

Common Scots pine deployment recommendations for Sweden and Finland



Abstract

For the past decade, Sweden and Finland have been collaborating on research and development of a joint system for deployment recommendations of Scots pine. Recently, joint transfer effect models covering both countries were developed (Berlin et al. 2016), simultaneous with joint work to define seed orchard characteristics of both countries in a common framework. The main aim has been to provide common Scots pine deployment recommendations and to update and expand the web tool across both countries (Planter's Guide).

This report describes how the transfer effect models and climate data developed in Berlin et al. (2016) and Barring et al. (2016), together with a common framework defining seed orchard characteristics, have been formalized into joint Swedish-Finnish deployment recommendations for Scots pine.



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Introduction

A number of components were important in the development of climate adapted joint Swedish-Finnish deployment recommendations for Scots pine (Figure 1).

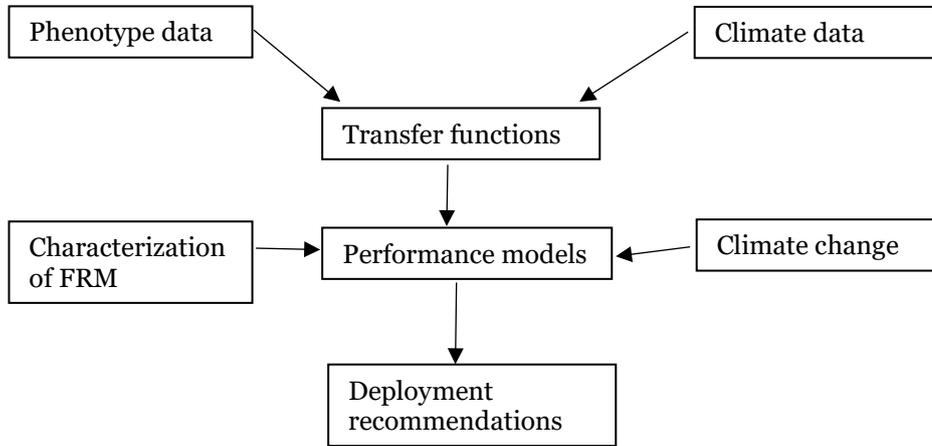


Figure 1. Schematic overview of the different components in the development of climate adapted deployment recommendations for Scots pine.

The development of transfer functions (i.e. models that describe the reaction patterns for forest reproductive material) requires both appropriate phenotypic data and climate data. Phenotypic data should span a sufficient range of growth conditions in terms of both field trial sites and genetic entry origins to capture the transfer effects / reaction patterns. Climate data needs to fulfil certain requirements in terms of both spatial and temporal resolution and must also contain tailored climatic indices known to be associated with desired properties of the species under study. Transfer functions that include climate indices as independent variables can be used to predict reaction patterns in future climatic conditions if they fulfil the requirements above. Different approaches are used in modeling the transfer effects, varying according to purpose and data available. For Scots pine, the phenotypic data and development of transfer functions for growth and survival are described in detail in Berlin et al. (2016) and the climate data in Barring et al. (2016). However, as these components are crucial to the development of deployment recommendations, they are also briefly described in this report.

The main aim of this report is to describe the development of joint Swedish-Finnish deployment recommendations based on the climate adapted transfer functions. To develop deployment recommendations, a model or method is required that can predict performance of contemporary forest reproductive material (FRM) at an arbitrarily selected regeneration site and rank the FRM according to this measure of performance. Such performance models need input from several different components. In the case of Scots pine, input needs include the transfer functions for survival and growth, climate change signals for the climatic drivers in those functions, and a characterization of key properties of the Swedish and Finnish FRM. The performance models then combine all this information and provide a ranking of contemporary FRM. As a final step, deployment recommendations are developed based on these performance predictions, but they also include both biological (e.g. model validity ranges) and administrative (e.g. current legislations) limitations.

This report is structured as follows (see Figure 1). First, the transfer functions are briefly described (section 1) and then the inclusion of climate change is reviewed (section 2). The characterization of FRM is divided into two sections (3 and 4), where the transfer functions are adapted to manage genetically improved FRM and methods/rules are developed for calculating key performance indicators of the FRM. The performance model for Scots pine is described in section 5, limitations of the model in section 6, and limits in the practical deployment recommendations in section 7.

1. Transfer functions for survival and growth

Models for survival and height were developed in Berlin et al. (2016).

For an arbitrary site, logit-transformed survival of a (possibly transferred) autochthonous stand is estimated at 2.5-meter height as

$$\text{logit}(S) = \mu_s + \delta \cdot d + \alpha_{1s} \cdot TS_s + \alpha_{2s} \cdot \ln TS_s + \beta_{1s} \cdot \Delta LAT + \beta_{2s} \cdot \Delta LAT^2 + \gamma_{1s} \cdot ALT \cdot \Delta LAT + \gamma_{2s} \cdot ALT \cdot \Delta LAT^2$$

And at the re-transformed scale (i.e. in %) as

$$S = 100 \cdot \frac{e^{\text{logit}(S)}}{1 + e^{\text{logit}(S)}}$$

where TS_s is the temperature sum of the selected site used for estimating survival (see section 2, 'Climate adaptation') and ALT is the altitude at the selected site, $\Delta LAT = LAT_{orig} - LAT_{site}$ is the transfer in latitude where LAT_{orig} is the (estimated) latitude of origin of the transferred stand and LAT_{site} is the latitude of the selected site, and d is a dummy variable where 0 represents Sweden and 1 Finland. The coefficient values are given in Table 1.

For an arbitrary site, height transformed by the natural logarithm of a (possibly transferred) autochthonous stand is estimated as

$$\ln H = \mu_h + \alpha_{1h} \cdot \ln AGE + \alpha_{2h} \cdot \ln(EY - 1945) + \alpha_{3h} \cdot \ln TS_h + \beta_{1h} \cdot \Delta LAT + \beta_{2h} \cdot \Delta LAT^2 + \gamma_{1h} \cdot TS_h \cdot \Delta LAT + \gamma_{2h} \cdot TS_h \cdot \Delta LAT^2$$

and at the re-transformed scale (in meters) as

$$H = e^{\ln H + \varphi}$$

where TS_h is the temperature sum of the selected site used for estimating height (see section 2, 'Climate adaptation'), AGE is the tree age, EY is the year of establishment, φ is a bias-correction term, and the other variables are as described above. The coefficient values and φ are given in Table 1.

Table 1. The model coefficients for survival and height from Berlin et al. (2016)

Survival		Height	
Coefficient	Value	Coefficient	Value
μ_s	-86.3416	μ_h	-6.0063
δ	-0.9286		
α_{1s}	-0.01082	α_{1h}	1.6279
α_{2s}	14.2905	α_{2h}	0.156
		α_{3h}	0.995
β_{1s}	0.1626	β_{1h}	0.02907
β_{2s}	-0.05642	β_{2h}	-0.1714
γ_{1s}	0.000864	γ_{1h}	-0.00005
γ_{2s}	-0.00007	γ_{2h}	0.000011
		φ	0.047865

In the height model, AGE=30 years to represent the highest possible age without extrapolating model performance, and EY=1980 to represent the mean establishment year for all trials.

In the survival model, $d=0$ for sites located in Sweden and $d=1$ for sites located in Finland. In practice, this means that Swedish sites have a higher survival than analogous sites in Finland. The reasons for this are discussed in detail in Berlin et al. (2016) but the main factor is thought to be differences in the establishment and early management of the test sites. In general, we contend that Swedish test sites received a more intensive monitoring and management than the Finnish sites, which were managed more like operational plantations, so the predicted survival levels in Sweden assume that the plantations are established and managed according to good practice as described in www.skogsstyrelsen.se/skogsskotselserien.

2. Climate adaptation

2.1 CLIMATE REFERENCE DATA

The climate reference data used in this study was derived from meteorological observations interpolated into high-resolution gridded data combined from the two national data sets for Sweden and Finland. For Sweden, the PTHBV dataset had a spatial resolution of 4×4 km and, for Finland, the FINADAPT dataset had a spatial resolution of 10×10 km (Barring et al. 2016). Climate indices considered important for Scots pine performance in boreal conditions were calculated for each grid from daily mean temperature and precipitation observations. These indices were then converted to averages spanning the period 1961-2007, which was considered to represent the current climate in both modeling work and in the deployment recommendations (Barring et al. 2016). This period also corresponds to and encompasses the climate encountered by the genetic entries in the selected field trials. Based on a modeling approach described in Berlin et al. (2016), where each trial site and genetic entry origin was assigned the climatic indices from the corresponding grid, transfer functions were developed for survival and height. The only climatic index included in the functions was temperature sum (TS_{ref}).

2.2 FUTURE CLIMATE

This climate reference data was used for calibrating the regional climate projections. An ensemble of six regional climate projections produced by global climate models was used to account for climate change. The derived climate scenario was the SRES A1B, which was considered well established and known to the Scandinavian forestry sector. It implies medium greenhouse gas emissions and thereby intermediate projected climate changes compared to other SRES scenarios (Nakicenovic and Swart 2000), and projects an increased global temperature by 2100 of around $+2.5^\circ\text{C}$ (Knutti and Sedláček 2012). This process is described in detail in Barring et al. (2016). From the derived SRES A1B scenario, a climate signal that could be added to the reference data was calculated as the average between the years 2035-2065. By adding the climate signal (ΔTS_{A1B}) to the reference data, the projected climate at year 2050 is obtained as

$$TS_{2050} = TS_{ref} + \Delta TS_{A1B}$$

2.3 INCORPORATING CLIMATE CHANGE IN THE TRANSFER FUNCTIONS

This region will experience a warmer climate that will increase forest growth, so it is important to exploit these conditions to maximize volume production per unit area over a rotation. However, at the same time, survival is and will be a key characteristic in a region with a relatively harsh environment. Climate-related Scots pine mortality predominantly occurs in the early developmental phase, from planting up to 2.5-meter height, (Persson and Ståhl 1993), so we use the current climate (TS_{ref}) in the model estimates of survival. To make use of the improved growth conditions with a warmer climate, we consider the time of maximum mean annual increment (MAI), which is around mid-rotation. In northern Sweden and Finland, an average rotation is approximately 80 years and for models describing growth we use the projected climate at year 2050 (TS_{2050}). We consider this combination of survival and growth to provide the best climate adapted compound estimate of volume production per unit area.

2.4 LOCAL CLIMATIC ADJUSTMENTS

As the models used in predicting growth/survival are based on climate data averaged over grids with the size of 4 x 4 (Sweden) and 10 x 10 km (Finland), climatic conditions on a local/planting site scale vary within the grid. We therefore introduced the possibility to adjust the modeled climate index (temperature sum) to reflect the local climatic conditions at the planting site, from harsher to milder than the grid average. Examples of milder conditions are southerly aspect, well-drained soil, and proper scarification, while harsher conditions include frost-prone sites, northerly aspect, poorly drained soil, and poor or no scarification. This harshness/mildness is expressed by adjusting the grid average temperature sum in steps of 75 day degrees as:

$$TS_{adj} \in [-150, -75, 0, 75, 150]$$

Consequently, for survival, the temperature sum used in predicting FRM performance is:

$$TS_s = TS_{ref} + TS_{adj}$$

and for height/growth, the temperature sum used in predicting FRM performance is:

$$TS_h = TS_{2050} + TS_{adj}$$

3. Seed orchard calculations

3.1 POLLEN CONTAMINATION

For seed orchard crop calculations, the first step is to calculate the standardized latitudinal origin (LAT_{st}) of the seed orchard crop. One part of this calculation is the estimated origin of the seed orchard clones (LAT_{clone}), calculated as the average of the origin of all clones (not considering ramet frequency). Pollen contamination level (PC) is then estimated as 40% (Eriksson 1996) in a ‘mature’ orchard (with full pollen production) and 100% in a ‘young’ orchard (with no pollen production, only cone production). The transition between a ‘young’ and ‘mature’ orchard is given by a function where y_p is the year from pollen production start, based on Almqvist et al. (2010). If the start of pollen production is given by $y_p=1$, then:

- When $y_p < 0$: $PC=100$

- When $y_p \geq 0$ & $PC > 40$:

$$PC = 100 - 100 \cdot (0.13932 \cdot y_p^2 - 0.142285 \cdot y_p + 0.33264) / 25$$

- When $y_p \geq 0$ & $PC < 40$: $PC=40$

The shape of the pollen contamination development curve is shown in Figure 2.

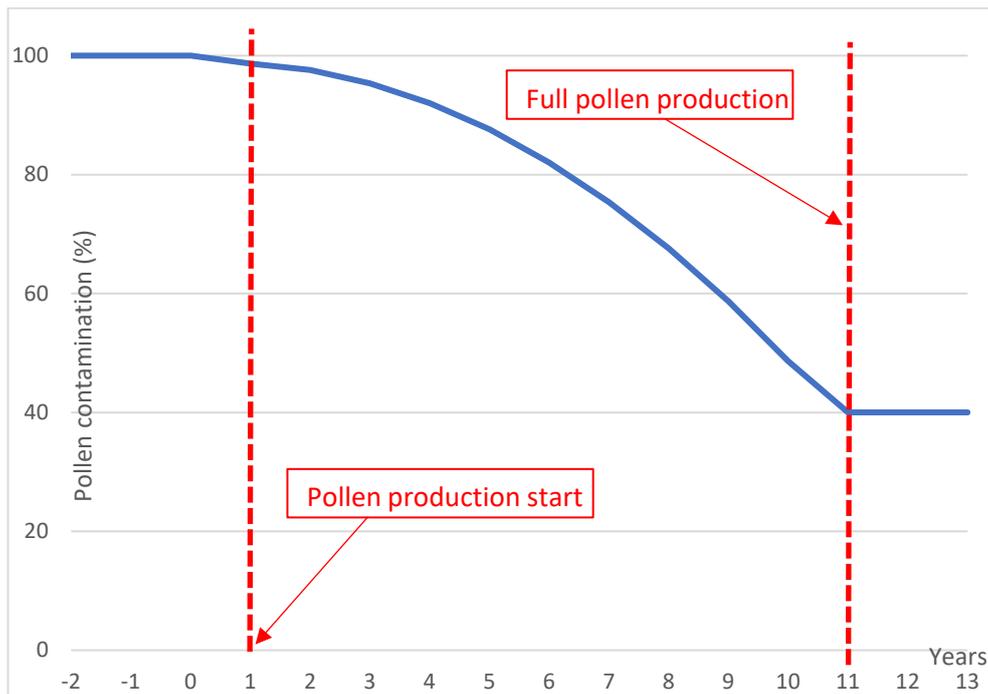


Figure 2. Pollen contamination in the years after pollen production start until full pollen production.

Pollen production start can vary due to different conditions in the establishment and early management phase, and is therefore given for each seed orchard individually when the first pollen is visible.

Consequently, external pollen contamination level (i_{PC}) can vary between values 0.4-1, where 1 represents a young and 0.4 a mature SO.

3.2 STANDARDIZED LATITUDINAL ORIGIN

Contaminating pollen is considered to have its origin half a latitudinal degree south of the seed orchard location (LAT_{SOL}), so $LAT_{vPC} = LAT_{SOL} - 0.5$ (Andersson and Ericsson 2002)¹. Other sources of pollen influx to the orchard (i.e. from adjacent seed orchards) with origin (LAT_{xPC}) contribute to the total pollen contamination as:

$$LAT_{PC} = LAT_{vPC} \cdot (1 - i_{xPC}) + LAT_{xPC} \cdot i_{xPC}$$

where i_{xPC} is the proportion of additional sources of pollen influx, with values between 0 and 1.

