), 8 – (Oleksyn 1988), 9 - (Oleksyn, Rachwał 1994), 10 – (Barzdajn 2000), 11 – (Rzeźnik 1989), 12 – (Barzdajn 2003), 13 – (Żybura 2003), 14 – (Sabor 2003).

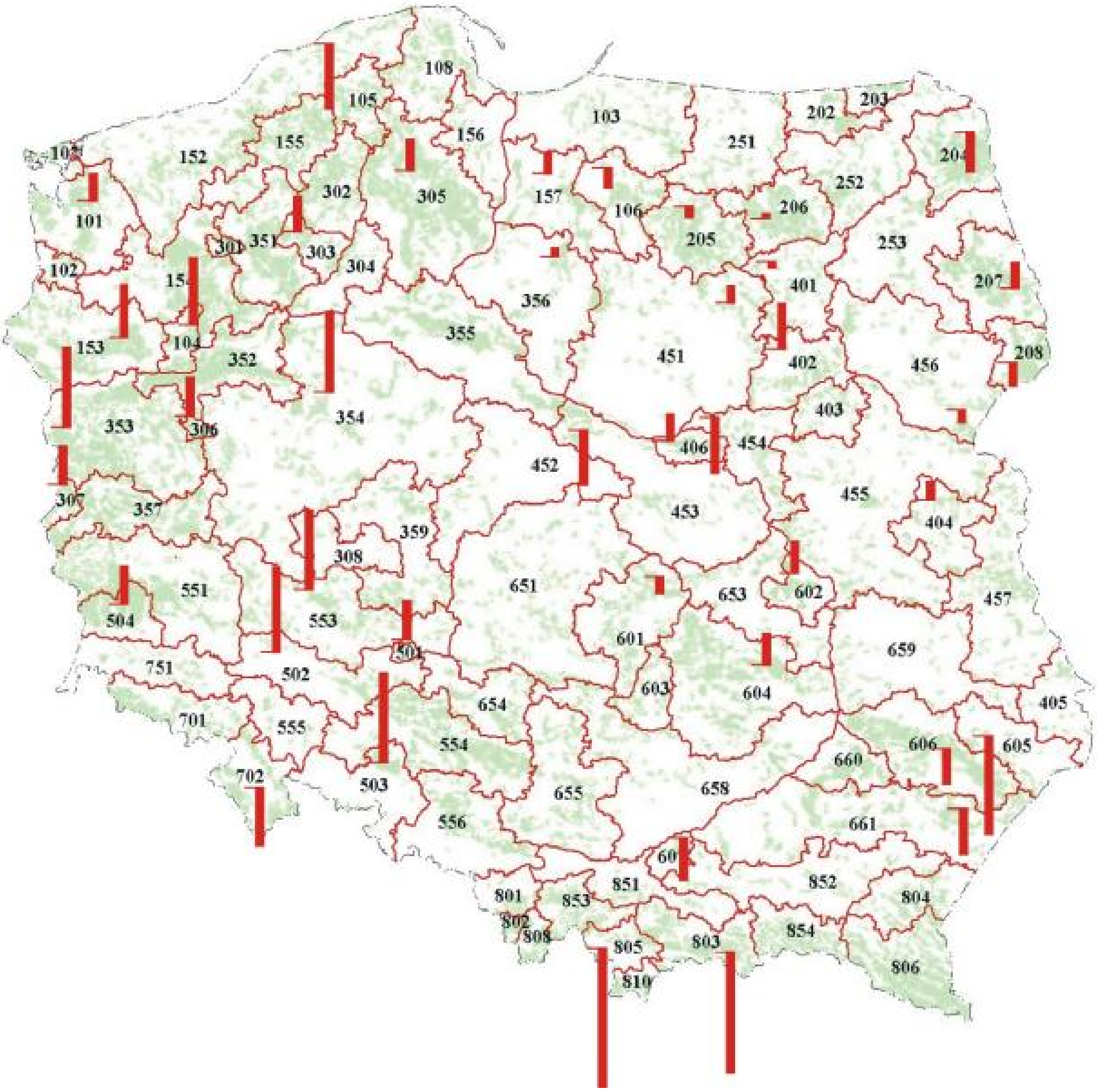

Figure 1. Average value in standards deviations unit of Scots pine Polish provenances.

Discussion

Presented results of the Scots pine growth analyses are giving us the general image of variability of Polish provenances. However this image is painted with the thick brush. That summarizing is useful in the scale of the all country. The value of presented results is variable. It depends on the trait, the age of analyzed trees and number and of experimental plots locations. When we look from the present perspective methodology of some experiments is not free from mistakes. The seeds sampling method for some experiments could not be made in the representative way. Sometimes seeds were collected only from a few trees. Also it happens that detailed information about the origin of tested provenance is not available. It results in difficulties to relate results to particular forest stands.

On the other hand however, it is possible to separate provenance regions where Scots pine is characterized with good growth confirmed on several experimental plots. Sometimes the best provenances characterized with good growth traits, the same time have bad quality. For example the pine from Bolewice in Sκkocin experimental plots (IBL 1966) is the best with volume and the same time characterize the worst stem straitens (Kowalczyk et al. 2000). It is also not possible to estimate breeding value of provenance taking into account only one trait. The research on pine provenance evaluation was indicated by many authors (Giertych 1993, Shutyaev, Giertych 2000, Stephan, Liesebach 1996, Sabor 1994). However the whole sense of provenance experiments concerns on looking for better foreign populations compare to local. Usually such populations have been possible to find (Giertych 1993).

Scots pine selection in Poland is based mostly on population selection. It assures lower genetic gain than selection based on family selection, but in the some way is more secure, providing bigger lever of genetic variability.

Conclusion

- In Poland until now, 27 experimental plots with Scots pine were established, with 76 proveniences tested from 41 regions of provenances.
- The best origins of pine concerning the quantity traits grow in western Poland.
- The detail data concerned grows of the particular provenances can be fond in table 1.

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PROGENY GROWTH CHARACTERISTICS IN 34-YEAR-OLD GEOGRAPHICAL TRIAL PLANTATIONS OF SCOTS PINE (*PINUS SYLVESTRIS*) AT JДRVSELJA, ESTONIA

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Abstract

This paper analyses height and diameter increments in 33-35-year old pine plantations established at Jдrvselja, Estonia, using seeds from 34 different regions of the former Soviet Union. The northernmost seeds were obtained from Arkhangelsk Province (lat.63°N), the southernmost from Georgia (lat.42°N), the westernmost from Lithuania and Lviv (long.24-27°E) and the easternmost from Khabarovsk (long.126°E). It appeared that height increment differed considerably for trees of different geographical provenance. The shortest were pines grown from seeds originating from Georgia (average height 12.5 m at 33.5 years of age) and the tallest were those grown from seeds collected in Lithuania (20.1 m), in Latvia (19.6 m) and in Mari El Republic (20.0 m). The breast height diameter of pines growing in Estonia depended on the north latitude of the seed collection site: the higher the latitude the smaller the diameter. The influence of the east longitude of the seed collection site on progeny height increment proved insignificant. Apart from north latitude, progeny height increment also depended on the local conditions of the seed collection sites.

Introduction

Scots pine (*Pinus sylvestris*) grows on a large area in Europe and Asia. Compared to other pine species the natural habitat of Scots pine is the most extensive, reaching northwest Norway in the north, the British Isles in the west, the Pyrenees in the south and the Sea of Okhotsk in the east (Laas, 1987). Within this extensive habitat, the characteristics of the species evidence a high geographical variability, which must be taken into account in seed transferrals from one region to another. On account of its high intraspecific variability and extensive geographical spread a number of forms are distinguished in Scots pine based on crown shape, stem height, bark, needle length, cone size and other properties.

More information about the variability of different pine populations can be obtained from provenance trials, which are of high importance in forest tree breeding. Eriksson and Ekberg (2001) define provenance as «a group of populations or individuals occurring within the same species and originating from a more or less strictly specified geographical region». Provenance trials are designed to compare the development of trees growing on identical territorial conditions but having different provenances. The primary objective of provenance research is to identify the provenances that are the most productive on a particular growth site. As soon as the best provenances are identified in the trials it is possible to select the best stands for seed collection in the respective geographical regions.

In the provenance trials of Anderson et al. (2003) pine height evidenced no significant dependence on growth site conditions, seedling transfer distance or tree age. Research results from Lithuania (Danusevиius, 2000) show that Scots pine local populations were more tolerant towards extreme environmental conditions and towards damage than introduced pines. Scots pine plantations grown from seed brought in from more southerly regions, particularly those of forest-steppe, had higher growth rates than local provenances yet evidenced lower viability, were knottier and had more crooked stems. Provenances more to the north had earlier growth seasons, were shorter by height and grew shorter needles, narrower crowns and fine twigs. Abraitis and Eriksson (1996) observed that populations of northerly provenances always exhibited slower growth than those originating from southerly regions. Nevertheless, some provenances that were introduced, mostly from the Baltic region, grew better than local ones. However, they were more vulnerable to the environmental stress than local plantations. In terms of timber mechanical properties, northerly provenances had no advantages over local ones.

There are reports that seed may without risk be transferred over distances of 1500 km from east to west, 100 km from north to south or 500 km from south to east (Kupchinskii et al., 1982). According to J. Wright (1976), however, differences in hereditary properties may already be observable over a distance of 50 miles (about 80 km). It has been observed in provenance trials that height gain is the greater and crown development is the better the greater the distance from the original habitat towards northeast or east (Gut et al., 1991). It is also held that provenance trials reflect fairly accurately the genetic structure of parent populations, and it has been concluded that morphological variability of populations is due to modifications caused by environmental conditions (Szweykowski et al., 1994).

The objective of the present study is to compare Scots pine trial plantations of different geographical provenances based on their growth characteristics by analysing the data obtained from the geographical trial plantations established under the guidance of E. Pihelgas in 1964–1965 using more modern statistical methods. The results obtained would help to determine the suitability of different subspecies of Scots pine for Estonian circumstances, which may contribute to the organisation of forest seed management, the development of nursery management and the purposeful establishment of forest plantations in Estonia.

Material and methods

Material

The geographical trial plantations of Scots pine in Estonia were established by E. Pihelgas, who in the winter of 1961/1962 turned to a number of educational establishments and research institutions dealing with forestry in the then Soviet Union with a request to send pine seed collected from their respective regions to Estonia for experimental purposes. The request drew 34 Scots pine seed shipments from various regions (Figure 1). The northernmost seed was received from Arkhangelsk Province (lat.63°N.) and the southernmost from Borjomi Forest Enterprise, Georgia, situated 800 m above sea level (lat.42°N). The westernmost seed was sent in from Lithuania and Lviv (long.24-27°E.) and the easternmost from Khabarovsk (long.126°E.). The Estonian pine seedlings originated from the forest districts of Jдrvselja, Valgejxe, Sxmeru and Koorkыla (Pihelgas, 1970).

The seed shipment from Arkhangelsk Province comprised the subspecies *lapponica* Fries, the Georgian seed belonged to the subspecies *hamata* Fomin and the seed sent from Amur Province were of the subspecies *sibirica* Ledebour. All the remaining seed represented ecotypes of the subspecies *sylvestris* L. According to the senders most of the seed was collected from stands of quality class II, with the exception that the Arkhangelsk seed was obtained from stands of

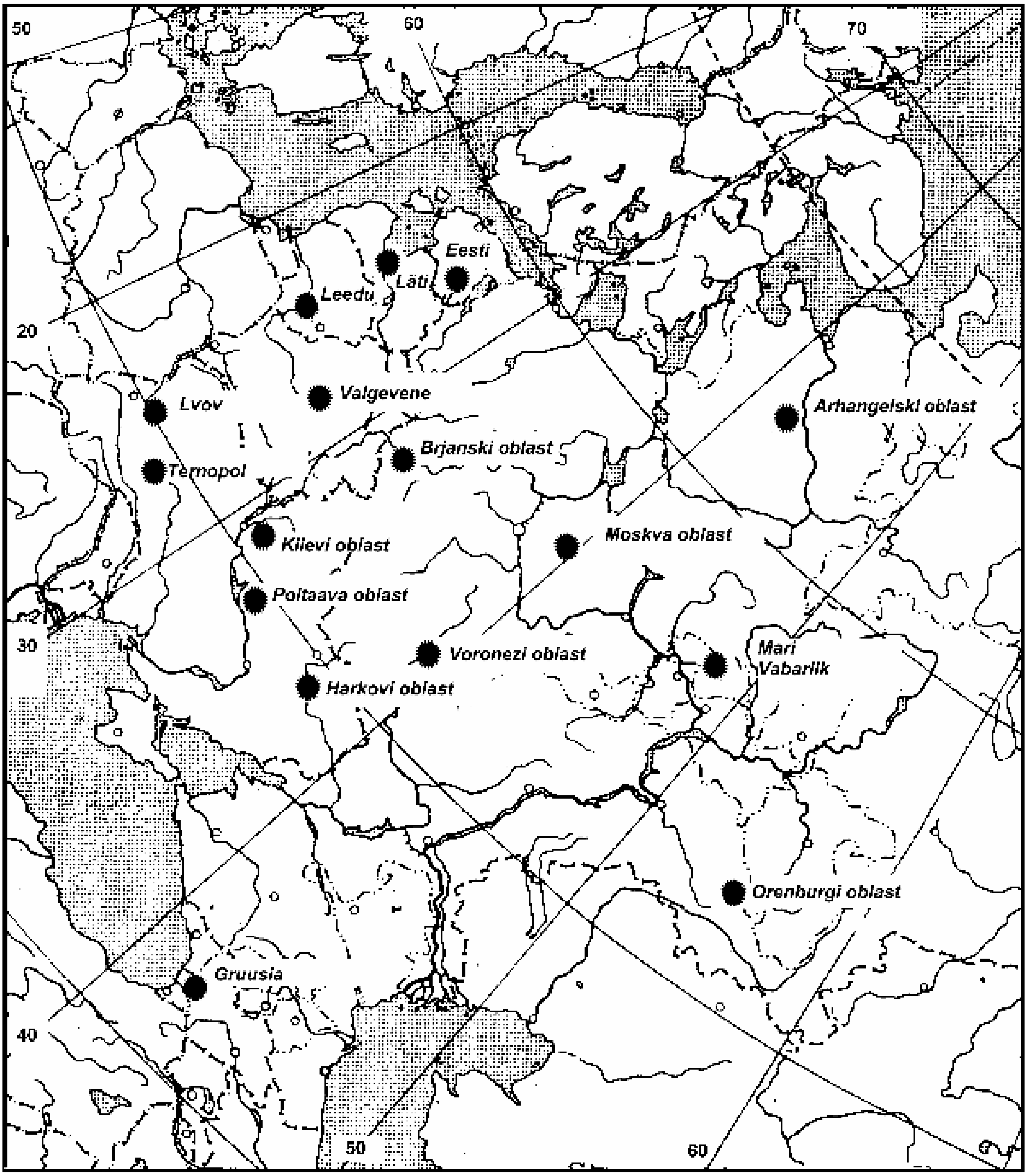

Figure 1. The geographical distribution of the seed collection sites.

quality class IV and the Lviv seed from those of quality class I. Most of the stands from which the seed was collected fell into the age classes III and V (Pihelgas, 1965, 1971).

In the spring of 1964 the plants were used to establish the trial plantations in compartment 35 and compartment 35A at Jдrvselja. The trial sites had a slightly podzolic sandy soil. Altogether, 185 trial variants were established in the 9.9-ha area. Bigger seed shipments were also used in end of April 1965 to establish trials on compartment 35, on a trial plot having a slightly to moderately podzolic sandy soil. Two-year pine seedlings were planted in a ground prepared by full ploughing in a 1.25Ч1.5 m arrangement. Each trial square comprised 300 planting spaces.

New measurements of the trial plantations established by E. Pihelgas were launched in 1998. All the 2278 progeny trees under study were measured for breast height diameter (at the height of 1.3 m) using a calliper with a 1-cm accuracy. Based on the mean diameters of each trial variant 15 model trees were selected, which were measured using a laser altimeter Vertex for tree height, breast height diameter in the directions NS and EW and live crown length. In the subsequent statistical analysis the breast height diameter measurements were averaged and designated simply as breast height diameter ($D_{1,3}$).

Statistical methods

The measurement results were statistically analysed with the SAS package, version 8.2, mostly using the procedure MIXED (SAS Institute Inc., 1990, 1997), which performs the dispersion analysis of multifactor mixed models.

Two similar models were used for analysis. In the comparison and estimation of particular provenances, provenance was taken as a discrete fixed factor; another factor treated as fixed was progeny tree age, which was considered continuous. This model, hereinafter referred to as Model 1 (see Appendix 1) was used to describe tree growth through third-degree age polynomial, which was taken to depend on provenance (site). Year of planting was taken as a random discrete factor. The selection of Model 1 corresponded to the concrete goal set – to study the effect of seed provenance on the development of progeny trees grown in Estonia.

In the second analysis, which was performed using Model 2 (see Appendix 2), the objective was to study the effect of the geographical location of seed collection site on progeny tree growth characteristics. In this analysis, seed collection site and year of planting were taken as discrete random factors whereas progeny tree age and seed collection site geographical coordinates (north latitude and east longitude) were treated as continuous fixed factors. Before the statistical analysis of height increment tree height was raised to the s power, which resulted in the dependence of tree height on tree age becoming more linear, the distribution of prediction residuals becoming more normal and the dispersion of prediction residuals being less dependent on mean value. The final results of the analysis were reconverted to the original height scale (into meters). The parameters characterising tree growth were modelled with tree age *a* and geographical north latitude *p* third-degree polynomials as follows:

$$X = c_0 + c_1 a + c_2 a^2 + c_3 a^3 + c_4 p + c_5 p^2 + c_6 p^3 + c_7 ap + c_8 ap^2 + c_9 a^2 p + e \ ,$$

where X is the characteristic of the tree under study, $c_0 - c_9$ are model coefficients that are dependent on characteristic X and are estimated according to the data, and e is an error term (residual term), which is assumed to be of roughly normal distribution. Based on the respective model progeny tree characteristics were estimated and checks were performed on whether tree growth parameters at that particular age had been dependent on the geographical location of the seed collection site.

Considering the specifics of the data progeny tree height increment was based on tree height at the age of 33.5 years (so-called control age) – at that age the predictions calculated from the model proved to have the highest statistical accuracy. In reality, predicted heights were used to compare the height increments of progeny trees planted at different times, irrespective of whether or not the trees were actually measured at the corresponding age. Such an approach was adopted due to the fact that predictions are more accurate than simple means as they take into account, via the model, all the data, not only selected measurement results and provenance data separately.

Results and discussion

It appeared from our previous data (Kurm et al., 2003) that pines grown from seed of Estonian origin, collected from Sxmeru and Vihula, were twice taller than the lowest trees, of Georgian origin, at the age of 35. The control height of the latter was just 12.5 m. By the use in this paper of another control age (33.5 years), an updated database, which was supplemented with measurement results from earlier growth stages, and the improved model, which, based on the yield table, also took into account measurements made at earlier tree ages, it was possible to produce more precise estimations of progeny control height. Table 1 presents tree height estimations at the selected control age of 33.5 years by provenances. By way of comparison, the table includes the means of height and breast height diameter for the most extensively studied age groups – 33 and 34 years. It appears from the table that the growth characteristics of trees grown from seeds collected in Estonia are somewhat inferior to those of progeny trees of southerly origin.

The dependence of tree height increment on north latitude is illustrated in Figure 2, which has been derived from Model 2. It appears from the figure that in Estonian circumstances the latitude most favourable for progeny growth is 50-58є. According to literature (Shutajev, Giertych, 2003[1], 2003[2]) the Baltic Region populations show good growth rates in European regions between 50-60є north latitude.

Table 1. Progeny tree heights at 33.5 years of age predicted by Model 1 compared to growth parameters at tree ages of 33 and 34 years obtained by simple averaging

Seed origin	Height predicted by Model 1 (m) ± standard error	Mean height at 33 years, m	Mean height at 34 years, m	Mean $D_{1,3}$ at 33 years, cm	Mean $D_{1,3}$ at 34 years, cm
Georgia	12.75±0.34	–	12.55	–	20.8
Arkhangelsk	16.46±0.10	16.13	16.60	16.4	15.0
Moldova	17.13±0.32	–	16.43		23.2
Sxmeru	17.23±0.17	17.03	–	16.8	–
Perm	17.60±0.32	–	16.99	–	16.7
Vihula	17.88±0.17	17.96	–	17.7	–
Poltava	18.15±0.11	18.62	17.78	21.6	24.0
Kirov	18.34±0.32	–	17.95	–	20.2
Kyiv	18.61±0.11	19.48	18.00	26.9	22.4
Latvia (Kalns)	18.64±0.14	–	18.82	–	19.5
Sagadi	18.65±0.14	18.96	–	18.0	–
Kharkiv	18.66±0.07	18.81	18.61	22.1	23.1
Valgejxe	18.71±0.11	–	18.79	–	19.4
Jдrvselja	18.82±0.09	19.03	18.15	18.1	22.4
Ternopil	18.88±0.09	19.17	18.41	23.0	24.1
Koorkьla	18.89±0.17	19.14	–	18.6	–
Voronezh	19.08±0.09	–	19.29	–	23.2
Zhytomyr	19.09±0.08	19.89	18.23	21.1	21.7
Bryansk	19.35±0.10	18.73	19.68	17.3	21.3
Orenburg	19.42±0.09	19.79	19.11	19.7	18.7
Byelorussia	19.45±0.08	–	19.67	–	20.6
Lviv	19.49±0.10	20.37	19.16	22.3	20.4
Latvia (Jelgava)	19.49±0.11	18.94	19.98	18.5	18.7
Latvia (Tukums)	19.58±0.09	19.63	19.43	18.1	20.7
Moscow	19.58±0.09	–	19.60	–	20.0
Mari El Republic	19.97±0.08	20	19.95	20.3	21.7
Lithuania	20.04±0.09	20.03	20.06	19.0	21.4

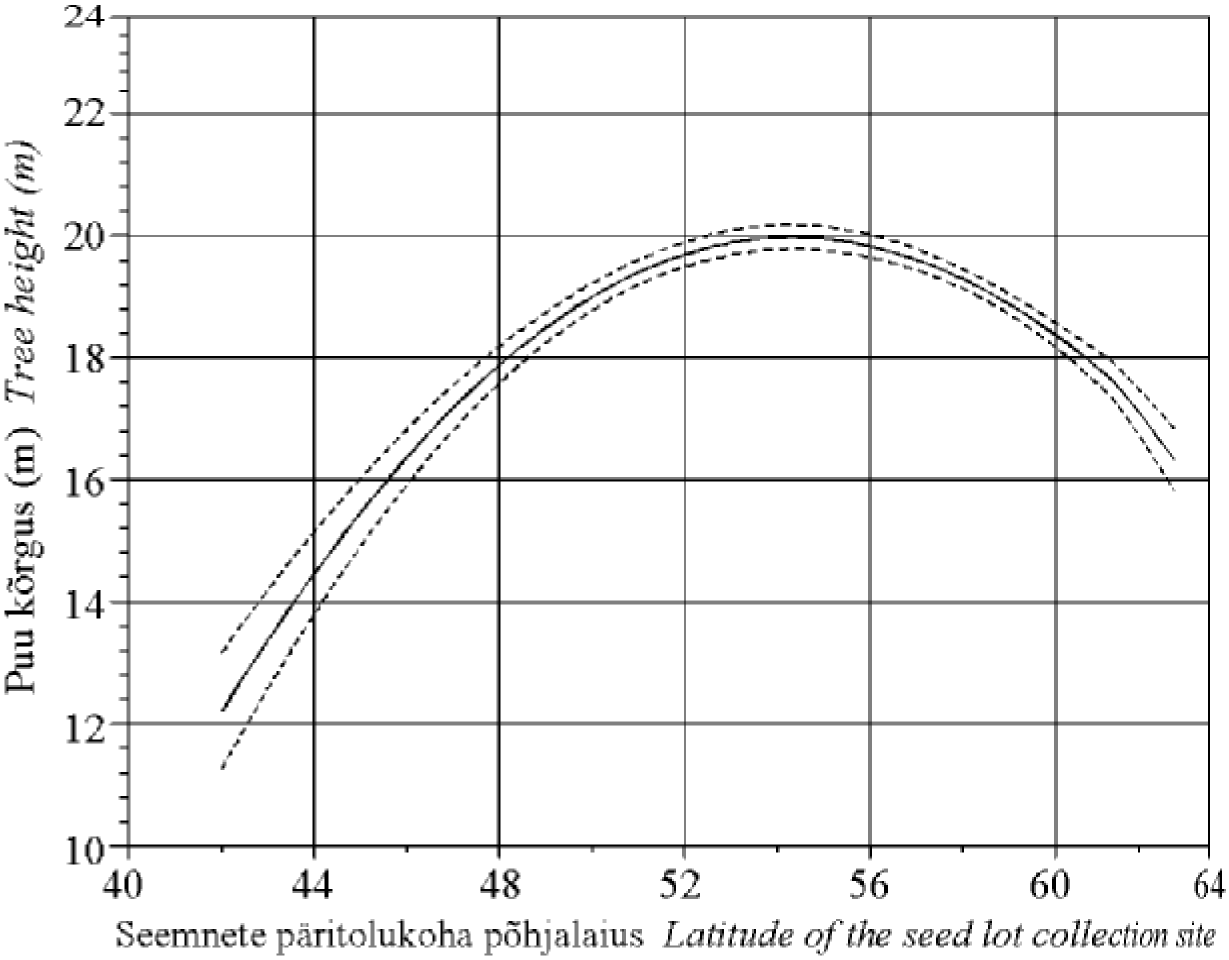

Figure 2. Progeny tree height at 33.5 years as dependent on the geographical north latitude of seed collection site. The east longitude is adjusted to 32.7є. Dotted lines stand for height prediction 95% confidence limits.

