

# SKOG FORSK

Stiftelsen Skogsbrukets Forskningsinstitut

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## **BREEDING PROGRAMMES IN SWEDEN**

**Corrected reprint from: Lee, S. J. (ed.). 1993. Progeny testing and breeding strategies, Proceedings of the Nordic group of tree breeding, October 1993, 184+pp. Edinburgh: Forestry Commission.**

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### Contents (25 pp):

Danell, Ö. 1993. Breeding programmes in Sweden:	
1. General approach.	1
Wilhelmsson, L. & Andersson, B. 1993.	
2. Breeding of Scots pine ( <i>Pinus sylvestris</i> ) and lodgepole pine ( <i>Pinus contorta</i> ssp. <i>latifolia</i> ).	5
Karlsson, B. & Rosvall, O. 1993.	
3. Norway spruce.	16
Werner, M. 1993.	
4. Breeding broad-leaved tree species in Sweden.	22

# Breeding programmes in Sweden

## 1. General approach

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### Introduction

Since the start of tree breeding in Sweden some 50 years ago, a vast base material of plus-trees has been collected, and progeny and clonal tests have been initiated. A large part of these tests have already evaluated and the rest of the evaluations will essentially be finished during this decade. Parallel to this, the collected material is used for mass-propagation of afforestation material, mainly in seed orchards.

The approach for the future is to continue the breeding by long-term recurrent selection programmes with the multiple purposes of securing adequate conservation of genetic variation, preparing for possible climatic changes and improving the material as efficiently as possible. The general structure includes meta-populations for each of the more important species composed by breeding populations with different adaptation targets and improvement goals. As an optional intermediate step prior to mass-propagation, intensive breeding in 'elite lines' is suggested.

The long-term plans are currently under further development and are gradually implemented in the various species.

### Long-term breeding programmes

#### *The background motives*

Most tree breeding programmes today acknowledge genetic conservation as an important objective along with breeding for economic goals. Quite commonly, however, these are suggested to be kept separated in the programme, such that long-term conservation needs are met by keeping large resource populations where only weak selection for commercial objectives is performed, and the main improvement efforts are concentrated to relatively small breeding populations. Propagation of afforestation material is based on improved materials from the breeding populations. Unless breeding populations are not large enough to manage inbreeding at an acceptable level and to secure a sustainable breeding as well as a sufficient level of long-term conservation, this approach makes it necessary to renew breeding material in advanced generations of breeding by introducing 'new' material from the resource population. The obvious draw-back is that the already achieved genetic improvement is at least partly lost.

Therefore, our approach for long-term breeding plans is to integrate (1) conservation efforts, (2) preparedness for future climatic changes and (3) intensive breeding for general purpose goals in the same material. This is done in a meta-population consisting of essentially closed nucleus breeding populations with different adaptation profiles. In short, the various objectives are considered within this general approach as follows.

## *Conservation for evolutionary needs and sustainable breeding*

The extremely long-term conservation of allelic variation for 'evolutionary development' is managed in the meta-population composed by the nucleus breeding populations. For the two major species, Scots pine and Norway spruce, a meta-population size of 1000 individuals sampled in each generation (selected parents of next generation) are considered sufficient (see Danell, this proceeding). For foreign species and species where the use of bred material is expected to be small in relation to natural regeneration, this level of conservation is considered less motivated and smaller meta-population sizes are considered acceptable. Thus for lodgepole pine and birch, a total of about 500 sampled individuals per generation is considered appropriate. For minor species, with limited breeding efforts and use of bred material, considerably smaller total populations are acceptable.

Conservation of genetic variation to secure sustainable breeding is done within each nucleus breeding population. With appropriate management, 50 parents selected in each generation will be fully sufficient. With this population size, the losses of 'common' alleles, being the main contributors to selection gain, will be low. Inbreeding is expected to be a more restricting problem due to the commonness of lethal and detrimental alleles in forest trees. With a restricted within-family selection (e.g. double pair mating and exactly one family member selected in each) the increase of inbreeding is low (about 0.5% per generation), and unrestricted within-family selection will just double this rate. That means effective population sizes kept at about 100 and 50, respectively.

## *Adaptation to current and future climate*

The nucleus breeding populations are allocated to different adaptation targets defined by measurable parameters describing light and temperature climate, rather than by their intended use in geographic terms. The reason for this is to enable testing and selection for adaptation under controlled and definable conditions in the future breeding work, rather than to run adaptation tests under temporary weather conditions on test sites defined by their geographic location.

The distribution of adaptation targets over the temperature climate covers an area which is broader than the current temperature climate range of Sweden (Fig. 1). When future changes occur, whether they are towards warmer or colder climates, there will be improved material ready to be propagated for afforestation purposes.

## *Recurrent selection programmes for gain generation*

For the main species, the breeding is based on recurrent selection programmes. The main structure for each breeding population is shown in Fig. 2.

Long-term breeding is carried out within each nucleus, which is maintained with about 50 parents per generation, selected essentially on a within-family basis and crossed e.g. according to a double-pair mating design. As the nucleus populations are intended to be a sustainable base for the breeding, the breeding objectives should be general.

The breeding programmes intend to promote both testing accuracy and selection intensity, as these are the major determinants to breeding efficiency along with the generation interval. As a main strategy, the testing is assumed to be based on progeny (pines) or clonal (N. spruce, broadleaves) testing of the new generation and typically selecting one out of 10 and 40 family members, respectively. When possible, early screening or testing and phenotypic selection could precede this. A problem with this approach is, however, that flowering/crossing or the vegetative multiplication in order to produce test material from the new generation will increase the generation interval. Therefore, phenotypic within-family selection is a reserve alternative until flowering stimulation or vegetative propagation for generation of test materials are further improved.

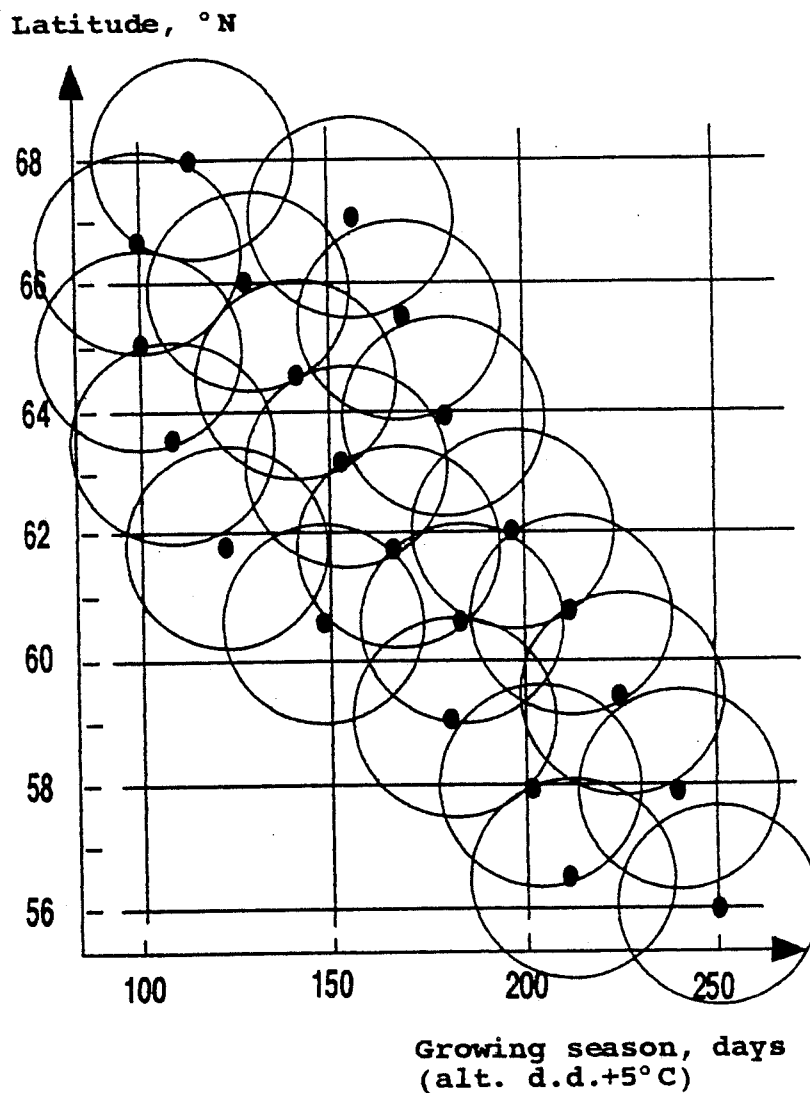


Fig. 1. Distribution of breeding populations over light and temperature climate gradients. Due to the inherent genetic variation the populations overlap and, especially on temperature climate, cover a considerably broader range than Sweden covers today.

