The Swedish Scots Pine Seed Orchard Västerhus A study of linear deployment

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Abstract

The Scots pine seed orchard Västerhus is a seed orchard in the 2nd round of orchards in Sweden, but since the clones were selected after progeny testing, it is genetically comparable to the 3rd round of seed orchards. It contains 28 clones which were selected from clones used in six plus tree seed orchards and used in different numbers. The clonal selections and deployed clonal proportions were worked out by Dag Lindgren and Bengt Andersson in an attempt to apply advanced designs in an operational orchard. The gain should then be increased while constrains would be kept on the genetic variation, a strategy later named linear deployment. In this deployment, the strategy was that the clones with the highest breeding values should be represented in higher numbers. In addition, flowering capacity was considered to predict gene contribution from each clone for the clonal deployment. The seed orchard was established 1991. In the summer 2007 16.1% of the grafts were dead and for 0.9% of the grafts, the root stock had replaced the grafted clone. The gain in breeding value by the linear deployment was initially estimated to 5.7-6.2% as compared to a comparable hypothetical seed orchard with equal clonal representation. The estimated gain by linear deployment at establishment did not change much due to loss of grafts. It is assumed that in this young seed orchard pollen contamination from the surrounding stands may have a larger and reducing effect on the genetic gain than loss of grafts and thus changed clone proportions.

Introduction

In the beginning of the Swedish forest tree breeding much progeny-testing was done by controlled crosses in seed orchards, and therefore the clones in the different seed orchards were tested in different sets. Utilizing selections from such progeny-tested clones makes Västerhus to the most advanced seed orchard of this age in Sweden. The areas where Västerhus according to Planter's guide (Hannerz and Ericsson 2007) seem to be among the best available seed sources, and more than around 12% better than optimally transferred stand seeds, are given in Table 1.

For Västerhus, six sets of clones corresponding to six seed orchards constituted the start material. The seed orchards and clone numbers are given in Table 2.

Table 1. Suitable areas for Västerhus seed orchard crop

 Table 2. Seed orchards from which the clones were
 selected

Latitude (°N)	Altitude (m.a.s.l.)	Seed orchard no.	Seed orchard	Tested clones	Available clones	Selected clones
61	300-800	412	Domsjöänget	52	42	7
62	50-500	410	Robertsfors	12	10	2
63	0-300	18	Brån	34	27	4
64	0-100	403	Nedansjö	40	32	5
		411	Domsjöänget	50	40	7
		426	Holm	20	16	3
			Total	208	167	28

Clonal deployment

An additional genetic strength and novelty at the time of establishment of the seed orchard is that the number of grafts of the different clones was deployed on the basis of the genetic capacity of the clones, i.e. their breeding values. Then, the genetically best clones were used in higher proportions. The clonal selections and deployed clonal proportions were worked out by Dag Lindgren and Bengt Andersson in an attempt to apply advanced techniques in an operational orchard, to increase gain while keeping constrains on genetic variation. This technique was suggested by Lindgren & Matheson (1986), and was later named linear deployment. In addition to the breeding value has the flowering capacity been considered, and adjustments has also been made to reduce the risk for inbreeding. Although established in the 2^{nd} round of seed orchards, having clones selected after progeny testing and furthermore deployed with the genetically best clones in higher proportions, Västerhus should be genetically better than the other 2^{nd} round seed orchards, actually one of the most advanced seed orchard of this age in Sweden.

When determining the clonal proportions, it was assumed that the average breeding value in the six clone sets (one set per seed orchard) was equal. To reach this, the assigned breeding value for each clone was the expected value from a normal distribution for the rank of the clone within its set. In a set with many clones, the top ranked clone thus get a higher assigned breeding value than the top ranked from a set with few clones. The aim of this study is to analyze whether the genetic improvement that was obtained by the linear deployment remains after 16 years, or if losses of grafts had reduced the advantage. Another aim is to make a documentation of the status of a seed orchard under development. This is the initial stage of a project which molecular tools will study the pollination pattern and contamination in the seed orchard.

Material and methods

The study was performed in the seed orchard Västerhus (Tab. 3). During June and August 2007, survival in the seed orchard was registered. Occurrence of cases where the root stock had replaced the graft was also registered. Three data sets of number of clones and clone frequencies were obtained: *i*) the intended number and frequencies of grafts per clone when designing the seed orchard, *ii*) the actual number and frequencies at planting, and *iii*) the number and frequencies in August 2007. The second data set differ from the first due to non-successful grafting, availability of scions etc, and the third from the second due to death of grafts or root stocks replacing the graft. By comparing the clonal proportions and assigned breeding values, the change in breeding value of the seed orchard can be estimated.