The latitudinal (standardized) origin of the seed orchard crop is then calculated according to Andersson and Ericsson (2002) as:

$$\begin{aligned} LAT_{sto} &= \underbrace{0.5 \cdot LAT_{clone}}_{\text{Mother contribution}} + 0.5 \cdot \underbrace{\left(\frac{\text{Seed orchard clones}}{LAT_{clone} \cdot (1 - i_{PC})} + \frac{\text{Wild pollen}}{LAT_{PC} \cdot i_{PC}} \right)}_{\text{Father contribution}} \\ &= LAT_{clone} \cdot (1 - 0.5 \cdot i_{PC}) + 0.5 \cdot LAT_{PC} \cdot i_{PC} \end{aligned}$$

The transfer distance (in latitude) between the standardized origin of the seed orchard crop and the planting site (*site*) is then calculated as:

$$\Delta LAT_{SO} = LAT_{site} - LAT_{sto}$$

3.3 TRANSFER FUNCTIONS FOR SEED ORCHARD CROPS

For an arbitrary site, logit-transformed survival of a (possibly transferred) seed orchard crops (not including genetic gain) is estimated at 2.5-meter height as

$$\begin{aligned} \text{logit}(S_{SO}) &= \mu_s + \delta \cdot d + \alpha_{1s} \cdot TS_s + \alpha_{2s} \cdot \ln TS_s + \beta_{1s} \cdot \Delta LAT_{SO} + \\ &\quad \beta_{2s} \cdot \Delta LAT_{SO}^2 + \gamma_{1s} \cdot ALT \cdot \Delta LAT_{SO} + \gamma_{2s} \cdot ALT \cdot \Delta LAT_{SO}^2 \end{aligned}$$

and at the re-transformed scale (i.e. in %) as

$$S_{SO} = 100 \cdot \frac{e^{\text{logit}(S_{SO})}}{1 + e^{\text{logit}(S_{SO})}}$$

¹ The reasons for this are (i) pines transferred from the south start to flower earlier in the spring than local pines, and (ii) the predominating wind direction in Sweden and Finland is from the south.

For an arbitrary site, ln-transformed height of a (possibly transferred) seed orchard crop (not including genetic gain) is estimated as

$$\ln H_{SO} = \mu_h + \alpha_{1h} \cdot \ln AGE + \alpha_{2h} \cdot \ln(EY - 1945) + \alpha_{3h} \cdot \ln TS_h + \beta_{1h} \cdot \Delta LAT_{SO} + \beta_{2h} \cdot \Delta LAT_{SO}^2 + \gamma_{1h} \cdot TS_h \cdot \Delta LAT_{SO} + \gamma_{2h} \cdot TS_h \cdot \Delta LAT_{SO}^2$$

and at the re-transformed scale (in meters) as

$$H_{SO} = e^{\ln H_{SO} + \varphi}$$

All terms for both the survival and height functions are as described in earlier sections.

The formulae above only account for the transfer effects of the seed orchard crops, and all extra gain from genetic improvement must be added.

The estimated level of survival (at 2.5-meter height), S'_{SO} , for an orchard at an arbitrarily chosen site is given as

$$S'_{SO} = S_{SO} + \Delta S \cdot S_{SO}^{adj}$$

where S_{SO} is the survival transfer effect of the orchard and S_{SO}^{adj} is an adjustment factor to calculate survival gain at other base levels than 50% (which is the level for which all survival gains are standardized). ΔS is the extra gain in survival from genetic improvement.

The factor S_{SO}^{adj} is calculated as (Andersson and Ericsson 2002):

$$S_{SO}^{adj} = 0.1883 + 0.03434 \cdot (50 + |S_{SO} - 50|) - 0.0003622 \cdot (50 + |S_{SO} - 50|)^2$$

Survival adjustment term

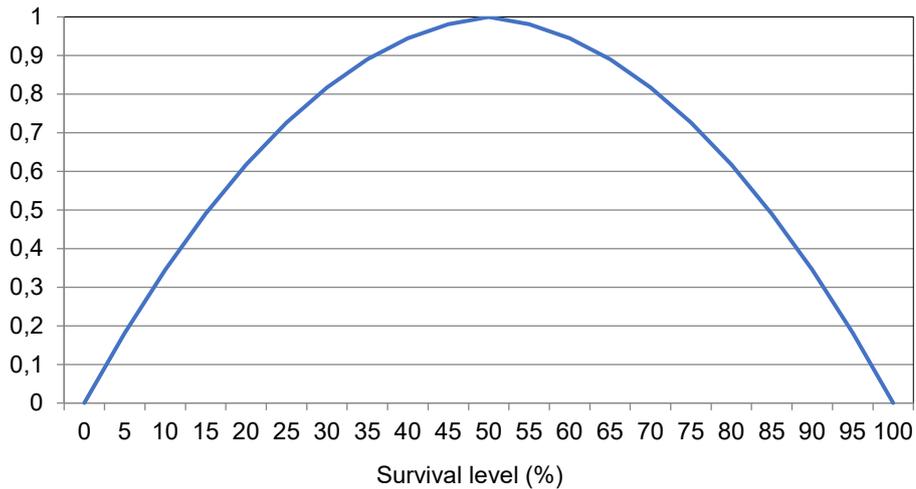


Figure 3. Adjustment of the gain in survival at different levels of survival.

Furthermore, it is assumed that 85% is the long-term, practically feasible survival. If the calculated value exceeds 85%, the expected survival is set to 85%.

The estimated level of height in meters at age 30, H'_{SO} , for an orchard at an arbitrarily chosen site is given as

$$H'_{SO} = H_{SO} \cdot \Delta H$$

where H_{SO} is the height transfer effect of the orchard and ΔH is the extra gain in height from genetic improvement.

4. Effects of genetic improvement

To compare and rank performance of seed orchards from both countries, genetic gain levels of survival and growth for Swedish and Finnish seed orchards must be calculated using the same methodology. Using breeding values to calculate genetic gain would have provided individual values for each seed orchard and ostensibly a higher resolution. However, breeding value estimates are only valid within the population in which they are calculated (in this case, a field trial series) and the genetic model design, handling large sets of data, also differs. Consequently, to obtain standardized gain estimates comparable in both countries, we used a genetic parameters approach rather than breeding values in calculations (See Appendix A1).

We identified five categories, all of which were assigned baseline genetic gain values based on the calculations and assumptions from Rosvall et al. (2001). The default levels of genetic gain for both height and survival were set to be equal for both countries.

Within each category we identified management regimes that would affect the baseline genetic gain by adding adjustment terms where these could be quantified in a transparent and general way. We identified four such management regimes:

- Selective harvesting (currently only applied in Sweden).
- Contribution of improved pollen from adjacent seed orchards.
- Genetic thinning (currently only applied in Finland).
- Linear deployment.

We used a standardized analysis structure using general genetic parameters to analyze the different management regimes. It turned out that all regimes except 'extra pollen source' could be assigned a set of fixed values. We believe that the trade-off of assigning fixed values is no greater in magnitude than the trade-off already made by categorizing the SOs.

The calculations of the values of ΔH and ΔS for the orchards and all variables needed for this calculation are given in the subsequent sections.

Table 2: Summary of all variables required to calculate ΔH and ΔS

Variable description	Variable name
Plus-tree effect (proportion)	r
Seed orchard effect (proportion)	$1-r$
External pollen contamination (proportion)	i_{PC}
External pollen contamination that originates from a surrounding older seed orchard (proportion)	i_{xPC}
Baseline survival gain (percentage)	S
Gain in survival from selection from all orchard clones (percentage)	S_{tot}
Gain in survival from selection from extra pollen (percentage) (including all gain)	S_{xPC}
Extra gain in survival from selective harvesting (percentage)	S_s
Extra gain in survival from genetic thinning (percentage)	S_t
Extra gain in survival from linear deployment (percentage)	S_{ld}
Baseline height gain (percentage)	H
Gain in height from selection from all orchard clones (percentage)	H_{tot}
Gain in height from selection from extra pollen (percentage) (only additional gain besides H)	H_{xPC}
Extra gain in height from selective harvesting (percentage)	H_s
Extra gain in height from genetic thinning (percentage)	H_t
Extra gain in height from linear deployment (percentage)	H_{ld}

The calculations needed to obtain ΔH and ΔS were divided into several different parts described below. Some parts describe the general gain for a set of seed orchard categories and other parts describe additional effects that are unique for each seed orchard.

4.1 GENERAL SEED ORCHARD EFFECT (FIXED VALUES)

A general seed-orchard effect is considered to be a combination of release of inbreeding depression prevailing in natural stands and seed physiological effects. These effects are only apparent in height and are not affected by pollen contamination. For height, H is the total baseline genetic effect of phenotypic selection and is assumed to be 10%. This effect is divided into the effect of plus-tree selection r and a general seed orchard effect $(1-r)$; for background to and level of these effects see Wilhelmsson et al. (1993) or Rosvall et al. (2001). For survival, no effect of phenotypic selection or seed orchard effect is assumed, although recent investigations have shown a slight decrease in survival (Andersson et al. 2007).

Therefore:

$$H_A = (1 - r) \cdot H$$

$$S_A = S = 0$$

Plus-tree effect: $r=0.6$ (corresponding to 6%)

General seed orchard effect: $1-r=0.4$ (corresponding to 4%)

4.2 SEED ORCHARD CATEGORIES (FIXED VALUES)

This structure is based on three main SO categories, two of which have additional distinct extra categories when survival has been an important breeding objective. Thus, there are five categories:

1g

Phenotypically selected plus trees. This corresponds to Swedish EttO (first round) seed orchards and those TvåO (second round) seed orchards that are based on phenotypic plus tree selection (Rosvall et al. 2001). In Finland this category corresponds to 1g seed orchards. These orchards are assumed to have the baseline genetic effect for growth and no effect on survival.

$$H_{tot} = 0\%, S_{tot} = 0\%$$

1.25g

A category representing those Swedish TvåO seed orchards with a proportion of tested plus trees (often based on early measurements with less accuracy) but also including new (untested) plus trees and forward selections from field trials. Although this group is more heterogeneous, we assume that there is an extra gain in growth (if forward selections are included) but none in survival.

$$H_{tot} = 2.5\%, S_{tot} = 0\%.$$

1.25gS

Corresponds to 1.25g but also includes a selection for survival. When selecting for two traits at the same time, the growth gain is lower compared to selecting solely for that trait, but there is a gain in survival instead. We therefore assume baseline genetic gain for growth but a gain in survival.

$$H_{tot} = 0\%, S_{tot} = 2.5\%.$$

1.5g

Orchards consisting of only tested and selected plus trees. This corresponds to the Swedish TreO (third round) seed orchards and the Finnish 1.5g. If selection has been primarily for growth, there is a substantial gain in growth but none in survival.

$$H_{tot} = 15\%, S_{tot} = 0\%.$$

1.5gS

Corresponds to 1.5g but also including a selection for survival. Same principle as for 1.25g, so gain in growth is lower than for 1.5g but there is a gain in survival.

$$H_{tot} = 10\%, S_{tot} = 5\%.$$

4.3 SELECTIVE HARVESTING (FIXED VALUES)

Selective harvesting is currently only performed in Sweden and is used to boost the level of genetic gain for a fraction of the seed orchard crop. This is done by only collecting cones from a sub-set of clones with the best breeding values. The effect of selective harvesting was calculated for all nine Swedish seed orchards, and the gain levels were very stable for both height and survival and for both A and B fractions (see Appendix A2). As the SOs include both 1g and 1.25g categories and are located and intended for all parts of Sweden, we conclude that fixed gain values are also suitable for selective harvesting. Note that all values shown in the tables have been calculated in the same standardized way using genetic parameters.

The additional effect of selective harvesting (an increase in mother clone effect in the same father clone environment) is

$$\begin{aligned}H_E &= 0.5 \cdot H_S \\S_E &= 0.5 \cdot S_S\end{aligned}$$

where:

Fraction A: $H_S = 6\%$, $S_S = 4.5\%$

Fraction B: $H_S = -2\%$, $S_S = -1.5\%$

4.4 GENETIC THINNING (FIXED VALUES)

Genetic thinning is currently only performed in Finland and is used to boost the level of genetic gain for an orchard by thinning out grafts so that the average performance of the orchard increases. The effect of genetic thinning could be calculated according to the formula for selective harvesting, but this requires a complete genetic thinning of exactly all ramets of the clones to be culled. If an orchard is to be productive, it is likely that the thinning will also need to consider practical aspects such as avoiding excessively large empty patches within the orchard. In Rosvall et al. (2001) an example is given where an imaginary orchard (similar amount of ramets/clone) of 200 clones is to be thinned to 100 (i.e. removing 50%). In that case the selection intensity would be

$$i_B = 0.795$$

However, if each row of trees is imagined to be divided into groups with two trees per group, each group is to be thinned individually so that one (the worst) of the two trees is thinned. This would be a practical restriction to prevent creation of large patches (there will never be a larger patch than the space between two trees). This would reduce the selection intensity to

$$i_B = 0.589$$

However, this is a purely theoretical calculation, and most practical genetic thinnings have been performed in Finland. Studies were undertaken to ascertain the actual gains in practical situations. First, up to two thinnings were performed where the number of removed grafts (compared to the original number of grafts) was around 50% in the first thinning and 75% in the second (see Appendix C).

For height, two SOs were studied in more detail to investigate what kind of selection intensities are obtained in practical situations. Results showed that selection intensities varied between 0.3-0.4 after the first thinning and around 0.6 after the second thinning. By using 0.3 for first thinning and 0.6 for the second, we get:

$$\Delta G_{TH1} = i_B \cdot r_{AI} \cdot r_{jm} \cdot CV_{Am} \cdot r_{mt} = 0.3 \cdot 0.80 \cdot 0.7 \cdot 0.125 = 0.021$$

$$\Delta G_{TH2} = i_B \cdot r_{AI} \cdot r_{jm} \cdot CV_{Am} \cdot r_{mt} = 0.6 \cdot 0.80 \cdot 0.7 \cdot 0.125 = 0.042$$

For height, two fixed values are given: 2% after the first thinning and 4% after the second thinning.

For survival, the effect of genetic thinning was studied on a number of SOs, where both response to breeding values for survival and calculated selection intensity based on progeny test results (survival) were investigated (Appendix D1 & D2). The effect on survival proved to be sensitive to simultaneous selection for other traits, and selection intensity varied between 0.4-0.6 after first thinning. By using 0.5, we get (where survival is transformed into normal scores and expressed in standard deviations relative to the 50% level):

$$x = i_B \cdot r_{AI} \cdot r_{jm} \cdot \sigma_A \cdot r_{mt} = 0.5 \cdot 0.80 \cdot 0.9 \cdot 0.20 \cdot 0.707 \approx 0.0509$$

This is expressed as percentage points by calculating the cumulative normal distribution function at x :

$$\Phi(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^x e^{-\frac{t^2}{2}} dt, \text{ and } 100 \cdot \Phi(0.0509) - 50 = 52.03 - 50 = 2.03$$

(i.e. $S_X = 2.03\%$ -points)

This is the same effect in percentage points as for height, and it is reasonable to assume that the effect of a second thinning also would be similar to that of height.

In summary, the additional genetic gains from genetic thinning are

<u>First thinning:</u>	$H_t = 2\%, S_t = 2\%$
<u>Second thinning:</u>	$H_t = 4\%, S_t = 4\%$

4.5 LINEAR DEPLOYMENT (FIXED VALUES)

Linear deployment is a method used in recent (1.5g) orchards to increase the level of genetic gain, given a pre-defined level of genetic diversity (Bondesson and Lindgren 1993). This is done by including more clones in the orchard and allowing for non-equal frequencies of ramets per clone increasing the frequency of the best performing clones and reducing the frequency of the worst performing clones.

To analyze the extra gain effect of linear deployment compared to a baseline 1.5g-orchard, we used a set-up where the total number of grafts in the orchard was 6000, and we also assumed that all clones would be present in the orchard with a ramet number between 50-500 (i.e. maximum 8.3% of the orchard). This would resemble the actual approach to LD in current Swedish SOs. We analyzed four newly established orchards using this approach, ranging from very harsh conditions in northern Sweden to mild conditions in central Sweden. We tested a

number of different comparisons (all designed to be fairly similar to actual approaches). In all cases, breeding values for a compound index (Volume production over a rotation) were used for ranking and selecting the clones for the orchards. We applied OPSEL (Mullin 2017) to perform linear deployment, given a certain status number of the orchard. We tried status numbers of 20-25 (selected from 30-35 clones) and calculated an average breeding value of height and survival for the LD-orchard. This value was compared to a baseline 1.5g with equal ramet frequency at the same status number (as all but one of the orchards had no related clones, this status number is the number of unrelated clones and simply the average BV of those). For height, this value varied around 1-1.5% and for survival the value varied around 1-1.5% (see Appendix A5). However, this extra gain depends on obtaining the suggested ramet frequencies in the orchard (which is unlikely due to difficulties in collecting enough scions, grafting success and mortality). Consequently, this gain value is slightly lowered to better correspond to real-life conditions, so was set to 1%.