Short- and medium-term flexibility in goals, more hazardous breeding objectives and 'elite' breeding to exploit the best parts of nucleus populations for specific propagation purposes is suggested to be met by intensive breeding of diverging lines. Still they should provide sufficient genotypic diversity in propagated material. Each elite line could be initiated with intensively selected clones from one or several nucleus populations, and successively renewed later on. As long-term breeding is secured by the nucleus populations, the long-term conservation aspects can be relaxed and there is a large flexibility in size, longevity and how the elite lines could be set up.

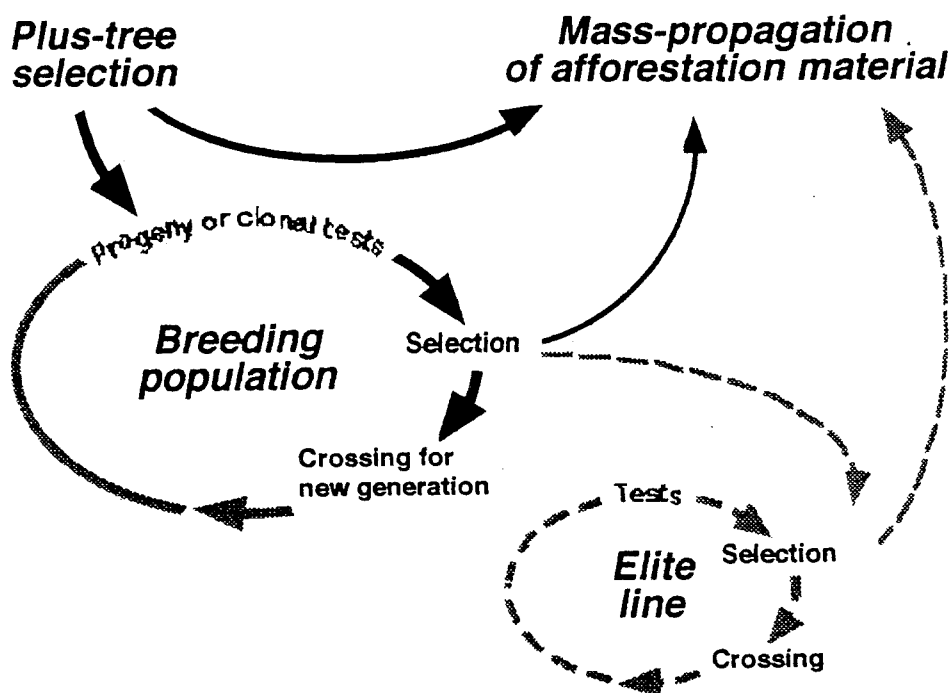


Fig. 2. General outline of recurrent selection programme for nucleus breeding population for long-term breeding and elite lines for medium- and short term breeding.

Conventional seed orchards and cutting propagation are currently the main propagation methods. In the future, many different propagation techniques are assumed to be used, allowing for an efficient and fast propagation of superior material. This includes controlled pollination for seed production and cell- and tissue culture techniques. In general, a sufficient genotypic diversity in propagated material is easy to achieve, also from small elite lines.

## Literature

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

## 2. Breeding of Scots pine (*Pinus sylvestris*) and lodgepole pine (*Pinus contorta* ssp. *latifolia*)

by

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### Introduction

Scots pine (*Pinus sylvestris*) is one of the most important tree species in Swedish forestry. This species accounts for about 33% of the annual national wood production (95 million cubic meters stem wood over bark) (Skogsstyrelsen, 1992). Lodgepole pine (*Pinus contorta* ssp. *latifolia*) is, without question, the most utilised exotic species in Swedish forestry. Annually between 1980 and 1990, an average of 30000 ha of pine was planted north of latitude 59°30'. This represents about 15% of the area planted with forest trees in Sweden during that decade (Skogsstyrelsen, 1992).

Efforts to breed Scots pine started in the 1940s (Werner et al. 1981). Since then a number of reports have covered with various aspects of pine breeding, i.e. Arnborg (1948); Johnsson, Andersson & Stefansson (1949); Kiellander (1949); Andersson (1960), Johnsson (1964) and Andersson (1966). Most studies dealt with programs for the establishment of seed orchards of Scots pine, but to some extent questions regarding further breeding were also addressed. A tree improvement and seed production program for lodgepole pine in Sweden was presented by Rosvall (1980). This was followed by a more detailed breeding plan for Scots pine, Norway spruce and lodgepole pine, presented by Werner et al. (1981).

During the last 10 years, many genetic parameters have been derived from assessments in progeny tests, and long-term breeding strategies have been extensively discussed by Gullberg & Kang (1985), Lindgren (1989), Eriksson (1991), Danell (1991;1992a) and Danell et al. (1993), among others. This information, together with general population genetics and economic analyses, have provided the foundation for a new general breeding strategy (Danell, 1992a), upon which the breeding plan described here is based.

### Breeding goals

The approach to genetically improving goal-traits is, to a certain extent, similar throughout Sweden and roughly the same for Scots pine and lodgepole pine. However, there are some important differences in the general conditions for forestry in different parts of the country that affect the relative importance of different traits. By analysing known and assumed sources of genetically and environmentally induced variation that affect the economic yield, the relative importance of the various breeding goals can be determined. A generalised overview of the goal-traits is presented in Table 1. Selection indices will be used to identify the best predictor of the total economic yield, calculated on assessments of several traits. The selection indices will be based on genetic variation, correlations between assessed traits and goal-traits, and economic weights of the different goal-traits.



Table 1. Generalised presentation of goal-traits considered for breeding pines in different regions of Sweden. II = Most important trait, I = Important trait, 0 = Trait of minor importance, unchanged values accepted, - = Unimportant trait, decreased values accepted.

<u>Goal traits, improvement of</u>	<u>Main regions</u>	<u>Harsh regions</u>	<u>Mild marginal regions</u>
<u>Adaptation, survival</u>			
Climatic adaptation (temp., photoperiod)	I	II	II
Disease resistance	I	II	II
Stability over environmental gradients	I	0	I
<u>Yield (survival rates excluded)</u>			
Growth capacity (total production of stem dry-matter)	II	0, -	II
Growth efficiency (N-productivity, allocation, etc.)	II	0, -	II
<u>Stem &amp; wood quality</u>			
Stem straightness	II	0	II
Branch types	II	0	II
Fibre properties affecting sawn-timber strength & pulp yield, etc.	I	0	I

### Founder populations of Scots pine

The base material (about 6000 plus-trees) used for establishing the founder populations of Scots pine consisted of two main categories of plus-trees, "old" and "new", selected in Sweden (Fig. 1.) and, to a limited extent, also in Finland, Norway, Germany, Poland, Estonia, Latvia, and Russia.

#### "Old" plus-trees

A first selection of around 1300 "old" plus-trees was made in good-looking, naturally regenerated stands at full rotation age (not always even aged) in different parts of Sweden during the 1950s to early 1960s. Many plus-trees were immediately used to establish the first-generation seed orchards. Testing of the progeny of these trees from the mid-1960s to late 1970s was based on partial dialleles consisting of between five and eight crosses per parent distributed into single-tree plot experiments.

#### "New" plus-trees

A second selection of about 4700 Scots pine plus-trees was made in the early 1980s. The trees were selected mainly in well developed, even-aged, planted (or sown) stands at an age of about 1/3 to 1/2 of the total rotation time. Presumably stands of this kind are suitable for use in discriminating between branch types, degrees of stem straightness, etc. Genotypes of some plus-trees from Finland, Norway, Russia, Estonia, and Latvia have been introduced to Sweden by planting either their progeny or plus-tree ramets. Since around 1980, open pollination has been used as the main tool for testing the progeny of new plus-trees of Scots pine

### Founder populations of lodgepole pine

The base material for lodgepole pine (Fig. 1.) consists principally of open pollinated progenies from around 1300 Canadian plus-trees (Rosvall, 1980). The selections were geographically distributed to correspond to a subdivision of Sweden into seed orchard zones, where progeny testing was carried out (Ericsson, 1993). Some 200000 individual trees in the test plantations are now available for use in establishing founder populations. However, the initial delineation of lodgepole pine seed orchard zones in Sweden was only used during the introduction phase and will not be employed in defining founder populations for future breeding.