According to E. Pihelgas (Pihelgas, 1980) the pine plantations established using seed brought in from Latvia, Lithuania and Byelorussia exceeded the local plantations by growth rate already at younger ages.

As an improvement on a previous height increment analysis (Kurm et al., 2003), this study additionally analyses progeny tree breast height diameter and stem volume at the control age of 33.5 years as depending on seed geographical origin (Figures 3 and 4). It was statistically proved that in pines growing under Estonian circumstances all the above parameters are dependent on seed geographical origin ($P<0.001$).

Statistical analysis of our data revealed that in pines growing under Estonian circumstances breast height diameter depended on the north latitude of seed collection site, being inversely proportional to it (Figure 3). The largest breast height diameter (over 21 cm) was observed in pines grown from seed collected in the regions of Kharkiv, Zhytomyr, Ternopil, Voronezh and Poltava. The smallest breast height diameter (16-19 cm) was measured in pines originating from Arkhangelsk, Perm and Estonia (particularly Sxmeru).

It is possible to try to explain all the regularities observed with the hypothesis that as solar radiation is reduced competition for light between trees intensifies and taller trees stand better chances of adaptation. At the same time the volume of photosynthesis and, accordingly, annual tree mass increment, reduce. As a result, it follows from natural selection that the tree phenotype adaptation that occurs in northerly populations comes as a compromise between increased

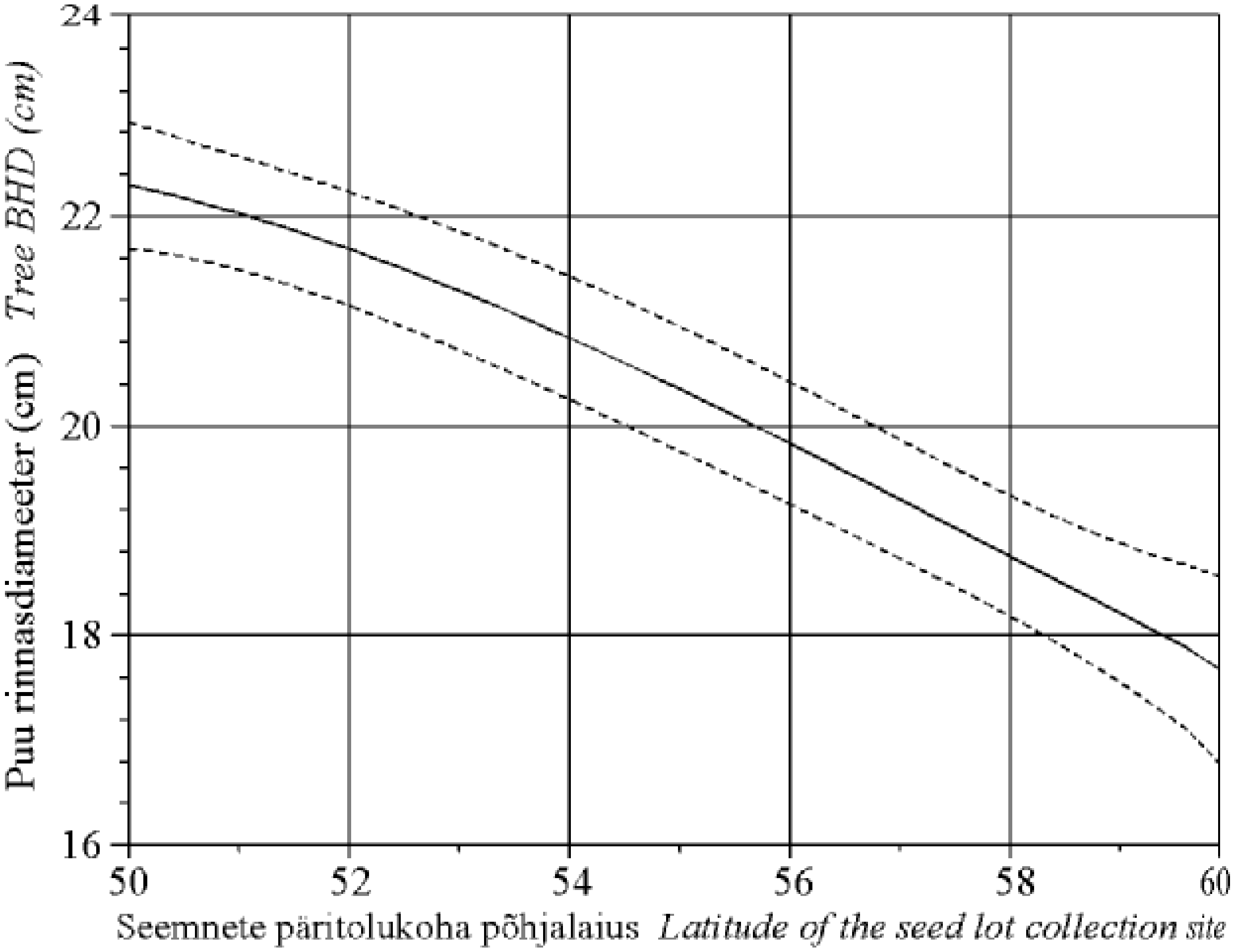

Figure 3. The diameter of 33.5-year-old progeny trees at the height of 1.3 meters as dependent on the geographical north latitude of seed collection site. The east longitude is adjusted to 32.7є. Dotted lines stand for breast height diameter prediction 95% confidence limits.

stem length and decreased stem diameter. Such phenotypic compromises are ingrained in tree genetic or epigenetic heredity and stored into its seed. When the seeds are transferred to Estonia, the tree ontogeny program is realised under Estonian circumstances and may be manifested precisely as observed in the present paper. At the same time, the ontogeny suitable for more southerly circumstances may not be optimal in northerly environments of lesser light and colder climate. It may be assumed that in such harsh conditions the higher growth rate of trees of southerly origin runs increased risk against other factors (windbreaks, pathogen resistance, etc.). An indirect proof of the assumption is the fact that the pines of Amur provenance have all died and that only two pines of Georgian provenance planted in 1964 have been found. In like fashion, pines originating from Stanislav, Zhytomyr, Kharkiv and Poltava (49-51є north latitude) have suffered substantial losses. Consequently, all the pines originating from Far East and from the south have died, the cause being, according to E. Pihelgas (1980), low resistance to pine needle cast fungus and other fungal diseases. It appeared that Scots pine subspecies *hamata* Fomin and *sibirica* Ledebour had proved unfit for Estonian circumstances. Apart from local plantations, one established using seed from Arkhangelsk (*P. silvestris* subs. *lapponica* Fries*)* has survived; however, it is growing at a relatively slow rate.

Conclusion

The results of this study enable the determination of the regions from where it would be reasonable to bring in seed for use in Estonia, as well as the identification of the regions from where it would be unreasonable to bring in seed to Estonia to avoid errors like those made in the past with the plantations of Darmstadt pine. Statistical analysis of our data showed that in Estonian circumstances the seed provenance latitude most favourable for progeny growth is 50-58є. Already at younger ages pine plantations established using seed brought in from Latvia, Lithuania and Byelorussia exceeded local plantations by growth rate. The breast height diameter of pines growing in Estonian circumstances depended on the north latitude of seed collection site, being inversely proportional to it. It appeared that Scots pine subspecies *hamata* Fomin and *sibirica* Ledebour had proved unfit for Estonian circumstances. Similarly, the plantation established using seed from Arkhangelsk (*P. silvestris* subs. *lapponica* Fries*)* is growing at a relatively slow rate.

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Appendixes

Appendix 1.*Core of the SAS program for predicting the height of progeny trees at the age of 33.5 (Model 1). Abbreviations: geogr – initial dataset, where the height of trees or the average of heights has the pover of s (the corresponding variable is H075), koht – the seed collection site, N – number of the averaged trees, age – the age of the trees, istutusA – the year when a tree was planted, preds – the file that contains predicted heights of the trees*

```
proc mixed data=geogr covtest;
     class koht istutusA;
     weight N;
     model H075= koht age(koht)|age(koht)|age(koht)
          / noint solution htype=3 outpm=preds;
     random istutusA ;

    title “Prognoosid 33.5a”;
     estimate “ARHANGELSKI”
               koht              1
               age(koht)         33.5
               age*age(koht)     1122.25
               age*age*age(koht)  37595.375 / cl;
. . . . .

     estimate “LEEDU” koht       0 0 0 0 0 0 0 0 1
               age(koht)         0 0 0 0 0 0 0 0 33.5
               age*age(koht)     0 0 0 0 0 0 0 0 1122.25
               age*age*age(koht)  0 0 0 0 0 0 0 0 37595.375 / cl;
. . . . .
run; quit;
```

Appendix 2. *Core of the SAS program for analyzing the dependence of the growth of progeny trees on the northern latitude (Model 2). Abbreviations: puudkoos – the initial dataset, where the height of trees, or the average of the heights, has the power of s (the corresponding variable is H075), koht – the seed collection site, N – number of the averaged trees, age – the age of the trees, pl – northern latitude, preds – the file that contains predicted heights. In order to get some additional predictions, a fictitios dataset has been added to the initial data. Instead of H075, abbreviations RD or TR have been respectively used in the evaluation of the geographical dependence of breast height diameter (RD) and the volume of the trunk (TR)*

```
proc mixed data=puudkoos covtest;
     class koht;
     weight N;
     model H075= age|age|age|pl|pl|pl@3
          / solution htype=3 outpm=preds;
     random koht;
run; quit;
```

UNBALANCES IN TREE BREEDING

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Abstract

Applications of unbalance in tree breeding are discussed. Unbalance has the potential to make the breeding more efficient. But management of unbalance is not fail-safe and requires often considerable competence. The benefits of unbalance may sometimes appear larger than they are in the long run and in the real world. On the other hand, unbalance is practically unavoidable and thus breeders have to deal with it anyway, and moderate unbalances are unlikely to have significant negative effects and thus seem fail-safe. It could be a good idea to apply unbalance with some moderation compared to what may seem optimal from individual simplified studies. When appreciable benefits seem likely, the implementation of moderate unbalance seems recommendable.

Why unbalances?

It is desirable to maintain genetic variation in breeding stock. Gene diversity is a quantitative measure of how well genes are conserved; from a conservation point of view it does not matter if they are good or bad, but to obtain high gain it is of course important to increase the representation of the good genes. Thus balanced breeding with equal contributions is not expected to be theoretically optimal.

In the gene mass of future breeding stock and propagation populations, the best part of the current breeding population will be overrepresented. It is thus more important to improve the better part of the gene mass than the worse. More resources can be spent on improving better gene mass than worse. Such a strategy will increase the realized average gain.

Unequal genetic distributions are the standard in Nature, and cannot be avoided. This is the driving force for evolution and a fundament for existence of life. It is the essence of genetic improvement that some are selected, while others are not.

Unbalanced selection offers more degrees of freedom and a more optimal consideration of essential elements of breeding (gain, diversity, time and cost).

Even a limited extra increase in efficiency (e.g., 5% increase of gain) may correspond to a huge sum of money for an expensive and important crop. Even if it is mathematically difficult and practically impossible to optimize the degree of unbalance, used with common sense and some care it ought to be possible to apply unbalance so the result become better than balance in situations when the added gain makes it worthwhile.

Utilizing unbalance may mean more gain faster, and it may be worth that even at the cost of a reduced potential for more gain later.

Against unbalances

In a closed ideal population, the gene diversity is maximized if different genetic components are equally represented. It is not fail-safe to apply unbalance; efforts may result in a worse situation than perfect balance. Breeding goals, genetic parameters and environments change over time, are difficult to predict and predictions has errors, while the effect of the unbalances may remain. Optimization of unbalance requires knowledge of certain parameters which are not accurately known and draws resources to get estimates of, larger resources the better estimates. Gains of using imbalance may be evident when measurement characters are considered, but the effects on other characters are less predictable. That means creation and optimization of unbalances may appear more favorable than it really is in the long run. Studies are often set up to demonstrate an effect and use simplifications. Results indicating considerable effects tend to be published and get more attention by both authors and readers compared to absence of effects or small effects. Therefore, if an effect is found, studies tend to overestimate the size in the real World. Safety bids that one does not change drastic at once from one extreme complete balance to the opposite extreme of strong unbalance based on a few undigested studies without much consideration about possible loopholes. It would not be politically correct to suggest the extreme, it would probably be counter-productive and raise suspicion and make it more difficult to implement a less drastic version. Striving for balance is a clear and simple strategy. Unbalance is demanding on competence and it takes time, effort and management skills to consider unbalances. Considering practicalities and difficulties to find the optimum, balanced breeding may still sometimes be regarded as best from an operational point of view when the advantage of unbalance appears marginal or doubtful.

Different unbalances

There are different types of unbalances, which will be discussed to a varying degree:

- Unbalance in components (parents);
- Unbalance in resources;
- Structure of breeding population (e.g. mating probability; PAM, Positive Assortative Mating, which means that similar parents are mated)

Unbalances in the propagation population

The simplest case is the propagation population, where only unbalance in components (clones) matter. The basic idea that unbalanced representation of genetic materials could offer advantages in forest tree breeding was first introduced for deployment of clones in seed orchards. The first speculation that unbalances may be favorable was done by Lindgren (1974). The propagation population was a seed orchard, which is the most common propagation population. Mathematical development showed that a linear relation between the amount of deployed genetic units (clones) and their breeding value resulted in an optimal balance between effective number (status number, gene diversity) and breeding value, the first suggested application was formulated by Lindgren and Matheson (1986). It was widened to deployment of clones for clonal forestry (Lindgren, Libby and Bondesson 1989) and developed to be applicable for genetic thinning by Bondesson and Lindgren (1993) and Prescher et al. (2004). The advantage and characteristics of the method have been mathematically quantified (Lindgren 1991, Lindgren 1993).

Further on to the production population

The production population is generated from the propagation population, but there are some steps between propagation population and production population. The propagation population is typically an open pollinated seed orchard. Unequal number of ramets will occur even if it is not directly intended, e.g. current clonal seed orchards are usually characterised by unequal number of ramets of different clones (Kang 2001). Thus equal representation is hardly a realistic alternative, neither does it offer advantages. It may be true that - given the clone number - the effective clone number is highest if clones have equal number of ramets, but a moderate increase in clone number is almost always a better way to meet a demand for increased effective clone number. Many other factors than ramet number contribute to the unbalance in seed orchard crops (Bila 2000, Olsson 2001, Kang 2001). Genotypes in a seed orchard differ in reproductive success, and there are differences between the male and female success, and male and female may be correlated to different degree. There is pollen migration into the seed orchard. Related genotypes may occur. Only some clones may be harvested. There are phenomena also after the cone harvest contributing to unbalance: seed extraction, seed fractionation, germination, nursery mortality, field mortality, naturals in plantations... The details about these phenomena occurring in the steps between the propagation population and production and possible responses are beyond the scope of this study.

Unbalances at the set up of a tree improvement program

Given a population with a structure of unrelated families it was possible to identify an optimum unbalance in selecting individuals from different families (Lindgren, Wei and Bondesson 1993). Optimum unbalance in deployment of individuals from different families is close to linear deployment, thus the number of selected from a family will be approximately linear related to the breeding value of the family, for at least some cases (Wei and Lindgren 1995).

The optimal number of families at the start of a breeding program was calculated as a function of cost components, heritability and desired effective population size (Lindgren, Wei and Lee 1997). The optimization allowed for unequal contribution from families, but the calculations were keeping the effective number constant and did not focus on unbalance. If the price of families (plus trees to use for crosses) is high, it may be worth investing a large share of available resources to get many unrelated families to start with. If the cost per family is low, it is advantageous to have a much larger number of families at the start than the effective number headed for.

Some studies mentioned below have been done more or less based on the Swedish breeding program, thus some information about that is given. The Swedish breeding stock is structured in 46 subpopulations of Scots pine and Norway spruce, the long term breeding population size (number of trees contribution to the next generation breeding stock in one of the populations) is planned to be 50. Ruotsalainen (2002, popularized in Swedish by Rosvall et al. 1999) studied the possible advantage of different contributions from different plus trees at the establishment of the breeding population. A comparison between unbalanced and balanced is done in Table 1. In the example there are 200 tested plus trees available for a population, which is rather typical. The highest ranking ones are used as founders and the contribution of the founders to the subsequent F1 breeding population is either 1, 2 or 3 (the standard variant of the Swedish tree improvement program is 2). The contribution of plus trees which are not used as founders and do not contribute to the breeding population is of course 0. This was organized so that one and only one individual was foreseen selected in each full sib family (within family selection). The compared alternatives (unbalanced versus balanced) use the same amount of resources: the

Table 1. Comparison of unbalanced versus balanced initiation of tree breeding

Unbalanced		Balanced	
Rank of plus tree	Progenies (full sib families)	Rank of plus tree	Progenies(full sib families)
1-10	3	1-50	2
11-30	2	-	
31-60	1	-	
61-200	0	51-200	0
Gain	1.368		1.271

same number of crosses (full sib families); the same number of test plants; the same number of F1-selections. The alternatives result in the same gene diversity. But the gain differs. The gain is given as selection intensity of parents.

The gain will be 7.63 per cent higher for the unbalanced alternative. This difference is likely to remain in the future and cause an improvement of the magnitude of 0.5% of forest production from future seed orchard crops at a given time in the future. Another way of expressing the advantage is that 15 % less plus trees need to be selected and tested. That means that 15 % less trees can be tested and still the same gain and gene diversity can be obtained, thus the costs of the most essential part of the initiation of long term breeding can be cut by 15% by using unbalance resulting in the same size of breeding population, the same gain and the same diversity.

Ruotsalainen (2002) studied other cases. Slightly more optimal solutions can be found, but the suggested one is near the optimum for Scandinavian pine and spruce and simple to express. A «heuristic rule» is suggested for the number of offspring to different founders depending on their breeding value (cf Table 1). Founders are here plus trees with known breeding values, which transmit progeny to establish a breeding population generation with trees with known parents. The number of offspring transmitted to the breeding population is depending on the breeding value of the parent. The top 1/6 of the selected founders contributes three offspring, the 1/3 with intermediate ranking contributes two and the 1/2 with low ranking contributes one.

Andersson (1999) found, based on selection in a Scots pine progeny test, that selection resulting in different number of selections from different families with more selections from the better families had advantages (more gain at the same gene diversity) compared to within family selection.

Rosvall (1999, see below) indicated only a minor and somewhat doubtful advantage of unbalance even at the first generation of breeding. This study was not set up to investigate the initiation and this is not in focus. Thus it does not directly contradict the results by Ruotsalainen (2002) indicating that the benefits of an unbalance in the initiation of the breeding can be substantial, although it gives a reminder that the gain in seed orchards which constitutes a more intensive selection than the breeding population, may be somewhat reduced.

There are other arguments than the extra gain to let a larger number of parents by represented in the first generation of the breeding population. It remains an option to derive larger gene diversity from the F_1 population if that would appear desirable. There is a larger flexibility to respond to changes in breeding goals. The results by Andersson (1999) suggest that group merit may be higher if the F_1 breeding population is refreshed by including fresh plus trees rather than confining the selections to the related progenies of those initially selected. That may indicate a way of increasing the number of founders and to introduce unbalance if it was not done immediately.

Unbalances in long-term breeding

Since some decades the major idea in creating unbalances in breeding is by «nucleus breeding». Nucleus breeding refers to the stratification of the breeding population into distinct groups based on estimated genetic value, usually a two-tier elite and a main subpopulations. The key idea is to concentrate more of the breeding effort on the elite, where maximum gain will be achieved, with less emphasis placed on the main, which is mainly for preserving genetic variation. This system was initially used in sheep breeding (James 1977), but has later been incorporated into forest trees (Cotterill 1989). This basic idea of structuring the breeding population can be developed into something more sophisticated, e.g. PAM combined with breeding effort related to breeding value.

Short-term gain is maximized by selection for breeding value. Breeding value can be estimated based on information from relatives. A simple case is to form an index (thus calculate predicted breeding value) of the individual performance and family performance. Selection for that can be called index selection and maximizes gain. But in long term breeding the loss of gene diversity will cause a loss of additive genetic variance and thus a reduction in the response to selection. Thus maximizing genetic gain in the short term will cause reduced genetic gain in the long term. It is a matter of optimization. The longer breeding program is considered, the more important for genetic gain at the end it is to conserve gene diversity. In the real long term, the assumptions for the used models break down (e.g. as mutations occur). Novel approaches to genetic improvement are likely to take over a century ahead. Current breeders responsibility may be restricted to keep options open for the foreseeable future. Management of genetic resources of forest trees may include guarding the genetic resources for gene diversity and other aspects so a reasonable situation a century ahead seems likely, but it is debatable if the responsibility stretches beyond that. Therefore it does not seem meaningful to consider more than five generations when cycling time is several decades.