In summary, the additional genetic gains from linear deployment are

Linear deployment: $H_{ld} = 1\%, S_{ld} = 1\%$

4.6 POLLEN SOURCES (CALCULATED AND FIXED VALUES)

The part of the genetic gain that is affected by pollen contamination (i.e. excluding the general seed orchard effect) can be divided into effects relating to: (i) internal pollination, comprising the seed orchard clone contribution from both father and mother; (ii) external pollination, where extra gain is only achieved through the mother contribution from the seed orchard clones; and (iii) external pollination from surrounding seed orchards, which in addition to (ii) includes the father clone effect from the surrounding orchard.

The effects in (iii) occur when there is an adjacent older seed orchard next to or surrounding the new orchard, intended to reduce the effect of wild pollen by adding an additional source of genetically improved pollen. With the aim of standardizing as many calculations as possible to obtain fixed values, we investigated whether that was also possible for extra pollen sources. However, at the time of this analysis, there were only three SOs considered to have extra pollen sources, and they varied considerably, as the surrounding old orchards were very different. As the pollen gain levels were all calculated according to the standardized system using general genetic parameters (see Appendix A1.3), we decided to allow those values to be variable rather than fixed. Detailed background and calculations for all orchards having this extra gain is necessary.

Gain from extra pollen sources is therefore calculated separately to obtain values H_x, S_x . The formulae for the different effects are given below.

Effect relating to internal pollination

The part consisting of SO clones with internal pollination (i.e. the mother and father clone effect)

$$H_B = (r \cdot H + H_{tot} + H_t + H_{ld}) \cdot (1 - i_{PC})$$

$$S_B = (S_{tot} + S_t + S_{ld}) \cdot (1 - i_{PC})$$

Effect relating to external wind pollination

The part consisting of SO clones with external wind pollination (only the mother clone effect)

$$H_C = 0.5 \cdot (r \cdot H + H_{tot} + H_t + H_{ld}) \cdot (1 - i_{xPC}) \cdot i_{PC}$$

$$S_C = 0.5 \cdot (S_{tot} + S_t + S_{ld}) \cdot (1 - i_{xPC}) \cdot i_{PC}$$

Effect relating to external pollination from surrounding seed orchards

The part consisting of SO clones with external pollination from surrounding seed orchards (the mother clone effect of the orchard in question and the father clone effect from the surrounding orchard).

$$H_D = (r \cdot H + 0.5 \cdot (H_{tot} + H_t + H_{ld} + H_{xPC})) \cdot i_{xPC} \cdot i_{PC}$$

$$S_D = 0.5 \cdot (S_{tot} + S_t + S_{ld} + S_{xPC}) \cdot i_{xPC} \cdot i_{PC}$$

4.7 SUMMARY OF GENETIC GAIN ESTIMATES

The total gain from genetic improvement is then:

$$\Delta H = H_A + H_B + H_C + H_D + H_E$$

$$\Delta S = S_A + S_B + S_C + S_D + S_E$$

Table 3 summarizes the different seed orchard categories with their respective genetic gain levels and management regimes that supply additional gain.

Table 3. Genetic gain levels for the seed orchard categories and management regimes.

	B		SG		SH		EP		GT		LD	
Category	H	S	H _{tot}	S _{tot}	H _s	S _s	H _{xPC}	S _{xPC}	H _t	S _t	H _{ld}	S _{ld}
1g	10	0	0	0	A	B	*	*	C	D	-	-
1.25g	10	0	2.5	0	A	B	*	*	C	D	-	-
1.25gS	10	0	0	2.5	A	B	*	*	C	D	-	-
1.5g	10	0	15	0	A	B	*	*	C	D	E	-
1.5gS	10	0	10	5	A	B	*	*	C	D	E	E

B=Baseline, SG=Selection gain, SH>Selective harvesting, EP=Gain from extra pollen sources, GT=Genetic Thinning, LD=Linear deployment

Asterisks (*) could have values ≠0 that are calculated separately.

A = [-2, 0, 6] (from left to right: Fraction B, no selective harvesting, Fraction A)

B = [-1.5, 0, 4.5] (from left to right: Fraction B, no selective harvesting, Fraction A)

C = [0, 2, 4] (from left to right: No genetic thinning, 1st genetic thinning, 2nd genetic thinning)

D = [0, 2, 4] (from left to right: No genetic thinning, 1st genetic thinning, 2nd genetic thinning)

E = [0, 1] (from left to right: No linear deployment, Linear deployment)

5. Performance index

Based on our methods and calculations, growth (height) and survival performances can be estimated for seed orchard crops at an arbitrarily selected site. However, in order to rank and recommend seed orchards (and stand seed), a measure of performance on a common scale is required. We therefore developed a performance index in which growth and survival are combined into an estimate of areal production over a rotation. The calculations for stand and seed orchard crops are given below.

To estimate the performance of the local stand (P_{lok}), survival at 2.5-meters height (S_{lok}) is multiplied by the average height at 30 years of age (H_{lok}) and a correction term, taking the patchiness of mortality into account (C_{lok}) (Appendix F, Berlin et al. 2009a).

$$P_{lok} = S_{lok} \cdot H_{lok} \cdot C_{lok}$$

where $S_{lok} = S(\Delta LAT = 0)$ and $H_{lok} = H(\Delta LAT = 0)$.

For transferred stands the performance is estimated as

$$P_{prov} = S_{prov} \cdot H_{prov} \cdot C_{prov}$$

where $S_{prov} = S(\Delta LAT \neq 0)$ and $H_{prov} = H(\Delta LAT \neq 0)$.

A relative performance index (local stand $I_{lok=100}$) is then estimated as

$$\begin{aligned} I_{pr} &= 100 \frac{S_{prov} \cdot H_{prov} \cdot C_{prov}}{S_{lok} \cdot H_{lok} \cdot C_{lok}} = 100 \frac{S_{prov}}{S_{lok}} \cdot \frac{H_{prov}}{H_{lok}} \cdot \frac{C_{prov}}{C_{lok}} \\ &= 100 \cdot S_{prov_{rel}} \cdot H_{prov_{rel}} \cdot C_{prov_{rel}} \end{aligned}$$

For seed orchard crops, the performance index is estimated as:

$$P_{SO} = S'_{SO} \cdot H'_{SO} \cdot C_{SO}$$

where S'_{SO} , H'_{SO} , and C_{SO} are survival at 2.5-meters height, average height at 30 years of age and a correction term for the (possibly transferred) seed orchard crop respectively.

A relative performance index (local stand $I_{lok=100}$) is then estimated as

$$\begin{aligned} I_{SO} &= 100 \frac{S'_{SO} \cdot H'_{SO} \cdot C_{SO}}{S_{lok} \cdot H_{lok} \cdot C_{lok}} = 100 \frac{S'_{SO}}{S_{lok}} \cdot \frac{H'_{SO}}{H_{lok}} \cdot \frac{C_{SO}}{C_{lok}} \\ &= 100 \cdot S_{SO_{rel}} \cdot H_{SO_{rel}} \cdot C_{SO_{rel}} \end{aligned}$$

The relative performance index is used to rank and recommend stand seed and seed orchard crops in the deployment recommendations. Both survival and growth measures are given as additional information.

5.1 SITE CLASS ESTIMATES

Instead of using the average height at age 30 as an indicator of growth potential as additional information in the deployment recommendations, a site class estimate is used. This is calculated in two steps. First, a site index is calculated and then the site class.

The site index (i.e. H100) for a stand seed (SI_{prov}) or seed orchard crop (SI_{SO}) is based on the height growth functions from Elfving (1982):

$$H(t) = \frac{SI}{e^{(7+\ln(t)\cdot(-0.57-0.05\cdot SI))+(-0.28+0-0094\cdot SI)\cdot\ln(t)^2)} + 1}$$

where t is assigned the value 30 years, $H(t) = H_{prov}$ or H'_{SO} and $SI = SI_{prov}$ or SI_{SO} . As SI cannot be solved analytically, an iterative process has been used. Based on a large amount of sampled data points from the function above, a simplified model was estimated by least square methods:

$$SI_{prov/SO} = m + k \cdot \sqrt{H_{prov/SO}}$$

where the coefficients $m=-2.47825399671574$ and $k=8.41064589021619$. The deviations between functions from Elfving (1982) and the simplified model was less than 0.1 m. Given the average height at age 30, $SI_{prov/SO}$ is the estimated site index for either stand seed or seed orchard crop.

$SI_{prov/SO}$

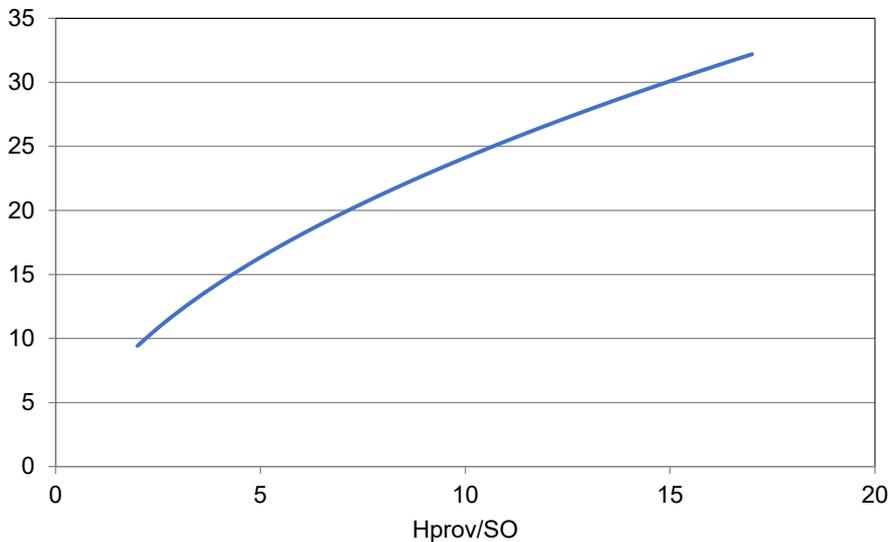


Figure 4. Estimated site index for various average heights.

Given this site index, the site class is estimated as:

$$SC_{prov/SO} = B \cdot SI_{prov/SO}^A + C$$

where the coefficients are $A=2.07983283100267$, $B=0.00637471892431809$ and $C=-0.138813738043048$ (Rosvall and Wennström 2008). This implies that a genetic improvement in growth can be considered as an increased site class (cf. Rosvall and Lundström 2011).

6. Model limitations and validity

The previously derived deployment recommendations and performance indices do not cover the entire geographic area of Sweden and Finland and are limited by two main factors: (i) non-forest lands, i.e. not suitable or too harsh for forest regeneration; and (ii) model range limitation. For (i), no recommendations are made for sites not considered suitable for planting; for (ii), recommendations are still made (southern Sweden) but a set of thresholds govern the transition region where the models are phased out and replaced with static zones.

6.1 SITES VALID FOR PLANTING/SEEDING

To exclude sites that are not suitable for planting or direct seeding (i.e. too harsh and non-forest land, e.g. mountains), a combination of latitude and altitude define suitable and non-suitable areas by:

- $TS_{lok} > 500$.
- $ALT_{lok} < 100 \cdot LAT_{lok} - 5\,300$.
- $ALT_{lok} < 3\,566 - 43 \cdot LAT_{lok}$

The following figure illustrates locations suitable for planting.

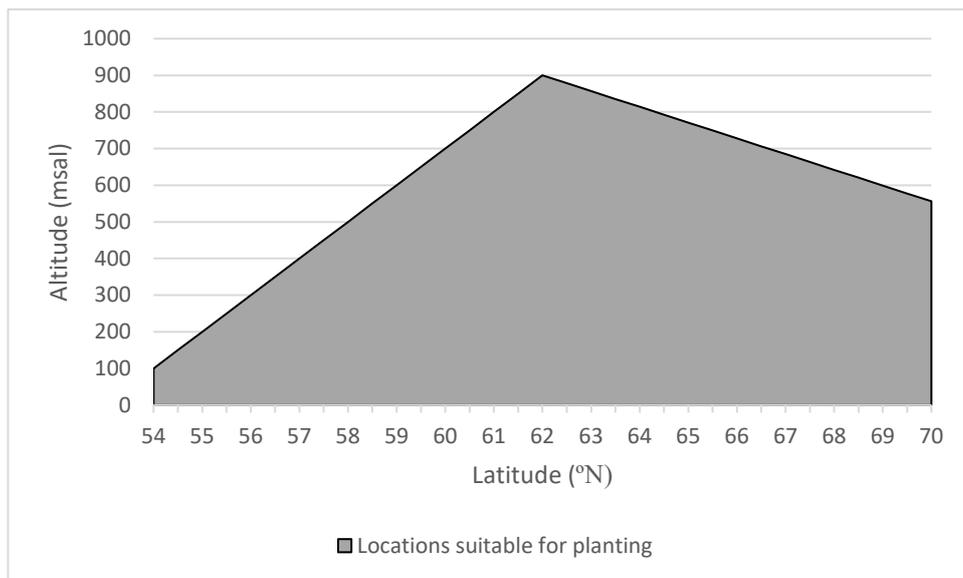


Figure 5. Illustration of suitable and unsuitable locations for planting.

If the selected locations of planting fall within the white area no recommendations are given.

6.2 RECOMMENDATIONS OUTSIDE THE MODEL RANGE

The transfer effect models are only valid northwards from latitude 60°N, which covers the whole of Finland and the northern parts of Sweden. Below that latitude, no field trial data and a smaller number of genetic entries (to describe northward transfer) were used in the model development (Berlin et al. 2016). Earlier studies have shown that the variation in survival and the transfer effects are much smaller in southern Sweden than in northern Sweden (which has a strong clinal trend in both survival and growth) and that transfer of seed has a wide optimum range around the local stand seed (e.g. Prescher 1986). Consequently, current deployment recommendations in southern Sweden are divided into larger zones where no effects of transfer are assumed.

For practical purposes, the transition between the region where the model is valid and southern Sweden, where we have assumed no transfer effects, is governed by a set of triggers and separate calculations of the performance index. The triggers depend on both the latitude of the selected site and the standardized latitude of the seed orchard.

First, planting sites are divided into three regions:

- $LAT \leq 59^\circ N$: Götaland
- $59^\circ N \leq LAT < 60^\circ N$: Svealand
- $(LAT \geq 60^\circ N \mid \mid \text{Finland})$: Norrland and Finland

Then, seed orchards are divided into three classes:

- SO_{Gota} - Seed orchards for Götaland ($LAT_{sto} \leq 59$).
- SO_{Svea} - Seed orchards for Svealand ($59 < LAT_{sto} \leq 60$).
- SO_{North} - Seed orchards for Finland/Norrland ($LAT_{sto} > 60$).

As there are no transfer effect models available for southern Sweden, a fixed index value is given as

$$I_{SO}^{fix} = 100 \cdot (1 + \Delta H)$$

There are therefore no transfer effects and only the genetic gain in growth affects the index. Furthermore, survival is assumed to be so high that no gain can be achieved.

In addition, adjustment terms ($dGota$, $dSvea$) are used to reduce the gain of orchards that are not primarily intended for use in an adjacent region.

$dGota/dSvea$ can have any of the values [0, -1, -2]. $dGota/dSvea = 0$ is used for SOs that are adapted to the Götaland/Svealand region, $dGota/dSvea = -1$ for SOs that are not optimal for Götaland/Svealand, and $dGota/dSvea = -2$ for SOs that are not well adapted for Götaland/Svealand.

For the different seed orchard categories, the following applies:

SO_{Göta} - Seed orchards for Götaland

- $LAT \leq 59^\circ N$: $I_{SO} = I_{SO}^{fix} + dGöta$
- $59^\circ N \leq LAT < 60^\circ N$: $I_{SO} = I_{SO}^{fix} + dSvea$
- $(LAT \geq 60^\circ N \text{ || Finland})$: $I_{SO} = I_{SO}^{fix} + dSvea$

1) When the standardized latitude $LAT_{sto} \leq 59$ (SO-Götaland)

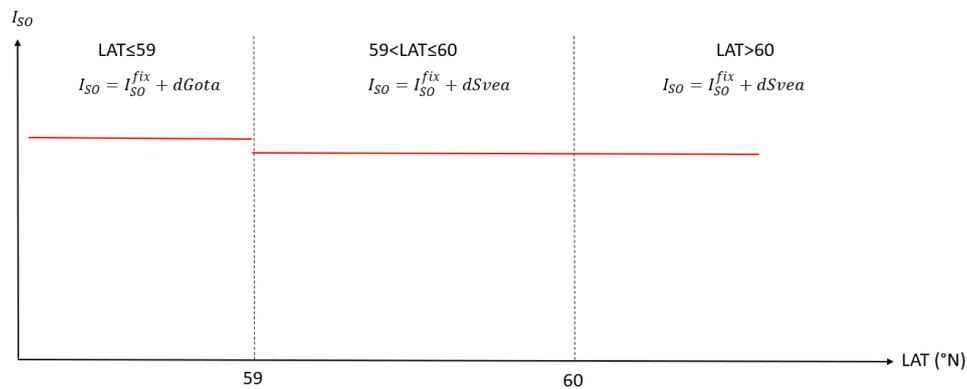


Figure 6. Example of the behavior of a Götaland SO.