Pinus sylvestris base materials

Pinus contorta base materials

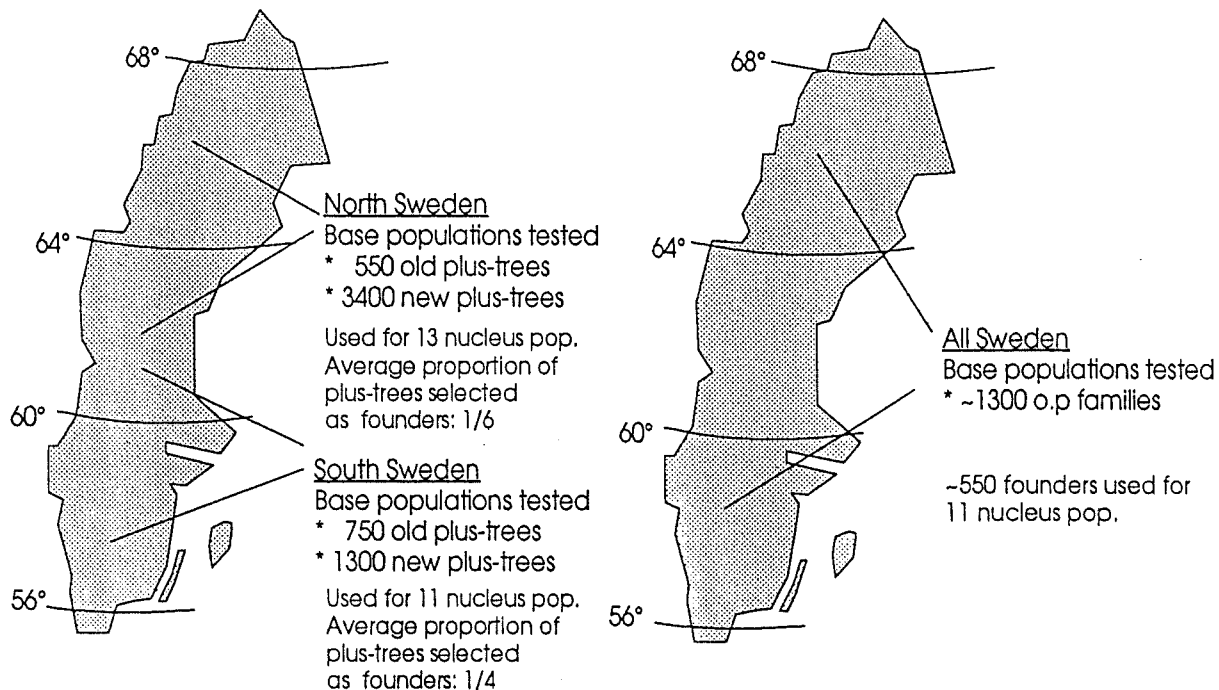


Fig. 1. Base populations from which trees will be selected for use in establishing founder populations of Scots pine and lodgepole pine.

Latitude °

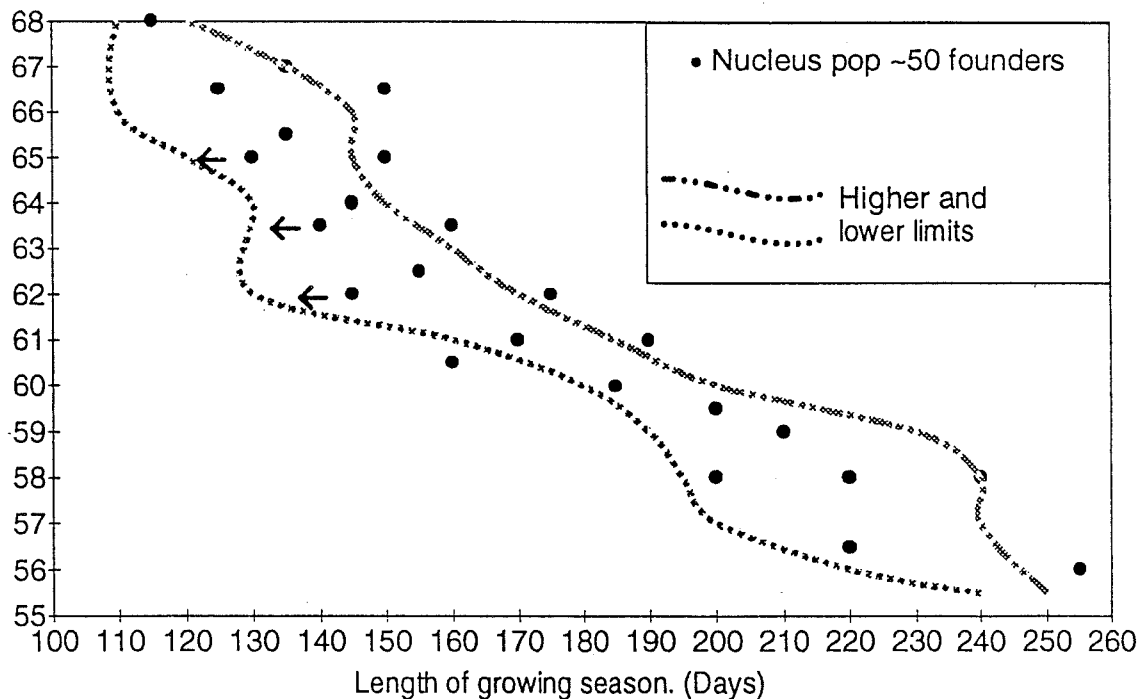


Fig. 2a. Proposed distribution of Scots pine nucleus breeding populations according to target latitude and length of growing season (number of days when mean daily temperature persistently exceeds +5°C). Limits of higher and lower values recorded within Sweden during 1961-76 (Odin et al., 1983).

# Formation of long-term breeding populations

## Scots pine

The general strategy for forming breeding populations is to delineate the total material into 24 nucleus populations. Each nucleus population will consist of around 50 founders, and is to be adapted to a specific combination of latitude (photoperiod) and temperature climate (length of growing season or temperature sums in day-degrees over +5°C). The distribution of the Scots pine nucleus populations is shown in Figs. 2a and 2b. To some extent the same founder may be represented in more than one population, but the sum of all founders used will probably exceed one thousand. Thus there should be sufficient genetic variation in the Scots pine breeding program to ensure the capability for both long-term breeding and the conservation of potentially important genes (Danell, 1992a; 1992b). In total, the base material includes around 6000 plus-trees, 3950 designated for use in northern Sweden and 2050 aimed for southern Sweden. Based on results of progeny tests, a total of around 650 founders will be selected to establish 13 nucleus populations in northern Sweden; thus the initial number of selected plus-trees will comprise about 1/6 of the base material. The corresponding figures for southern Sweden are 550 founders used to establish 11 nucleus populations, and the initial number of selected plus-trees represents about 1/4 of the base material.