Once the breeding population is closed, the ultimate long-term response is maximized by balanced within family selection (Dempfle 1975). However this ultimate limit is irrelevant for trees, as it lies a large number of generations ahead.

Breeding can be seen as a balance between gain and gene diversity. Earlier the needed number crunching power did not exist and that put strong constraints on what could be done, much of the theoretical basis some decades ago appeared rather abstract. For forest tree applications an essential landmark was the PhD thesis of Wei (1995). It become evident that tree breeding maximizing breeding value and not considering loss in gene diversity (build up of relatedness) had the potential to erode the diversity severely. For managing unbalances the application of «status number» (group coancestry) was essential (Gea 1997, Lindgren and Kang 1997).

Rosvall (1999) used the breeding simulator POPSIM (Mullin and Park 1995) to simulate a case relevant for the planned Swedish long-term breeding of Norway spruce. (The latest version of POPSIM is referred to in Lstiburek, 2005). The value of the breeding population was seen as its capacity to support seed orchards. Higher gene diversity in the breeding population makes it more able to support selections with high breeding value to seed orchards (Figure 1). Different ways of introducing unbalance was used. Unbalance appeared to offer only minor advantages (e.g. Figure 1).

Rosvall (1999) assumed testing of the recruitment population, which means high heritability. Balance is more favorable when heritability is high as then the family component of selection becomes unimportant. An option for long term Swedish Scots pine breeding is selection of untested genotypes for the breeding population, and in that situation the advantage of unbalance can be

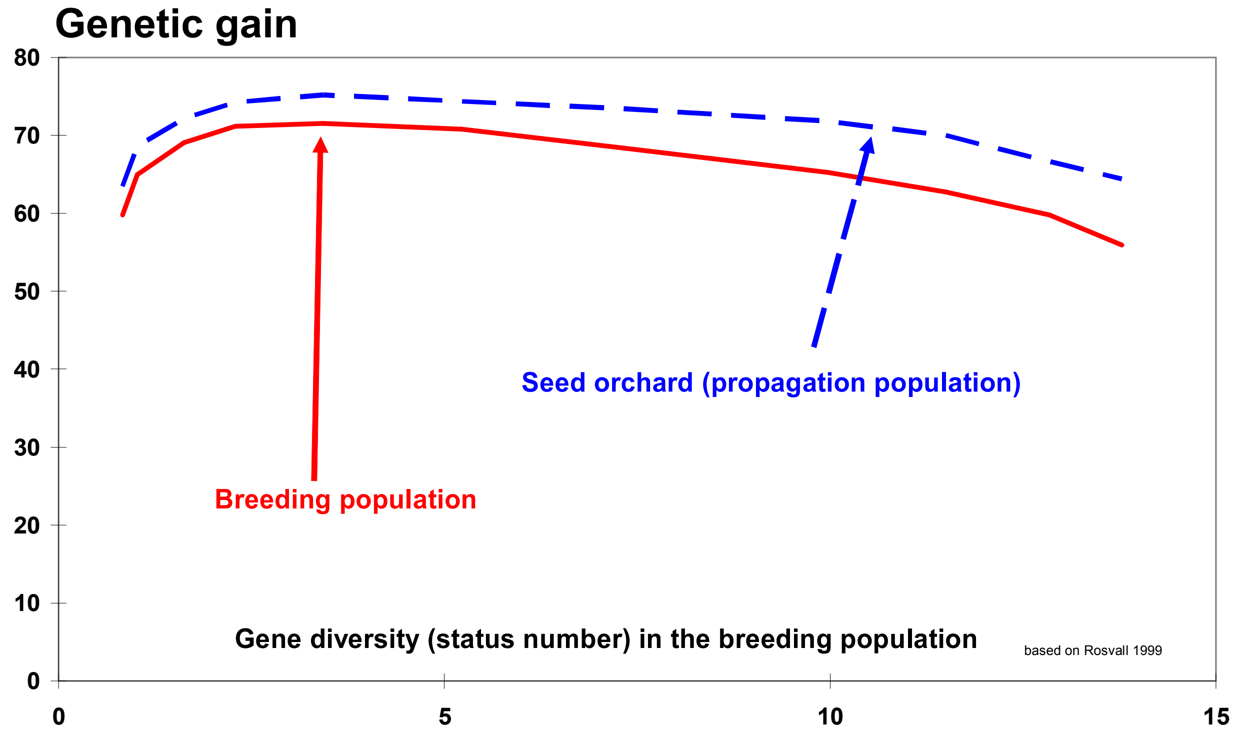

Figure 1. Genetic gain as a function of gene diversity remaining after five generations in a simulation of a program similar to Swedish Norway spruce breeding. (Single pair mating, progeny size 50, high heritability with clone testing.) The rightmost diversity values correspond to maximizing balance (strict within family selection, each member in the breeding population get exactly two offspring transferred to next breeding population generation). Some of the genetic gain lost in the breeding population, when that is run for high genetic gain, is recovered then forming seed orchards. The extra genetic gain obtained by applying unbalance becomes rather small. The figure is based on Rosvall (1999).

expected to be larger. An advanced generation «seed orchard» is likely to be designed in a complex and sophisticated way, thus the idea of classifying the «goodness» of an advanced breeding population by a seed orchard derived from it could be developed and it does not seem impossible that unbalance in the breeding population will carry a smaller penalty with such a more developed measure.

It may be noted that the balance becomes less important the higher the breeding population size is, thus unbalance may be more justified in breeding programs using large breeding populations.

Sanchez (2000) concluded, based on quantitative simulation, that a slight unbalance could be more favorable in breeding than complete balance, as it leads to more gain without a corresponding loss of genetic diversity.

Lindgren and Wei (1994) studied the effect of selection in a population composed of an infinite number of equally sized unrelated families. The selection criterion was a weighted average of family value and individual value. By using different weights of family versus individual, a gain/diversity relation was developed. Among family selection and within family selection appeared as extremes, and index selection where family and individual are optimally weighted to maximize gain of cause appears as a peak. They got results, which indicated an unfavorable gain/diversity relation for completely balanced within family selection. Their study was based on infinite populations and normal distributions, while later studies have used limited population and populations truncated by selection, and also other inputs closer to forest tree breeding. Even if a drop in efficiency has been observed also in later studies, its magnitude seemed smaller that noted by Lindgren and Wei (1994).

It is practically easier, more transparent, less competence demanding and more fail-safe to manage balanced selection than intentionally unbalanced in the first breeding generations, so advantages of the magnitude observed by Rosvall (1999) may not be regarded as sufficient motive to apply intentional unbalance in the long term breeding.

Population-wide PAM appeared, based on POPSIM simulations, to offer advantages compared to structuring of the breeding population in elite and main (Lstibщrek 2005). The advantage of PAM was emphasized if test effort was linearly related to breeding value (see below).

Change per generation at a given breeding population size does not say everything

Perhaps it should not be the loss of gene diversity per generation but the annual loss, which should be in focus. Both annual gain and annual diversity loss are affected by both the degree of unbalance and the duration of a generation. More unbalance and longer generation time may possible result in both higher gain and less loss in gene diversity at a certain time. A high degree of balance is one they of increasing gene diversity but another way is to increase breeding populations size, and there may be trade-offs. An optimization e.g. maximizing gain per year at a given gene diversity loss per year allowing variation in testing time, breeding population size and degree of unbalance simultaneously has never been done and unbalance may appear favorable. Using fixed generation times and breeding population size may be somewhat misleading. Application and extension of the methods used by Wei and Lindgren (2001) and Danusevicius and Lindgren (2005) could be helpful in more sophisticated studies. Multi-generation studies usually assume that the breeding population is managed in the same way over generations, but the optimum may be to deal with them differently, and that may give larger room for unbalance.

Rolling front breeding

Forest Tree breeding is almost certainly better made in a rolling front system (Borralho and Dutkowski 1998) than in discrete generations turned over at the same time. It just does not work to get all needed crosses and other operations done at the same time in an operative breeding program. For Swedish breeding, the status of the breeding populations are annually reviewed (Sonesson et al. 2005), the problem of managing a breeding population synchronous is evident. In advanced breeding it will turn out advantageous to mate individuals from different generations. In rolling front breeding perfectly balanced breeding become rather meaningless and does not appear simple any more. A rolling front strategy may be optimized by using group merit annual progress as the criterion on efficiency (Wei and Lindgren 2001, Danusevicius and Lindgren 2005)

Stratified sublines with and without unbalance

Stratified sublines (Ruotsalainen 2002, Lindgren et al 2004) can be described as positive assortative mating driven to its extreme, where the process is continued several generations forming separate small sublines. Stratified sublining makes it possible to get orchards with more than 10% superior gain compared to conventional sublining, it ought to get still higher improvement by using higher breeding efforts on the highest ranking sublines, while the low ranking sublines could have a still stronger emphasis on diversity.

Stratified sublining will be implemented in the recently developed Finnish breeding strategy (Lindgren et al. 2004). To further boost the effect of stratification and to obtain additional genetic gains from future seed orchards, the Finnish breeding strategy involves the idea of distributing breeding, testing and selection efforts unequally, making the effort positively dependent on genetic value of the material being improved. This principle is implemented throughout the breeding cycle. In the first generation turnover, the founders forming the first-generation breeding population are single-pair mated with regard to breeding value (in the way described above). Those of the founders that are ranked to the highest quarter are, however, double-pair mated to allow more options for recombination of their gene mass and reduce the risk that their gene mass is degraded by an unfortunate choice of partner, as well as a way to increase the number of offspring. Furthermore, the target sizes of F_1 families are larger for the best quarter of the parents than for the average parent or for the lowest quarter of parents. The F_1 families (the recruitment population) are grown in forward selection trials that last from 5 to 10 years depending on species. At this age, the best individuals within each full-sib family are phenotypically selected for further testing. Roughly three times as many selections (candidates) are drawn from within the larger families (representing offspring of the best parents) than from the smaller ones. The number of candidates selected from each full-sib family to the new breeding population varies in relation to the mean breeding value; three individuals are selected from the best full-sib families (determined as the mean breeding value of the top 3 candidates), two individuals from the average families, and one (possibly none) individual from the lowest ranking families (Ruotsalainen 2002). As a result, the second generation breeding population, will have an unbalanced structure where the size of the stratified subline is six, four or two trees for the highest ranking, the average and the lowest ranking candidates, respectively. This method results in an overrepresentation of the gene mass of the best founders whereas a high number of low ranking founders will still be represented, but with relatively small genetic contributions.

Unbalances in deployment of resources to families

Lstibщrek (2005, a popular presentation in Swedish by Mullin et al 2005 is based on Lstibщrek's thesis) made a study with the tree-breeding simulator POPSIM. The recruitment population was created by PAM single-pair among selected tested parents. The family size was linearly related to the families breeding value (thus a form of «linear deployment»). The next breeding population was selected by within-family selection. The criteria of goodness of the strategy were the genetic gain of the best share of the breeding population selected for mass multiplication (seed orchard) at a given diversity. The comparisons were done at the same resource (the same number of trees planted). Different degrees of unbalance were used; on one extreme was balanced selection when all families are of size 30 and the other extreme strong unbalance when family sizes varied between around 2 and 60. Moderate unbalance implied differences among family sizes of the magnitude 20-40. The gain compared to balanced selection increased by 20% using strong unbalance and 10% if intermediate unbalance was used. There is no associated disadvantage from increased resources or lost diversity for these gains. It seems very logic that allocating more resources to improving the genotypes which are more likely to be selected to seed orchards and less to those which are there more for assuring diversity in long time breeding will boost seed orchard selections. The advantage is large compared with what was indicated by earlier similar efforts, e.g. Rosvall (1999). That is probably explained by that Lstiburek (2005) in the simulation used REML and BLUP, thus more precise methods making more efficient use of available information (like a modern breeder would do).

Arguments against to employ tree improvement efforts depending on the breeding value

A model predicting the profit of some action deviates always from the real world. Those deviations may be more or less severe. Unequal representation of families can have direct negative effects if the model assumptions are not full-filled. A simple example is given to illustrate one problem (Table 2). A field test has 10 trees belonging to two families. The best individual in each family is selected by within family selection.

Table 2. Average selection intensity for within family selection. The candidate population consists of two families of different sizes where the best tree is selected

	Balanced		Moderate unbalance		Strong unbalance	
	Size	Sel int	Size	Sel int	Size	Sel int
Large family	5	1.163	6	1.267	9	1.485
Small family	5	1.163	4	1.029	1	0
Average selection intensity		1.163		1.148		0.742
% of balanced		100		98.7		63.8

Genetic gain is proportional to selection intensity. The selection intensity will decrease if there is unbalance. Average gain by within family selection will be lower. The decrease in selection intensity will be marginally small if the family sizes vary intermediate, but may be important if there is large variation in family size. As the goodness is only counted on the best selections and as the best families are larger, the within family selection intensity will be higher for the selected part, and that effect is much larger in the simulation than that caused by the loss in selection intensity. But simulations differ from the real world. It is assumed that the family sizes (decided before establishment of the trial) concern exactly the same character as the selections (decided when trials are mature for selection). That is certainly not so, e.g. environments used where the propagation population is deployed will not be the same as the test environments. Sampling effect is one reason but there are many more which are likely to cause differences. The preferred selection index (selection criteria) as a combination of characters used for deciding breeding values of parents probably changes over time till progenies are selected. It might actually be optimal to use different index for different purposes. The breeding targets are probably somewhat different for the breeding population and the seed orchard population (which is used as a measure of the value of the breeding population).

If one invests resources in creating offspring from parents, it seems bad breeding economy to field test very few individuals for any families. Breeding population members and families are expensive and these costs are not neglectable compared to costs related to family size. There are costs connected to parents like clone archives and pollen management. It does not make sense to create families which are so small so all individuals have to be selected resulting in no gain at all. Just for safety reasons as an assurance against irreversible loss, it seems advisable to use a minimum size of families, so there exist some selectable trees when it is time. Linear deployment need not be optimal for deployment of the recruitment population even if it was proven good, it seems likely it is more optimal to make the smallest families a bit larger, at least in a real world.

In the simulations an average under an idealized situation is considered. The results favoring PAM and variations in breeding effort are probably less robust and more depending on the idealized conditions than Random Mating and uniform breeding effort in a single run in the real world than under simulations.

In the real world the PAM are not as perfect as assumed in simulations. Besides practical considerations reducing the degree of PAM, PAM is for the index used over the environments used, and that degree of PAM will be lower for the selection index and environments in the progeny generation. The breeding stock is often not propagated under the same conditions or tested in a single test. The crosses are usually done at different occasions and places, which may cause asymmetries. The individuals will often be selected in several steps, first based on the phenotype and later based on some test.

The uncertainties are small with intermediate unbalance. The intermediate unbalance is not larger that usually occurs unintentionally. It does not seem to exist a good reason not to apply moderate unbalance immediately (say decreasing within family selection intensity by 2%). The risk that this results in a considerable loss seems neglectable. The implementation in Finnish breeding mentioned above seems to be such a moderate application with limited risk.

It seems illogic that unbalance in testing effort should be strongly positive while unbalances in contributions small, that indicates a better balance between these two types of unbalances can be found.

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USING SEED ORCHARD SEEDS WITH UNKNOWN FATHERS

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Abstract

The natural pollen cloud moving around with the winds in early summer may account for 50% of pollinations in mature seed orchards with high internal pollen production. The background pollen is genetically different from seed orchard pollen produced by selected plus trees. This may affect the adaptation of the seed crop and justify a modified use of the seeds, e.g. the best place to use the crop. However, even seeds from young seed orchards without pollen production may usually be useful forest regeneration material and there are reasons to limit or eliminate demands on high internal pollen production when seed orchard clones and contaminating pollen do not differ much in adaptation. Artificial freeze testing seed orchard crops of Scots pine for autumn cold hardening is often performed in Sweden to determine the area of utilization. In the same way the hardiness of the natural pollen cloud can be experimentally estimated using artificial freeze testing of progenies obtained from controlled wind pollination of selected clones. Therefore a number of permanent small clone archives of Scots pine have been established in central and northern Sweden as a basis for evaluating geographical and daily variation in the hardiness of the background pollen cloud. An archive of mobile grafts is also under establishment. One application may be long-term mapping of changes in the natural pollen cloud following climate changes and large-scale seed transfer in Swedish forestry.

Background

The major wind-pollinated Swedish forest trees (Scots pine, Norway spruce, birch) produce large quantities of pollen able to be transported wide distances by the wind. This pollen will influence seed orchards, the issue was discussed at a Nordic Genetic meeting 1991 (Lindgren 1991). Seed orchards trees produce pollen as well as seeds. In the early days of seed orchards, the hope was that once the pollen production in seed orchard started, it would outcompete pollen sources outside the seed orchard. Calculations indicated that a pollen production around 20 kg/ha would be well compatible with other pollen sources and harvest has often not been recommended until that pollen production has been reached. Later research showed that even in seed orchards with a considerable pollen production, fertilizations with fathers outside the seed orchard were important, and today we assume and accept 40-50% pollen contamination in mature seed orchards. Still cone harvest is often not recommended until the pollen production has reached 20 kg/ha, that is common in Swedish seed orchards of Scots pine and Norway spruce. A detailed evaluation of the likely quantitative consequences of utilizing the contaminated crops from young and mature seed orchard crops has never been done.

Differences between seeds fertilized by inflowing pollen versus «seed orchard pollen»

Today almost all practically used seeds in Sweden come from seed orchards with phenotypically selected plus trees. The superiority of the first generation seed orchard seeds compared to stand seeds is estimated to 10% and probably there are three sources for the superiority: (i) selection of plus trees (6%), (ii) release of inbreeding (2%) as there are relatives in a stand but not in a seed orchard (can also be expressed as hybridization as plus trees are selected from a wide area, range 100 km or more) and (iii) seed orchard seeds are more «vital», or better programmed or «physiological effects» or has a higher weight and maturity which leads to an estimated 2% «gain» (Rosvall et al 2001).

The «physiological» effects are at least in the first approximation expected to be the same whether the pollinator is a seed orchard clone or contaminant. «By definition» we define trees in *different* stands as non-related, relatedness must be «recent», the more generations back we go, the more common ancestors there will be. In advanced seed orchards, clones may be relatives and the inbreeding higher because of relatedness.

More improved seeds

Insufficient pollination can cause early conelet abortion, empty seeds and reduced production of filled seeds. In Sweden there is usually sufficient Scots pine pollen for full seed production even in absence of seed orchard pollen. But in other situations, like in environments where Scots pine is not among the dominating species, the pollen from the seed orchard can give an increased seed production of improved seeds.

Pollen from native or transferred populations

In Swedish forestry large-scale transfer of trees has been carried out by forest owners for many decades. For Scots pine the transfer direction has been mainly from north to south, which is in the opposite direction to the main wind direction and natural pollen flow during the flowering period. As the transferred forests grow up and become fertile their pollen will contribute to the natural pollen cloud with a different genetic composition compared with pollen released from native stands in the same region. Today pollen from transferred forests does contribute much to the natural pollen cloud, and its influence on the seed orchard crops should still be relatively small, although this influence is increasing.

Breeding value

The seed orchard parents are selected while the parents of the background pollen are not selected. Breeding value of a seed with a plus tree mother and a father from outside the seed orchard is expected to be exactly half of that if the father was a seed orchard clone. If the outside father has a different geographical origin than the seed orchard father, the genetic value of the seed might be either higher or lower than half of that of a seed obtained from pollination with a plus tree father. However, unlike pollen from forests transferred by man, tree breeding has not yet advanced long enough to make contribution from bred trees in the general pollen cloud important. For the breeding values in the 3rd-batch seed orchards estimates by Lindgren and Prescher (2005) were considered.

Selfing

Trees of the most relevant species produce both pollen and seeds and are able to self-fertilize. As male and female structures are not very distant an estimated amount of 10% self pollination seems reasonable. Most selfed zygotes die and most selfings results in reduced production of filled seeds. The selfing frequency among germinating seeds or young seedlings is measurable and it is likely to be in the magnitude 4 percent (although figures such high as 25% has been reported), different in different investigations and under different circumstances. The selfed individuals are discriminated during the whole life cycle and few remain to the mature stand.

Selfing in a clonal seed orchard can occur in two ways, either selfing with a ramet's own pollen, or one ramet pollinates another of the same clone. The chance that the later will occur depends on the number of clones in the seed orchard. Lindgren and Prescher (2005) have developed methods for estimation of selfing effects. The estimates of the influence of selfing within ramets on a production compatible scale for Scots pine by Lindgren and Prescher (2005, 1.6%) in table 1 are in hyphens. Rosvall et al (2001) makes estimates which are half as high. The analysis by Lindgren and Prescher was for evaluating suitable clone number and to reduce the risk that the recommended clone number is too low and may overestimate selfing, so the production loss is assumed 1%.

Contaminating pollen can not cause self-fertilization in seed orchards; the rate of selfing will increase when the internal pollen production increases. The lower situated cones get higher rate of selfing than the higher, as the male reproductive structures are in the lower part of the crown. Because lower cones are easier to harvest, the selfing rate in a harvested seed orchard crop may be higher than in the biological crop.

Diversity Loss

The biological production in a forest may decrease if it is insufficiently diverse. Diversity also has an immaterial PR-value. The diversity losses for seed orchard crops in Table 1 are estimated by methods developed by Lindgren and Prescher (2005) and using their quantifications for Scots pine seed orchards.

Table 1. Summary of quantitative estimates for stand seeds and seeds from young and mature 1st batch and 3rd batch of seed orchards.

Parameter	Stand seeds	1st batch seed orchard		3rd batch orchard	
		Young	Mature	Young	Mature
Contamination (%)	50	100	50	100	50
Clones number	?	50	50	20	20
BV-clones	0	6	6	20	20
BV-seeds	0	3	4.5	10	15
Physiological	0	2	2	2	2
Selfing – within ramets	-1.0 (-1.6)	0	-1.0 (-1.6)	0	-1.0 (-1.6)
Selfing – among ramets	0	0	-0.2	0	-0.7
Relatedness	-2	0	0	0	0
Diversity loss	0	-0.2	-0.4	-0.5	-1.1
Adaptation uncertainty	0	-2	-1	-2	-1
Sum	-3.0 (-3.6)	2.8	3.9 (3.3)	9.5	13.2 (12.6)

Adaptation loss and uncertainty

The seed orchard crop is made up of one seed crop from internal pollination and one seed crop from background pollination. Because the two seed lots are in practice impossible to separate a seed orchard crop can be considered and handled as a single seed lot with a wider adaptation than a seed orchard crop from pure internal pollination. With the wider adaptation follows that pollen contamination reduces the maximum adaptation of the seed orchard crop to a specific climate.