SO_{Svea} - Seed orchards for Svealand

- $LAT \leq 59^\circ N$: $I_{SO} = I_{SO}^{fix} + dGöta$
- $59^\circ N \leq LAT < 60^\circ N$: $I_{SO} = \max\{I_{SO}^{fix} + dSvea, I_{SO}\}$
- $(LAT \geq 60^\circ N \text{ || Finland})$: $I_{SO} = I_{SO}$

2) When the standardized latitude $59 < LAT_{sto} \leq 60$ (SO-Svealand)

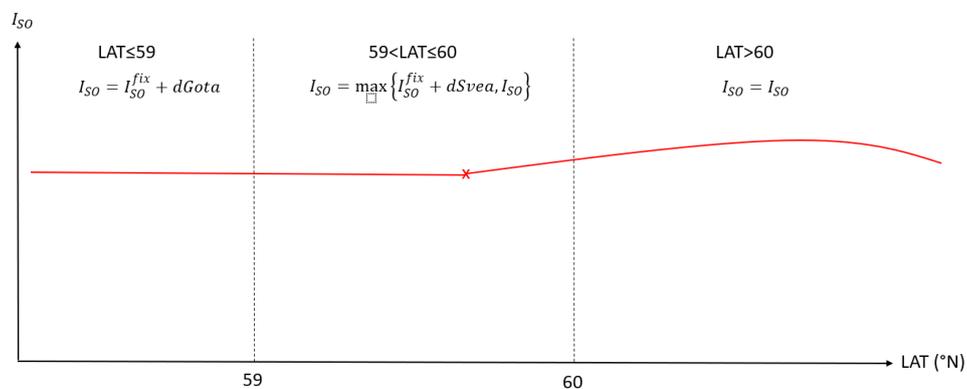


Figure 7. Example of the behavior of a Svealand SO.

SO_{North} - Seed orchards for Finland and Norrland

- $LAT \leq 59^\circ N$: $I_{SO} = I_{SO}$
- $59^\circ N \leq LAT < 60^\circ N$: $I_{SO} = I_{SO}$
- $(LAT \geq 60^\circ N \ || \text{Finland})$: $I_{SO} = I_{SO}$

3) When the standardized latitude $LAT_{sto} > 60$ (Finland/Norrland-SO)

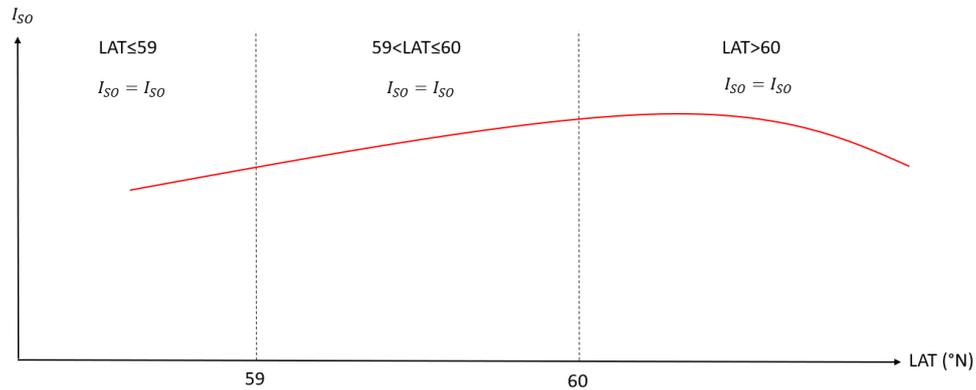


Figure 8. Example of the behavior of a Finland/Norrland SO.

As the performance index in southern Sweden is driven by growth only, the ranking list comprises only the index value below latitude 60°N (not the separate growth and survival levels). In Finland, all values are always given.

7. Limits to transfer and deployment zones

There are also limits relating to transfer and deployment that differ between stand seed and seed orchards, but also between the two countries.

7.1 LIMITS TO STAND SEED TRANSFER

For stand material the limits are given as a combination of latitudinal transfer and site harshness (temperature sum):

- When $TS_{lok} > 1\ 433$: $-1 < \Delta LAT_{prov} < 3$
- When $900 < TS_{lok} < 1\ 433$: $0.00375 \cdot TS_{lok} - 6.375 < \Delta LAT_{prov} < 3$
- When $TS_{lok} < 900$:
 $0.00375 \cdot TS_{lok} - 6.375 < \Delta LAT_{prov} < 0.00625 \cdot TS_{lok} - 2.625$

In Figure 9, valid transfers are shown by the grey area and non-valid transfers by the white area.

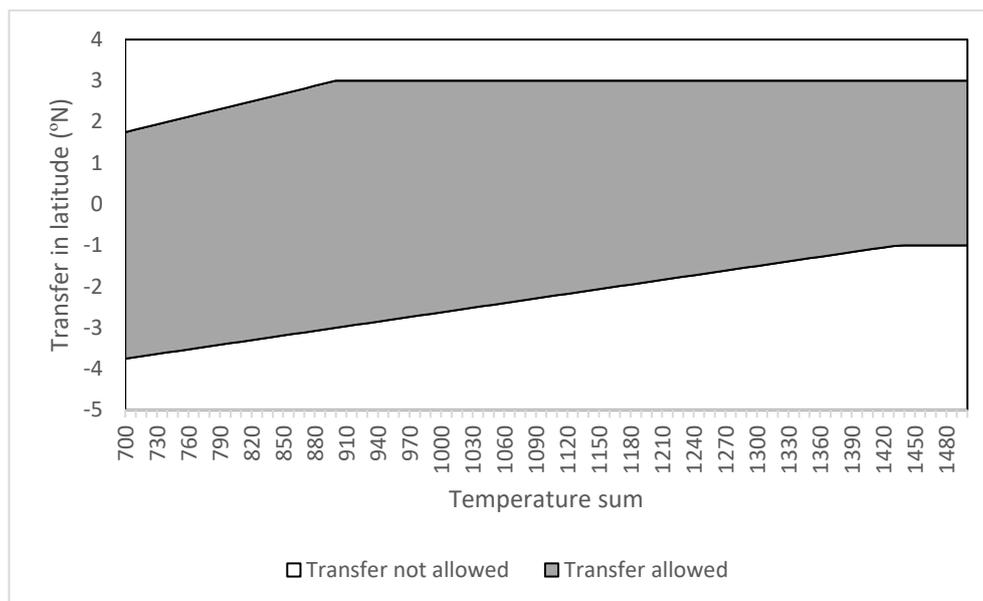


Figure 9. Illustration of the valid range of transfer for stand seed.

If the selected locations of planting fall within the white area no recommendations are given.

7.2 DEPLOYMENT ZONES FOR SEED ORCHARD CROP

The deployment zones for use of seed orchard crop are set by different rules/systems in Sweden and Finland. Those limits are developed based on a combination of biological information, administrative regulations, demands on seed orchard crop performance, and ranges of model validity.

Finnish deployment zones

New deployment rules were developed in Finland based on the deployment recommendations, but with a slightly different parameterization of the models to produce the predictions of growth, survival and areal production (Ruotsalainen et al. 2016).

The Finnish deployment zones are based on a number of SO categories (groups), where each has a given performance index threshold (sometimes with additional delimitations) governing the allowed geographical delineation. The performance indices, $I_{SO}^{(FIN)}$, and survival values, $S_{SO}^{(FIN)}$, providing the thresholds for zoning were calculated with a different parameterization of the model than the one used in the deployment recommendations. For details about the parameterization, see Appendix G and (Ruotsalainen et al. 2016).

There are four main categories.

- Category 1: First generation SO. Basic case.
- Category 2: First generation SO where the target area is northern Finland. They are defined by having $LAT_{clone} > 66.56^{\circ}N$ and $LAT_{SO} < 64^{\circ}N$.
- Category 3: First generation SO where $LAT_{SO} < 64^{\circ}N$ and the clones were selected for hardiness (i.e. 1.25gS).
- Category 4: 1.5 generation SO. Basic case.

In addition, Swedish seed orchards considered too southern for use in Finland were excluded (see Appendix G).

For each SO category, valid deployment zones are described in Appendix G. This model structure will provide individual SO deployment zones in accordance with the official maps in terms of geographic extension. Within these allowed zones, all index values and SO ranking are calculated according to the default calculations as described earlier.

Swedish deployment zones

In Sweden, the geographic range where different seed orchard crops are considered feasible to use as regeneration material is governed by a latitudinal span that varies according to site harshness. This span is also related to the transfer span covered by a majority of the field data. At harsh sites, a longer southward transfer and a shorter northward transfer is allowed. At mild sites, the opposite applies. The following applies for SO crops in Sweden.

- If $TS_{lok} > 1\ 200$: $-2 < \Delta LAT_{pl} < 3$
- If $900 < TS_{lok} < 1\ 200$: $0.00375 \cdot TS_{lok} - 6.375 < \Delta LAT_{pl} < 3$
- If $TS_{lok} < 900$: $0.00375 \cdot TS_{lok} - 6.375 < \Delta LAT_{pl} < 0.00625 \cdot TS_{lok} - 2.625$

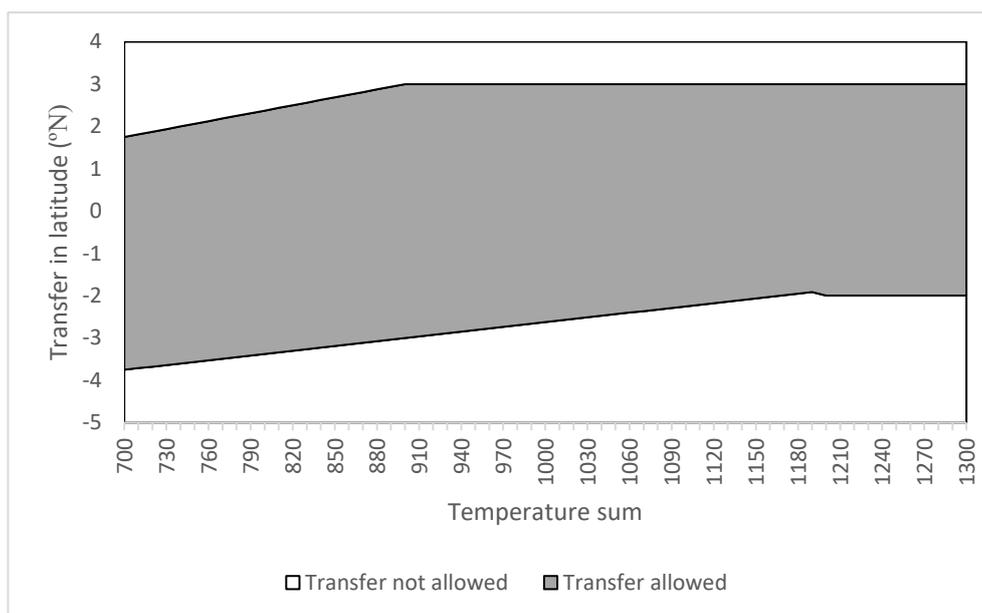


Figure 10. Illustration of the valid range of transfer for seed orchards in Sweden.

If the selected locations of planting fall within the white area no recommendations are given.

For seed orchards with a very long transfer of northern clones to southern orchard locations (i.e. category 3 in the Finnish deployment zones), adjustments to the orchard characteristics are made compared to the 'default' orchards. First, seed orchard crop is considered to originate from two distinct populations rather than one joint population, which is the default. Second, external contaminating pollen is considered to originate from 1.5 latitude degrees south of the orchard locations as compared to 0.5 degrees for the default case, due to phenological difference in flowering. These adjustments are made to provide a more conservative estimate of the hardiness of these orchards, and are described in detail in Appendix H.

7.3 DEPLOYMENT MAPS FOR THE SEED ORCHARDS

Swedish maps

In addition to the limits described above, no index values where the index is below 100 or the survival is below 50% are shown in the deployment maps. These deployment areas are more conservative than the Forestry Board's official rules on legal transfer (Skogsstyrelsen 2011).

Finnish maps

Index values (i.e. index values calculated according to the default calculations) can be lower than 100 in Finland due to pollen contamination. The main effect seems to be that the standardized latitude can vary considerably when pollen contamination rates are high (and there is a large difference between clonal origin and SO location). However, this will be a transient effect and index values will rise quickly as pollen contamination levels go down.

Nevertheless, we have therefore allowed index values below 100 in Finland (not in Sweden) so that deployment areas are not affected and still comply with the official maps. This meant that the color scale for the maps needed to be slightly adjusted to allow for a difference in color nuance also below 100 (earlier values were cut off below 100).

Map color scale and design

In order to indicate the variation of seed orchard performance in an optimal way, the color scale used is non-linear, where most of the color span is focused on the index range 100-120. This will help differentiate performance in the most relevant range (see Figure 11).



Figure 11. A deployment map for the seed orchard T7 Slåttholmen, illustrating the performance of the orchard and its different limitations in Sweden and Finland.

Furthermore, the deployment maps are based on Google Maps, where the climate grids from each country (4 x 4 km in Sweden and 10 x 10 km in Finland) are used and provide the resolution of the map.

8. Future implementation and development

A main aim has been to implement the Scots pine deployment recommendations in a web tool, serving as a decision support tool for forestry across both countries. The current web-tool for Sweden, Plantval (Planter's Guide) (<https://www.skogforsk.se/produkter-och-evenemang/verktyg/plantval-tall/>), will be expanded and made available in both languages. The process of securing acceptance, obtaining design feedback from stakeholders in each country, is vital for making the tool operative, and this has already been started.

Besides the implementation in a web tool, there are a number of pressing development projects that have been started or are planned to start.

In the current deployment recommendations, only one climate scenario has been used to predict future FRM performances. However, several different scenarios are currently available, and it is not clear how they will affect the predicted FRM performance and how this uncertainty should be managed. This is a main focus within the Horizon-2020 B4EST-project (2018-2022).

The local climatic adjustment is included in the deployment recommendations in an attempt to consider the within-grid variation and specific growth conditions at the planting site. However, this adjustment is currently coarse and lacks direct support, as there are no models available to capture this phenomenon. Using high-resolution DTM (Digital Terrain Models) and advanced topographic indices, the prospect of developing such models will be investigated in a national project (2019-2020).

The web tool, Plantval (Planter's Guide), in its current form provides FRM deployment recommendations one site at a time and is not adapted to the requirements of large forest owners and/or plant producers. Therefore a system to optimize the use and distribution of genetically improved forest reproductive material (FRM) for large forest owners with many regeneration sites and access to several different seed sources was developed in a pilot study (Davidsson et al. 2018). Results implied that large Swedish forest owners could substantially increase forest production by optimizing the use and distribution of their available plant material.

However, there are several additional research topics that could be analyzed. (1) The objective function in the optimization was very simple (maximize mean annual production per hectare) and could be refined to include, e.g., net present value and logistical costs. (2) Only one company was studied, and results indicate that including other companies (from both countries) would yield additional gain by trading seed/plants. (3) By integrating the deployment recommendation platform with stand simulators like Heureka/Motti, optimization could include alternative/adapted silvicultural regimes (e.g. varying stand density, time of and intensity of thinning, mixing improved plants with natural regeneration and/or other species).

All the above implementations and developments have been focused on Scots pine, as the development of transfer functions and deployment recommendations have progressed much further compared to Norway spruce. However, as these two species totally dominate the economic importance of forestry in Fennoscandia and the Baltic States, climate adapted deployment recommendations will also be developed for Norway spruce. Following the analysis structure described here and in Berlin et al. (2016), new climate indices, transfer functions and deployment recommendations will be developed for Fennoscandia and the Baltic States in the Horizon-2020 B4EST-project (2018-2022).

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Appendix A.