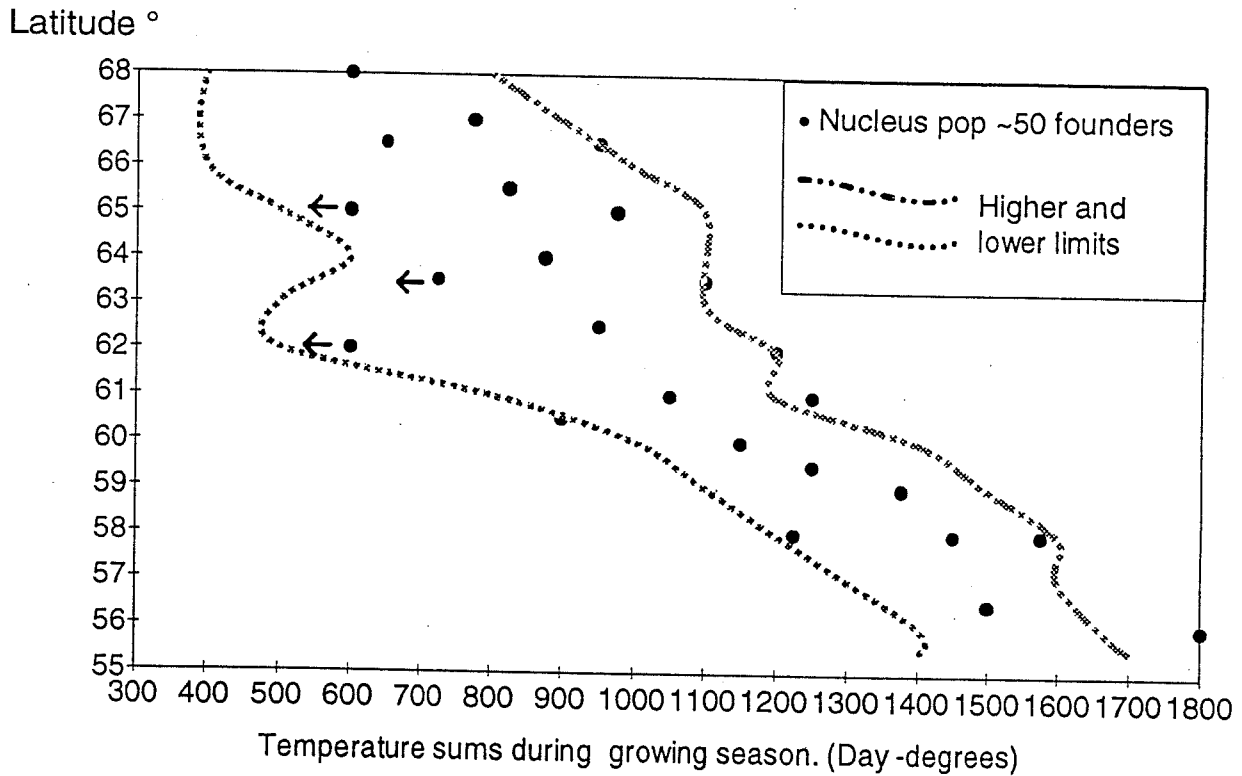


Fig. 2b. Proposed distribution of Scots pine nucleus breeding populations according to target latitude and temperature sum (days x degrees when mean daily temperatures persistently exceeds +5°C). Limits of higher and lower values recorded within Sweden during 1961-76 (Odin et al., 1983).

## Lodgepole pine

The general strategy for forming breeding populations of lodgepole pine is similar to the one used for Scots pine. However, lodgepole pine seems to be less sensitive to transfers. Additionally, gene conservation is considered to be a lower priority in lodgepole pine than in Scots pine. Thus 11 nucleus populations are considered to be sufficient. With 50 founders constituting a nucleus, 550 trees are to be selected from half-sib progenies of around 1300 progeny-tested mother trees. Unrelated trees with superior mothers will be given highest priority. The final choice between individuals may be based on their phenotypes or on the results of further progeny testing. The distribution of the lodgepole pine nucleus populations is presented in Fig. 3.

### Long-term breeding

The basic strategy for long-term breeding is to maintain an effective population size ( $n_e$ ) of about 50 in each nucleus population. This will be achieved by aiming for two crosses per individual according to a pattern that does not strongly increase the differences between best and worst family means and provides a balanced selection of new individuals to a very high proportion of the families.

Latitude °

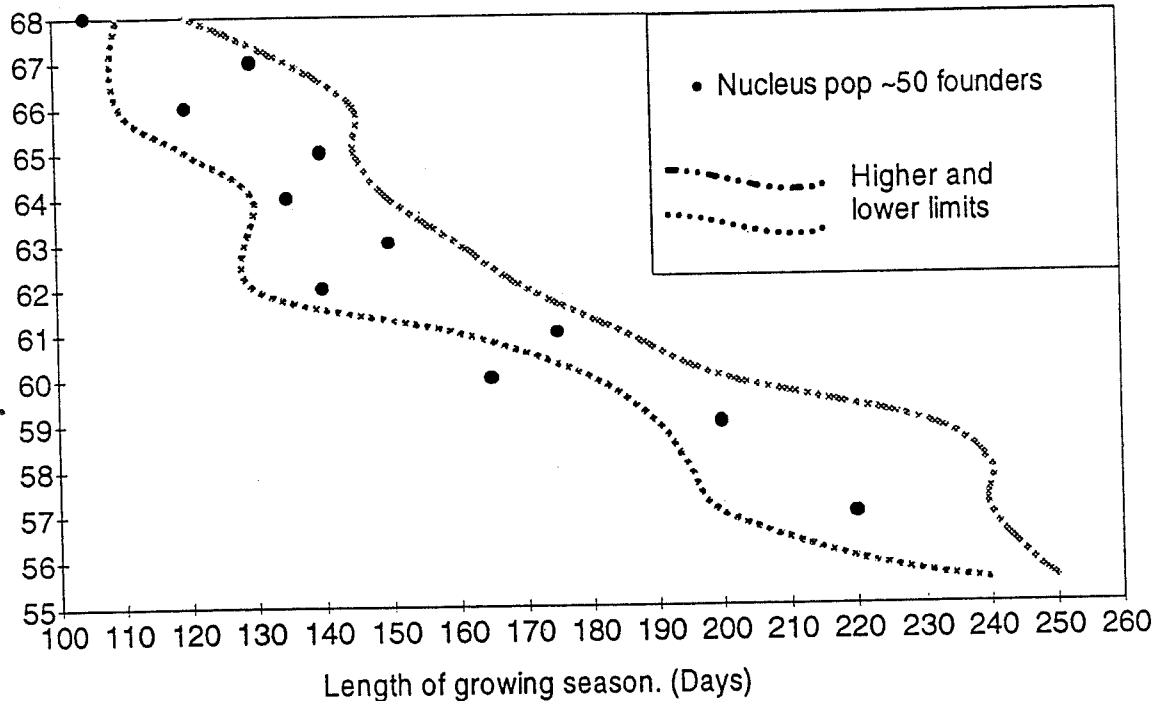


Fig. 3. Proposed distribution of lodgepole pine nucleus breeding populations according to target latitude and length of growing season (number of days when mean daily temperature persistently exceeds +5°C). Limits of higher and lower values recorded within Sweden during 1961-76 (Odin et al., 1983).

### Creation of new breeding generations

The continuous breeding work will include different phases in each generation. Without taking time and costs into account, it can be assumed that the largest gain per generation will be achieved by progeny-testing using strategy 1, described below.

**Strategy 1.** Selection of trees for use in next generation based on progeny testing. Source: Seed from controlled crosses between selected parents

<u>Phase of breeding cycle</u>	<u>Estimated duration years</u>
A1. Screening of young phenotypes in nursery before progeny tests	1 - 5
B1. Stimulate production of female flowers in phenotypes in archive collections or field tests. Polycross or open pollination (field tests)	3 - 20
C1. Progeny testing of the phenotypes	2 - 15
D1. Evaluation & selection of genotypes (based on progeny tests)	1 - 2
E1. Stimulate male and female flowering	2 - 5
F1. Recombination of selected genotypes. 2 crosses/genotype.	2 - 5
Total time, years/generation	11 - 52

If progeny-testing may considerably delay the creation of a new generation, selection of phenotypes without progeny-testing may be an cost-effective alternative. This is referred to as strategy 2 below.

**Strategy 2.** Phenotypic selection of trees for use in the next generation. Source: Seed from controlled crosses between selected parents

<u>Phase of breeding cycle</u>	<u>Estimated duration years</u>
A2. Establish trials designed for selection forward (including possibilities to check the breeding values of the parents)	7 - 15
B2. Evaluation & selection of phenotypes	1 - 2
C2. Grafting (if necessary), stimulate production of male & female flowers	3 - 15
D2. Recombination of selected phenotypes. 2 crosses/phenotype	2 - 5
Total time in years/generation	13 - 37

Calculations of the rate of genetic gain per year for the two principle strategies (1 and 2) have been made by Danell (in this volume). These calculations indicate that the results of the two strategies are similar. There is at least one other alternative that looks very promising for pine breeding, i.e. "the clonal method". It resembles the strategy used for spruce "Testing with cuttings" described by Danell (in this volume) and the procedures described in the flow-chart for Norway spruce presented by Karlsson & Rosvall (in this volume). However, the methods used for vegetative propagation (cuttings, tissue culture and somatic embryo genesis) of Scots pine, and even lodgepole pine, are still under development. Efforts up to now have met with limited success, even with very young seedlings. Furthermore the "clonal effects" may be considerable and are not sufficiently well known.