Because the contaminating pollen may vary in origin and frequency due to changes in weather conditions (temperatures, winds, rain etc.) before and during female receptivity, crops from a seed orchard exposed to pollen contamination are more uncertain and less reproducible than a crop from a seed orchard less affected by contamination.

Nilsson (1991) presented a model to estimate effects on survival of seed orchard crops planted on different latitudes/altitudes from varying background pollination rates and origins. The model can handle daily variations in both rate and hardiness of the contaminating pollen (assuming a normally distributed quantitative trait) as well as for pollen and female gametes in the seed orchard. By careful studies of timing of pollen dispersal and female receptivity and estimation of breeding values of the seed orchard clones relevant parameters for the seed orchard genotypes can be determined for input into the model. However, little is still known about what parameter values are relevant for the complex background pollen.

Daily variation in origin and adaptation of background pollen

In a seed orchard female receptivity may be extended over a period of one week or more. It is reasonable to assume that changes in weather condition and wind directions might cause significant changes in the origin of long distance pollen invading a seed orchard in different days of the receptive period. Nilsson (1995) found that the background pollen in a coastal clone archive of Scots pine had a geographical origin and cold hardiness (estimated from artificial freeze testing of progenies from controlled wind pollination and progenies from pollination with reference pollen) approximately one degree latitude north of the archive. The most likely explanation was that immediately before female receptivity occurred in the clone archive a heavy rain washed out pollen from the air and the earlier southern winds were changed to northern ones carrying pollen from early flowering non-coastal northern localities. With a more interior localization (less influence of the cold Gulf of Bothnia on early summer temperatures means earlier receptivity) or if the sudden change in weather conditions had occurred a few days later more southern pollen would probably have contaminated the archive and reduced the hardiness of the seed crop.

Discussion

Today it is usually recommended for Scandinavian conifer seed orchards to start seed collection when pollen production is above 20 kg/hectare to assure a sufficient reduction of pollen contamination from outside the seed orchard. It is suggested that the demand is relaxed for seed orchards where the contaminating pollen is not drastically different from the seed orchard clones. The seed orchard material can often be assumed to be the best available for reforestation even in cases with 100% non seed orchard pollen.

The gain from a young 3rd batch of seed orchards compared to a mature first batch seed orchard is considerable when adaptation pattern of the contaminating pollen is the same as the orchard clones, and is thus not likely to be inferior as long as there are not large problems with the adaptation of the contaminating pollen.

Selfing

Estimates of selfing are mainly done on rather young seed orchards, whereas pollen production per graft and thus selfing may be larger in mature seed orchards. It is possible that the 3rd batch of seed orchards will be subject to more selfing as they are planned for more intensive pruning. The repeated pruning may raise the male strobili in the tree crowns and move them on average closer to the female strobili and thus increase selfing, as has been found a problem with lodgepole pine seed orchards in British Columbia (Owens et al. 2005).

Testing seed orchard crops

The adaptation pattern of each actual crop could be tested. Such tests are sometimes done routinely, e.g. artificial freeze testing of seed orchard crops during autumn cold acclimation using seeds of known adaptation pattern as references. There may also be variations among years due to variable contribution from different clones, the effect of this would be decreased by freezing tests. This problem will increase with the 3rd round seed orchards as they will have fewer clones, and there may thus be a larger variation among years. A possible problem with progeny testing of young seedlings occurs if the testing method catches up «after-effects» which are physiological rather than genetic. One way to circumvent this problem is to postpone testing of seedlings until possible after-effects are insignificant. In freeze testing for autumn cold acclimation after-effects have been found small already for one-year progenies, and non-significant for two-year progenies. Anyway, we suggest a mixture of reliance of test results and predictions based on origin and common sense when deciding the area of use of tested seed orchard crops.

Adaptation correction

The seed orchard parents are selected as they are expected to match the adaptation demands in the target area for the seed orchard. The target area can be where the average of the seed orchard clones is best adapted. However, the pollen contamination is so large in mature seed orchards, so the matching of seed source and intended area of use will assume 40-50% pollen contamination. If the orchard clones have different adaptational pattern than the contaminating pollen, the target area can be modified considering the adaptation. For Scots pine the adaptation can be expressed as latitudes, and the adaptation of origins could be modified by one degree latitude for 300 m difference in altitude of origin. The target area of the mature seed orchard crop could be calculated as the average of the target area for the clones and the contaminating pollen.

If the difference in adaptation of the seed orchard clones and the contaminating pollen is not much larger than what corresponds to one latitude of origin, it is suggested that the loss is neglectable. If it were 1 latitude, the mature seed orchard adaptation would be changed 0.25 latitudes because of the contamination, now the adaptation would change 0.5 latitude instead, thus a difference in the adaptation peak of the seed orchard crop of 0.25 latitude. Clone origins in a seed orchard typically have a range of 1.5 latitudes. The intended target area of the orchard ranges slightly more than one latitude.

Individual seed crops from the same seed orchard vary. Let us assume that adaptation varies with a standard deviation of 0.4 latitudes. Seen against these ranges and fluctuations and also uncertainty, a change in adaptation caused by the decreasing amount of pollen contamination seems marginal. The contaminating pollen is also variable among years, both in extent and in origin, so that is a disadvantage with a larger share of contaminating pollen. Quantitatively the production loss is likely to be below one percent, as the loss of adaptation by recruiting plus trees from a range of two latitudes instead of recruiting from the same latitude is less than one percent (Lindgren and Ying 2000).

Lindgren and Cheng (2000) calculated adaptational loss as a function of seed orchard size using data for Swedish Scots pine. The worksheet is found at:

http://www.genfys.slu.se/staff/dagl/Breed_Home_Page/SiteNrRange/ADAPTATION.XLS

The math discussed here should be valid for Scots pine plantations on adjusted latitudes 59 and 66.5 (thus not the highest elevations in the far north). Some figures are derived from that which a perfectly adapted provenance is assumed to perform 100%. To indicate adaptedness latitude is used, but this latitude is to been seen as adjusted for altitude. Seed orchards are composed of a mixture of provenances; the plus trees are assembled over a range assumed to be two degrees latitude. That means that if the seed orchard material is used where it has its adaptational peak it produces 99.3% of its production capacity because of the heterogeneous origin of the plus trees, while a provenance at its adaptational peak produces 100%. A seed orchard crop used over a range of 1.5 latitudes (± 0.75 latitudes from where it is «targeted») has an adaptational value of 98.9 % on average over the range of use of the seed orchard material. But 0.75 latitudes away from the target the value is 97.4% and one latitude away from the target it is 95.6 %. Let us say that the contaminating pollen has an adaptation for X latitudes south of the adaptation of the seed orchard clones (designed X0). This would change the adaptational goal for the seed orchard. For 50% and 100% contamination the goal would be changed (X0-0.25*X) and (X0-0.5X), respectively. If seed usage assumes 50% contamination but the contamination is 100%, the seeds would be out of target with 0.25X. The consequences are summarized in Table 2.

Table 2. Expected effect from differences in geographical origin of seed orchard clones and contaminating pollen assuming 50 % pollen contamination (model from Lindgren and Ying, 2000)

Difference between seed orchard average and contaminating pollen	Difference between recommendation for mature crop and best use of young crop	Value if young seeds are used based on an area assuming a mature 50% contamination (%)	Expressed as loss (%)
0 latitudes	0	99.6	0.0
1 latitude	0.25	99.4	0.2
2 latitudes	0.50	98.6	1.0
3 latitudes	0.75	97.4	2.2
4 latitudes	1.00	95.6	4.0

The losses expressed by this method give approximately the same but marginally larger losses compared to suggestions by «Val av skogsodlingsmaterial» www.skogforsk.se). A few percent can be seen as marginal. There are few cases where the difference between the orchard clones and the contamination origin is likely to be larger than 3 latitudes and even if it is not expressed in official recommendations it is still likely that some considerations may be done. The «loss» will lead to a higher increase in mortality but that is partly compensated for by a better growth. However, the losses will be relatively larger if the area of use is on the fringe already with assumption of 50% contamination.

Conclusion: it should usually be possible to generalize so the recommended seed use is the one assuming 50% contamination even for the early crops.

Localization of seed orchards

Seed orchards are preferably established on localities that favors rich flowering, large seed crops and high seed quality. For northern latitudes this usually means more southern localities at lower elevation and closer to the coast than the plus tree origin. A consequence of the southern location is an increased risk of exposure to pollen populations that are poorly adapted to northern environments. The increased risk of southern localization has two sources: shorter geographical distance to southern pollen sources, and less time separation between flowering in the seed orchard and the timing of pollen dispersal in southern stands. Coastal localization of seed orchards may delay flowering about one week compared to localization in the warmer, less costal localities on the same latitude. Except for the mountain areas in the west that are unsuitable for abundant seed production for other reasons, the coolest early summers in central and northern Sweden are probably found on islands in the sea. Such localization of a seed orchard should mean that female receptivity can be delayed another week or more compared today's localization in coastal mainland (Figure 1).

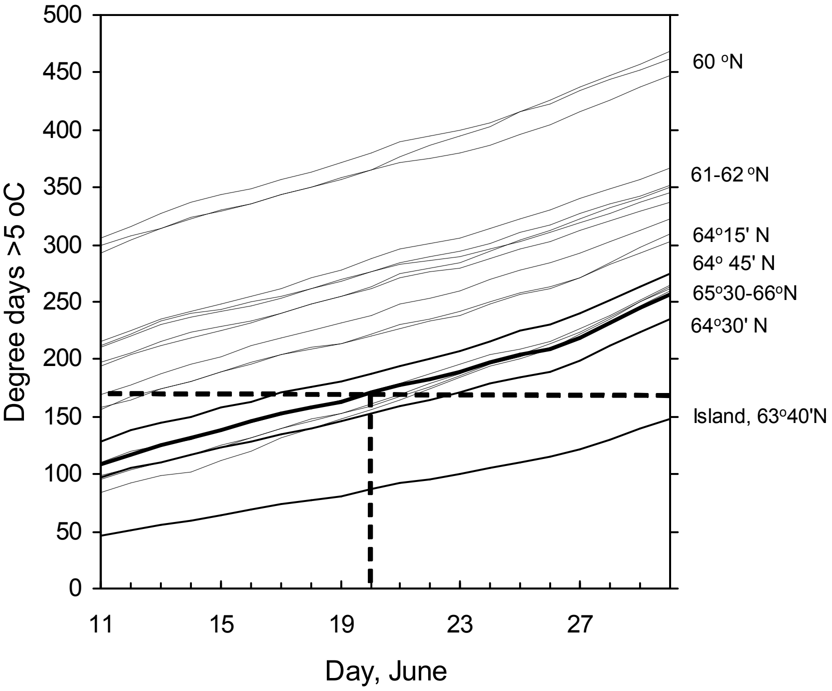

Figure 1. Degree days (> 5°C) in June 1998 on 19 weather stations (SMHI) between latitudes 60 and 66 °N Sweden. The bold curve indicates Umee (lat 63°48'N), the dotted lines indicate date and degree days for onset of pollen dispersal in mature seed orchards close to Umee.

Localization on islands in outer archipelagoes would usually reduce the influence of southern background pollen and enhance the influence of northern background pollen on the seed orchard crop. However, so far we have too little knowledge about how the geographical origin and genetic composition of the background pollen are affected by weather and winds to make more than very approximate statements about effects of seed orchard localizations on the adaptation pattern of seed orchard crops.

Clone archives for pollen cloud observations

In the early 1990's nineteen small clone archives of Scots pine, each with the same ten clones, were established in central and northern Sweden between latitudes 61 and 67°N with the intention that the female flowers would catch up the background pollen on the different localities. From the seeds produced by wind pollination, progeny testing can be performed to study geographical variation in adaptation patterns between pollen clouds. To reduce pollination from neighboring stands the archives were established in areas without adjacent Scots pine forests. The ten clones originating from between latitudes 62 and 67°N in Sweden are represented by five grafts in each archive. Clone selection was made in mature seed orchards for abundant female flowering but no pollen production. In addition an archive of potted grafts of Scots pine clones was recently initiated as a mobile complement to the permanent field archives allowing future studies of background pollen on any places.

Some of the permanent clone archives on mild localities up to latitude 64°N have now started to produce female flowers and seeds to allow progeny testing of background pollinated progenies. Therefore the first artificial freezing experiments for autumn cold acclimation are now performed to give experimental indications on differences in cold acclimation patterns between natural pollen clouds of Scots pine on different localities in Sweden.

Norway spruce

With Scots pine and northern Norway spruce «origin» can be related to mainly «latitude» and that makes the contamination rather manageable. With Norway spruce in southern Sweden the critical factor is flushing phenology in early summer which is more a question of longitude of origin. Long pollen transports ought to be less frequent for Norway spruce as the pollen is heavier and less likely to stay airborne for many hours. «Local» pollen originating some kilometers from the seed orchard may cause the same contamination rate; but it would at least be somewhat more reproducible. On the other hand there may be larger variations in «local» contamination, in particular considering the large variation in origin of spruce in southern Sweden. There are observed effects in seed orchards with Eastern European clones which could indicate that the large phenological genetic differences matter for contamination. Could it be some sort of physiological effects rather than contamination?

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SEED PRODUCTION IN SCOTS PINE SEED ORCHARDS

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Abstract

Earlier studies show that seed orchards have considerable heavier cones and seeds, but not necessarily more seeds per cone and fluctuations in seed production are smaller than in stands. Harvest statistics are often available for seed orchards; usually the amount of harvested cones and seeds drops by age of the orchard. However, the harvest statistics seldom reflects the actual biological seed production. Biological seed production in some Swedish Scots pine seed orchards was calculated. No decrease in seed production when the orchard gets old was indicated. A case was reported when dense spacing did not increase seed production at age 30. Few of the cones were registered in a fast cone count in two mature seed orchards, indicating that manual observations are unreliable. Reasonable estimates of variation in female fertility among grafts seem possible with simpler measures than actual seed count. A considerable variation in female fertility among grafts was observed. The variation in seed weight among ramets was rather moderate.

Keywords: Seed orchards, cone production, seed production, seed weight, fertility variation, visual estimation.

Introduction

Prognoses of seed set in seed orchards are needed for projections about future seed production, for operational decisions and also for estimates of effective population size. There exist, however, a considerable difference between different meanings of seed production, which complicates these procedures. Reports about seed orchard harvests are frequent, but actual seed production is more rarely reported. Even when seed production per graft is reported, it is seldom converted to area production and often considers young grafts where seed production per area still is raising. There is a biological seed production potential, but the seed available for operational harvest is another thing, harvest statistics further another, and seed production observed in experimental settings may not be representative for operational seed orchards. Here some aspects of this will be discussed. Some estimates of biological seed production in actual mature seed orchards will be presented. Methods for estimation will be discussed.

Seed production in nature and its relevance for seed orchards

The Scots pine stand seed production has been carefully investigated in Finland; the main important studies were initiated by Heikinheimo in 1920's (Heikinheimo 1932, 1937) and continued, by Sarvas (1962) and Koski and Tallqvist (1978). There are also important Swedish studies like Hagner (1957). In natural stands, seed crop (on areal basis) is higher in rather sparse seed tree stands as compared to dense forests (Heikinheimo 1937). The difference increases with time from the thinning treatment and is greater in poor seed years. On average 50 seeds/m^2 are produced in northern Finland, 100 in central Finland and 150 in southern Finland. In peak years it may be three times as high. Seed production increases with site class.

A comparison between natural stands and seed orchards reveals that there are at least sometimes differences in their cone and seed characteristics. The number of seeds per tree (graft) can be higher in seed orchards than in stands. The cone number and volume may be larger. Cone size is – not so surprisingly – clearly greater in seed orchards, but number of seeds per cone is about the same (20). Seed production per volume unit of cones is higher in stands than in seed orchards. Seed weight is considerably higher in seed orchards (see below). The annual variations are likely to be smaller in a seed orchard than in a stand.

There are differences between seed orchards and stands, which may explain differences in seed set. Scots pine seed orchards have often a more southern location than their utilization area, and a good site class; they are often situated on former farmland. Land preparation includes ditching and removal of competing vegetation. Sometimes they are fertilized. A natural stand under those conditions would probably produce 120-150 seeds/m^2. A mature seed orchard is similar to the top of an old stand, thus a similar seed production would be expected. Thus we may assume that biological seed production in old seed orchards would approach 120-150 seeds/m^2 (10 kg/ha in orchards, but only 6 in stands).

When trees are released in seed tree cuttings they react by setting more cones and producing more and heavier seeds (Karlsson 2000). The effect is largest 4-5 years after the release and may then pass 200 seeds/m^2. The seed production is still considerable higher 10 years after the release than before. Seed tree stand conditions may have some similarity with seed orchards.

Material

Observation of seed production

We report on seed production in mature Swedish Scots pine seed orchards. Information about the concerned seed orchards is given in Table 1.

Table 1. Basic information for considered Swedish Scots pine seed orchards

Seed Orchard	Year(s) established (planted)	Latitude, °N	Number of clones (main clones)	Intended (planted) grafts per ha	Description of the orchard, reference
Askerud	1966-69	60	43	400	Almqvist et al. 1995; Eriksson et al. 1998
Klocke	1968-72	62	60	318	Eriksson et al. 1998
Lustnäset	1969-72	60	69 (40)	278	Almqvist et al. 1998
Lengtora	1962-64	60	36	400	Jonsson et al. 1976
Skaholma	1958-1980 (+70-86)	64	42	(277-)625	Yazdani et al. 1995
Sävar, experimental seed orchard	1969 (-77)	64	51	158-625	Rosvall et al. 1983

Results

Observations of seed production

In Table 2, rather recent observations of actual biological seed production from mature seed orchards are presented. None of the observations has been used for estimation of per area seed production earlier, although some other aspects of the basic data utilized, have been published for Askerud, Klocke and Lustnaset.

Table 2. Observations of biological seed set (filled seeds)

Seed orchard (seed maturation year)	Seeds per m^2	Seeds per m^2, adjusted A)	Seeds per graft	Remaining grafts/ha; B)	Clones observed	Graft age Oldest, (likely) C)	Grafts observed	Reference
Askerud 2000-02	71		2130	335	40	36 (34)	240	D)
Askerud 1991	70		2000	350	6	26(24)	6	Eriksson et al. 1998
Klocke 1990	129		4781	270	12	22 (20)	≈ 30	Eriksson et al. 1998
Lustnдset 1993-94	179		6470	278	47	25(23)	96	Almqvist et al. 1996
Lengtora 2004	349	349	22340	156	12	42(41)	34	D)
Skaholma 2004	231	153	17761	130	14	46(40)	42	D)
Sдvar 156 – 1999	255	152		125	51	30(29)		
Sдvar 331 – 1999	321	191		269	51	30(29)		D)
Sдvar 625 – 1999	323	192		525	51	30(29)		

A) Adjustment made for cone set in pine forests in the region according to the Swedish Forest Survey (In the region around Savar 1999 it was 1.4 more than normal; 1.5 around Skaholma 2004; and 1.0 around Langtora 2004).

B) Could be arithmetic average of 2 or 3 years, refers to untreated grafts. Skaholma and Langtora are based on inventories of graft density 2004 to 2005 by the authors.

C) Refers to age at seed set.

D) Data not published before.

In seed orchard Askerud the same per hectare seed production is observed at age 24 and 34 (70 and 71 seeds/m^2 respectively). A considerably higher production is observed in Klocke (129 seeds/m^2) and Lustnaset (179 seeds/m^2) even though these orchards are younger than Askerud.

Skaholma and Langtora are mature seed orchards at the end of their service period (actually trees at Langtora were cut in connection with the cone harvest). The seed orchards have not been pruned or managed for the previous five years (Skaholma) or decade (Langtora). The cones may be typically growing 5 meters (Skaholma) or 7 meters (Langtora) from the ground. The seed production in Langtora is outstanding the highest in this study, 349 seeds/m^2, whereas Skaholma has about the same production (153 seeds/m^2) as the experimental orchard Savar at the same spacing.

An interesting result is, that at age 30, different spacings (269 and 525 grafts/hectare) in the experimental seed orchard Savar resulted in the same number of seeds/m^2 (191 and 192 respectively).

In Skaholma and Langtora the clonal variation in seed set was studied. All cones were collected 2004, and the seeds extracted, from 3 grafts per clone for 12-14 clones. The results are summarized in Table 3.

Table 3. Cones, seeds and seed weight per graft at Skaholma and Langtora 2004 and their variation among grafts. CV is coefficient of variation, thus the standard deviation divided by the mean

Seed orchard character	Lengtora		Skaholma	
	Mean	CV	Mean	CV
Filled seeds	22340	0.682	17761	0.845
Weight of filled seeds (g)	125.48	0.753	94.68	0.800
Volume of cones (dm^3)	21.14	0.707	14.13	0.852
Number of cones	1122	0.686	886	0.877
Cones observed from ground	83.5	0.577	80.1	0.721
Seed weight (mg)	5.47	0.153	5.56	0.120

Visual estimation of cone set

An effort to estimate the cone set of individual grafts by a fast visual inspection was done for grafts at Langtora and Skaholma, where also an exact count was done. A spot was chosen with a good view of the graft. Preferable spots to the south were chosen to get better illumination. Only unaided eye was used. Visible cones without moving were counted. Less than 10 per cent of the harvested cones were observed (Figure 1 and 2), which was a surprise for the observer.

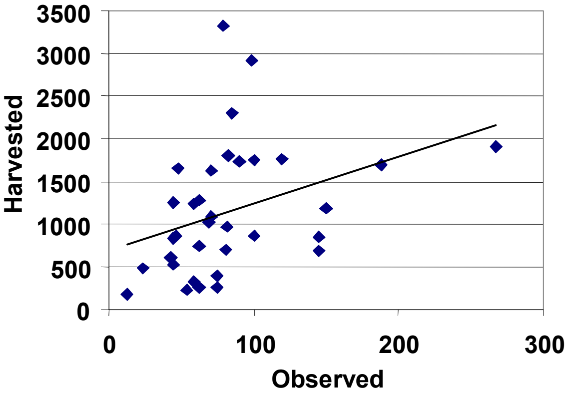

Figure 1. Relationship between visually estimated number of cones and harvested (= true number) cones per ramet in seed orchard Langtora 2004.

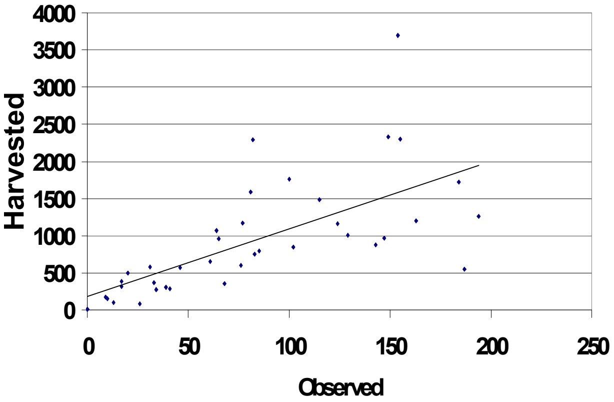

Figure 2. Relationship between visually estimated number of cones and harvested (= true number) cones per ramet in seed orchard Skaholma 2004.