Calculations based on genetic parameters

A1. CALCULATION OF ADDED GAIN FROM SELECTING A FRACTION OF CLONES IN AN ORCHARD

The added gain from selecting a fraction of clones in an orchard is approximated by calculating a selection intensity where the selected fraction p is the quotient between the total number of seed orchard clones n and the number of clones used in the selective harvesting j .

$$p = \frac{j}{n}$$

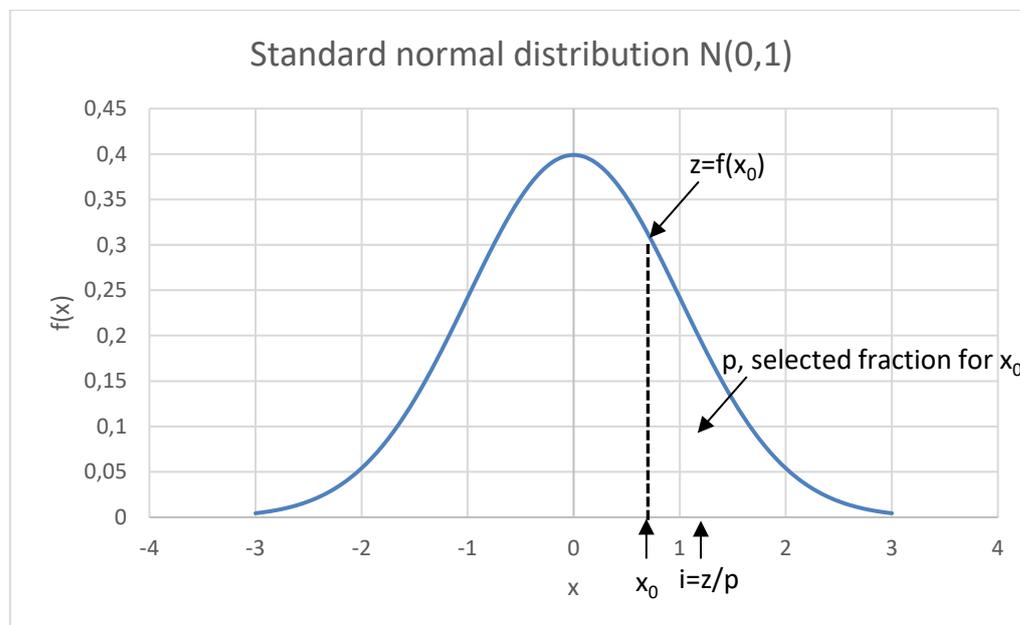
The selection intensity for samples of finite size can then be calculated as (cf. Burrows 1972; Lindgren and Nilsson 1985):

$$i_B = i - \frac{n - j}{2j \cdot (n + 1) \cdot i}$$

Where i is the selection intensity in the infinite case calculated as:

$$i = \frac{z}{p}$$

Figure A1. Illustration of the variables included in the calculation of selection intensity (i) from the proportion selected (p) for a standardized selection criteria x .



Given the selection intensity the added gain from selecting a fraction of the clones in an orchard can be calculated as (for height):

$$\Delta G_s = i_B \cdot r_{AI} \cdot r_{jm} \cdot CV_{Am} \cdot r_{mt}$$

And for survival

$$\Delta G_s = i_B \cdot r_{AI} \cdot r_{jm} \cdot \sigma_A \cdot r_{mt}$$

Where:

i_B = Selection intensity when selecting a fraction of the clones.

r_{AI} = testing accuracy

r_{jm} = juvenile-mature correlation

$r_{G \times E}$ = reduction for average G×E within deployment area = 0.8 (not added to the equation above as the CV_{Am} and σ_A has been corrected for G×E.

CV_{Am} = additive coefficient of variation for the target trait (areal production over a rotation)

σ_A = additive standard deviation for survival relative a 50%-level (this will be adjusted for to actual survival levels in other parts of the calculations in the deployment recommendations)

r_{mt} = reduction when selecting for multiple traits. $r_{mt} = 1$ when only growth is considered,

$r_{mt} = \frac{1}{\sqrt{2}}$, when both growth and survival is considered (simultaneously).

These genetic parameters have been assigned the following values based on Rosvall et al. (2001) (where a correction for a G×E of 0.8 has been taken into account):

Table A1. Genetic parameters used for calculation of genetic gain

Target trait	Areal production over a rotation	Survival	
Measurement trait	Height in field trials	Survival in field trials	Freezing tests
r_{AI}	0.80	0.80	0.80
r_{jm}	0.7	0.90*	0.7
CV_{Am}	0.125	-	-
σ_A	-	0.20	-

*Set to 1.0 in Rosvall et al. (2001). However, recent analyses from Treeplan runs state that the value should rather be 0.9.

A2. SELECTIVE HARVESTING – EXAMPLE

Assume that selective harvesting is performed in an orchard consisting (in this case selected for growth only, i.e. $r_{mt} = 1$) of 100 clones and that the 30 best clones are used for selective harvesting, which means that two fractions will be created. Fraction A collected in the best 30 clones (i.e. $j=30$) and fraction B collected in the remaining 70 clones. How will those gains be calculated (examples made for areal production)?

Firstly $i_B^A = 1.1490$ when selecting 30/100. Then Fraction A will be calculated as:

$$\Delta G_s = i_B^A \cdot r_{AI} \cdot r_{jm} \cdot CV_{Am} = 1.1490 \cdot 0.80 \cdot 0.7 \cdot 0.125 \approx 0.08 \text{ (i.e. } H_s^A = 8\%)$$

$$\text{For fraction B: } i_B^B = -\frac{j}{n-j} \cdot i_B^A = -\frac{30}{100-30} \cdot 1.1490 \approx -0.4924$$

$$\Delta G_s = i_B^B \cdot r_{AI} \cdot r_{jm} \cdot CV_{Am} = -0.4924 \cdot 0.80 \cdot 0.7 \cdot 0.125 \approx -0.035 \text{ (i.e. } H_s^B = -3.5\%)$$

A3. EXTRA POLLEN SOURCE – EXAMPLE

This example is based on the seed orchard 403 Nedansjö elit, which is considered to be an orchard of 1.5gS-category. Around it is the old (1g) orchard which was genetically thinned (completely thinned – disregarding spatial patchiness as it was only intended to serve as a pollen source for the new orchard). Thus, the gain from the extra pollen of the old, thinned, orchard is:

By thinning the old orchard to the best 28 of 57 clones (considering both height and survival from BVs that were now available): $i_B = 0.801$.

For height:

$$\Delta G_s = i_B \cdot r_{AI} \cdot r_{jm} \cdot CV_{Am} \cdot r_{mt} = 0.801 \cdot 0.80 \cdot 0.7 \cdot 0.125 \cdot 0.707 \approx 0.0396 \text{ (i.e. } H_x = 3.96\%)$$

For survival (where survival is transformed into normal scores and expressed in standard deviations relative to the 50%-level):

$$x = i_B \cdot r_{AI} \cdot r_{jm} \cdot \sigma_A \cdot r_{mt} = 0.801 \cdot 0.80 \cdot 0.9 \cdot 0.20 \cdot 0.707 \approx 0.0816$$

And expressed in %-units by calculating the cumulative normal distribution function at x :

$$\Phi(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^x e^{-\frac{t^2}{2}} dt, \text{ and } 100 \cdot \Phi(0.0816) - 50 = 53.25 - 50 = 3.25 \text{ (i.e. } S_x = 3.25\% \text{-units)}$$

A4. FREEZING TEST – EXAMPLE

This example is based on seed orchard T2 Alvik, where the clones were selected in the nursery based on freezing tests. It is assumed that the score of freezing damage is correlated to survival ability in the field $r_{f,s} = 0.3$ but also slightly unfavorably correlated with height $r_{f,h} = -0.1$ (values from Persson et al. (2010)). The gains in height and survival are thereafter calculated with the formulae for correlated response.

In this case 135 clones were selected from 1500 candidates so that $i_B = 1.8025$. The correlated response for survival (where survival is transformed into normal scores and expressed in standard deviations relative to the 50%-level) given selection in freezing damage is:

$$x_{s,f} = (i_B \cdot r_{f,s} \cdot r_{AIf} \cdot r_{AIs} \cdot \sigma_{Af}) \cdot r_{jm} = (1.8025 \cdot 0.3 \cdot 0.8 \cdot 0.8 \cdot 0.2) \cdot 0.9 \approx 0.0623$$

And expressed in %-units by calculating the cumulative normal distribution function at x :

$$\Phi(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^x e^{-\frac{t^2}{2}} dt, \text{ and } 100 \cdot \Phi(0.0623) - 50 = 52.5 - 50 = 2.5\%$$

And for height:

$$\Delta G_{h,f} = i_B \cdot r_{f,h} \cdot r_{AIf} \cdot r_{AIh} \cdot CV_{Am} \cdot r_{jm} = 1.8025 \cdot (-0.1) \cdot 0.8 \cdot 0.8 \cdot 0.125 \cdot 0.7 \approx -0.0101 \text{ (-1\%)}$$

Appendix B. Selective harvesting

For nine Swedish Seed Orchards, where selective harvesting has been performed, gains in survival (S_s) and growth (H_s) for both fractions were calculated using genetic parameters according to Appendix A1 (Table B1).

Table B1. Gains in survival (S_s) and growth (H_s) for both fractions of nine Swedish seed orchards when selectively harvested. The A-fractions are given in bold fonts and the corresponding B-fractions are given normal fonts.

Name	SO ID	Category	S_s (%)	H_s (%)
Domsjöänget	FP-411A	1g	5.17	7.06
Domsjöänget	FP-411B	1g	-1.14	-1.55
Domsjöänget	FP-412A	1g	4.87	6.65
Domsjöänget	FP-412B	1g	-1.31	-1.78
Tällby	FP-433A	1g	4.11	5.62
Tällby	FP-433B	1g	-1.77	-2.41
Våge	FP-125A	1g	5.05	6.9
Våge	FP-125B	1g	-1.21	-1.64
Hade T16:2	FP-610A	1.25g	0	5.67
Hade T16:2	FP-610B	1.25g	0	-0.83
Gnarp T12	FP-620A	1.25gS	3.94	5.38
Gnarp T12	FP-620B	1.25gS	-1.93	-2.63
Robertsfors	FP-886A	1g	3.85	5.25
Robertsfors	FP-886B	1g	-1.93	-2.63
Gotthardsberg T19:2	FP-606A	1.25g	0	6.6
Gotthardsberg T19:2	FP-606B	1.25g	0	-1.8
Lilla Istad T19:1	FP-604A	1.25g	0	5.8
Lilla Istad T19:1	FP-604B	1.25g	0	-2.3

As these orchards are both 1g and 1.25g and covers all parts of Sweden they can be considered to provide a general picture of gain levels. The data is compiled in the table B2

Table B2. Average gains in survival (S_s) and growth (H_s) for both fractions of nine Swedish seed orchards when selectively harvested.

	Average	Max	Min
S_s fraction A	4.5	5.2	3.9
S_s fraction B	-1.5	-1.1	-1.9
H_s fraction A	6.1	7.1	5.25
H_s fraction B	-2.0	-0.8	-2.63

The data show that for both height and survival the gain levels seem rather stable around 4.5% for survival and 6% for height regardless of the SO category and if one or two traits have been selected. The same goes for the loss of gain in the B-fractions.

Appendix C. Some observations on realised selection intensity in genetic thinning of seed orchards

By Seppo Ruotsalainen (2016-03-03)

In genetic thinning of seed orchards the grafts are removed using following most important criteria (Kinnunen and Karvinen 2010):

- growing space for the remaining grafts
- the genetic value of the clone: height growth and quality (and survival)
- seed production capacity of the clone
- phenotypic qualities of the graft (mainly related to seed production)

The genetic value of a clone is predicted using the progeny test results expressed as performance level values (Venäläinen and Ruotsalainen 2002). The weighing among the different criteria can vary from case to case.

The effect of genetic thinning on selection intensity was studied in two Finnish Scots pine seed orchards. The composition of the seed orchards is described in Table C1. A few clones, usually with a small number of grafts, did not have progeny test results for height growth, and they were omitted from the following analysis. [The proportions of grafts remaining after the first \(50 – 61%\) and second thinning \(27%\) are quite representative of operational thinnings made in Finnish Scots pine seed orchards \(Jukka Antola, pers. comm.\).](#)

Table C1. Basic information of the number of clones and grafts in the two studied Scots pine seed orchards during different stages of genetic thinning.

	SO No. 150		SO No. 282	
	Clones	Grafts	Clones	Grafts
No. at start (all)	138	4455	196	4480
No. at start (with height)	135	4406	190	4454
No. after 1 st thinning	121	2693	148	2244
% after 1 st thinning	89.6	61.1	77.9	50.4
No. after 2 nd thinning	-	-	85	1183
% after 2 nd thinning	-	-	44.7	26.6

An example of the effect of an operational thinning on the distribution of grafts in the performance level classes for height at seed orchard No. 150 is given in Figure 1. The proportion of the grafts in the best height classes has increased after thinning. However, some quite poor grafts have also remained due to the weighting by other selection criteria. If the selection with the same removal percentage had been conducted exclusively based on the height, the poorest classes would have been totally removed and the proportion of the best classes would have greatly increased (the “Threshold” category in Fig. C1).

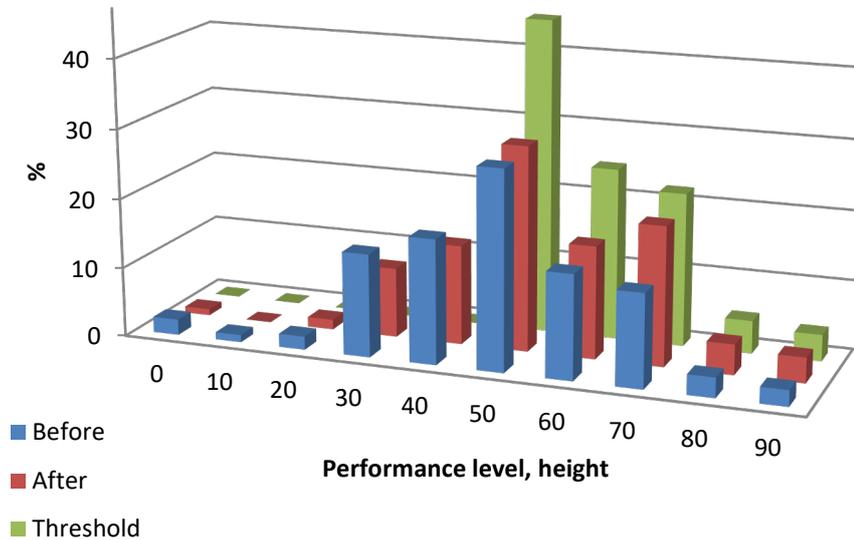


Figure C1. Effect of genetic thinning on the distribution of performance level values of the grafts in seed orchard No. 150. Distribution is shown also after using a simulated truncation selection with a fixed threshold value for height giving the same removal percentage.

To study the realised selection intensity in operational genetic thinnings selection intensity was calculated in two different ways. First a theoretical value was obtained using the proportion of the grafts that remained after thinning (Table 3 in (Lindgren and Nilsson 1985)). The realised selection intensities were derived from the equation $i = S/\sigma_p$ (S = selection differential, σ_p = standard deviation of the performance levels of heights for the clones in seed orchard). Both the averages and the standard deviations I calculated on a clonal mean basis weighting them with the number of grafts.

The standard deviations represent the situation before the first thinning of the seed orchard. The standard deviations for the performance level of height were 17.279 and 18.287 in the seed orchards No. 150 and 282, respectively.

The effect of genetic thinning on selection intensity was in the simulated cases close to the expectations in both of the seed orchards (Tables C2 and C3). This proves that the distributions of the performance level values follow closely the normal distribution. On the other hand, in the operational thinning the selection differential and, therefore, the realised selection intensity was only about half of those indicated by the simulations. This is evidently caused by the above mentioned multiple selection criteria used in genetic thinning, thus lowering the selection response for height.

Table C2. Effect of genetic thinning on the performance level of height and selection intensity in seed orchard No. 150. One operational thinning done in 1992 and three theoretical thinnings with truncation selection are shown.

	Operational thinning		Thinning based on truncation selection (simulated cases)	
Remaining, %	61	75	61	25
Height PL, remaining	54.36	56.71	60.03	71.02
Selection differential	4.99	7.34	10.66	21.65
i, obtained	0.289	0.425	0.617	1.253
i, theoretical	0.629	0.424	0.629	1.271
i, obtained. % of theoretical	45.9	100.2	98.1	98.6

Table C3. Effect of genetic thinning on the performance level of height and selection intensity in seed orchard No. 282. Two operational thinnings done in 1993 and 2013, and three theoretical thinnings with truncation selection are shown.