Results

Table 4 shows for each clone the number and proportion of planted grafts, dead grafts and root stocks replacing the grafts. It also shows the proportion of grafts for a hypothetical seed orchard without linear deployment. This comparison is made at the approximate same effective population size, and this implies 20 clones in the traditional orchard. In the linear deployment orchard, 17.0% of the grafts were lost between planting 1991 and August 2007. Either the graft had died (16.1%) or the root stock had replaced the graft (0.9%). Breeding values in Table 5 are expressed as deviation from average of all 167 clones mentioned in Table 2 in units of the standard deviation of the breeding value among the clones available for selection (thus as a fraction of the root of the additive variance). Table 5 shows also the breeding value for the hypothetical seed orchard at the same effective population size. The contribution of the different clones in terms of their breeding values is illustrated in Fig. 1. In spite of the losses, the relative breeding value remains similar (1,600 and 1,657, respectively). The results indicate that that the loss of grafts has negligible influence on the genetic quality of the seed orchard.

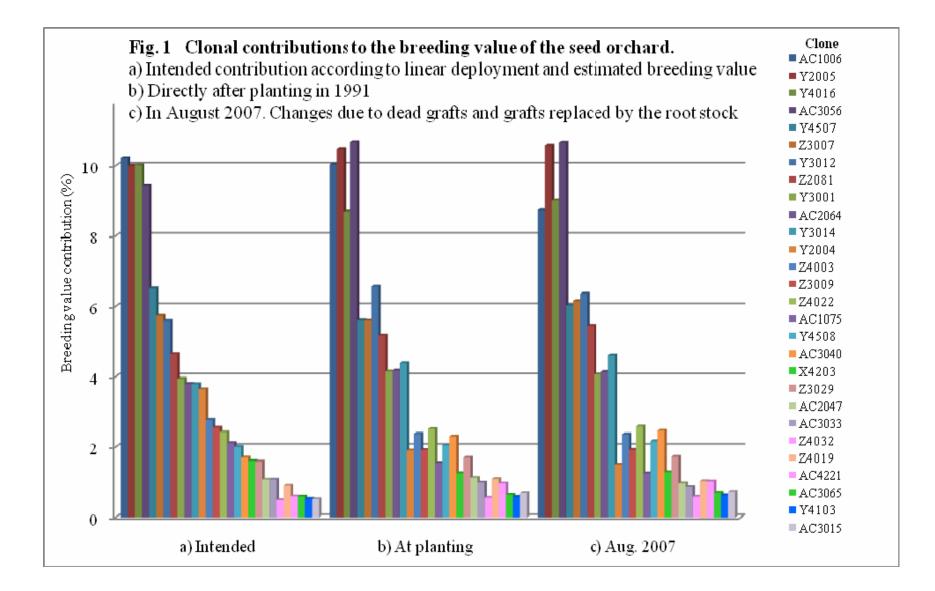
Table 3. Facts about Västerhus

ID no: S23FP100T10, T10A							
Location: 15 km NV from Örnsköldsvik, lat. 63°18'N, long.							
18°32'E, alt. 5-25 m.a.s.l.							
Establishment year: 1991							
Number of clones: 28							
Number of planted grafts: 4594 (plus 44 grafts of an							
unidentified clonal mixture).							
Included clones: From six seed orchards in north central							
Sweden (Tab. 2). The clones were							
deployed mainly according to linear							
deployment, i.e. the clones with highest							
ranking in highest number.							
Design: Spacing is 7 m between columns and 2.5 m between							
rows. Many plots are only partly filled with grafts.							

In the comparison between the linear deployment in Västerhus and the assumed traditional design in a hypothetical seed orchard that undergoes the same development (mortality etc.), the linear deployment shows its advantage. The breeding value of the linear deployment seed orchard is 5.7% higher than an assumed traditional seed orchard, when comparing breeding values after adjustment for graft mortality and at the same effective population size (Ne=19.7) (Tab. 5).