The visual estimates were regressed against the exact counts :

$Y = 695 + 5.50X$; $r = 0.359$ (Langtora)

$Y = 179 + 9.12X$; $r = 0.673$ (Skaholma)

where X is visible cones for a ramet, Y is harvested cones for a ramet, r is the coefficient correlation.

Seed weight

One motivation for seed orchards is the superior technical seed quality. One important factor is the seed weight, which is generally considerable higher than for stand seeds. Recorded values in Swedish Scots pine seed orchards for 16 years, are compiled in Table 4. After 1988 the series was broken for administrative reasons. The table is based on many individual annual reports from former «Institutet for Skogsforbattring» (list of these sources can be found at http://www.skogforsk.se/), which never have been compiled before. Table 4 also compiles some previously not published data with stand seeds analyzed in response to enquiries from practical forestry.

Table 4. Seed weights of Swedish Scots pine seeds (mg/seed or g per 1000 seeds) harvested in seed orchards and stands

Year	Seed orchard seeds				Stand seeds	
(seed maturation)	Northern Sweden	Middle Sweden	Southern Sweden	Average	Middle Sweden	Northern Sweden
1973	6.57	6.39	6.44	6.467	n/a	4.64
1974	6.08	5.55	6.33	5.987	n/a	4.23
1975	5.48	5.83	6.54	5.950	n/a	2.89
1976	6.32	6.53	7.31	6.720	5.36	4.30
1977	5.31	5.43	5.86	5.533	4.11	4.00
1978	5.37	6.09	6.12	5.860	n/a	3.47
1979	5.96	6.12	6.33	6.137	4.13	4.07
1980	6.07	6.47	6.25	6.263	3.77	4.03
1981	5.76	6.14	6.27	6.057	3.85	3.85
1982	5.51	5.76	6.33	5.867	4.03	3.67
1983	5.86	6.14	6.56	6.187	4.02	3.79
1984	5.88	6.07	6.34	6.097	n/a	3.63
1985	6.06	6.70	6.84	6.533	3.82	3.78
1986	6.28	6.16	6.20	6.213	n/a	3.89
1987	5.54	6.20	6.26	6.000	n/a	2.41
1988	6.93	7.15	6.97	7.017	n/a	4.47
Average	5.936	6.171	6.434	6.180		3.82
# Seeds/kg	168 457	162 058	155 415	161 801	-	261 706

Discussion

Observations of seed production

According to Table 2, there are annual variations in seed production and the observations may have been done unrepresentative years, therefore for some of the values we adjusted as if the seed orchard harvests had varied as observations on cone set made by the Swedish Forest Survey. However these adjustments are likely to be too large, the variations in cone set are likely to be smaller in seed orchards than in stands and the deviations in the seed orchards are likely to reflect real deviations from stands as well as annual fluctuations, but still the adjustments are given to give an idea of how unrepresentative the few observations may be. Another uncertainty is that the observations of the Swedish Forest Survey are done visually, c.f. the discussion below.

The Savar seed orchard was established as an experimental orchard situated physically adjacent to the Swedish Forest Research Institutes station, and this gives probably an advantage (higher per area seed production) compared to an ordinary operative orchard. From the beginning it has a better protection situation (better fencing; problems are noted and acted on faster; etc.). Lost grafts are usually replaced rather fast and the spacing at operation had not declined much compared to the initial.

The study shows that dense spacing does not seem to promote seed production beyond 30 years, however this is very scarce and difficult to interpret data. The experimental orchard has 16 large seed orchard plots, all with different treatments (thus no true replications). It is thus unreliable to separate a single factor like spacing, since many factors are confounded.

The high per area seed production in the more than 40 year old seed orchards, Skaholma and Langtora, with large grafts growing at a density of magnitude 150 grafts/hectare, strongly indicates that biological seed production does not decline when grafted seed orchards get old and large with widely spaced trees. That harvests often decrease in old seed orchards is more likely to be associated with lower accessibility of cones, lower priority in connection with higher costs of harvest and management actions, to get cones more accessible on large grafts. The seed orchards were not recently pruned, which probably contributed to the high seed production. Therefore the seed production can probably not be considered sustainable, at least if cones should stay within reach.

The estimated variation among grafts (CV) in fertility does not differ much if measured as any of the characters: filled seeds, weight of filled seeds, volume of cones, number of cones, or cone counts from ground. Thus probably all measures results in usable estimates of female fertility variation and the most cumbersome methods need not be generally used for that purpose.

Seed weights can probably be as variable among grafts in a seed orchard as among years. The seed weight 2004 was probably lower than average for Langtora. Probably this is connected to that no fertilization had been done for a long time and that the seed crop was high, but the seed weight is still much higher than in stands. For Skaholma the average seed weight 1973-88 was 5.59 mg, 2004 does not deviate from average.

Visual estimates of cone set

That few cones are visible in a seed orchard could be as the nourishment state is usually good in a seed orchard, the crowns could be rather dense and many cones could be hidden. In our study we saw only about 10% of all cones. The Swedish Forest Survey makes annual inventories of cone set (mentioned in Table 2). Trees are observed by a binocular from a point chosen to see many cones. Hagner (1957 p26-28) made such an inventory of 170 pines on different localities covering Sweden. The trees were felled and all cones collected. It was found that 23.1 % of the cones were seen. In a stand the crown is not so dense, so more of the cones may be visible. Also the use of binocular will increase the number of observed cones somewhat.

The coefficient correlation in this study is rather low, but still visual estimates seem good enough to get an impression about the variation among grafts, and thus probably also among clones. Even if the correlation is moderate, it is still high enough to be used as a guide about which grafts produce many or few cones.

Seed weight

Seed orchard seeds are considerable heavier than stand seeds, even in not well-maintained seed orchards. The reason why orchards produce seeds that is heavier than stand seeds seems to be complex. Seed orchards are generally established on fertile soils on agricultural land, they are located in mild locations with high temperature sum and the capillarity in the soils is normally good, but the difference is not dramatic and is larger among years than among parts of the country. Trees within orchards are widely spaced and commonly pruned, the use of fertilizer, herbicides and moving grass are regular treatments. Clones within northern orchards are often southerly transferred. Perhaps a contributing reason could be that plus tree selection is a selection of trees that produce higher seed weight. Perhaps top pruning, which breaks the apical dominance and forces more nutrition to branches and less to height growth, can be a contributing reason, but heavier seeds are observed also in non pruned seed orchards.

Acknowledgement

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RESULTS FROM GENETIC TESTS OF *BETULA PENDULA* AND ITS IMPACT ON FUTURE BREEDING IN SOUTHERN SWEDEN

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Abstract

Phenotypically selected plus-trees of silver birch (*Betula pendula* Roth) were tested in progeny and clonal tests in the southern part of Sweden. The report includes genetic evaluation of survival, growth and fibre/wood traits up to 11 years of age.

Growth traits were mostly under strong genetic influence, genetic variation was substantial indicating a high potential for genetic gain. The genetic age Ч age correlations were strong, suggesting that short test periods could be used. No transfer effects for clones of different origin was found and GxE correlations were strong indicating that southern Sweden can be treated as a single utilization zone.

Wood and fibre properties were under strong genetic control with broad sense heritabilities varying between 0.66 and 0.73. Their genotypic coefficients of variation were quite low (3.5 to 4.7 %). The genetic correlation between growth and wood/fibre traits were weak and not significant except between diameter and wood density showing an unfavourable, modest and significant correlation (r_g = -0.53).

Introduction

Using broad-leaved species as an alternative crop on surplus agricultural land increased interest in birch at the end of 1980"s and resulted in a re-start of birch breeding in all of Sweden. For administrative and biological reasons the country was divided into four breeding zones (Figure 1), where the most southern zone (latitude <60°), is of concern in this report.

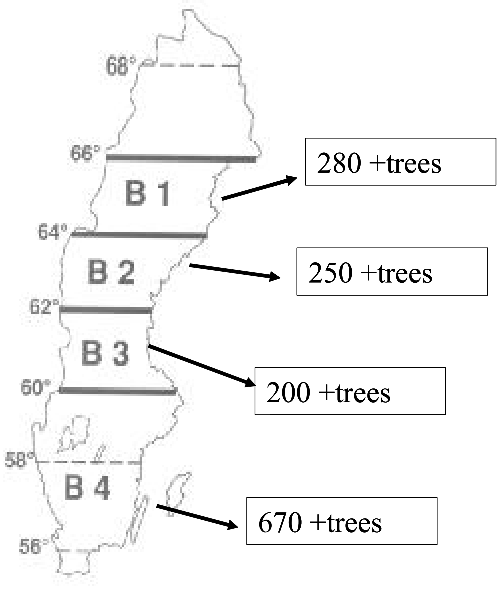

Figure 1. Basic birch breeding zones and number of selected plus-trees per zone.

The main objectives of birch breeding are improvement of vitality, yield and external stem quality traits (Danell & Werner 1989). A total of 670 plus-trees of silver birch (*Betula pendula*) were selected for southern Sweden during the years 1988-1990. The trees mainly originated from southern Sweden, but trees from southern Finland, Lithuania, Poland, Germany, Latvia, Holland and Estonia were selected as well.

The plus-trees were all supposed to be genetically tested in clonal tests after vegetative propagation by tissue-culture techniques. However, micro-propagation was only successful for 40 % of the plus-trees and a total of 20 clonal tests were established during the years 1990-1991. The remaining 60 % of the plus-trees were grafted, intensively cultivated in a greenhouse and finally planted in a clonal archive at the Ekebo research station (55°57'N, 13°07'E, 80 m). Totally 10 progeny tests based on open-pollinated seed from the grafts were established during the period 1992-1998.

In this report main results of genetic parameters and genetic correlations and its impact on future breeding of silver birch in southern Sweden are presented.

Materials and methods

The results are based on trials each including tests of at least 39 plus-tree clones of Swedish origin only (Table 1, Figure 2). The trials were established as single tree plots in a randomised block design with five (clonal tests) and up to 15 (progeny tests) replications per trial in a spacing of 2Ч2 m. In trials 1A-1C, 2A-2C, 3A-3B and 4A-4B respectively, the same set of clones were tested.

Table 1. Trial data. From Stener & Jansson (2005)

Trial no	Name	Planting year	Type of land	No of clones
Clonal tests				
1A	Hjuleberg	1990	Agriculture	78
1B	Hцreda	1990	Forestry	83
1C	Simonstorp	1990	Forestry	74
2A	Trollehom	1991	Agriculture	43
2B	Kavles	1991	Agriculture	45
2C	Harg	1991	Agriculture	41
Progeny tests				
3A	Вцkц	1995	Forestry	57
3B	Jдrpes	1995	Agriculture	59
4A	Hallsjц	1998	Forestry	44
4B	Striberg	1998	Forestry	39

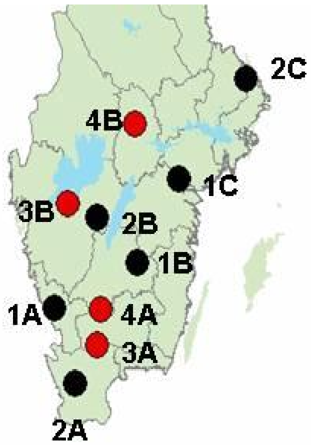

Figure 2. Location of the trials.

The statistical analysis was based on individual tree observations according to the models:

$$y_{ijk} = \text{м} + b_i + c_j + d \cdot h_{ijk} + e_{ijk} \qquad \text{(clones)} \qquad (1)$$

$$y_{ijk} = \text{м} + b_i + f_j + e_{ijk} \qquad \text{(open pollinated, half-sib families)} \qquad (2)$$

where y_{ijk} = observation k, in block i for clone or progeny j, м = trial mean, b_i = fixed effect of block i, c_j = random effect of clone j, f_j = random effect of family j, and e_{ijk} = random error term for observation ijk. The differences in height at the time of planting were considered in the analyses of the clonal tests by introducing initial height at age 1 or 2 years as a covariate represented in model (1) as d = regression coefficient h_{ijk} = height at age 1 or 2 years for observation ijk. Growth traits were analysed from assessments up to 10 years of age. Formulas and other additional information about methodology is given in Stener & Jansson (2005).

Results and discussion

Growth and survival

The survival was high (> 80 %) in all trials but two (Table 2). Mortality was mainly caused by competing weed but also by pine weevil (*Hylobius abietis*). The heritabilities (H^2 and h^2) were generally very low, i.e. the genetical control was weak, indicating that survival is of minor importance when breeding birch in southern Sweden.

Mean heritabilities of the growth traits were high (around 0.30). However, heritability varied a lot among trials (Table 2). It was high in trials where establishment was successful and low where establishment was poor. Heritability should be considered more as a measure of experimental efficiency than a robust parameter characterizing the genetic control. This is especially true for an extreme pioneer species like birch, which is strongly influenced by the conditions at establishment.

Table 2. Mean values, heritabilities, (H^2 and h^2) with standard errors (s.e.) for survival and growth traits and genetic coefficients of variation (CV_G and CV_A) for growth traits. The age at measuring was 10 years (clonal tests) and 7 years (progeny tests). From Stener & Jansson (2005)

Trial	Survival			Height				Diameter			
	%	H^2	s.e.	dm	H^2	s.e.	CV_G, %	mm	H^2	s.e.	CV_G,%
Clonal tests											
1A	95	0.07	0.04	95	0.25	0.07	4.9	81	0.42	0.06	11.7
1B	95	0.12	0.05	80	0.29	0.06	5.7	70	0.43	0.06	11.8
1C	82	0.03	0.04	71	0.21	0.08	5.2	62	0.22	0.07	9.2
2A	72	0.10	0.07	74	0.07	0.10	4.6	60	0.25	0.12	12.9
2B	86	0		80	0.47	0.09	9.6	67	0.46	0.09	16.1
2C	86	0.22	0.09	47	0.56	0.09	13.3				
Mean	86	0.09	0.06	75	0.31	0.08	7.2	68	0.35	0.08	12.3

Trial	%	h^2	s.e.	dm	h^2	s.e.	CV_A, %	mm	h^2	s.e.	CV_A,%
Progeny tests											
3A	79	0.12	0.08	56	0.08	0.10	5.1	47	0.11	0.10	11.1
3B	98	0.10	0.07	66	0.54	0.14	8.2	56	0.59	0.14	15.3
4A	91	0.09	0.08	50	0.47	0.15	14.0	34	0.33	0.13	20.5
4B	92	0		40	0.21	0.11	8.7	28	0.14	0.10	12.4
Mean	90	0.08	0.07	53	0.32	0.13	9.0	41	0.29	0.12	14.8

The broad sense heritability (H^2) is by definition supposed to be higher than the narrow sense heritability (h^2). This was not the case here and was probably an effect of the small sample size (2.7 to 4.3 ramets per clone on average in each of the clonal tests).

The mean estimates of the genetic coefficients of variation (CV_G and CV_A) varied between 7-9 % for height, and between 12-15 % for diameter (Table 2). Estimations of genetic gain are presented in figure 3. For instance, a selection of the best 10 % clones in respect of height from a total population of 300 clones resulted in a 10 % gain. The corresponding estimation for diameter was 18 %. In conclusion, the results from the genetic parameter estimations indicate that growth traits are mostly under strong genetic influence, they show substantial genetic variation and a high potential for genetic gain.

The efficiency of breeding depends very much on the age at which selection is carried out. Strong genetic age x age correlations for height were found. In relation to the target age of 10 years the

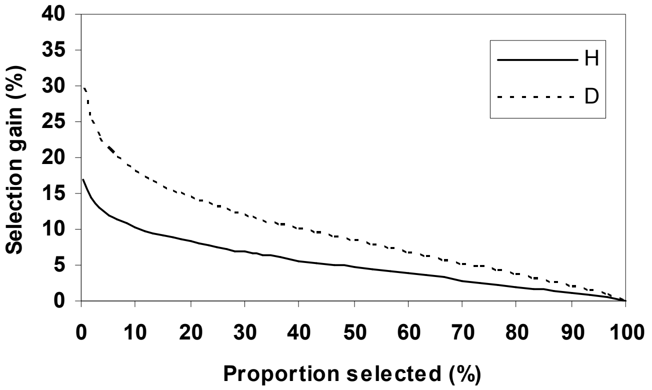

Figure 3. Predicted genetic gain for two growth traits after selection based on height or diameter at age 10 years from a population of totally 300 clones. From Stener & Jansson (2005).

mean genetic correlations for height were 0.60 at age 4 and 0.94 at age 5 or 6 years (Table 3). This suggests that short test periods (ages of around 6 years, i.e. at mean heights around 4 metres when establishment is successful) could be used. However, it is hard to make any general conclusion only from these findings, since the target age used only corresponds to around 25 % of the rotation time for birch. On the other hand we have the same indications for hybrid aspen (Stener & Karlsson 2004) at an age corresponding to 40-50 % of the rotation time. Furthermore, phenotypical estimations from other silver birch studies confirm our results (Johnsson 1967, Erkйn 1972). These results all together indicate that it should be possible to use short test periods.

Table 3. Genetic correlations between height at different ages (age in brackets). Significant correlations (P<0.05) are shown in bold. From Stener & Jansson (2005)

Trait 1	Trait 2	Trial			
		1A	1B	1C	2B
H(4)	H(6)	**0.85**	**0.93**		
H(4)	H(10)	**0.60**	**0.75**	0.47	
H(5)	H(10)				**0.92**
H(6)	H(10)	**0.93**	**0.96**		

How clones perform in different environments can be estimated from genotype x environment correlations (r_{GE}). These were in general strong (Table 4), indicating that the ranking of clones in respect of growth were quite similar at different sites.

Table 4. Genetic correlations (r_{GE}) between the same trait in different trials. The age at measuring was 10 years (clonal tests) and 7 years (progeny tests). From Stener & Jansson (2005)

Trial	Height	Diameter
1A x 1B	0.87	0.91
1A x 1C	0.81	0.89
1B x 1C	0.81	0.93
2A x 2B		0.98
2B x 2C	0.65	
3A x 3B	1.22	0.93
4A x 4B	0.52	0.50

Previous studies concerning transfer of birch in Sweden (Stener 1997) have shown that a few degrees of latitudinal transfer to the north or south does not affect vitality or growth. These findings are supported by the results in the present study (not presented). This all together with the findings of a strong GxE correlation indicate that southern Sweden can be treated as a single utilization zone and that few sites are needed for genetic tests.

Wood and fibre traits

In a separate study genetic parameters of wood, fibre and growth traits were estimated in trial 1A at an age of 11 years. From this trial, 30 clones were randomly selected and three ramets per clone were harvested. Wood density was determined from discs cut at 1.3 m above the ground by the standard water-displacement method. Fibre length and width were measured with an STFI FiberMaster. The wood samples tested included 8-9 annual rings. The same statistical model (1) as described previously was used, except from the term $dЧh_{ijk}$ which was excluded (Stener & Hedenberg 2003).

Wood and fibre properties were found to be under strong genetic control with broad sense heritabilities around 0.70 (Table 5). The genotypic coefficients of variation were quite low (3.5 – 4.7 %).

The genetic correlation between growth and wood/fibre traits were weak (ranging from -0.14 to 0.38) and not significant except between diameter and wood density (Figure 4) showing an unfa-

Table 5. Mean values and genetic parameters of different traits in the wood/fibre study. From Stener & Hedenberg (2003)

Trait	Unit	Mean	Min	Max	H^2	S.e. of H^2	CV_G, %
Height	dm	107	74	132	0.43	0.12	5.5
Diameter	mm	86	44	125	0.46	0.11	11.1
Density	kg m^{-3}	429	368	474	0.73	0.08	4.7
Fibre length	mm	0.873	0.748	0.994	0.68	0.08	4.5
Fibre width	µm	20.4	18.1	22.9	0.66	0.09	3.5

vourable, modest and significant correlation (r_g = -0.53). This suggests that density is likely to decrease when clonal selection is based upon diameter. However, the reduction in density was very modest when diameter was used as the selection criterion (a selection of the 10% best clones in respect of diameter decreased the density with around 2.5%, or 12 kg m^{-3},). Since lumber of birch is mostly used for furniture, parquet flooring and veneer, and not as construction timber, a minor decrease in density should not be a problem. Thus, introducing wood density as a selection trait in birch breeding cannot be justified from these results.

Final remark

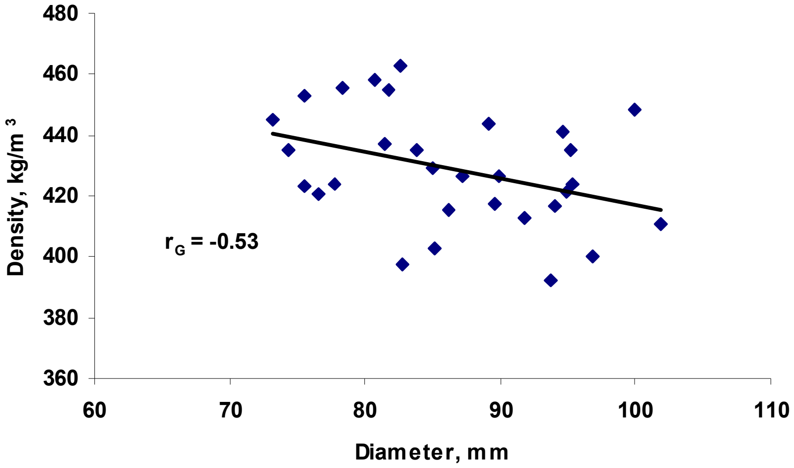

Figure 4. Genetic correlation between density and diameter. From Stener & Hedenberg (2003).

These findings suggest that developing an efficient birch breeding program for southern Sweden should be relatively straightforward. However, further investigations are needed to confirm the results.

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IMPROVED UTILIZATION OF THE INTERNAL POLLEN PRODUCTION IN A *PINUS SYLVESTRIS* SEED ORCHARD BY THE USE OF A MIST BLOWER

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Few experiments with the aim of more effective utilization of the pollen production in seed orchards without first collect the pollen have been reported. The number of filled seed has been reported to increase after mist blower treatment in *Pinus taeda* (Brown, 1987). The effect of using a helicopter to blow pollen around the seed orchard on pollen contamination in a *Pinus sylvestris* seed orchard varied from negative to slightly positive in a Finnish experiment (Antola et al. 1994).

The objective of this experiment was to evaluate the effect of treatment of a *Pinus sylvestris* seed orchard with a tractor-mounted mist blower during female flower receptivity. The aim was to increase the number of seeds per cone, and to increase the number of seeds having a seed orchard clone as father. This should be achieved by releasing the pollen produced in the seed orchard as soon as possible by the use of the mist blower.

The experiment were performed in a 14 hectare *Pinus sylvestris* seed orchard located in central Sweden (Lat 59° 53'. 80 m.a.sl.). The clones originated from approximately the same latitude but from higher altitudes, resulting in a mean transfer to a location with 400 d.d. higher temperature sum (+5°C).

The seed orchard was divided into four plots. Two plots were treated with the mist blower, and two plots were untreated controls. Treatment was carried out on five days each of three consecutive years.