	Operational thinnings		Thinning based on truncation selection (simulated cases)		
	1993	2013			
Remaining. %	50.4	27	75	50.8	27
Height PL, remaining	55.30	59.4	55.60	62.41	71.01
Selection differential	7.24	11.37	7.54	14.35	22.95
i, obtained	0.396	0.622	0.412	0.785	1.255
i, theoretical	0.782	1.271	0.424	0.782	1.271
i, obtained. % of theoretical	50.7	48.9	97.3	100.3	98.8

In all the operational thinnings studied, the selection intensities for height were about 50 % of that obtainable theoretically using the same removal percentage if the selection and thinning had been conducted solely on the basis of height. The selection intensities for the first thinning were in the range 0.3 – 0.4, whereas in the second thinning it was 0.62. These values could be used as guidelines when calculating the genetic gains obtained with genetic thinning of seed orchards.

When considering the total economic gain, these figures provide a conservative estimate, since some gain is obviously made in quality traits, although the magnitude of those gains cannot be quantified with this calculation.

Appendix D: Genetic thinning of seed orchards for increased survival

D1. THINNING SEED ORCHARDS BY HARDINESS – OBSERVATIONS ON THE EFFICIENCY

By Seppo Ruotsalainen (2016-05-03)

Introduction & Material & Methods

Due to the lack of comprehensive survival data from field trials, genetic thinning of seed orchards of northern Finnish origin has during the past years relied on freezing tests. Seeds are collected clone-wise from the seed orchard to be thinned (omitting usually clones with only a few grafts) and the freezing test is then conducted as described in Pulkkinen (1995). The hardiness of the seed orchard clones is expressed as estimated temperature sum of origin, which is then transformed to performance level scale to be used as an input variable in genetic thinning. In addition to the freezing test results also some variables describing the seed production capacity of the clones are usually used as criteria in genetic thinning.

As thinning by a freezing test represents a genuine case of indirect selection with unknown and/or variable correlation with the target trait (Fig. D1), there are difficulties to predict the response of it. However, in this study BLUP breeding values for survival, predicted from a comprehensive set of open-pollinated progeny tests of northern Finnish Scots pines, serve as a target trait. The breeding values are presented as deviations from the 50% expected mean survival level in each target area (defined by temperature sum). The material is from progeny tests with single tree plots, measured at about 10 years age. The average survival of the seed orchard clones for estimating the response to thinning was calculated by weighting the breeding values with the number of grafts.

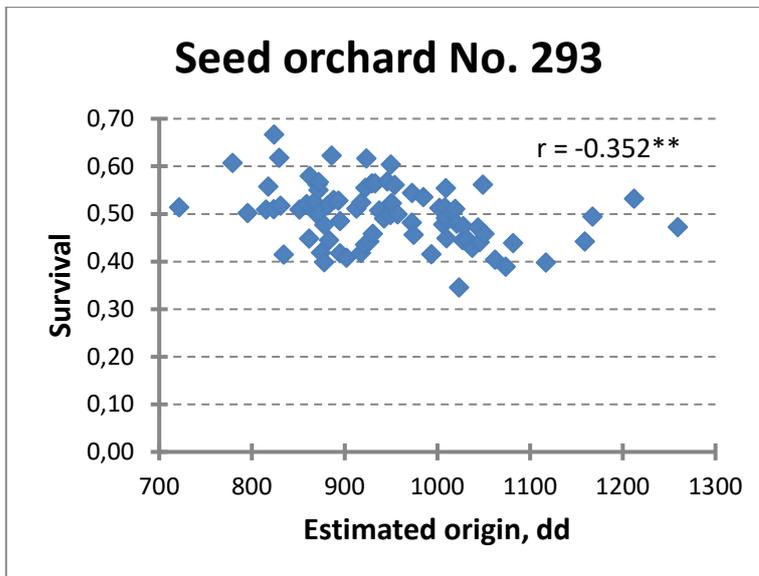
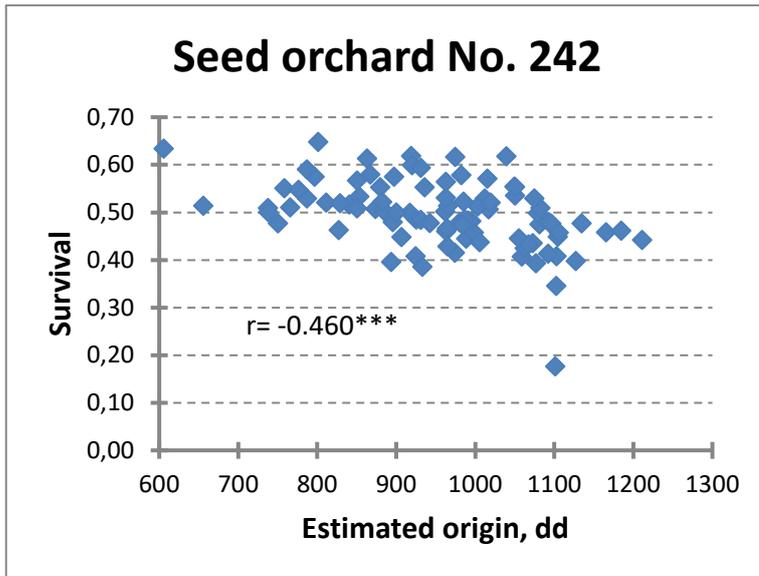


Figure D1. Correlation between survival in field tests and the temperature sum of origin estimated by freezing tests in two different seed orchards of northern Finnish origin.

Because the breeding values in each target area are predicted separately, comparison of them does not properly reflect the change in the mean hardiness in thinning if trees from several target areas are included. Therefore, mainly seed orchards with material from only one target area were chosen for the study. The seed orchards with the northernmost plus trees from the Inari region met best with this criterion (trees from the target area 6). There are four such seed orchards which were genetically thinned in 1998 or 1999 (Table D1). In addition, one seed orchard with more heterogeneous set-up was used. As a comparison also a second genetic thinning for one of the seed orchards conducted on the basis of progeny tests was studied. The seed orchard material describing the genetic thinning was provided by Jukka Antola and Ari Kinnunen. The earlier thinning was conducted on a mainframe VAX computer using the thinning procedure based on Nikkanen and Pukkala (1987), the last thinning in 2014 used a modern Excel programme based on the earlier procedure (Kinnunen and Karvinen 2010).

The information concerning the seed orchards (Table D1) is given considering only those clones which were both freeze and progeny tested. As can be seen, in all except one case the seed orchard material was covered rather well by the tests. However, as the presence of the plus trees in the single tree progeny tests is by no means connected to their genetic value, the results can in all cases be expected to be unbiased and representative to the whole seed orchard. For each thinning operation the efficiency of selection is roughly described by the coefficient of slope for each variable used (Table D1). These coefficients come from the parameters used to adjust the thinning operation. One example of them is given in Figure D2.

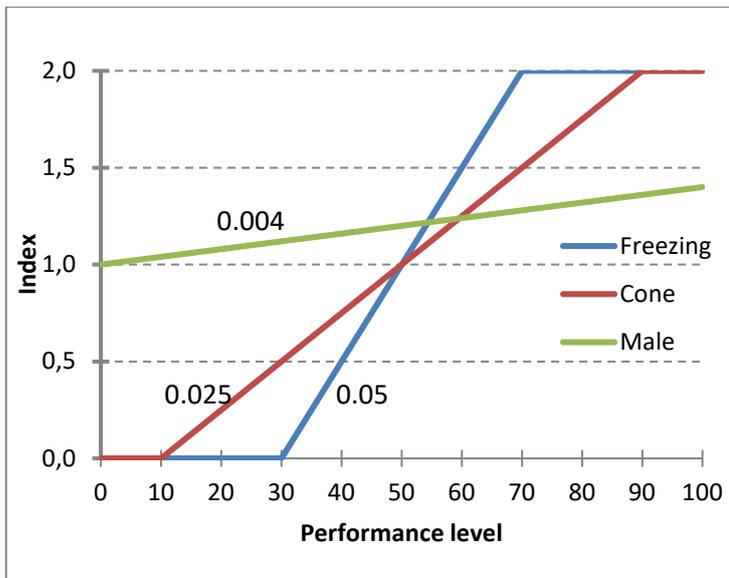


Figure D2. The indices for freezing test, cone crop and male flowering used in genetic thinning of seed orchard No. 242. The figures by the lines indicate the slopes of the indices.

Table D1. Information about the studied seed orchards, variables used in selection and selection results. The numbers of clones and grafts refer to that part of the material in the seed orchards, which was represented in the freezing and progeny tests.

	Seed orchard No.					
	144	241	242	293	297	297
Background information						
Target area	5, 6	6 ¹⁾	6	6	6	6
Thinning year	2000	1998	1999	1998	1999	2014
No. of clones	42	78	92	80	97	75
No. of grafts	3052	6459	3272	3311	4361	2264
Clones removed, %	54.8	15.3	28.3	27.5	25.8	21.3
Grafts removed, %	60.5	49.5	45.9	54.8	46.4	48.6
Grafts represented in tests, %	45.4	79.3	82.9	73.6	84.0	88.2
Selection characters; efficiency of selection (slope)						
Freezing test	0.033	0.02	0.05	0.02	0.033	
Cone crop	0.027	0.01	0.025	0.02		
Seed crop					0.033	0.02
Male flowering		0.003	0.004	0.005		0.008
Survival						0.025
Height growth						10 ²⁾
Quality						10 ²⁾
Mean breeding value in survival (adjusted to 50%)						
Before	46.6	49.0	48.6	49.0	48.4	50.2
After	45.4	51.2	52.2	50.0	50.2	54.8
Change	-1.2	2.2	3.6	1.0	1.8	4.6

¹⁾One clone from target area 4 excluded.

²⁾Selection threshold at PL=25

Results & Discussion

Genetic thinning based on freezing test and seed production or some flowering characteristics resulted in all but one case to increased survival in the material produced by the seed orchard (Table 1). The change in survival varied from -1.2 to 3.6 %-units. The average increase in survival was 1.5 %-units. The increase in survival predicted in this way presumes totally internal pollination within the seed orchard. As this is not the reality, the average increase with 50% background pollination can be assumed to be close to 1 %-units.

The seed orchard with the deviating negative change in survival as a result of genetic thinning was the only one having plus trees from two different target areas. It was also the seed orchard having the lowest proportion of material tested (Table D1). However, it is unlikely that these technical features are the reason for the inefficiency of selection for hardiness in this seed orchard. It is more probable that the improvement of survival in genetic thinning was restrained by the high weight given to cone crop in the thinning operation of this seed orchard, because the hardiest clones seem to be poorer cone producers (Fig. D3). The high weight given to cone production is illustrated by the coefficient of slope for it (0.027, highest of all seed orchards) which is high also in relation to the corresponding slope for freezing test (Table D1). This seed orchard also had the greatest thinning intensity of all the studied seed orchards with more than half of both the clones and the grafts being removed (Table D1). Heavy weighting of cone crop together with great percentage of grafts removed has obviously led to this poor outcome in improvement of survival.

The importance of the weight given for the freezing test in the genetic thinning is further emphasised, when studying the seed orchard No. 242 with the greatest improvement in survival. It has absolutely the highest slope for freezing test (0.05, Table D1). It has also relatively high slope for cone crop, but it is only half of that for freezing test.

The effects of the weights given for different characters in genetic thinning can be illustrated also visually, by studying which clones are totally removed in genetic thinning. The two compared seed orchards had been treated in rather different ways as regards the selection variables (Fig. D4). In seed orchard No. 242 the removal of the clones has occurred solely by the hardiness estimated by freezing test, whereas in seed orchard No. 293 both the hardiness and cone crop have been used for rogueing. These different weightings are well described also by the slope coefficients and are clearly visible in the outcome of the thinning operation (Table D1). Of course the removal of whole clones describes only the most extreme part of genetic thinning; much of the effect comes also from the changes of relative abundances of the remaining clones. Deeper discussion in this question is beyond the scope of this study, and is neither justified by the limited material.

In the only case where genetic thinning was made using directly the survival in progeny tests the improvement was naturally clearly higher than when using freezing tests, 4.6 %-units (Table D1). Also this prediction must be corrected to correspond to the real background pollination percentages, e.g. with 50% pollen contamination the gain would be 3.5 %-units. However, this value must be regarded as tentative, because it is based only on one studied thinning operation.

Conclusions

As a conclusion, based on this material, the average gain in survival using genetic thinning in seed orchards with freezing test and progeny test with the prevailing background pollination levels and the currently applied thinning procedures can be predicted to be roughly 1 and 3 %-units, respectively. If there are some contradicting selection goals, which are selected simultaneously, the achieved gains for survival can be lower or even non-existent.

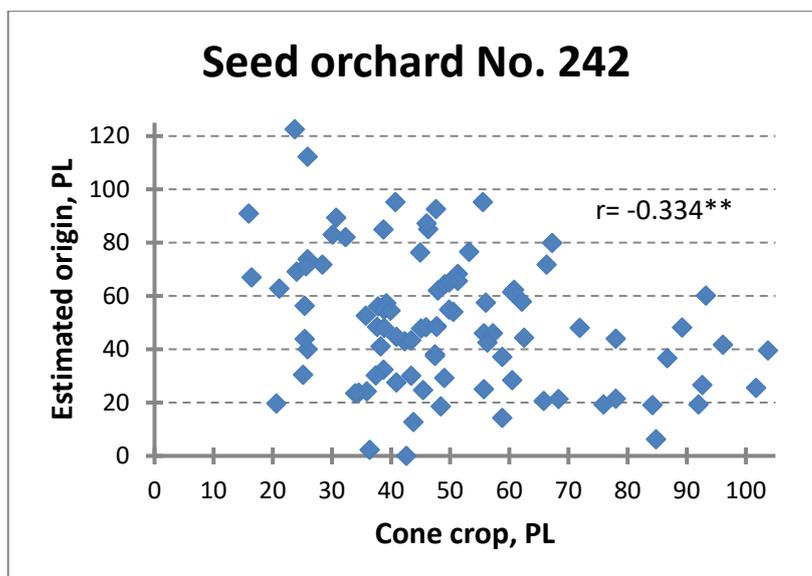


Figure D3. Correlation between the origin of plus trees estimated by freezing test and their cone crop. The estimated origin has been transformed to performance level values so that the lowest temperature sums get the highest PL values.

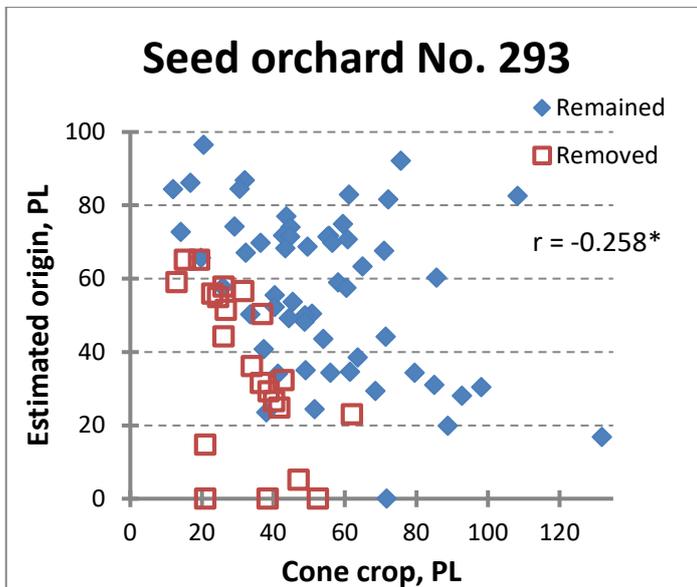
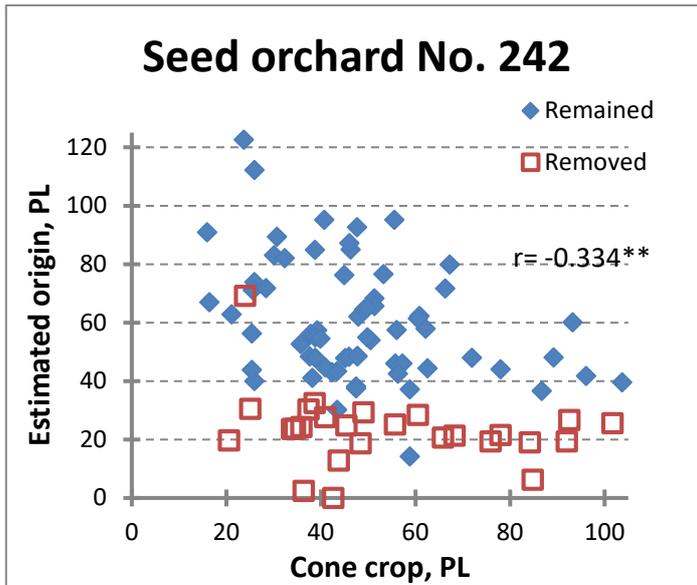


Figure D4. The clones which have remained and removed in genetic thinning of two seed orchards plotted against two major selection variables.