The potential for increasing the genetic gain per year is greater for strategy 1 than for strategy 2, but there are a number of problems concerning the stimulation of early flowering that have yet to be solved, and the intensive methods needed may be too expensive. Strategy 2 would

probably cost less, but it may require that the nucleus populations have to be located in their respective target environments. Thus, at least for some nucleus populations, it might later be necessary to graft the selected phenotypes into archives aimed for flower stimulation and crosses. The costs of grafting to produce clonal archives would then be compared with the costs for stimulating flowering, collecting pollen and accomplishing crosses between the selected phenotypes at the original test sites.

In practice, there are considerable differences in breeding stock available for different nucleus populations, e.g. differences in mating systems, age, and environment. For this reason both strategies 1 and 2 will be used, alone or in combination and with various modifications, depending on the situation and nucleus population concerned. A combined strategy allowing many options in cases where the probability of success in critical phases (e.g. seed production from young seedlings) is uncertain is described in Fig. 4. With this flexible strategy, progeny tests can be quickly made with individuals from a large number of families. Phenotypic selection can then be practised in all families in which only a low or medium-sized proportion of flower-stimulated individuals produced progeny at an acceptably rapid rate (A high rate of success will be required to avoid any problems with unknown correlations between early flowering ability and other traits). If the full-sib crosses produce sufficient amount of seed it may be possible to screen for traits that can be studied early. Selection intensity at the screening stage may vary greatly, depending on the power of the methods used for early screening. In breeding for hardiness, for example, it will be possible to use a selection intensity higher than that exemplified in Fig. 4.

### **Short-term breeding - elite lines**

The aims of long-term breeding are to achieve genetic gain while minimizing inbreeding and conserving a considerable amount of genetic variation within each nucleus breeding population. Therefore elite lines are suggested in order to maximise short-term genetic gain and to provide options in the selection and crossing of breeding stock where special traits (e.g. special emphasis on quality traits or maximised biomass production etc.) are desired. A typical elite line consists of the 10 best parent trees, judged in terms of the breeding goals for the line. If breeding goals and economic weights for the elite line are the same as those for the whole nucleus population and if the elite line is designed for use in the same target area as the nucleus population, then it will probably consist of the 10 best parents in the nucleus population. In such a situation some crosses may be combined for both short- and long-term breeding. However, since the crosses for long-term breeding will be distributed over all ~50 parents it is necessary to make additional crosses for short-term purposes. Another option is to combine material from different nucleus populations into an elite line. The number of elite lines desired will depend on the breeding objectives in the different regions and the availability of funding. If elite lines are bred for several generations inbreeding will reach unacceptable levels. For this reason, elite lines should be used for short-term breeding only.

### **Genetic gains**

Genetic gain in the breeding populations will be a function of the genetic variation in goal traits, genetic correlations between goal traits, genetic correlations between assessed traits and goal-traits and the selection intensity. Examples of breeding values have been used to calculate gains in assessed traits (Table 2). Corresponding gains from mother-tree selections could be estimated for lodgepole pine from breeding values presented by Ericsson (1992).

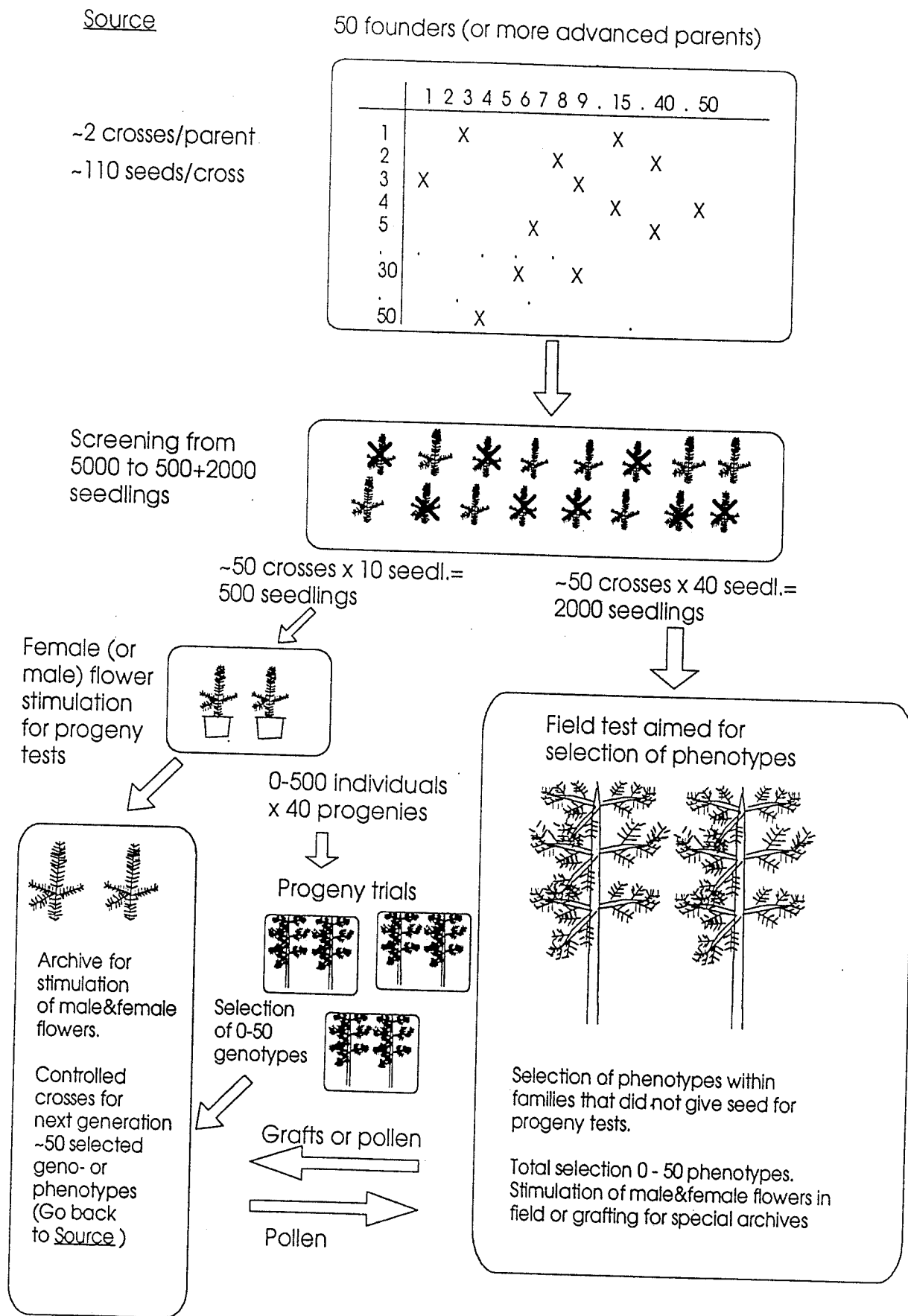


Fig 4. Example of combined strategy including options for progeny testing and/or phenotypic selection

Table 2. Examples of genetic gain in assessed traits after selection of given proportions of the tested parents in Scots pine progeny tests. Selection based on preliminary suggested selection indices. All values presented as deviations from population means. (Parent mean before selection = 0)

Series of progeny-trials	442 Sollerön 1	45 Saleby 2	56 Hens- backa <sup>3</sup>	42 Påarp <sup>4</sup>	466 Aspanäs <sup>5</sup>	1 Ska- holma <sup>6</sup>	10 Östteg <sup>7</sup>	462 Forn- Wij <sup>8</sup>
Target latitude	60-62	57-60	57-59	58-61	56-59	63-66	63-65	59-61
Selected proportion of parents	21%	24%	23%	30%	21%	17%	17%	13%
No. of field experiments	1	2	1	3	4	4	3	3
<u>Trait</u>								
1.Height %	4.0	8.0	5.0	4.8	12.6	8.3	10.8	7.2
2.Stem diameter %	2.7	7.5	3.7	1.4	10.6			3
3.Branch thickness %	2.6	1.9	-4.9	-1.8	0.6			-0.5
4.No of branches/whorl	0	0.4	-0.4	0				0.1
5.Branch angle	1.2°	1.2°	0.7°	0.3°	-0.7%			3.9°
6.Freq stems without spike knots %	0.3	2.4	-3.6	2.0		0.7	0.5	
7.Freq straight stems %	-0.9	0.6	7.1	3.5	-0.4%			+
8.Freq surviving trees %	0.6		0.0			-0.1	3.5	

For all traits except 3 and 4 high values are preferred. All frequencies (trait 6-8) are expressed as %-units. Figures in italics are not quite comparable to the others since they represent slightly different traits.