The amount of pollen in the air was measured with Rotrod samplers at 4 meters and 6 meters height. Cones were collected from all clones on all four plots. Seeds were extracted and seed parameters were recorded. Pollen contamination estimates were obtained by microsatellite analysis. We used five loci with 20 to 50 alleles per loci.

The results show that the mist blower treatment increased the amount of pollen in the air during the treatment time, figure 1. The amount of pollen in the air before and after treatment each day was not affected. There were no differences in number of filled seeds per cone or in percentage empty seeds per cone between the treated plots and the control plots, table 1.

The mist blower treatment did not change the amount of pollen contamination in the seed from treated plots compared to seed from the control plots, Figure 2. The level of pollen contamination

Table 1. Seed set data in the experiment

Year	Treatment	Number filled seed per cone	Percentage empty seeds
1999	Treated	16.9	24.7
	Control	17.5	24.6
2000	Treated	16.3	29.4
	Control	16.7	28.3
2001	Treated	21.3	21.9
	Control	20.4	20.3

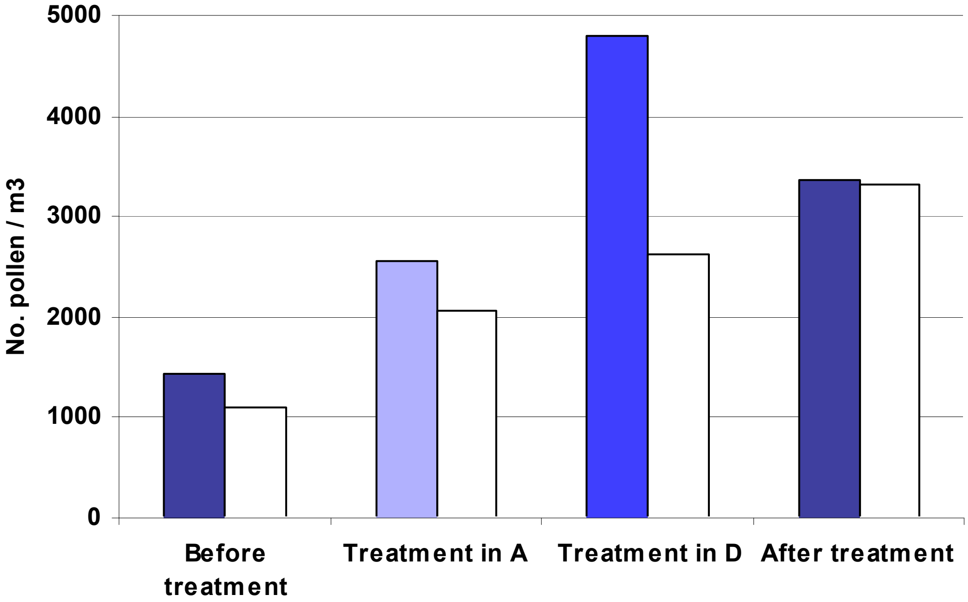

Figure 1. Amount pollen in the air at 4 meters height year 2000. Summary of the 5 measurement days. Unfilled bars are control plots. Checked bars before and after treatment are average for the two treated plots. Vertical lined bar are values for plot A during treatment of that plot, and horizontal lined bar are values for plot D during treatment of that plot.

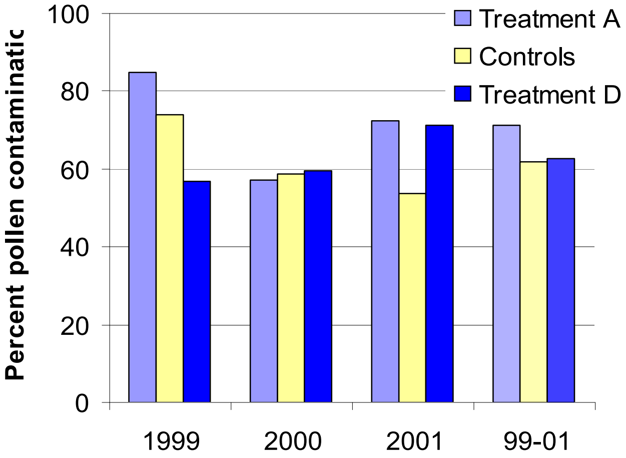

Figure 2. Pollen contamination in the experiment during the three years, and as a summary of the three years.

recorded in this experiment on the control plots were higher than contamination estimates made with izosymes previously reported from the same seed orchard (Almqvist et al. 1995). This indicates that earlier pollen contamination estimates made by izosyme technique may be underestimates of the true contamination level in *Pinus sylvestris* seed orchards.

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CONSIDERATIONS OF TIMING AND GRAFT DENSITY OF FUTURE SCOTS PINE SEED ORCHARDS

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Background

In Sweden and Finland, Scots pine seed orchards are usually established with initial density of around 400 grafts per hectare. By production time, this initial density is reduced by mortality and/ or thinning. Density in existing seed orchards is estimated at 267 and 318 grafts/ha in Finland and Sweden, respectively (Kang et al 2001). At present, newly established Scots pine orchards are planned to be at an initial density of 400 grafts/ha or slightly more with an expected operational lifespan of 40 years. Cone collection from new orchards is often recommended first at the stage where orchard's pollen production reaches 20 kg/ha, which typically occur after 15 years to reduce the influence of pollen from other sources. Seed production form newly established seed orchards is projected to reach 8 kg/ha between year 20 and 40.

Objectives:

The objective of this study was to explore some factors of relevance for advanced generations seed orchards, in particular those associated with planting density, start and end of seed collection, costs and cost components and the genetic value of the crop.

Methodological framework:

A program was developed that considers: 1) seed orchard area (size) 2) planting density, 3) establishment and management costs, 4) cone harvest and seed processing costs, 5) annual genetic progress available for new seed orchards, 6) impact of pollen contamination; 7) value of seed, expressed as a function of their genetic quality; 8) first and last year of operation (the productive period of the orchard). The developed program uses linear interpolation among a matrix of seed production and seed collection costs (approximated by different harvest costs on cones above and below 3m) as a function of graft density (160, 400 and 1000 grafts/ha) and orchard age. The orchard area was set to meet a projected demand of 10 million seeds annually over the life time of the seed orchard. The «benefit» was expressed as the value of a seed with the cost of production subtracted.

Runs

The estimate of inputs was based on experiences, suggestions and projections developed in discussion with a number of well informed people assuming intensive management adjusting to spacing and expected life time including branch and top pruning. Some basic information for the estimates is found in Rosvall and Eriksson (2002), Almqvist (2004) and Prescher et al. (2005). Different seed orchard sizes corresponding with the specific spacing was used and seed harvest periods ranging in the interval from age 8 (=early) to age 50 were tested to identify efficient designs.

Results and Discussion:

Benefit expressed in financial terms as a function of the orchard life time for 400 and 600 grafts/ha spacing and cone harvest starting at age 8 and 15, respectively, were compared (Figure 1). The comparisons showed the following: 1) to start the harvest early (age 8) was considerable superior to wait for pollen production (age 15), 2) the superiority declined as the life time of the orchard got longer, 3) the benefit as a function of life time peaked at 25 when harvest started early and at 30 when the first harvest was postponed, 4) for longer seed orchard life times the benefit sunk approximately proportional to the life time, 5) absence of an important difference between 400 and 600 grafts/ha.

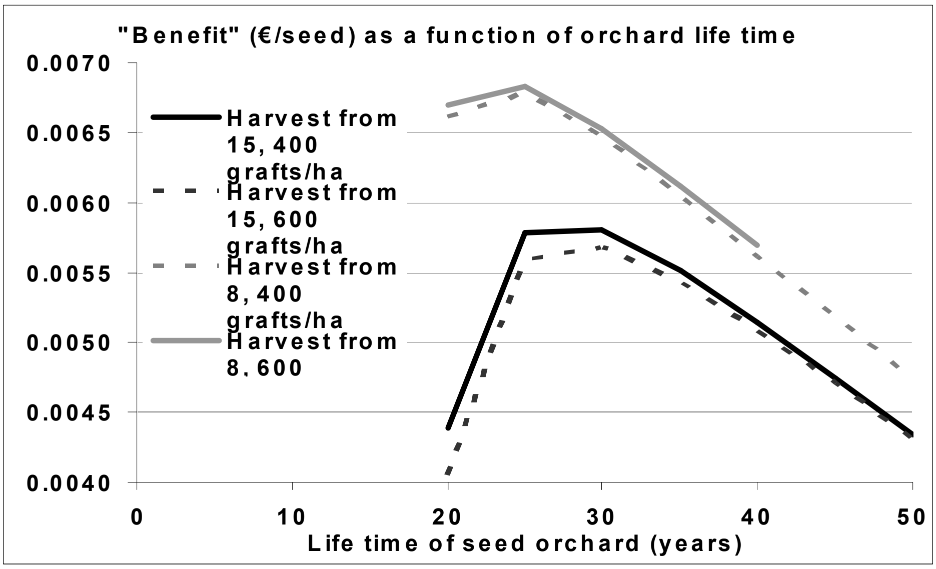

Figure 1. Benefit/seed (the «value» of a seed with production cost subtracted), comparison between 400 and 600 grafts/ha, for early (8 yrs) and late (15 yrs) initiation of harvest as a function of seed orchard life time. The genetic consequences of pollen contamination are considered.

The comparisons above favor faster turn-over of seed orchards. The advantage is that we can capture higher gain as seed orchard cycles are progressing with a pace closer to breeding population advancement and also that cone harvest becomes cheaper as younger trees are harvested. An advantage not considered in the calculations which could be visualized by adding an interest is that the return on investment in establishing seed orchard will appear earlier.

Cost breakdown comparison for the same production target is illustrated in Figure 2 for early (8 yrs) and late (15 yrs) harvest for 400 grafts/ha. The following points highlight the comparison between larger orchard with shorter productive time and early initiation of harvest (8 yrs) and smaller orchard with longer rotation and later initiation of harvest (15 yrs): 1) establishment cost is considerable higher for shorter rotation comparing to that of longer rotation orchards caused by larger orchard size and more frequent establishments, 2) management cost is slightly increased because of larger seed orchard area, 3) total harvest cost is lower, which is associated with more easily accessible cones, and 4) seed extraction cost is identical.

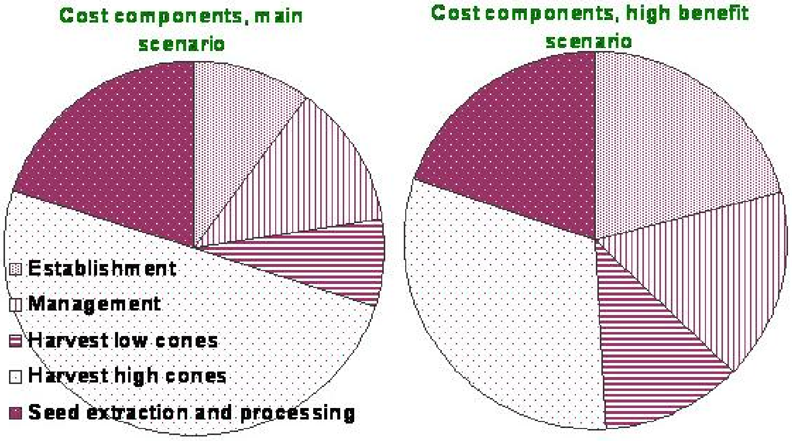

Figure 2. Cost breakdown comparison between a main scenario (400 grafts/ha) initiating cone harvest at age 15 and ending at age 40 (left figure) and a «high benefit» scenario initiating cone harvest at age 8 and ending at age 25.

Cone collection from younger orchards with low pollen production (<20 kg/ha) increases the vulnerability to high contamination rate. Longer rotation is expected to reduce pollen contamination by increasing the within orchard pollen cloud density. The current study suggests that early cone harvest is justified, at least if the contaminating pollen has similar adaptational characteristics as the seed orchard pollen. Per seed cost was marginally lower for 400 grafts/ha than 600 and about 5% lower for initiating the harvest early compared with waiting for pollen production.

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PRELIMINARY ASSUMPTIONS TO «THE PROGRAMME OF FOREST GENE RESOURCES CONSERVATION AND BREEDING OF FOREST TREES SPECIES IN POLAND IN THE YEARS 2010 – 2035»

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Prerequisites for the Preparation of the «Programme»

«The Programme of Forest Gene Resources Conservation and Selective Breeding of Forest Trees in Poland», which is under way in the State Forest, has been planned for the years 1991-2010. Data presented in previous papers show that material tasks of the «Programme» have practically been executed.

The pro-ecological forest management system and the increased role of other functions of the forest may by one of the factors causing the limitation of forest production functions.

Although the significant increase of the quantity of timber harvested in the last decade has been observed (the increase from 24 million mi to 32 million mi annually) the demand for timber is still significantly higher than its supply. At the same time, the production ability of Polish forests is used within the limited extent.

Global changes of climate and related threats should constitute an essential driver for the amendment to the new programme's strategic objectives. Activities related to the selective breeding of forest trees must guarantee the preservation of the total forest genetic diversity and durability in the changing environmental conditions. Counteracting the reduction of biodiversity of forest ecosystems, and biodiversity of stands in the first instance, is becoming an important objective. The principal goal of selective breeding of forest trees should, first of all, be the directed modification of the population increasing natural adaptation processes of forest trees to changing conditions. The most important features to be supported are flexibility and tolerance of species for changing environmental conditions, and only then there comes the timber increment.

Poland has become the European Union member state. Thus, we are obligated to implement essential changes in principles of functioning, establishment and use of the forest-tree seed resources – the forest basic material (FBM).

The adjustment of principles to the EU requirements means the simultaneous protection of Polish forests against seeds and cuttings of unknown origin, which may cause the erosion of individuality of our native stands and constituting danger to the durability and stability among forest ecosystems.

Basic Assumptions

The programme should be a continuation of programmes executed so far (both the principle objectives and tasks execution modes will be preserved). Only the actual changes of conditions of forestry may modify the execution of the programmes and tasks stipulated therein.

The programme should cover activities related to the conservation of forest biodiversity, including genetic diversity, as well as selective breeding of forest trees. Such approach to the breeding of forest trees will allow to achieve the regular progress in fulfilling various functions by managed forests, including the production function.

The programme should define the scope of meritoric and material activities, as well as additional activities such as:

- scientific research necessary for the execution of the «Programme»,
- establishment of technical infrastructure for the proper execution of the «Programme».

Strategic Objectives of the Programme

The strategic objectives adopted in 1991 for the «Programme» for the years 1991-2010 remained practically unchanged. Priorities of the «Programme» for years 2011-2035 should cover:

a. Conservation of forest biodiversity.
b. Selective breeding of forest trees.
c. Establishment and maintaining of the proper quality and quantity seed base for the purpose of reforestation and afforestation.

Specific Activities for Individual Priorities

Conservation of forest biodiversity, including genetic diversity

The proposed scope and scheme of activities within the conservation of forest genetic diversity has been presented in Fig 1. Basic activities planned within this programme cover the following:

Legislative activities:

- preparation of an act on the conservation of forest biodiversity or amendment to the act on the environment protection and the forestry act which would legally sanctions the application of the active methods of biodiversity conservation in forest management, for example: stands selected for the preservation of endangered tree populations or valuable clone archives,
- preparation and implementation of necessary measures in order to preserve the forest biodiversity,

Field activities:

- cultivation of selected stands in order to preserve the endangered tree populations chosen according to scope of former programme,
- establishment of next generations in selected stands for the in situ preservation of endangered tree populations,
- establishment and tendering operation in ex situ plots (based on the existing stands selected for the preservation of endangered tree populations),
- establishment of progeny plantations based on breeding populations,
- establishment and handling of seed plantations for the purpose of breeding and the preservation of endangered tree populations, plantation seed crops and clone archives (ex situ conservation of single genotypes),
- obtaining the propagation material from stands selected for the preservation of endangered tree populations, breeding populations and individual genotypes (seeds, parts of plants, pollens) for the long term storage in the Forest Gene Bank,
- complementary choice, based on systematic genetic-research, of subsequent populations and genotypes of specific genetic features complementing the forest genetic diversity gathered in stands selected for the preservation of endangered tree populations and breeding populations.

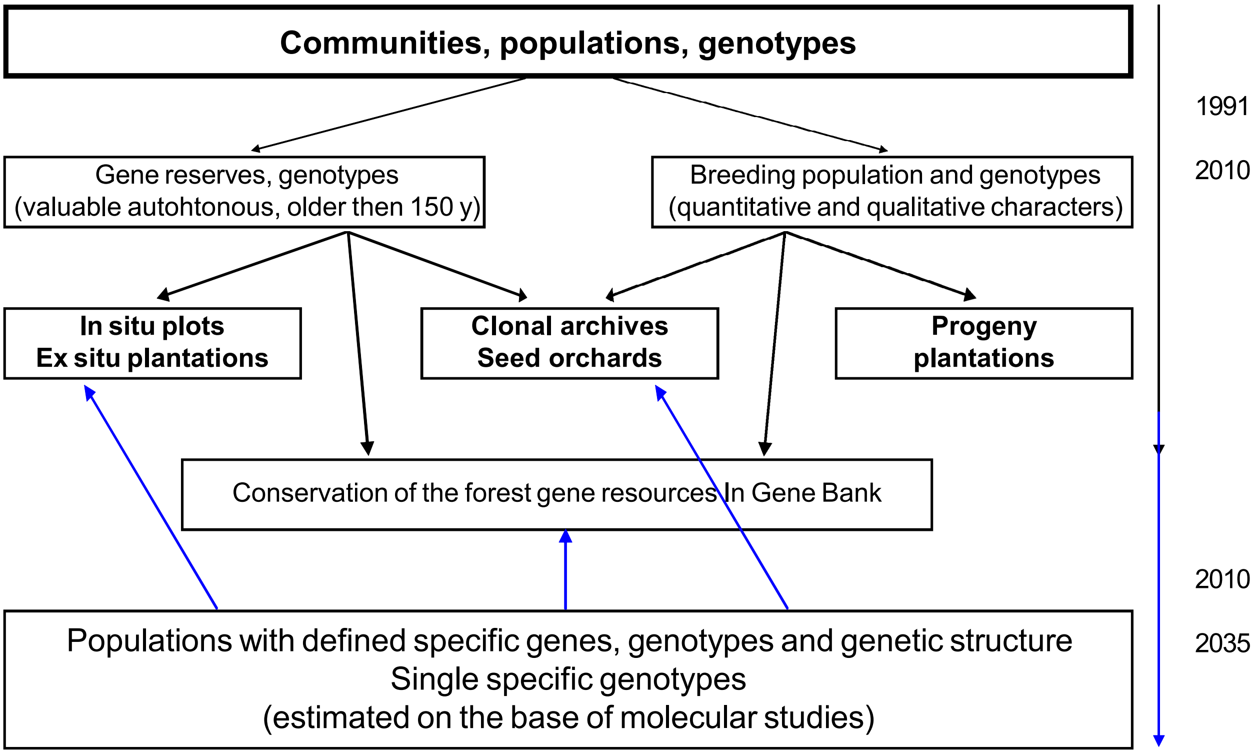

Figure 1. Conservation o f the forest genetic variability.

Laboratory activities:

- long-term storage of seeds, parts of plants, pollens in the Forest Gene Bank Kostrzyca, including the wider application of cryogenic methods,
- genetic characteristics (DNA, isoenzymes and other chemical compounds) of populations and genotypes selected for the conservation of forest-gene resources,
- monitoring of threats to forest genetic diversity,
- monitoring of changes of forest genetic diversity with special consideration of areas influenced by anthropogenic factors.

Breeding of forest trees

Breeding of forest trees and the establishment of seed resources shall be conducted in the same way as in programmes executed so far, i.e. by means of population and lineage selection. The population selection will play the key role and should fulfil the seed demand in 80%. The remaining seed supply will come from seed plantations. The programme of selective breeding of forest trees shall cover tasks realised so far, that is: the selection of stands chosen for the preservation of endangered tree populations (WDN), mother trees (DD), the establishment of derivative crops, seed plantations and first generation plantation seed crops for selected species in these RDSF (Regional Directorates of the State Forests), where the size of seed resources is insufficient for the proper execution of breeding tasks. Selective breeding of forest trees for already existing objects means testing selected stands, trees and seed plantations, and thus creating the category No IV of «Tested» FBM. The programme should also cover the permanent verification and updating of principles of application and transfer of forest reproductive material (seed regionalisation). The programme should also formulate the methods and means for the enrichment of genetic diversity of populations used for economic purposes (e.g. universal application of natural regeneration in specific conditions). Fig. 2 presents activities proposed within breeding of forest trees to be executed within the new programme.

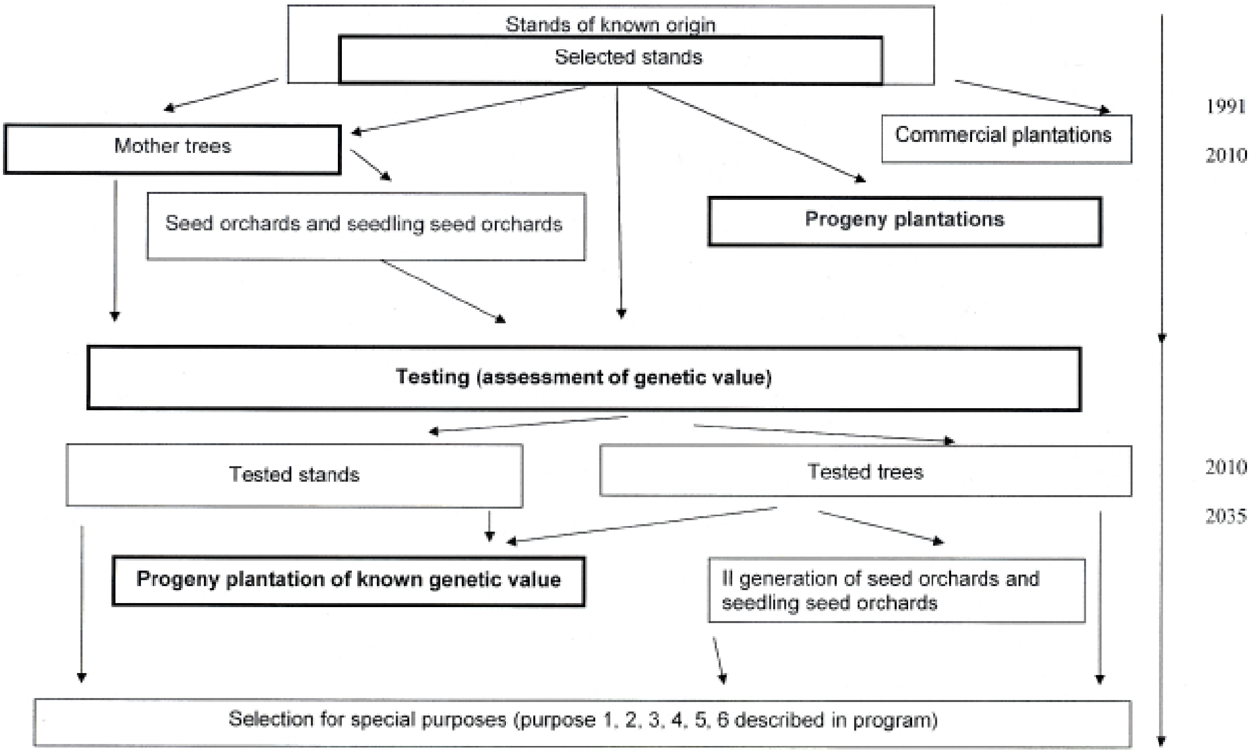

Figure 2. Breeding of forest trees.