D2. THINNING SEED ORCHARDS BY HARDINESS – OBSERVATIONS ON THE SELECTION INTENSITY

By Seppo Ruotsalainen (2016-09-16)

Introduction & Material & Methods

To predict the effect of genetic thinning of a seed orchard using results from freeze testing, selection intensities (standardised selection differences) were estimated for a number of northern Finnish Scots pine seed orchards. This study is a follow-up to an earlier study in which the effect of genetic thinning by directly observing changes in survival (Appendix D1). The seed orchards studied are the same as in that earlier study. As for the material and the freezing test method, the earlier study is referred to. Some basic information of the seed orchards is also repeated in Table D2.

Selection intensities for freeze testing were calculated in a similar way as for tree height in an earlier treatise (Appendix C). The variable selected for was the estimated temperature sum of the seedlot origin.

Table D2. Information on the seed orchards, realised selection intensities and selection results. The numbers of clones and grafts refer to that part of the material in the seed orchards which was represented in the freezing tests, except for the upper part of the table which only includes the clones which are also found in progeny tests.

	Seed orchard No.					
	144, all	144, tested	241	242	293	297
Background information for seed orchard and material in progeny tests						
Target area	5, 6	5, 6	6 ¹⁾	6	6	6
Thinning year	2000	2000	1998	1999	1998	1999
No. of clones	42	42	78	92	80	97
Grafts represented by tests, %	45.4	45.4	79.3	82.9	73.6	84.0
Selection by freezing test						
No. of clones	92	42	96	105	107	115
No. of grafts	6633	3052	8048	3820	4500	5143
Realised i	0.473	0.403	0.576	0.549	0.389	0.459
Theoretical i	0.89	0.97	0.83	0.72	0.83	0.77
Realised i, %	53.2	41.6	69.4	76.3	46.8	59.6
Grafts selected, %	44.2	39.5	48.2	55.0	47.6	51.6
Estimated hardiness, before th., dd	864	867	958	959	955	890
Estimated hardiness, after th., dd	819	829	913	892	919	849
Change of breeding value in survival						
Change	-1.2	-1.2	2.2	3.6	1.0	1.8

1) One clone from target area 4 excluded.

Results and discussion

The average realised selection intensity for hardiness (expressed as the temperature sum of seedlot origin) established in freezing tests in these five seed orchards was 0.489, ranging from 0.389 to 0.576 (Table D2). This is only about 60% of the theoretical selection intensity (0.81), which would have been obtained, if selection had been based on freezing test only, and the same thinning percentage had been applied. This intensity is roughly of the same order than the one obtained for genetic thinning based on tree height (50%), applied in some southern seed orchards (Appendix C).

The reduction in the realised selection intensity is due to two factors. First, cone or seed production capacity of the clone was used as another selection criteria in genetic thinning. Secondly, thinning decisions were affected by the need to provide sufficient growing space for grafts.

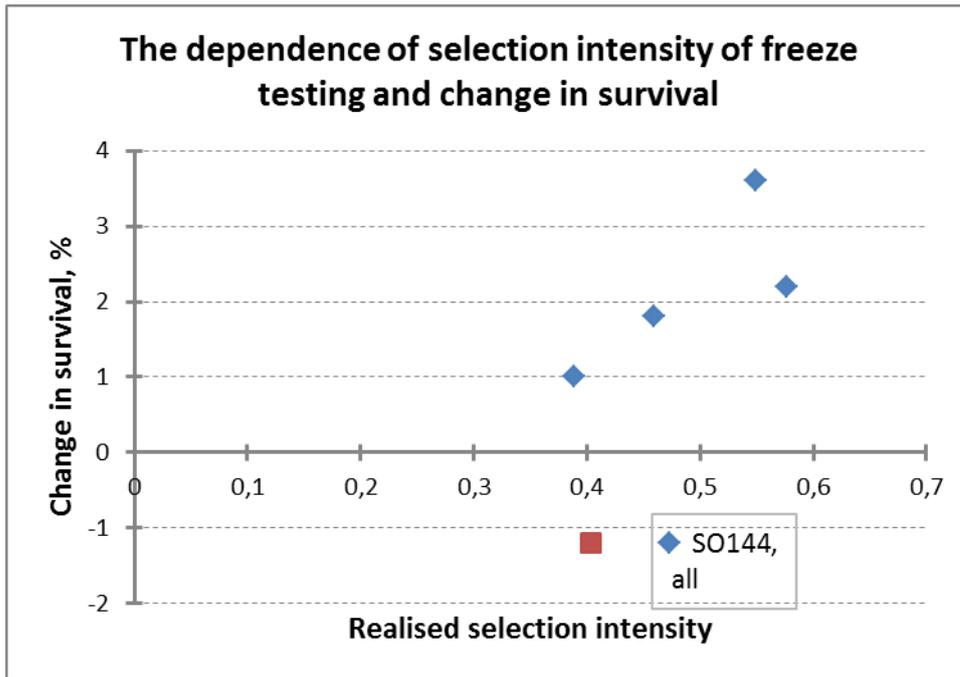


Figure D5. Relationship between the change in survival due to genetic thinning and realized selection intensity based on freeze testing. Results are presented for five seed orchards. For the seed orchard No. 144, selection intensity was calculated twice: for all clones (blue square) and only for progeny-tested clones (red square).

The selection intensity for estimated hardiness roughly correlates with the change in survival as a result of genetic thinning, with the exception of seed orchard No. 144 (Figure D5). In that single seed orchard thinning resulted in fact to a decrease in progeny survival in spite of modest selection intensity. Inclusion of only the clones in progeny tests resulted in slightly decreased realised selection intensity. As result, the relationship between selection intensity and the effect of genetic thinning slightly improved (Figure D5), but that change does not at all fully explain the negative selection effect in seed orchard No. 144. As discussed already earlier (Appendix D1), the obvious reason for this oddity is the great weight given for cone crop in the genetic thinning of this seed orchard, since a rather strong negative correlation was found between cone crop and survival (Figure D6).

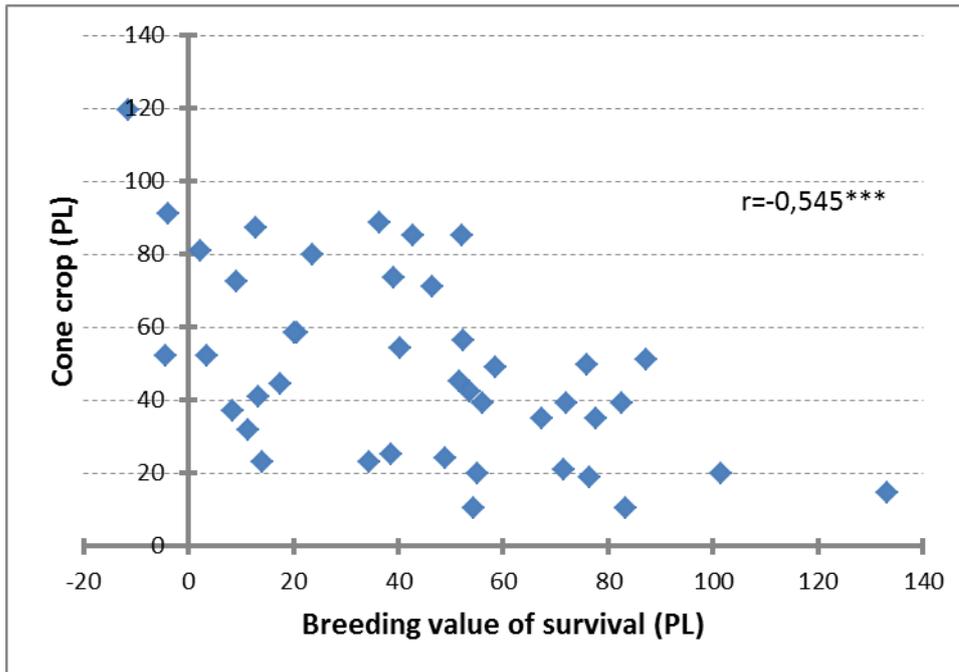


Figure D6. Correlation between cone crop and survival in field trials of clones in seed orchard No. 144. The values are expressed as standardised performance levels (mean 50, standard deviation 25).

Conclusions

As a conclusion, the average selection intensity when freezing test results are applied in genetic thinning of seed orchards, is approximately 0.5. However, the realised selection intensity does not very well predict the outcome of genetic thinning, if some other contradicting selection goals are simultaneously applied.

Appendix E. Linear deployment

We selected four 1.5g seed orchards where linear deployment has been performed. Three were in northern Sweden (TreOT3, TreOT6, TreOT10) and one in central Sweden (TreOT15). To conform with obtained performance given practical considerations (i.e. real life conditions) we parameterized the OPSEL system accordingly. The orchards were in the size of around 6000 grafts and as we do not allow one single clone to be more than 8% of the total amount of grafts we set the maximum number of ramets per clone to 500. On the other hand we wanted all selected clones to have some minimum frequency in the orchard and set the minimum value to 50. Furthermore, the target diversity of an orchard is a status number of around 20 and this often corresponds to selection of some 25-35 unique clones. We tested using 25, 30 and 35 clones but results were very similar so details are only given for the example with 30 clones. All results are taken from real life situations and the selection criteria was a compound index combining volume production (mostly) and quality. However, height and survival at age 30 was used for genetic gain calculations as they are the input values to the deployment recommendations.

Table E1. Results from OPSEL-runs for height at age 30 in the SO target area for four SO's.

	TreOT15	TreOT10	TreOT3	TreOT6
Maximum number of ramets per clone	500	500	500	500
Minimum number of ramets per clone	50	50	50	50
Total number of identities in pedigree	188 ^a	30	30	30
Number of unique selected individuals	41 ^a	30	30	30
Census number of selected group	6001	5998	6002	6001
Status number of selected group	20	20	20	20
Group coancestry of selected group	0.02	0.02	0.02	0.03
Proportional gene diversity of selected group	0.98	0.98	0.98	0.97
Average inbreeding of selected group	0.00	0.00	0.00	0.00
Average genetic value of selected group	129.49	127.53	118.89	108.67
Unweighted arithmetic mean (n=20, T15 n=41)	126.86	124.87	116.89	106.62
Adjusted average genetic value of selected group ^b	123.64	122.27	116.22	109.07
Adjusted unweighted arithmetic mean (n=20, T15 n=41) ^b	121.80	120.41	114.82	107.64
Additional gain from linear deployment	1.5%	1.5%	1.2%	1.3%

^aFor this seed orchard genetic material from advanced generations was used and induced a significant degree of relatedness among the selected clones. Therefore 41 individuals were selected instead of 30 (as there was no relatedness in the other orchard clones).

^bThe genetic value has been reduced by $r_{jm}=0.7$ as the trait under consideration was height at age 20.

For height the average gain level is slightly less than 1.4% with a small variation.

Survival was only used as a selection trait in the three northern SO's so only those were used for study.

Table E2. Results from OPSEL-runs for survival at age 30 in the SO target area for the three northern SO's.

	TreOT10	TreOT3	TreOT6
Maximum number of ramets per clone	500	500	500
Minimum number of ramets per clone	50	50	50
Total number of identities in pedigree	30	30	30
Number of unique selected individuals	30	30	30
Census number of selected group	5999	6001	6004
Status number of selected group	20	20	20
Group coancestry of selected group	0.02	0.03	0.02
Proportional gene diversity of selected group	0.98	0.97	0.98
Average inbreeding of selected group	0.00	0.00	0.00
Average genetic value of selected group	84.38	88.70	86.88
Unweighted arithmetic mean (n=20)	82.52	87.44	86.03
Adjusted average genetic value of selected group ^a	80.94	84.83	83.19
Adjusted unweighted arithmetic mean (n=20) ^a	79.27	83.70	82.42
Additional gain from linear deployment	1.7%	1.1%	0.8%

^aThe genetic value has been reduced by $r_{jm}=0.9$ as the trait under consideration was vitality at age 20.

For survival the average gain level is around 1.2% with a small variation.

Appendix F. Calculating the correction factor for the performance index

When estimating the correction factors for the calculation of the performance index, projection curves from a model which calculates the economic weight of survival relative to volume production was used (Berlin et al. 2009a). Using two sub-models (I & II), volume production is calculated as a function of survival (s) and patchiness (p_{rel}^2) based on a Scots pine stand growth model. In this case, the stand growth model was parameterized with a site class T24¹, rotation time of 100 years and an initial planting stand density of 2500 seedlings/hectare. This produced 3 projection curves for the patchiness coefficients (p_{rel}^2) 0.25, 0.5, 0.75, in addition to the analytically solvable curves for patchiness coefficients 0 and 1. Four cubic splines were fitted to each of the three projection curves. For each of the k splines, the function for the projection curves are:

$$V_{k,p_{rel}^2} = f(s)$$

To calculate the correction factors (c) the projection curve functions are divided with the linear function corresponding to patchiness coefficient 1 as:

$$c_{s,p_{rel}^2} = \frac{V_{k,p_{rel}^2}}{V_{p_{rel}^2=1}}$$

Results from field trials suggest a patchiness coefficient of approximately 0.25 (Berlin et al. 2009b) but in order not to reduce the relative importance of survival in the performance index too much, we have chosen a conservative calculation of the correction factor with a patchiness coefficient of 0.5. The different projection curves and spline function coefficients are described below.

¹ Site index is defined as the average height of the 100 stems per hectare with the largest diameter at age 100 years. T denotes Scots pine; thus, T24 indicates that the average height of 100-year-old Scots pine is 24 m

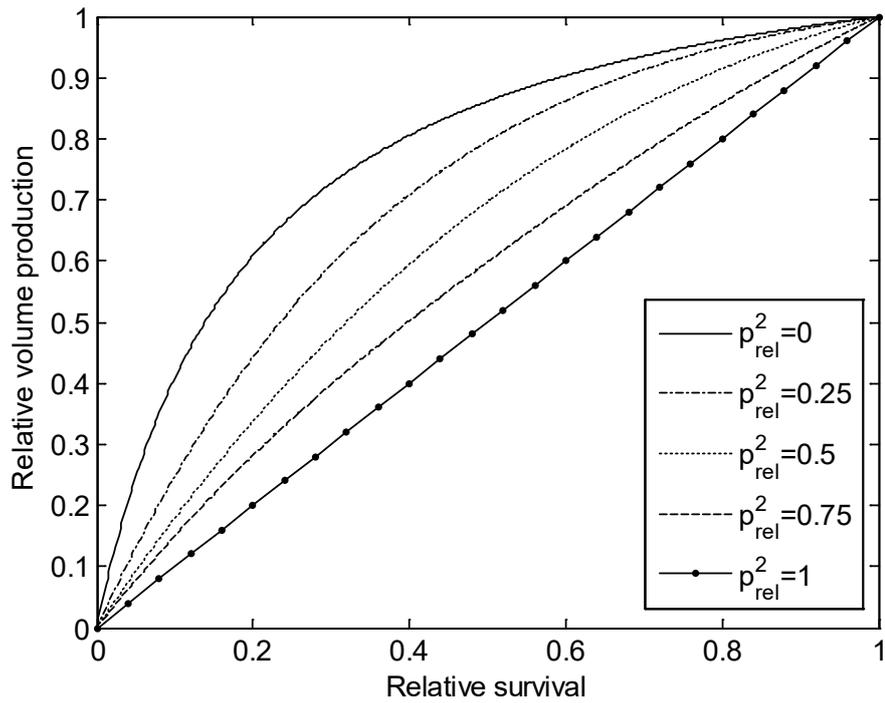


Figure F1.
Projection curves for different patchiness coefficients. From Berlin et al. (2009a).

The spline-functions for patchiness coefficient 0.5:

$$y = 0.2488x^3 - 1.1752x^2 + 1.9265, \quad 0 < x \leq 0.25$$

$$y = 0.2488x^3 - 0.9887x^2 + 1.3855x + 0.4121, \quad 0.25 < x \leq 0.5$$

$$y = 0.2488x^3 - 0.8021x^2 + 0.9378x + 0.7005, \quad 0.5 < x \leq 0.75$$

$$y = 0.2488x^3 - 0.6155x^2 + 0.5834x + 0.8887, \quad 0.75 < x \leq 1$$

Appendix G. Deployment zones in Finland

In order to provide the deployment recommendations with the functionality to impose the zoning rules used for the official Finnish maps/zones (Ruotsalainen et al. 2016), we have implemented a separate calculation structure with the sole purpose of producing zoning limits as close to the official maps as possible.