1	Calculations based on	Almqvist et al.(1992)
2	"	Almqvist(1992)
3	" " "	Almqvist(1993)
4	" " "	Hannerz(1993)
5	" " "	Högberg(1993)
6	" " "	Andersson(1993)
7	" " "	Andersson & Bäckström(1994)
8	" " "	Wilhelmsson(1990)



## Future research and development needs

Although knowledge concerning pine breeding has increased greatly during recent years, there is, nevertheless, an urgent need for research and development in certain areas:

- \* Develop methods for stimulating sexual maturation and flowering.
- \* Determine genetic correlations between flower characteristics and goal-traits.
- \* Develop procedures for vegetative propagation that minimise "clonal effects"
- \* Determine genetic correlations between assessable traits and goal-traits.
- \* Develop reliable methods for indoor and field testing in different environments.
- \* Determine relation between individual tree yield and yield per hectare.
- \* Estimate genetic and environmental variation in allocation of assimilates
- \* Determine the relation between growth efficiency and growth capacity.
- \* Evaluate the relative importance of different goal-traits from a long-term perspective.
- \* Estimate correlations between different goal-traits.

## Acknowledgement

Special thanks are due to Tore Ericsson for providing many helpful facts about lodgepole pine.

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### 3. Norway spruce

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#### Introduction

Norway spruce is one of the two main conifer tree species in Sweden and thus economically very important. It contributes about 50% of the annual total planting stock in south Sweden and 20 % in the north. Breeding activities, which were started in the 1940:s (Werner et. al. 1981), have been more intensive in later years, mainly due to more efficient breeding tools such as improved cutting technique and flowering stimulation (Werner 1993).

#### Founder population

The founder population can be divided into three categories.

A. "Old" plus-trees (approximately 1 000 trees) were selected and used directly to establish the first seed orchards in the 1950-60's. These plus trees were selected mainly in mature, often naturally regenerated stands, which resulted in a less accurate selection than expected. Progeny tests have been carried out mostly through controlled crosses. Due to irregularity in flowering some of them are tested with open pollinated families. The test results have been used to estimate genetic parameters and to predict breeding values and thus form the base of genetic knowledge for Norway spruce in Sweden.

B. "New" plus-trees, the next category, were selected in the 1970-80's in order to broaden the founder population. To accomplish a more accurate selection than the first one this selection was done in younger (20-40 years), of even age, and well developed stands. This choice of stands allowed a better judgement of branch quality since living or dead branches were present along the whole trunk. Furthermore, it allowed plus trees to be selected in optimally transferred provenances. In southern Sweden, this meant selection in provenances introduced from eastern Europe. In northern Sweden in the ideal situation this meant selection in provenances transferred one to three degrees of latitude to the north. In order to speed up the progeny testing, cones were selected from the trees directly in the stands. This material includes more than 5 200 trees of which 4 500 are or will be progeny tested with open pollinated progeny from stands or clone archives.

C. Clones from clonal test programmes are maybe the most potent founder population for establishing good breeding populations. The material originates from different clonal forestry programmes in different parts of the country. The oldest originates in south Sweden with clonal tests planted out from 1975 and onwards. Later programmes have started for middle and north Sweden. The clones represent provenances that are rare or absent in other materials, or offspring from bred material. They are tested in the field with several ramets each on at least two sites. The three clonal test programmes will finally include more than 18 000 tested clones.

The number of founders in different parts of the country are shown in Figure 1.

In addition there is another clonal test programme run by Hilleshög AB containing 15 000 clones in field tests. These clones could also be included in the breeding programme.

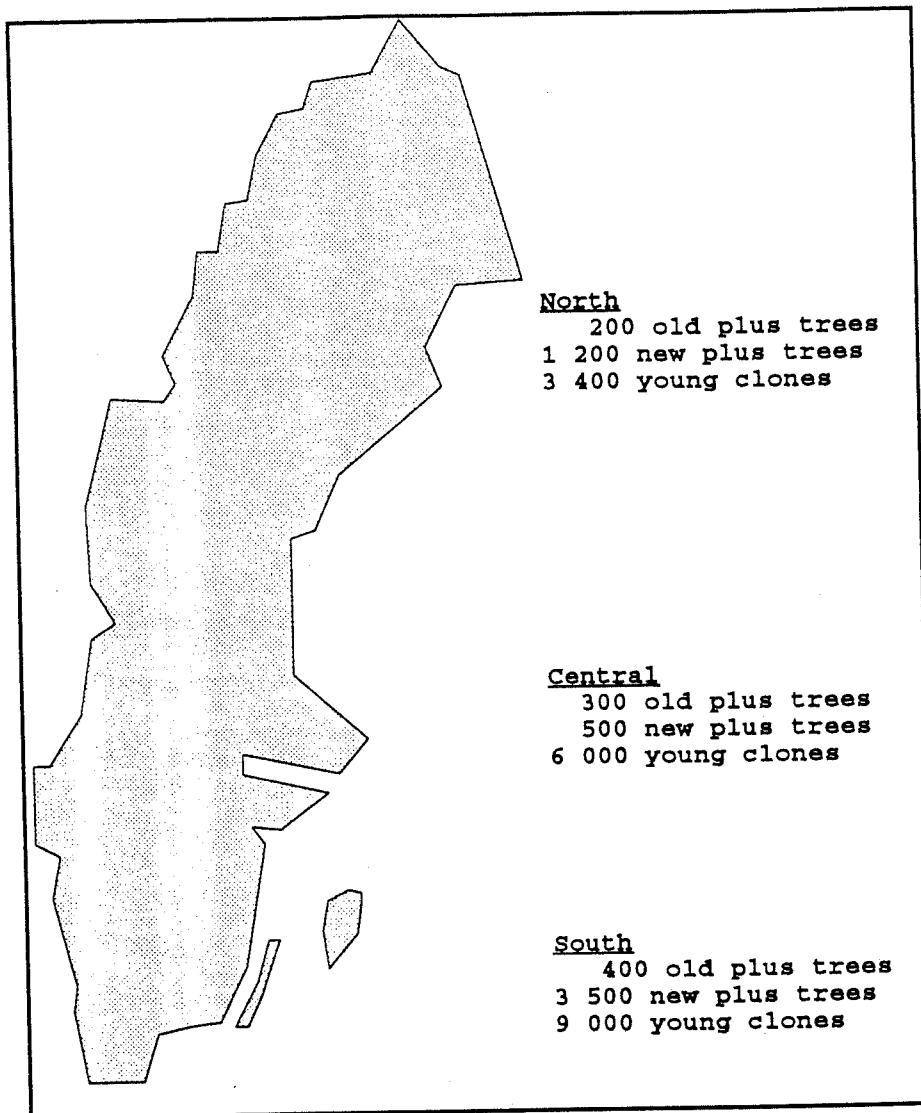


Figure 1. Founder population by type and number in different part of the country.

### Formation of breeding populations

The total founder population of 24 500 tested plus trees and tested clones, will be used to form the long term breeding populations. With the plasticity of Norway spruce, 20 populations are needed to cover the desired variation in photo period and temperature climate, including both warmer and colder climates than found at present (Danell 1992, Danell et al 1993). Assuming an effective population size of at least 50, more than 1 000 trees will be selected for the long term breeding programme for Sweden. The 20 populations will cover normal spruce sites from latitude 56° in the south up to 67° in the north, and a variation in temperature sum from 800 to 1800 day degrees over +5°. Some populations will be designed for specific conditions such as maritime climate and pronounced frost exposure. A graph showing the distribution of populations is shown in Figure 2.