The realisation of the following objectives has been planned within the following activities:

- improving of the quality and the quantity features of populations (stands) – population selection (choosing stands out of «selected» and «tested» categories),
- selection of populations and genotypes of high flexibility for the purpose of breeding in changing climate condition (population and individual selection),
- creation of artificial breeding populations based on seed plantations determined by a relatively high genetic diversity (individual selection – selection of various genotypes for the set of trees for plantations and plantation seed crops based on DNA analyses),
- improving the quality features of genotypes – individual selection – selection of genotypes representing specific features from the «tested» category – creation of artificial breeding populations for forest purposes (based on seed plantations),
- improving the resistance of genotypes to biotic and abiotic factors – individual selection – selection of genotypes of specific features from the «tested» category – creation of artificial breeding populations for forest related purposes based on seed plantations,
- improving the quantity features of genotypes – production of timber in short and average production cycles – individual selection – selection of genotypes of specific features from the «tested» category, creation of FBM resources to breed clones and mixed clones, creation of clone sets and establishment of seed orchards.

The following will be covered by the «Programme» activities related to the selective breeding of forest trees:

a) continuation of tasks executed so far:
- selection, handling and using of selected stands (WDN),
- selection and using of mother trees (DD),
- establishment of seed plantations and I generation plantation-seed crops,
- establishment of units of progeny plantations,
- evaluation of breeding features of derivative crops in a bearing period

b) new task related to the evaluation of the genetic value of FBM:

- establishment, handling and evaluation of FBM, used for production of FRM II and III (selected stands, mother trees, seed plantations, plantation-seed crops), in progeny tests,
- selection of FBM objects used for the production of "tested" FRM category,
- stipulation of principles for handling and usage in forests of FBM registered in the IVth part of the National Register,
- establishment of II generation of seed orchards and seedling seed orchards,
- establishment of units of crops with FBM of a known genetic value.

The following should be guaranteed by the execution of the programme:

a) within the conservation of genetic diversity:
- long term preservation of the existing genetic diversity,
- sustainability of ecological processes in forest ecosystems,
- durability of existing ecosystems and possibility of their sustainable use,

b) within the selective breeding of forest tree species:
- establishment of tested seed resources at the level of 10% of the national seed demand (expected profit from selection concerning growth features will reach 15% at the level of population, and 25% at the level of lineage in relation to growth features of materials originated from outside of these resources),
- maintenance of selected seed resources at the level of 30% of the national seed demand (the selection profit for growth features is expected to be 10% of population, and 15% at the level of lineage)
- maintenance of fixed seed resources originated from the identified source at the level of 60% of the national seed demand (the selection profit for growth features is expected to reach the level of 2-5% of population).

Ending

The assumptions of the new «Programme» presented above will be widely discussed in the coming years. Practically, only 4 years left for such a discussion gives still enough time to implement amendments to the «Programme» (if necessary) and to make the programme assumptions more feasible.

FORESTS AND FORESTRY WITH EMPHASIS TO TREE BREEDING IN KOMI REPUBLIC

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Forest resources

Total area of Komi Republic is 41.6 million ha. The state forest fund is 38.9 million ha (including wetlands, lakes and watercourses, non – regenerated clear felling areas and forest fire areas, roads etc.) or 95% of total territory. Forest fund is primarily owned by Agency of Forestry for Komi Republic. The forest covered land is 30.6 million ha, so forest land share of total land area is 72%. Total growing stock volume is 2 961 million m^3.

Distribution of forest covered land by species: Scots pine – 7.1 million ha, Norway spruce – 16.2, Siberian larch – 0.2, Siberian pine – 0.02, Silver and downy birch – 4.6, European aspen – 0.6 and the others species (Siberian fir, willow and alder) – 0.1. General age structure of forest covered land by age groups: young stands – 4.5 million ha, middle – aged – 4.5, pre – mature – 1.4 and mature and over – mature – 18.4.

Removals

The enable annual felling is 25.8 million m^3 on a sustained basis. Before 20th century the commercial harvesting was very limited (Figure 1). The clear cuttings were introduced in 1930th and

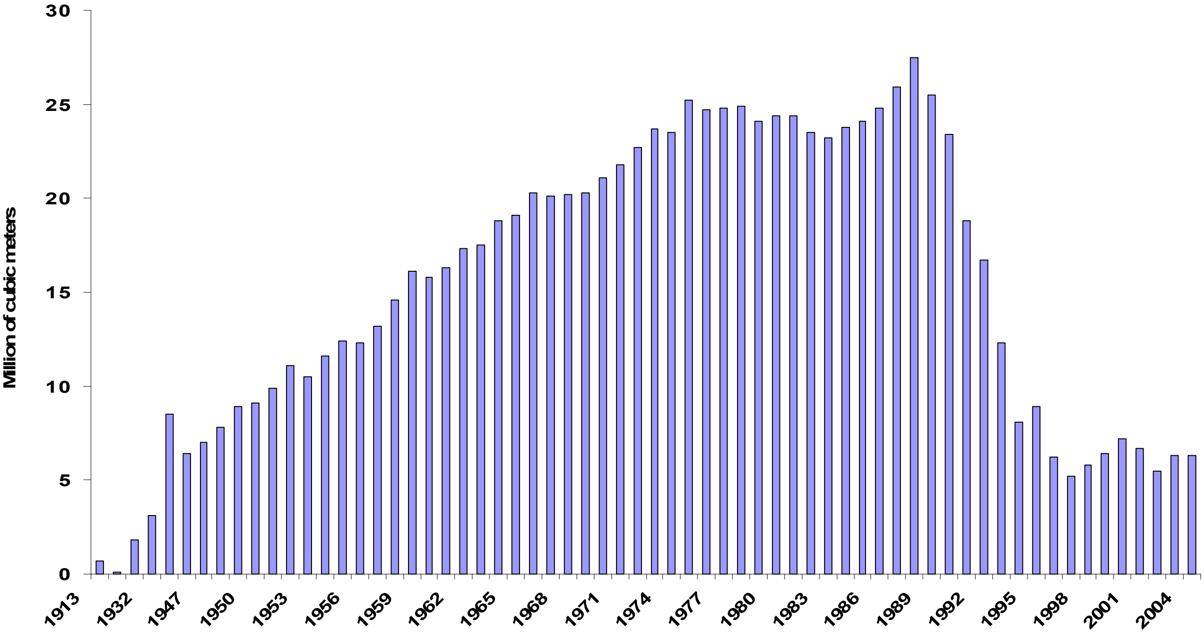

Figure1. History of commercial roundwood removals in territory of Komi Republic.

roundwood removals were increased. The serious decreasing of harvesting was in beginning of 90th due to political and economical changes in former Soviet Union.

Artificial regeneration

The artificial regeneration in Komi republic has not long history (Figure 2). The total area of plantations is about 720 thousands of ha. The main method of plantation establishment was direct sowing – 59.2%, planting – 39.2% and air sowing – 1.6%. The distribution of cultivated species: Scots pine – 49%, Norway spruce – 49%, Siberian pine – 1.6% and Siberian larch – 0.4%.

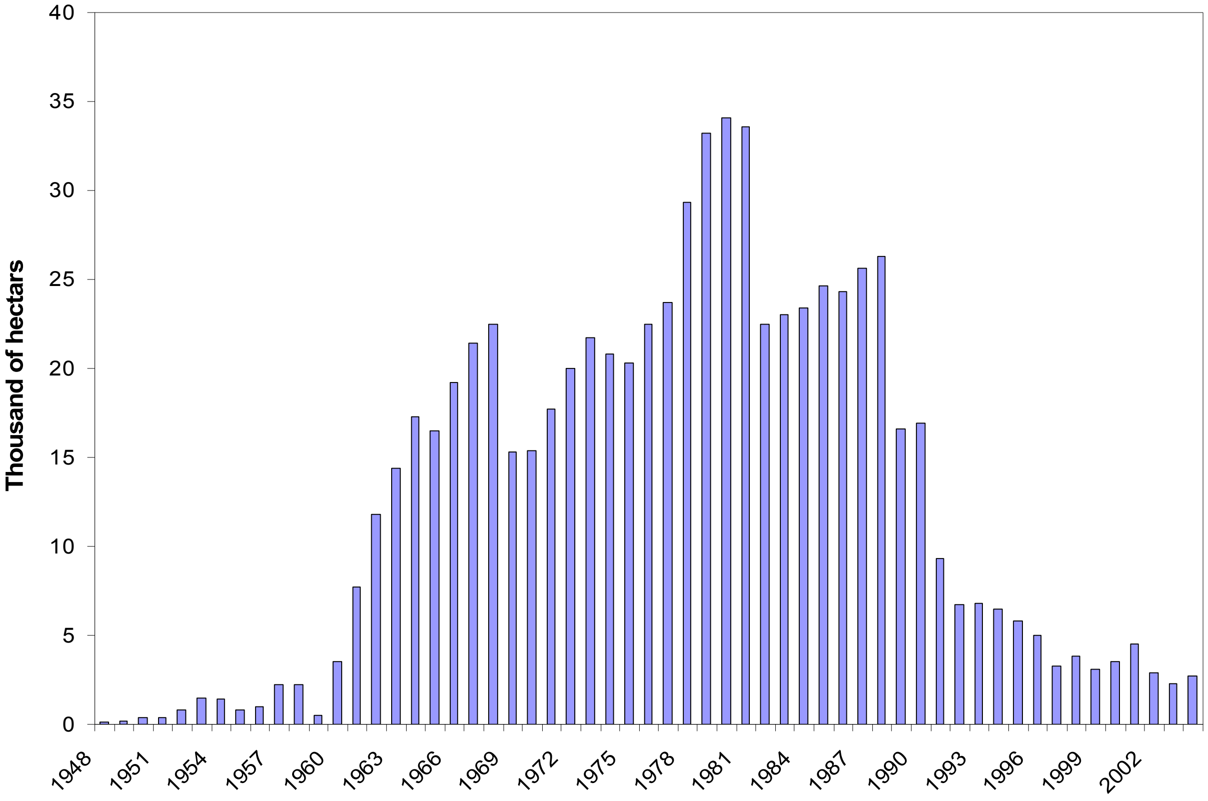

Figure2. History of artificial regeneration in Komi Republic.

Tree breeding

Tree breeding activity in Komi is managed and owned by Agency of Forestry for Komi Republic. ***The plus trees selection*** was started in end of 60th. The dominated initial effort has been to select plus trees in natural stands. Main emphasis was given to Scots pine, but altogether 4 tree species were included. Number of plus trees by 1.01.2005 are Scots pine – 1511, Norway spruce – 729, Siberian larch – 486 and Siberian pine – 320. ***The first generation seed orchards*** establishment was started in 1977. The general facts concerning seed orchards are given in Table 1. Seed orchards are located in southern part of Komi. About one third of Scots pine seed orchards area is a seedling seed orchards, other part is clonal ones. Seed collections were started in 1995.

Table 1. General facts about seed orchards in Komi Republic

Tree species	Area, ha	Number of clones/families	Total seed collection, kg (1995 – 2004)
Scots pine	160.3	614	311
Norway spruce	27.9	56	–
Siberian larch	1.0	13	–
Siberian pine	8.7	183	

Clonal archives

In order to conserve plus trees genotypes for future use in the breeding programme, four clonal archives were established in southern Komi. About one – third of the Komi plus trees (Table 2) are represented in seed orchards or clonal archives.

Table 2. General facts about clonal archives in Komi Republic

Tree species	Area, ha	Number of clones/families
Scots pine	15.9	65
Norway spruce	5.8	77
Siberian larch	1.6	13
Siberian pine	7.7	136

Progeny testing

As a whole, nearly half of the Komi plus trees are being tested in field progeny trials (Table 3). The one hundred half – sib progenies of northern Swedish Scots pine plus trees are also included in three field trials.

Table 3. General facts about plus trees progeny tests in Komi Republic

Tree species	Years	Number of trials	Area, ha	Number of half – sib families
Scots pine	1988 – 2005	15	21.1	858
Norway spruce	1998 – 2001	6	17.0	519
Siberian larch	2004	1	0.7	47

The major forthcoming task is to turn from the plus tree selection and retrospective testing phase to establishment seed orchards based on a superior fraction of the plus trees (1.5 generation orchards).

Provenance research

The first provenance trial was established in 1977 (Table 4). This trial was used mainly to design the seed collection zones in Komi. There are 3 zones for pine and 3 zones for spruce and 4 for Siberian pine and 3 for Siberian larch. The zones are also used as the regions of provenances in the trade of forest reproductive material.

Table 4. General facts about provenance experiments in Komi Republic

Tree species	1977	1980	1987	1993	1996	1997	2004	Total
Scots pine	$\frac{7.3}{24}$	–	–	–	$\frac{1.5}{3}$	$\frac{3.0}{9}$	–	$\frac{11.8}{36}$
Norway spruce	$\frac{12.8}{33}$	–	–	–	$\frac{0.9}{5}$	–	–	$\frac{13.7}{38}$
Siberian larch	–	$\frac{6.3}{7}$	$\frac{4.4}{10}$				$\frac{3.1}{12}$	$\frac{13.8}{29}$
Lodgepole pine	–	–	–	$\frac{4.3}{-}$			$\frac{4.6}{6}$	$\frac{8.9}{6}$

Most lodgepole pine seed material for the trials originated from Swedish seed orchards and was supplied by Svenska Skogplantor AB and SkogForsk.

ULTRASTRUCTURE, PHOTOSYNTHESIS AND RESPIRATION OF SCOTS PINE NEEDLE IN PROVENANCE EXPERIMENTS

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Introduction

The main function of leaf is photosynthesis providing a growth and productivity of plants. Leaf quantitative parameters of the same plant species have geographical, ecological, endogenous variety. For example, Scots pine and Norway spruce in southern and northern parts of natural area different in needle mass, length and anatomical characteristics (Mamaev, 1972). Mesophyll cells in herb leaves of southern and northern populations have differences in ultustructure parameters (Miroslavov et al, 1999). The aim of this study was to determine ultrastructure parameters of mesophyll cell, photosynthesis and dark respiration activity of Scots pine needle in province experiments.

Materials and methods

Table 1. General facts about Scots pine provenances used in study

Variant / year of planting	Region (republic), forest farm	Latitude	Subzone
1-77	Murmansk, Monchegorsk	67°51` N.	extreme-northern taiga
2-77	Komi, Syktyvkar	61°40` N	middle taiga
3-77	Udmurtia, Votkinsk	57°03` N	southern taiga
1-97	Komi, Usinsk	65°36` N	extreme-northern taiga
2-97	Komi, Syktyvkar	61°40` N	middle taiga
3-97	Kirov, Vjatskie poljany	56°17` N	southern taiga

This study was carried out in Kortkeros and Syktyvkar provenance experiments, established in 1977 and 1997. Provenances used in experiments ate shown in Table 1. For ultrastructure study transver segments of 2d year needle were fixed in a solution of 2.5 % glutaraldehyde for 8h at cool temperature. Speciments were postfixed in 1 % osmium tetroxide. Tissue was aspirated several times during ethanol and acetate dehydration and embedded in Epon. Ultrathin sections were examined with electron microscope Tesla 500. Needle photosynthesis and dark respiration were measured by gas analysis system LiCor 6400 in field conditions.

Results and discussion

According to this study there are differences in needle sizes and needle mass among Scots pine provenances (Table 2). Northern provenance pine trees have smaller shoots and less number of needles. The volume of mesophyll tissue in needle is about 50 % (Figure). Mesophyll cells of southern, local and northern ecotypes have the same sizes, but some distinguishes are observed.

Table 2. Morphological parameters of experimental pine needle

Variant	Length of 2d year shoots, mm	Total number of needle per one shoot	Length of needle, mm	Cross sectional surface of needle, mm^2
1-77	94±15	128±33	41±8	0.39±0.03
2-77	109±28	153±46	51±4	0.64±0.24
3-77	128±23	185±32	52±2	0.57±0.23

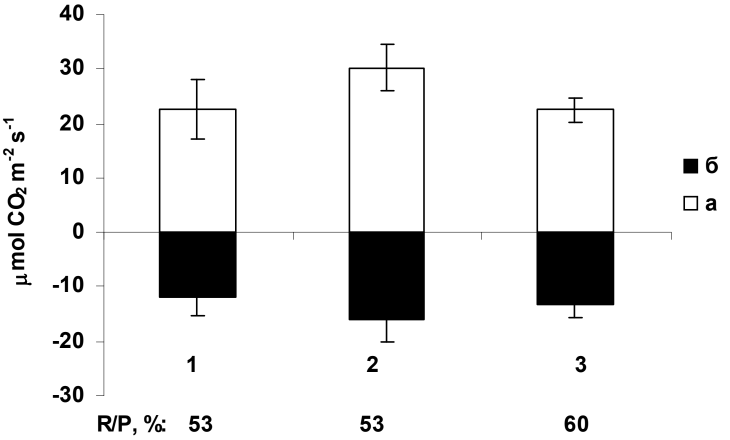

Figure. Photosynthesis (a) and dark respiration (б) of pine needle in provenance experiments. Origins: 1 – Usinsk, 2 – Syktyvkar, 3 – Vjatskie poljany.

Table 3. Parameters of chloroplasts and mitochondria in mesophyll cells of pine needle

Parameters	Variant		
	1-77	2-77	3-77
Chloroplast number per cell section	20±5	20±5	24±6
Chloroplast section area, μ^2	6.0±1.1	7.7±1.5	6.9±1.7
Long axis of chloroplast, μ *(a)*	5.4±0.7	5.7±1.0	6.7±0.6
Short axis of chloroplasts, μ *(в)*	1.7±0.4	1.5±0.4	1.7±0.5
a/в ratio	3.2	4.2	4.3
Number of granum per chloroplast section	28±10	20±6	37±10
Thylakoid number per granum	4±1	6±2	6±2
Total thylakoid number per chloroplast section area	112	120	222
Plastoglobul number per chloroplast section area	21±10	19±4	19±2
Mitochondria number per cell section	35±14	30±7	32±9
Diameter of mitochondria section, μ	0.7±0.1	0.7±0.2	0.8±0.1
Number of lipid droplets per cell section	70±20	62±26	49±17

Experimental variants differ in parcel volume of intercellular space, thylakoid number in chloroplasts and lipid droplet number per cells section (Table 3). At the same time local pine has maximum photosynthesis. The transfer of provenance from north to south did not result in increasing of photosynthesis. Southern provenance has lower photosynthesis and higher ratio of respiration to photosynthesis.

According to climatic theory of organic substance synthesis the differences in oil, protein and carbohydrates contents in plants of different geographical origins is a result of climate effect (Ivanov, 1961).

Cultivating of the plants in the same conditions have leaded to disappear of the distinctions. As for Scots pine in our provenance experiments, differences of needle some physiological, morphological and anatomical parameters remained. The results agree with investigations carried out in other regions of Russia (Rjazantseva, Shutjaeva, 1977). Long-term investigations in the middle taiga resulted in assumption about more activity growth of local origin trees (Nakvasina et al, 1990; Tarkchanov, 1998). According to these investigations high life state of northern ecotypes connected with their steady to damage by frosts, diseases and insects.

Good survival of northern provenances seems to be correlated with synthesis in their needle high level of reserve metabolites protecting cells from low temperature damage. According to Savva et al, 2002 Scots pine provenances had differences in growth of ring width of trunks. The fact proves heritage of growth reaction of ecotypes to environmental change effects. We can suppose that photosynthesis and growth connection in sink-sours system of plants is a reason of lower photosynthesis in the northern ecotype in provenance experiment planting in middle subzone of taiga. At the same time adaptation of plants results in increasing of respiration and photosynthesis ratio (Semichatova, 2002). High conservative of physiological processes of the northern pine provenances demonstrates their stress tolerance by moving from north to south. At the same time high ratio of respiration and photosynthesis of the southern provenance seems to be a result of its higher sensibility to environment change.

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CHARACTERISTICS AND SUSTAINABILITY OF GENETICALLY IMPROVED NORTHERN SCOTS PINE

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Genetic differences between improved and unimproved Scots pine (*Pinus sylvestris* L.) in 36 north Swedish field tests, covering wide geographical and climatic gradients (latitude 62.3-67.8°N; temperature sum 496–1056 day-degrees), are presented. Improved trees were represented by progenies (controlled crosses) from first generation phenotypically selected plus trees (selected mainly for superior height growth), while unimproved trees originated from unselected natural stands. Improved trees were superior in height, stem diameter, and stem volume at the age of 19-33 years. Height growth of improved trees demonstrated sustainable development and was in accordance with height growth at different site indices. Furthermore, improved trees were more slender (height/diameter) than unimproved, while differences in survival and frequency of ramicorns and stem breaks were only minor. Lack of interaction between tree categories and site conditions for growth characters imply that the results are generally applicable. No difference in response to competition was detected. However, improved trees showed a deviating reaction to southward transfer, where survival increased more and height growth decreased less compared to unimproved trees. The results support specific growth and production functions for improved trees. The use of competition and height indices based on neighbouring trees to adjust for bias and site variability in single tree plots significantly improved the estimates.

GENETIC PARAMETERS IN APPLIED TREE BREEDING

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We intend to describe Swedish forest trees in terms of genetic variation, heritability, and genotype by environment interaction for growth and adaptive traits. Knowledge about genetic structure is needed to predict the effect on populations due to changes in environments as well as to optimise breeding programmes. Additive genetic variation is a prerequisite for response to selection. With access to numerous populations, which grow in trials all over the country, investigation of general genetic structure and environmental response is possible, contrasting to more fragmented earlier studies. We expect to reveal general relationships as well as spatial and environmental trends in the expression of genetic characters.

The objective of the ongoing study is to determine the genetic structure of Scots pine and Norway spruce in Swedish environments. It will be studied through genetic parameters such as additive coefficient of variation, heritability and genetic correlations for growth traits and adaptive traits. The aim is to answer questions such as:

- Are there basic differences between Norway spruce and Scots pine?
- Do genetic parameters change over different environmental conditions?
- How does assessment age affect genetic parameters?
- How is the pattern of genotype by environment interaction?
- How may populations be characterised due to potential for evolvability?
- How will the result affect future breeding and conservation strategy for the two species?

So far, about two thirds of available estimates regarding growth and adaptation are assembled in a database. Some basic scatter graphs were presented with heritability and CV_A values plotted over, for example, site characteristics (latitude, altitude, temperature sum) and tree development stage (tree age, mean height). The presentation is very preliminary and there has been very little data quality control.