It is important to recognize that this separate calculation is not used for producing index values and ranking within the allowed zone. There, our commonly agreed modeling structure applies (albeit with different survival levels – “land factor”).

Changes in the transfer functions

In the Finnish zoning calculations, a few parameters and input data were different than in the deployment recommendations. Firstly, the establishment year was set to 2020 (1980 in the deployment recommendations) in the height function and then “current climate” was set to the climate in 2020 (in the deployment recommendations current climate is given as the average of the observed values 1961-2007). This was addressed by simply setting the establishment year to 2020 in the code and to update the database with an estimate of the climate 2020. These values were taken directly from the Luke-excel sheet where such values were given (in order to replicate the official maps).

Those inputs were then changed in the parallel calculations for local and transferred height, $H_{SO}^{(FIN)}$, survival, $S_{SO}^{(FIN)}$ and production index, $I_{SO}^{(FIN)}$.

Changes in standardized latitude and additional gains

In the deployment recommendations, pollen contamination varies with age after pollen production start and full production equals 40% contamination level. In addition, the origin of the background pollination level is assumed to be 0.5 latitude degrees south of the SO-location.

In the Finnish zoning calculations background pollination is set to a static value of 50% for all orchards (no difference depending on developmental phase). Furthermore, the external pollen origin is assumed to come from the SO-location (no southward adjustment).

In the deployment recommendations a number of additional genetic gains are added to the base SO gain level, such as selective harvesting, extra pollen from adjacent old SOs, genetic thinning and linear deployment. No such effects are included in the Finnish zoning calculations.

In the parallel calculations, background pollination level and pollen origin were adjusted and all extra genetic gains were omitted.

Another set of SO-categories

In the deployment recommendations, the SOs were categorized according to a common platform based on 1g, 1.25g, 1.5g (and whether selection was based on hardiness or not). In the Finnish zoning system 4 distinct categories were used. Furthermore, a dummy SO was developed to provide an additional restriction on SOs with clones of northern origin and a southern SO-location (to ensure that the allowed deployment zone does not extend too far north). In addition, a sixth category for the Swedish SO's that have been considered to have a too southern origin for safe use in Finland, was introduced.

In the table, provided by Luke, the 4 categories (group 1-4), the dummy SO (group 5) and the introduced group 6 (for s. Swedish SOs) are shown in the table G1.

Table G1. The five seed orchard categories (and the dummy) and their characteristics and threshold values used in the delineation of deployment zones in Finland.

Category	Type of SO/ model SO	Genetic gain, growth, %	Genetic gain, survival, %	Production index limit for the deployment area	Description	Other restrictions
1	1 st generation Sv124	12.5	0	110	The basic case	No
2	1 st generation, north Sv239	12.5	0	110	Latitude of origin >66.56°N; Latitude of seed orchard location <64°N	Northern limit is that of the dummy SO
3	1 st generation, north, new Sv409	10	5	110	Latitude of seed orchard location >64°N, clones selected for hardiness	Survival > 50%
4	1.5 generation Sv404	25	0	120	The basic case	No
5 ¹⁾	Dummy SO	12.5	0	110	Used for defining the northern limit of the deployment area for northern SOs (group 2)	
6	South Swedish SO	-	-	-	Considered too southern for use in Finland	Not used in Finland.

¹⁾Parameterized as a 1g SO with a clonal origin of LAT=66.56°N and SO location of LAT=62°N, with full pollen production.

Consequently, all SOs must be assigned a group value according to the table above. This has been implemented in the deployment recommendations database and orchards must be categorized with care.

First note that the basic gain levels differ from the deployment recommendations and for zoning purposes in Finland the SO-performances are calculated with those values depending of the grouping value. Furthermore, in the Finnish zoning calculations, the effects of pollen contamination have only been used to calculate the standardized latitude. For the additional genetic gain levels given in the grouping table there is no reduction of those values due to pollen contamination.

Thus, using the index $I_{pl}^{(FIN)}(SOx)$ and survival $S_{pl}^{(FIN)}(SOx)$ values from the parallel calculations for each seed orchard category (SOx) the restrictions on deployment zones are given as:

Category 1:

If $I_{SO}^{(FIN)}(SO_1) < 110$ No index value
 Else Index value calculated

Category 2:

If ($I_{SO}^{(FIN)}(SO_2) > 110$ & $I_{SO}^{(FIN)}(SO_{DUMMY}) > 110$) Index value calculated
 Else No index value

Category 3:

If ($I_{SO}^{(FIN)}(SO_3) > 110$ & $S_{SO}^{(FIN)}(SO_3) > 50$) Index value calculated
 Else No index value

Category 4:

If $I_{SO}^{(FIN)}(SO_4) < 120$ No index value
 Else Index value calculated

(The “Category 2” threshold is actually a bit more complicated as the “dummy” orchard should only delimit/cut the allowed zone to the north).

The above values should also be applied for Swedish seed orchards in Finland. The 1.25 generation seed orchards do not appear in the table, because there are no examples of such orchards in Finland. However, the Finnish SOs in category 3 are classified as 1.25gS in the deployment recommendations and all Swedish 1.25gS SOs are assigned to category 3. The Swedish 1.25g SOs are considered to belong to category 1.

All the previously mentioned steps, together with the system of thresholds given above should provide individual SO-deployment zones that should be in accordance with the official maps in terms of geographic extension. Within these allowed zones, all index values and SO ranking are calculated according to the “ordinary” system/model structure.

Thus, $H_{SO}^{(FIN)}$, $S_{SO}^{(FIN)}$ and $I_{SO}^{(FIN)}$ are only used to produce the valid deployment zones. Within those valid zones, H'_{SO} , S'_{SO} and I_{SO} are used to calculate performance of height, survival, production index and all ranking.

Removal of Swedish orchards adapted to southern Sweden in Finland

The current system entails a grouping category “6” that simply deletes seed orchard with that category in Finland (no effect on deployment/performance in Sweden). Currently, only Swedish SO’s with southern origin aiming for seed zones in southern Sweden have been set to category “6”.

Map color scale and index values

Index values (i.e. index values calculated according to the deployment recommendations) can be lower than 100 in Finland due to pollen contamination. The main effect seems to be that the standardized latitude can differ quite a lot when pollen contamination rates are high (and there is a large difference between clonal origin and SO-location). However, this will be a transient effect and index values will raise quickly as pollen contamination levels go down.

Nevertheless, we have therefore allowed index values below 100 in Finland (not in Sweden) so that deployment areas are not affected and still follow the official maps. This meant that the color scale for the maps needed to be slightly adjusted to allow for a difference in color nuance also below 100 (earlier values were cut below 100).

Appendix H. Deployment zones for seed orchards with long southward transfer in Sweden

In the Finnish deployment zones a number of seed orchards (from both countries) where the clonal origin is substantially more northern than the orchard location have been assigned a specific category (2) that limits their use in Finland, especially in harsh/northern areas. This delimitation is done from concerns about the hardiness performance due to the long southward transfer of northern clones and the effect of southern contaminating pollen. Originally, no such limitation was applied in Sweden but there are theoretical and practical reasons why similar delimitations should be enforced also in Sweden. Those reasons include origin of contaminating pollen and population assumptions which are reviewed below.

Origin of pollen contamination

For the default seed orchards, contaminating pollen is assumed to originate 0.5 latitude degrees south of the seed orchard location. The reasons being: (i) pines transferred from the south start to flower earlier in the spring than local pines and; (ii) the predominating wind direction is from the south. However, the southward transfer of clones in the default orchards is smaller than the category 2 orchards and it is therefore reasonable to assume that the contaminating pollen for the category 2 seed orchards is even further from the south due to phenological characteristics in flowering. Another hypothesis could be that strongly transferred orchards could be “isolated” from pollen contamination due to their strong off-set in flowering compared to the surrounding natural forests. However, there is a strong body of evidence that viable Scots pine pollen can spread over very long distances (e.g. Franzén et al. 1994; Lindgren et al. 1995) and therefore, the category 2 orchards are not considered isolated but affected by pollen contamination to the same degree as the default orchards. We have decided to assign the contaminating pollen one and a half latitudinal degree south of the seed orchard location (LAT_{SOL}). Thus, $LAT_{vPC} = LAT_{SOL} - 1.5$.

Population assumptions

For the default orchards the latitudinal (standardized) origin of the seed orchard crop is calculated as:

$$\begin{aligned}
 LAT_{sto} &= \underbrace{0.5 \cdot LAT_{clone}}_{\text{Mother contribution}} + 0.5 \cdot \underbrace{\left(\frac{\text{Seed orchard clones}}{LAT_{clone} \cdot (1 - i_{PC})} + \frac{\text{Wild pollen}}{LAT_{PC} \cdot i_{PC}} \right)}_{\text{Father contribution}} \\
 &= LAT_{clone} \cdot (1 - 0.5 \cdot i_{PC}) + 0.5 \cdot LAT_{PC} \cdot i_{PC}
 \end{aligned}$$

Where the father contribution is divided into the internal pollination from the seed orchard clones and the external wild pollen. Theoretically, the seed orchard crop consists of two separate populations with different standardized latitudes. One population exclusively consists of the seed orchard clones and the other population of the hybrids between seed orchard clones (mothers) and the external wind pollen (fathers). The assumption for the default orchards (and the formula above) is that the difference in standardized latitude between the two populations is small enough for them to be approximated with one common population (see figure H1).

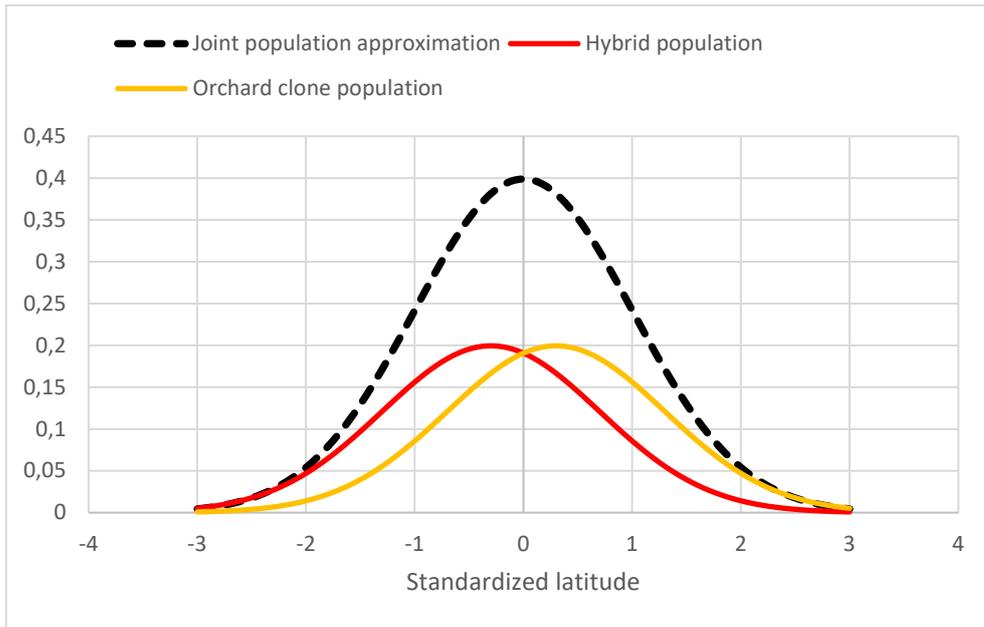


Figure H1. Illustration of the joint population approximation for the default seed orchards.

However, for the category 2 orchards, we consider this assumption not valid as the difference in standardized latitude between the seed orchard clone population and the hybrid population is so large that the two populations cannot be approximated with one joint population (figure H2).

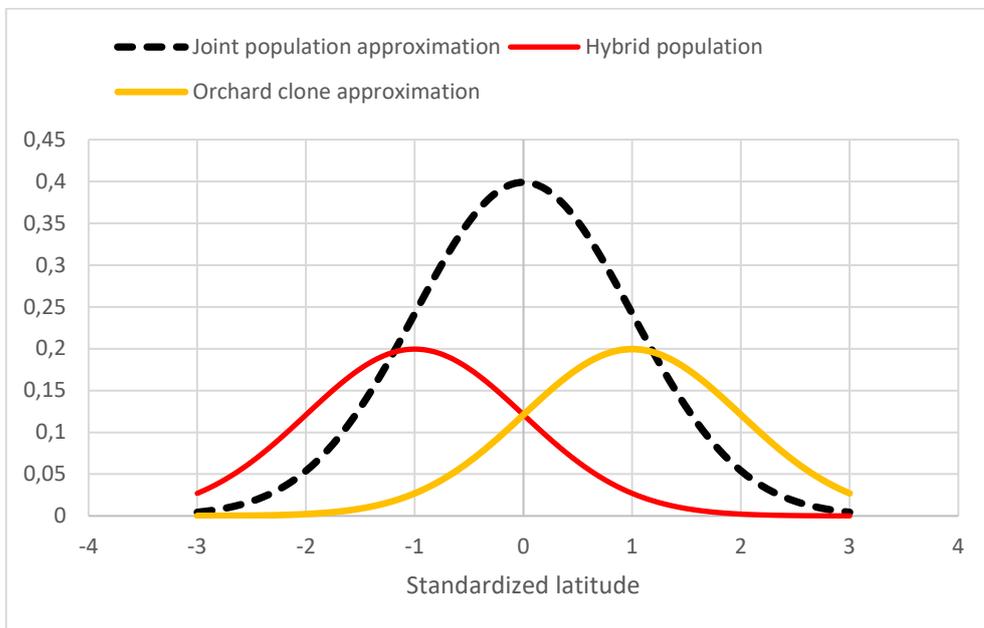


Figure H2. Illustration of the difference between the orchard clone and hybrid populations in the category 2 orchards.

Calculation of growth, survival and standardized latitude

Thus, for the category 2 orchards the standardized latitude for the seed orchard crop is considered to originate from two distinct populations where the standardized latitude is

$$LAT_{sto}^{SOclone} = LAT_{clone}$$

for the orchard clone population, and

$$LAT_{sto}^{Hybrid} = 0.5 \cdot LAT_{clone} + 0.5 \cdot LAT_{PC}$$

for the hybrid population.

Survival and growth are then calculated separately for each population. For the orchard clone population

$$S'_{SO}^{(SOclone)} = S_{SO}(LAT_{sto}^{SOclone}) + \Delta S(i_{PC} = 0) \cdot S_{SO}^{adj}(LAT_{sto}^{SOclone})$$

$$H'_{SO}^{(SOclone)} = H_{SO}(LAT_{sto}^{SOclone}) \cdot \Delta H(i_{PC} = 0)$$

And for the hybrid population

$$H'_{SO}^{(Hybrid)} = H_{SO}(LAT_{sto}^{Hybrid}) \cdot \Delta H(i_{PC} = 1)$$

$$S'_{PC}^{(Hybrid)} = S_{PC}(LAT_{sto}^{Hybrid}) + \Delta S(i_{PC} = 1) \cdot S_{SO}^{adj}(LAT_{sto}^{Hybrid})$$

For the total seed orchard crop survival and growth (height) are calculated as the sum of each population weighted by their proportion as:

$$S'_{SO} = (1 - i_{PC}) \cdot S'_{PC}^{(SOclone)} + i_{PC} \cdot S'_{SO}^{(Hybrid)}$$

$$H'_{SO} = (1 - i_{PC}) \cdot H'_{SO}^{(SOclone)} + i_{PC} \cdot H'_{PC}^{(Hybrid)}$$

In practice, the separate population method will result in a less hardy performance of the seed orchard crop than the joint population approximation, for the category 2 orchards in most situations (except in situations with very low survival, which is probably not feasible for planting anyway).

The standardized latitude of the seed orchard crop is not used for calculations but needs to be estimated as it is a key characteristic. To calculate the standardized latitude, we have used the fact that seed orchard survival is a function of latitudinal transfer as:

$$S'_{SO} = f(\Delta LAT_{SO}) = f(LAT_{site} - LAT_{sto})$$

Since we have the survival and latitude of the planting site (LAT_{site}), a standardized latitude (LAT_{sto}) can be obtained by interpolation of the survival function.