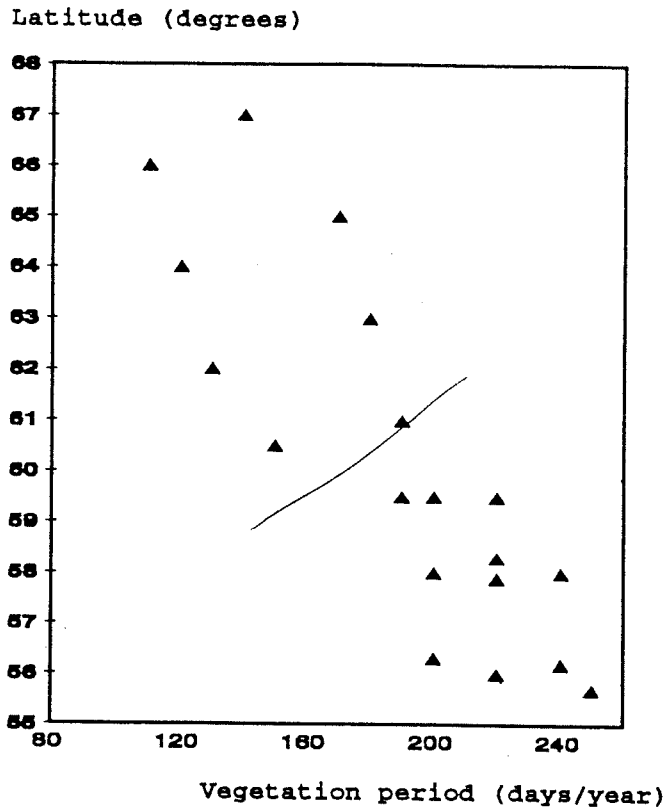


Figure 2. Distribution of breeding populations.

### Long term breeding

The long term breeding will be carried out in such a way that genetic diversity will be ensured and sufficient genetic gain will be reached, and to achieve freedom of action in the far future.

The selected trees of each population will be treated with gibberilin to promote flowering as early as possible. They will be mated so that each parent will be represented in at least two fullsib families. Approximately 100 seedlings will be produced from each of the full sib families. 40 of these seedlings will be selected based on their growth rhythm and growth.

In order to test this new generation of 2000 seedlings, they will be vegetatively propagated. (Today this is done by rooted cuttings, in a foreseeable future micro propagation may be used.) Full sib clonal progeny tests will be planted out on 4 different test sites with 3-4 ramets/site. The sites will be located over gradients of photo- and thermoperiod and in environments of special interest e.g. frosty sites. The ortets and a few ramets/clone will be kept in crossing archives to be used as parents for the next generation. Depending on design and geographic location the field tests will be finally evaluated at age 10-15 years and a new selection for the next breeding generation will be carried out. An approximately equal representation of each original founder should be aimed at in order to keep the intended effective population size and to minimise the increase of coancestry and inbreeding. A scheme for the long term breeding activities is shown in Figure 3.

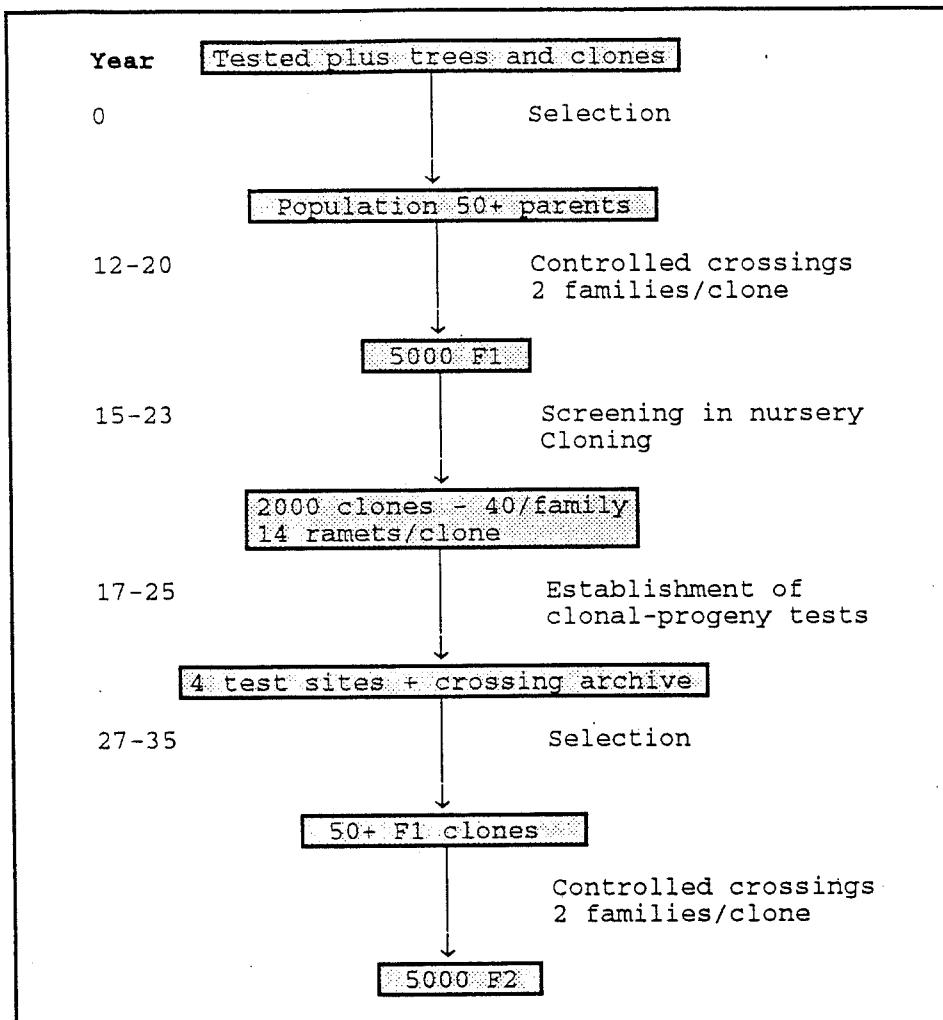


Figure 3. Scheme for long term breeding in Sweden

### Short term breeding - elite lines

Short term breeding will be carried out to capture maximum genetic gain in forest regeneration activities in the near future. Elite lines will be formed by mating the top 10 within each population. The very best ones will also be crossed with adjacent populations. The breeding goals will be the same as for the long term breeding unless special interests are expressed for and funded by e.g. forest owners. These lines, which will be open and can be abandoned at any time, will be the basis for selection of mass propagation for a few generations before the genetic base will become too narrow.

### Breeding goals

As good adaptation to climatic conditions is most essential for all tree breeding, the main selection criteria when forming the breeding populations will be growth rhythm characteristics, giving optimal synchronisation to the vegetation period of the intended planting site. Other breeding goals must be defined to carry out a successful long term breeding. Main goals still not perfectly defined are:

- **Vigour** Resistance to biotic and abiotic stress and ability to repair and recover from damages are very important characteristics.

- **Stem dry matter per hectare production.** Efficient resource acquisition and use as well as stem-wood allocation and high specific density.
- **Wood product quality.** As the main value for Norway Spruce is in saw timber, traits as straight stems as well as small knot size and low percentage of knot wood, are very important.
- **Good fibre characteristics.** It is discussed whether or not fibre morphology should be considered in the breeding programme.

## Mass propagation

Today, commercial mass propagation is carried out by clonal seed orchards. Sweden has 224 hectares of phenotypically selected old clonal seed orchards with a potential to produce seed. Since 1982 about 256 hectares of new clonal seed orchards have been established. Some of these are composed of genetically selected tested clones, while others are phenotypically selected and designed for later genetic thinning when breeding values will be available. In the future however, time between realised genetic gain and mass propagation has to be decreased if forestry should have the opportunity to be "up to date" with their reforestation material. From now on the following alternatives for mass propagation are available:

### Bulk propagated full sib crossing families

Bulk propagated full sib crossing families is the fastest way of mass propagating the new material in each new breeding generation. The genetic level will be the same as the parent generation, unless some nursery selection can be carried out for traits as e.g. growth rhythm. The time from crossing to commercial stock is 6-7 years.

### Multiclonal varieties

Assuming that at least the expected best part of the clones are kept juvenile during clonal progeny test, there will be a possibility of mass propagating a mixture of the very best clones in the new generation. Time from crossings to mass propagation will, due to at least 6 years testing, be 15-16 years.