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GENETIC PARAMETERS FOR WOOD DENSITY IN SCOTS PINE

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Scots pine (*Pinus sylvestris* L.) breeding is mainly focused on volume growth. The genetic correlations between wood density and growth traits have, however, in many studies been negative. A breeding gain in volume thus implies less gain in terms of wood biomass. The wood has furthermore a considerable heterogeneity where the different types of wood have different wood and fibre properties. As trees grow older, there is a change from juvenile wood to mature wood with their certain properties, and within an annual ring, the density of earlywood is 30-40% of the the density of latewood. This heterogeneity and the indications on negative correlations with growth traits make it even more important to include wood density in genetic analyses. Our study aims to elucidate the phenotypic and genetic relationships between wood density and growth traits for Scots pine and their changes by age. The trees studied were around 30 years old and we make an attempt to estimate correlations of wood density between juvenile and mature wood. So far we concentrate on whole ring wood density without making separate estimates for earlywood and latewood. Those wood types will be in focus in coming studies.

Wood density and annual ring width were measured on increment cores from 1400 trees in a 30-year-old full-sib progeny test of Scots pine in north Sweden. Genetic parameters for wood density were analysed separately for ten outer annual rings, and average wood densities were similarly calculated for the five most recent years. The evaluation included genetic correlations with height and stem diameter at breast height. Heritabilities of density, estimated separately for each annual ring, varied between 0.14 and 0.26 without any age trend, and was jointly for the ten or five latest around 0.3; for height growth it was 0.3-0.4 and for stem diameter slightly above 0.1. Additive genetic correlations with height and stem diameter were -0.4 and -0.5, respectively, in a straightforward analysis but vanished or at least diminished when ring width was used as a covariate. Yearly density breeding values, which were calculated for the parent trees for each of ten rings separately, varied considerably between parent trees and years. The tendency was increasing breeding values by increasing age, with a substantial increase between ages around 14 to 16 years from the pith. This age fits reasonably well to literature data on the change from juvenile wood to mature wood. The high genetic correlations for wood density between years, above 0.8 in all comparisons up to ten years apart, may indicate high covariation between juvenile and mature wood.

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FOREST TREE BREEDING 2050 – FINLAND'S NEW TREE BREEDING PLAN

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Finland's recently developed tree breeding plan, *Forest Tree Breeding 2050*, replaces the former long-term plan which was taken into action in 1989. The plan aims at improving the cost-efficiency of tree breeding while maintaining a broad base of genetic variation from which sustainable genetic gain may be derived. Moreover, it attempts to guarantee long-term response from breeding in changing circumstances (market demand, climate). To fullfill these objectives, various aspects of breeding, e.g., breeding goals, metapopulation sizes (a reduction from several thousands of trees to less than a thousand), population structure and selection and testing designs, have been revised.

Following the principles of the Multiple Population Breeding System, the breeding material will be distributed to multiple independent populations with different climatic and product goals. Climatic differences are accounted for by dividing Finland into six climatically uniform (mainly with respect to temperature sum) target areas which, to alleviate the transition process, roughly correspond with the former Norway spruce breeding zones. The new target areas are common to all the species.

A breeding population comprises 160 superior general performers selected for a «mainstream index» of growth, quality and vitality, with trait-weightings set appropriately with respect to the target area and the species. Apart from this basic setting, the plan reserves an option to breed for more diverse product goals within each climatic target area by means of Specific Goal Subpopulations. These comprise a small group of trees (recommendation is 20) which excel in specific characteristics but may not necessarily rank high on the standard selection criteria. Such specific traits can include resistance to pests and diseases, crop traits (narrow-crowned trees), and certain wood quality traits (e.g., heartwood content). Specific Goal Subpopulations may also be formed applying a selection index with economic weights that are modestly different from those of the mainstream index.

Controlled matings are used to create the recruitment population from which advanced generation selections (within families) will be made. The parents for single-pair matings are selected in the order of breeding value (positive assortative mating). Additional matings (2-3) are performed with the 1/4 of the highest-ranked trees, which allows some additional genetic gain to be made from between-family selection. Here as in several other steps of breeding, the allocation of efforts will be positively dependent on the genetic value of the material, i.e., the highest-ranking parents will have a larger representation of their offspring in the recruitment and candidate populations than the rest of the tested parents. In subsequent generations, the breeding population will be subdivided into small sublines stratified by breeding value, that are very effective in supplying future seed orchards with unrelated highly-bred trees.

The genetic evaluation of the breeding material is primarily based on clone testing (whenever possible) or the combination of phenotypic preselection and progeny testing. The genetic field trials will be replicated in 5–6 locations which sample a wide continuum of climatic conditions, extending to adjacent target areas and even neighbouring countries. Simple recurrent phenotypic selection is an option that can be used in connection with minor tree species with little commercial interest.

LOW COST IMPROVEMENT OF COASTAL DOUGLAS-FIR (*PSEUDOTSUGA MENZIESII* VAR. *MENZIESII* (MIRB.) FRANCO) BY APPLICATION OF THE BREEDING SEED ORCHARD APPROACH IN DENMARK

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An evaluation of a seedling seed orchard in Denmark of Coastal Douglas-fir showed variation between open pollinated families in their susceptibility to windthrow, height and diameter growth, stem straightness, number of forks at age 10 and bud burst at age 9. Individual narrow-sense heritability was 0.63 for bud burst, 0.40 for height and diameter, respectively, 0.48 for stem straightness, 0.20 for number of forks and 0.17 for windthrow susceptibility. Fast growing families were characterised by late bud burst and poorer stem straightness. Predicted gains concerning a reduction of windthrow susceptibility were poor due to low genetic variability. In multi-trait selection scenarios aiming to improve growth, stem straightness and reducing windthrow susceptibility, the approach of using seedling seed orchards demonstrated that it might be possible to obtain gains in height above 5% combined with significant improvements of stem straightness while retaining an effective population size above 50.

SCOTS PINE BREEDING STRATEGY IN LATVIA

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Ongoing research in Scots pine breeding in Latvia has two aims – select best trees for 1.5 generation seed orchards and develop long term breeding strategy. Both of them are based on evaluation of plus-tree open pollinated progeny trials that have reached age 25-35 years.

Breeding strategy should be ready for implementation after 3 years, when all data from previous trials will be collected and analyzed – in order to avoid time-gap in continuous breeding process and inefficient efforts.

Strategy should ensure continuous development, so all three sustainability cornerstones will be included.

<u>Economical effect</u> of breeding is proven in experiment, where growth and quality of progenies from average seed sample from 24 first generation seed orchards and 8 stands were compared. Experiment was placed in 3 distant places in Latvia and measures made at the age of 21 year. Seed orchard progenies were superior both in yield, m^3/ha (19%) and quality (stem straightness 6%, branchiness 1%). Since average pine stand yield in cutting age (?101 year) is 290 m^3/ha, and areas suitable for pine growth are 60% from total forest area, gain by using selected seed source is proven to be significant.

Single pair positive assortative mating as cheapest alternative is suggested for future development of breeding population. It could be done for 2 sets of 20-30 best clones. For the rest of clones phenotypic forward selection within open-pollinated families could be an alternative.

<u>Ecological aspect</u> is safeguarded with large initial material – roughly 900 phenotypically selected plus trees. From these material open-pollinated progeny tests as well as 697 ha first generation seed orchards have been established. Based on test results since 1983 in total 135 ha 1.5-generation seed orchards from 2 sets with 64 clones each have been established.

For both – experimental and gene pool preservation reasons – 3 population seed orchards containing 140-220 clones each have been established in superior pine stands. Genetic diversity is preserved also in natural regeneration that occupies ? 10% from total area regenerated by pine and in gene reserves.

Renovation of old clone archives as well as establishment of new ones is started with general idea to preserve at least half of initially selected plus trees. Besides, special archives are made and will be maintained for trees selected as average in growth, but superior in resin production.

<u>Social aspect</u> is also included with main idea to be in dialogue with society. It is important since half of forests in Latvia are state owned and most of breeding efforts are allocated to them. Questionnaire about recreational value has been chosen as first step, since with breeding general view of trees is (and will be) changed. Recreation is growing part of forestry-use and changes in visual view of forest influence everyone in country. Results of questionnaire could give useful information of what society wants and how to regard it in allocation of target areas for growth of forest from improved seed source.

Another important aspect to take into consideration – use of improved seed sources in forest regeneration leads to increasing yield (m^3/ha) that creates possibility maintain total wood production in the same level despite of increasing share of forest areas for nature protection and recreation.

WOOD DENSITY, ANNUAL RING WIDTH AND LATEWOOD CONTENT IN LARCH AND SCOTS PINE

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The wood density and late wood content in five different species of larch (*Larix* Mill.) and in Scots pine (*Pinus sylvestris* L.) were investigated using direct scanning X-ray densitometry. In total 106 trees were investigated. Old, 120-150 year, Siberian larch (*Larix sibirica* Ledeb. and *Larix sukaczewii* Dyl.) grown in Krasnoyarsk and Archangelsk and 105 year-old European larch (*Larix decidua* Mill.) grown in Sweden had on an average 20-25 % higher wood density than Swedish Scots pine. The variation in density between different trees of the same species was big. Average dry wood density of larch trees was 618 (535-670) kg m^{-3} in old Siberian larch, 621 (550-665) kg m^{-3} in mature European larch timber grown in Sweden. Average wood density for the young, 30-35 years-old, larch trees was 536 (515-560) for European larch (*L. decidua* Mill.*)*, 451(410-490) for hybrid larch (*L. x eurolepis* Henry) and 452 (420-490) for Japanese larch (*L. kaempferi* Lamb.*)*. Corresponding figures for mature Scots pine was 504 (510-590) kg m^{-3}. The density within the mature zone of the heartwood was 20-40 % higher than in the juvenile wood zone. The density in mature European and Siberian larch heartwood, usually reached 650 kg m^{-3} after 25-30 annual rings from the pith.

The density of larch heartwood increased with annual ring width up to 2.5 mm and decreased with annual ring with wider than 3 mm. On an average the latewood content was 40-50 % in old European larch, around 40 % in mature Siberian larch and 20-40 % in young hybrid larch (*L. × eurolepis* Henry.). The late wood content of mature Scots pine was approximately the same as in mature European larch.

The density of 35 year old European larch with narrower ring widths up to 4 mm had a higher wood density than old slow growing Scots pine.

GENETIC DIFFERENCES IN SCOTS PINE HEIGHT-DIAMETER RELATIONSHIP

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The aim of tree breeding is to genetically improve economically important traits as efficient as possible. Usually volume production is one such important target trait. Still, tree height is often used as the selection trait. It is usually easier to measure, has high heritability, and besides, there is also a positive correlation to stem quality. Selection for height alone could, however, cause us to select more slender (height/diameter) stems than average, which per see might be positive or negative, but also affect volume production through correlated response. The height-diameter relationship is therefore an important variable to study, and few studies are conducted in this area.

The environmental impact on diameter is high and the heritability is often lower than for height. Competition effects from neighboring trees therefore need to be controlled. Further, modeling an allometric relationship like the ratio between variables, may suffer from difficulties with size dependency and the slenderness ratio (height/diameter) is not constant over size. As a logic and simple measure of the slenderness of the stem we have instead tried to model the diameter among families when adjusting for height. This was done in a material of 10 progeny trials of Scots pine (*Pinus sylvestris* L.) in the Swedish tree breeding program. The progenies originated from controlled pollination in a partial diallell mating design with parents from three seed orchards in northern Sweden. A linear mixed model with covariates was fit to the data. Competition and micro-heterogeneity was also adjusted for in order to diminish the differences from those effects. To evaluate the impact on gain in volume production the families were ranked and selected with different selection intensities.

The main results showed that there was a considerable genetic variation in slenderness among the parents in the study. However, selection based on height alone only had minor influence on the volume gain.

NEW SEED ORCHARD PROGRAMME IN FINLAND

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The first seed orchards were established in Finland in the early 1950's. However, the major activities in this field did not start until more than a decade later. In 1963 an official report was issued about the total area of seed orchards required for the production of genetically improved reforestation seed in Finland. The large-scale realization of seed orchards started some years later, and was completed by the mid 1970's. The target of the first seed orchard programme was to produce all the seed needed in forest cultivation, also in direct seeding, in seed orchards. In all more than 3000 ha of orchards were established. At the moment there are 141 (2202 ha) Scots pine and 25 (282 ha) Norway spruce registered first generation seed orchards in Finland.

In later seed orchard programmes the target to produce all the seed needed in the whole country has been revised, especially concerning seed production for the northernmost part of the country and for direct seeding. The main target of the new generation seed orchards is to produce genetically as good quality seed as possible. A new master plan for forest tree seed production, made in 2003-2004 by a working group appointed by the Ministry of Agriculture and Forestry, was based on earlier programmes carried out in 1989 and 1997.

The task of the new, broad-based working group was to evaluate the need for forest tree seed in 2005-2030, and based on this evaluation to revise the existing seed orchard programme. Need for forest tree seed was thoroughly evaluated using the current area of annual cuttings, objectives of regional forestry plans, and the national forest inventory data. In addition, the visions of forestry professionals about trends in forest regeneration were taken into account. Annual need for Norway spruce seed orchard seed for nursery use was 1827 kg, and that for Scots pine 542 kg, but in addition, 3416 kg of Scots pine seed orchard seed was needed for direct seeding. The total seed orchard area needed for Norway spruce was 290 ha from which still 190 ha has to be established, and the total area for Scots pine was 610 ha from which 270 ha has to be established. There is also need for Silver birch seed in Finland, annually 39 kg for nursery use and 99 kg for direct seeding. All the birch seed is produced in green house seed orchards.

Because of the high establishment costs and long waiting time for the first crops, seed production in seed orchard is not a tempting business investment. That is why the working group recommended that the state should subsidy by 85 % the costs caused by establishment of seed orchards (excluding land costs) and tending of young orchards. Also decentralized seed production strategy, i.e. several independent seed producers, was recommended.

SIMILARITY BETWEEN AUTUMN FROST HARDINESS AND FIELD PERFORMANCE IN NORTHERN *PINUS SYLVESTRIS*

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During the 1980's and 1990"s six Scots pine (*Pinus sylvestris* L.) seed orchards were established, which were intended to produce material for reforestation in harsh regions of northern Sweden, and may supply around 50 percent of the productive forestland in these regions. The clonal selections in the orchards were mainly based on the results of juvenile freezing tests in climate chambers. It is clearly important, therefore, to establish how the initial freezing-test based screening of the orchard clones will influence the performance of new forests originating from these seed orchards.

The data analysed in the study were the results of artificial freezing tests of the autumn frost hardiness of 1-year-old seedlings and field measurements of 9- to 13-year-old saplings representing (in both cases) the progenies of first-generation Scots pine plus-trees. The field traits analyzed were survival, tree height, spike knot frequency, branch diameter, branch angle, stem straightness, and resistance to the pathogens *Phacidium infestans*, *Gremmeniella abietina*, *Melampsora pinitorqua* and *Lophodermella sulcigena*. The genetic material was clustered in four independent test groups, each of which comprised a separate set of half-sib families replicated in one freezing test and five field trials. The total number of half-sib families included in each test group ranged from 303 to 360. The material was grown from open-pollinated seed collected from the plus-trees in the forest stands. Stand locations of the plus-tree mothers and positions of the field trials ranged from approximately 61° to 68° N in Sweden.

There was considerable variation in both sign and significance among estimated additive genetic correlations between frost hardiness and the tested field characters. After sub-grouping based on the harshness of the field sites, positive and fairly high correlations were observed between frost hardiness and field survival from the trials located in the harshest environments. In the milder environments, no clear association was found, probably because genes associated with hardiness traits were expressed at low levels. In addition, estimated correlations between frost hardiness and tree height were negative in 9 out of 10 cases for trials located in relatively mild environments, and non-significant for trials in the harshest environments. Thus, the expression patterns of genes associated with tree height may differ between sites, depending on the harshness of the environment. The genetic correlation between frost hardiness and quality characters/pathogen resistance were in most cases non-significant and no clear trends were detected.

In conclusion, selection based on juvenile freezing test results should improve field survival, reduce height growth and have minor effects on quality and pathogen resistance.

MITOCHONDRIAL DNA VARIATION AND POSTGLACIAL COLONIZATION ROUTES OF SCOTS PINE

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Knowledge about the history of Scots pine is important in understanding its genetics and especially mechanisms of adaptation during the colonization. The exact routes of colonization and origins of different Scots pine populations are not known. Different composition of mitochondrial haplotypes in different populations can reflect the colonization history the species. In this study we used two mitochondrial regions with polymorphic structural rearrangements to get more resolution on post glacial history of the Scots pine. 26 European Scots pine populations and 29 single trees (total 546) were sampled, covering a large part of its present day distribution. Mitotyping was conducted by PCR and PCR-RFLP. There was a strong geographical differentiation in mitochondrial haplotypes. G_{ST} among all the sampled populations was 0.727, which is much higher than previous estimates of F_{ST} from nuclear data. The most striking result was that the previously undetected mitotype *c* was present in Central Europe, Scandinavia and Eastern Europe. Several populations in the Iberian Peninsula have a private haplotype *b*, which is in accordance with the previously postulated hypothesis that there have been isolated populations in the Iberian Peninsula, and that they have not contributed to the colonization of rest of Europe. The origin of the Turkish population is also different to the European populations, since it has a private haplotype *d*, which is not present anywhere else in Europe. The results of this study support the view that during the last glacial maximum there have been populations of cold tolerant tree species such as *P. sylvestris*, outside the Mediterranean peninsulas and these populations have a large contribution to the present day populations of the species.

UTILIZATION OF SCOTS PINE SEED ORCHARD SEED IN DIRECT SEEDING

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Background

Direct sowing of Scots pine is an important forest regeneration method in Finland. Annually some 30 000 ha of forest is regenerated by sowing. This comprises more than half of Scots pine cultivation and about 1/4 of all artificial regeneration.

Direct sowing is mechanised to a high degree. In 2003 sowing by machine in connection to soil scarification was done on 59 % of all sowing area. The easiness in mechanisation and lower costs compared to planting have helped to maintain the amount of direct sowing at a rather constant level, although planting of Scots pine has decreased drastically during the last two decades.

Sowing consumes rather great amounts of seed. In 2003 about 9500 kg seed (mainly Scots pine) was used for direct sowing, when at the same time the nurseries used 1740 kg seed (all species). About 1/3 of the Scots pine seed used in direct sowing is produced in seed orchards. There has been discussion whether this proportion should be increased. In order to find out the usability of seed orchard seed in direct sowing a research project was initiated at Finnish Forest Research Institute in 2002.

Study methods

The study was accomplished by establishing field experiments where seed lots from several seed orchards were compared to stand seed lots in three years at four localities in southern and central Finland (in the first year only at two localities). There were two types of seed orchards included in the material: seed orchards with southern and northern origin, but all the tested seed lots had their 0defined utilization areas in southern or central Finland.

Sowing was done on mineral soil on shallow holes made by a special tool. 16 seeds were sown on each sowing spot and covered by a thin layer of mineral soil. The experimental design was randomised blocks with one sowing spot of each entry in each of the 30 blocks.

The plant establishment was monitored 3 to 5 times during the first growing season and later the number of the plants was counted and their condition evaluated at the end of growing season. Also the height of the tallest plant in each sowing spot was measured at the end of the growing season.

Observations from the experiments

The better the germination of the seed lot was in laboratory, the better was also the plant establishment result in the field (r = 0.855**). Plant establishment was 5 %-units higher with seed orchard seed than with stand seed, but the plant yield per equal weight unit of seeds was 15 % lower with seed orchard seed because of its greater weight. Plants from seed orchard seed were 15 % taller than plants from stand seed. The height difference decreased with age in relative terms, but increased in absolute units. The difference between seed orchard and stand seeds in plant establishment rate varied greatly depending on year and site, whereas in height growth the differences were consistent in different years and sites.

There was great variability between seed lots within each seed type as regards plant establishment rate, so no general conclusions can be drawn if only a few seed lots are tested. In some cases the seed lots from seed orchard with northern origin had delayed germination which could extent to the next spring.

Preliminary conclusions

Due to the young age of the experiments no final conclusions can be drawn yet, but at this stage seed orchard seed seems not to offer any great advantage compared to stand seed as regards plant establishment rate. The better height growth of the seed orchard material will of course result in genetic gain in wood production as is also shown by planted material. It remains to be seen what is the long term effect of this better height growth as regards the competition with ground vegetation and thus to the density of the stand.

The monitoring of the experiments will be continued to get more reliable results. There has also arisen a question whether the tested seed lots are representative to their classes and could there be some benefit of combining differently germinating seed lots.

GENETIC GAIN IN AREA-BASED PRODUCTION IN NORWAY SPRUCE

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Results are presented from a series of 55-60 year old field tests with Norway spruce (*Picea abies* (L.) Karst.) in Sweden. The aim with the present study is to estimate genetic parameters in area based production (coefficient of additive variation, CV_A), the genetic correlation (r_{jm}) between juvenile height and mature production and the genetic gain in production when selecting for early height.

Area-based production is defined as the total production of stem volume per hectare. The production includes living trees, dead or damaged trees and thinned trees. The field tests were established during the 1940's and has almost completed a full rotation-period. In total 14 test sites are studied – seven in mid-Sweden and seven in northern Sweden. On all sites half-sib progenies were planted in multiple tree plots. Multiple tree plot designs are advantageous for studies of production but the low number of parents tested and the low number of replications used, lowers the precision of the estimates.

The progenies originate from trees selected for various reasons: phenotypically selected plus-trees based on superior height growth, randomly selected trees and trees selected for uncertain reasons. The material, especially at the northern test sites, involves considerable latitudinal transfer. As transfer effects are expected on early tree height and production, it is considered in the analysis. Genetic connections exist over sites but is too small to be considered significant.

Early measurements are re-used to study the early performance in height and production. New measurements are performed to study current production based on diameter or stump diameter of all trees and tree height on sample trees. Approximately 16 sample trees are used to create volume functions for each family and site. Incomplete data are evident on several of the test sites due to clear-cuttting, snowbreakages and non-existing early height measurements.

Results of early survival show high survival rates on most sites. Late survival is also high which makes it possible to trace most of the planted trees. Trees not possible to trace are trees lost mainly due to uncontrolled historic thinnings or loss of small sized trees. Data on production per hectare and early tree height are analyzed with a unisite univariate model and a unisite bivariate model using the AsReml software. The results show CV_A's at similar levels for both early height and production. The genetic juvenile-mature correlation was moderate. The range in CV_A and juvenile-mature correlations were both wide.

The genetic gains are calculated as: selection intensity × $CV_A \times r_{AI} \times r_{jm} \times r_{GE}$. Based on the results in this study the anticipated genetic gain in production when selecting for early height is high. The genetic variation (CV_A) appears to be higher than generally expected, which further increases the gain in production. On the other hand the moderate genetic correlation (r_{jm}) appears to be lower than generally expected which reduces the gain somewhat.

СОСТОЯНИЕ, МОНИТОРИНГ И ЗАДАЧИ СЕЛЕКЦИОННЫХ ПРОГРАММ

Материалы совещания лесных генетиков и селекционеров северных стран Европы

STATUS, MONITORING AND TARGETS FOR BREEDING PROGRAMS

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