### Seed orchards

Seed orchards could be established either by cuttings or grafts propagated after evaluation of clonal-progeny tests, or else by genetic thinning of the actual clonal-progeny test. Neither of the alternatives give sufficient harvests before 30-35 years after material is generated, which is a severe delay compared to the clonal options. In fact this means a delay in time comparable to one whole breeding generation before the genetic gain can be brought into operational forestry and should therefore not be of great interest.

## Breeding gains

Calculations of expected breeding gains give the results shown in Table 1 (Danell 1990). The figures are based on selection for one single character. When selection will be carried out for more than one character, the single trait gain will be reduced, but overall gain will be maximised.

Table 1. Expected genetic gain for a single trait,  $\Delta G$ , in different stages of breeding. The level of unselected stands or seedling stocks is 100.

Material, stage in breeding	$\Delta G$
Selected plus trees and clones	106
Selected parents for breeding population	116-118
Selected clones in breeding population F1	123-125

## Problems

To carry out an effective breeding of Norway spruce we have to broaden the knowledge and get a better understanding of Norway Spruce. Some problems are listed here.

- In order to keep breeding generation time within acceptable limits (15-25 years) we need reliable tools for flowering stimulation.
- To improve the results from breeding work we need to define the most important basic traits which are and will be important in the future. We also need to know what characters in young trials that correspond to these desired traits.
- We need to know if there are cloning effects involved in the results from the clonal-progeny tests.
- What influence does free growth have when evaluating rather young tests?
- We are using single tree plots with a rather narrow spacing. Do we measure trials too early? Norway spruce is a secondary species. Do we evaluate it as primary species?
- There might be a problem in achieving flowering in all clones in acceptable time (20 years from seed).

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## 4. Breeding broad-leaved tree species in Sweden

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### Abstract

All broad-leaved tree species, used in forestry in Sweden, will be improved. However, resources and intensity will depend on the species. Various levels of improvement strategies and conservational ambitions will be applied. Clones will be used wherever possible in the improvement work. Different options of mass propagation methods will be applied depending on species and level of ambition.

### Introduction

The interest in breeding broad-leaved tree species has varied considerably over time. When forest tree breeding started, these species were focused on first of all. Later however, for a period of 25 years, no work was undertaken at all. Since 1985 activities have restarted, and the directives are now to "improve or breed" all species used within forestry.

Compared to conifer breeding, resources available are very small. This is quite natural as the use in reforestation of most species is very limited. The total demand for seedlings of broad-leaved trees in south Sweden is predicted to about 7 million, of which birch and alder are 5 million. Within the same area 155 million conifer seedlings will be used.

However, some species as birch and alder, could probably be used still more, if an improved reforestation material was available. For aspen and poplars, a certain interest is already there, due to a high yield and a short rotation time. For indigenous species such as oak, beech, ash, lime trees and several others, the interest is limited mainly due to a long rotation time and a limited market for this specific wood for the time being. These species are also often self-regenerated, which decreases the demand for plants.

### Breeding outlines

#### General remarks

The breeding work of broad-leaved trees follows the general outlines put forward by Danell et al 1993, and by Danell in this publication. Therefore, only a short summary is given, pointing out the main features of the different alternatives used.

Since all broad-leaved tree species used in forestry are on the list, the following three restraints are valid:

- discontinuous work within species
- restricted resources per species
- intensity - depending on species

As a consequence of the restraints above, all species can not be handled in the same way, neither in terms of level of improvement nor concerning conservation aspects. The different levels of intensity will be:

#### Improvement

- multi-generation breeding
- one - two generation breeding
- clonal selection

## Conservation

- sufficient variation for evolution
- sufficient variation for breeding
- appropriate variation for propagation

Of the above six listed degrees of intensities, "variation for evolution" is the only one that will not be used. This is because natural regeneration of the species which will be intensively improved will take care of that task. Variation for breeding is the conservation level for all species running through multi-generation breeding and most species in the group one - two generation breeding. However, some of the species in this last group and the species for clonal selection have variation for propagation as the conservation goal.

One important technical remark is, that whenever possible, clones (propagated by cuttings or tissue cultures) will be used in the testing procedure. This decreases the number of individuals needed for testing, increases the speed and precision in the breeding, and also opens up an intensive option for clonal forestry already from the beginning, giving the best possible genetic gain in the shortest time.

## Multi-generation breeding

This line includes long-term breeding within a sufficient number of breeding zones covering the entire country (Danell & Werner, 1991). After tissue culture propagation of selected plus trees (200 - 600 per zone), clonal tests are established. The 50 clones per zone with the best clonal values are appointed parents in the breeding population and crossed together, each clone being a parent in two families. Within each full-sib family 15 individuals are propagated as clones which are established in clonal tests. This gives 1500 clones under testing. The very best of these can be used for mass propagation. However, at the selection of the 50 parents for the next breeding generation, an equal representation of parentage of the clones must be taken into consideration.

The only species following this line of breeding so far is the European birch (*Betula pendula*). Breeding is in progress within 4 breeding zones of which the southern one covers a little more than four degrees of latitude. Six breeding populations are planned, of which two take maritime climate and drought into consideration.

Other future candidates for this intensive breeding are Black alder (*Alnus glutinosa*) and Silver birch (*Betula pubescens*).

## One - two generation breeding

This strategy is used for most species. As a base for each future breeding population at least 100 plus trees are selected. If possible, these are propagated vegetatively for establishment of clonal tests. If this is not possible due to pronounced c-effects or other reasons, the selected trees are progeny tested by means of open pollinated families. To save money, the selected plus trees are planted out as clones in a combined clonal archive and seed orchard designed for a 50% genetic thinning, after results from progeny- or clonal tests. The 50 best parents are appointed parents in the breeding population and full-sib families as clonally propagated individuals are planted out in tests as above. For many species the full-sib families as seedlings, or more often open pollinated families form the seed orchard, are planted out in repeated family line plantings with 10 - 16 individuals per row plot. These plantings should first of all serve breeding purposes, in which the next generation of parent candidates are selected, but can easily be converted into future seed stands, either using available genetic information or just by phenotypic thinning.

Almost ten species, as e. g. oak, beech and ash, are successively taken care of as described here.

## Clonal selection

Species hybrids as most Poplars, Hybrid aspen and Alder hybrids are above all improved by establishment of field tests for clonal selection. For the *Populus spp* resistance breeding should have been advantageous, but unfortunately the costs for such a programme can not be justified in relation to the predicted use of this material. Such a programme also consumes a lot of genotypes and requests a crossing programme as well. But production of new hybrids can only be made occasionally.

Although clonal forestry is an intensive method, and many of these hybrids have a remarkable potential for growth, the improvement efforts must be characterised as fairly extensive.

## **Aspects on mass propagation**

### Clonal forestry

For the species hybrids, clonal forestry is quite obviously the only mass propagation method of any interest. This opens up the future perspective to grow defined fiber qualities for the pulp industry. However, high quality wood of many of the species is very well paid. Clonal forestry could perhaps be a valuable tool in improving production of excellent wood quality. Therefore, investigations in cutting propagation and tissue propagation techniques may be good investments for the future.

### Bi-clonal seed orchards and few clone seed orchards

In most species, such as birch, natural regeneration will be the predominant way of regeneration. Therefore, genetic variation is not threatened by the future areas planted with improved material. To achieve a good result in spite of the limited resources available, bi-clonal- and few clone seed orchards (5 - 10 clones) ought to be tried. One possibility always open, if genetic diversity should need to be increased, is to bulk seed from several bi-clonal or few clone seed orchards. This need should really be questioned as mass propagation only covers one generation and even a natural regeneration from such stands will involve surprisingly large quantities of remote pollen.

The possibilities of growing seed orchards indoors increases the gain and should be developed for the species with intensive improvement programmes.

### Multi-clonal seed orchards

Extensively improved species are handled in clonal archives which are genetically thinned into multiclonal seed orchards with about 50 clones.

### Family seedling seed orchards

The minor extensively improved species and species like oak and beech producing very limited amounts of acorns and nuts per hectare, should after the multi-clonal seed orchard stage, be planted out in family seedling seed orchards. These contains half-sib or full-sib families from the clonal seed orchard planted in ten individual row plots replicated several times. This is a way of spreading out the responsibility for seed production and of making improvement less sensitive to changing future trends. Different options to thin in these "orchards" from genetic thinning between families to phenotypic thinning within the row plots, increases flexibility and allows different managers to make their own future decisions.

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