Clone	Assigned breeding value based on ranking (std dev)	Planted grafts (no.)	Dead grafts (no.)	Root stock replacing the graft (no.)		Clonal proportions (%)			Clonal proportion in an balanced seed orchard seed	
						Intention	At planting	August 2007	20 clones	After adjust- ments (see text)
AC1006	2,180	352	82	16	254	7,8	7,66	6,66	5.00	4,27
Y2005	2,161	370	60	0	310	7,7	8,05	8,13	5.00	5,28
Y4016	2,070	321	43	2	276	8,1	6,99	7,24	5.00	4,49
AC3056	1,998	408	69	1	338	7,9	8,88	8,87	5.00	5,64
Y4507	1,776	241	26	0	215	6,1	5,25	5,64	5.00	4,62
Z3007	1,766	242	19	2	221	5,4	5,27	5,80	5.00	5,36
Y3012	1,753	286	56	0	230	5,3	6,23	6,04	5.00	5,69
Z2081	1,647	240	28	2	210	4,7	5,22	5,51	5.00	5,86
Y3001	1,563	203	38	0	165	4,2	4,42	4,33	5.00	5,15
AC2064	1,542	207	36	1	170	4,1	4,51	4,46	5.00	5,43
Y3014	1,539	218	27	1	190	4,1	4,75	4,99	5.00	6,07
Y2004	1,517	96	32	1	63	4,0	2,09	1,65	5.00	2,06
Z4003	1,400	130	22	1	107	3,3	2,83	2,81	5.00	4,25
Z3009	1,370	107	16	2	89	3,1	2,33	2,34	5.00	3,76
Z4022	1,344	143	21	0	122	3,0	3,11	3,20	5.00	5,33
AC1075	1,306	91	27	3	61	2,7	1,98	1,60	5.00	2,96
Y4508	1,285	122	13	2	107	2,6	2,66	2,81	5.00	5,39
AC3040	1,232	143	16	0	127	2,3	3,11	3,33	5.00	7,24
X4203	1,217	79	12	0	67	2,2	1,72	1,76	5.00	3,99
Z3029	1,203	108	15	2	91	2,2	2,35	2,39	5.00	5,42
AC2047	1,115	77	22	0	55	1,6	1,68	1,44	0	0
AC3033	1,114	68	17	2	49	1,6	1,48	1,29	0	0
Z4032	1,083	40	5	0	35	0,8	0,87	0,92	0	0
Z4019	1,067	78	14	3	61	1,4	1,70	1,60	0	0
AC4221	1,009	73	8	1	64	1,0	1,59	1,68	0	0
AC3065	1,001	50	4	1	45	1,0	1,09	1,18	0	0
Y4103	0,990	46	5	0	41	0,9	1,00	1,08	0	0
AC3015	0,977	55	7	0	48	0,9	1,20	1,26	0	0

Table 4. Numbers and proportions of the clones, intended according to linear deployment, at planting, in August 2007 and for an assumed seed orchard with equal number of clones per graft. Assigned breeding values based on the normal distribution (see text).



Discussion

Breeding value of the seed orchard

Although clonal differences in mortality and in root stock dominance (8-33% and 0-4.5%, respectively) (Tab. 4), there is no decrease in genetic quality in the seed orchard (Tab. 5) and graft mortality seems thus not correlated with the breeding value of the clone. Linear deployment seems in addition to be a satisfactory efficient approximation for optimal deployment when considering occurrences of selfings (Prescher at al. 2006), and when thinning a balanced seed orchard linear deployment can optimize both production and genetic diversity (Prescher et al. 2007). The advantage with designing the seed orchard with linear deployment is therefore worthwhile.

 Table 5. Clonal frequencies, breeding values and effective population sizes for the five seed orchard alternatives.

		seed orchar r deploymer	Traditional seed orchard with truncation selection		
	Intended according to linear deployment	At planting	In August 2007	20 clones in equal pro- portions (%)	Adjusted due to mortality (%) ¹⁾
Clonal fre- quency (%)	0.8-8.1	0.9-8.9	0.9-8.9	5.0	2.1-7.2%
Breeding value (in standard deviations) ²⁾	1.665 (106.2%)	1.600 (105.9%)	1.657 (105.7%)	1.593 (101.6%)	1.568 (100%)
Effective population size (Ne)	19.93	19.75	19.68	20	19.7

¹⁾ Adjustments of clonal proportions were made on the basis of registered graft mortality and root stocks replacing the graft in Västerhus, i.e. in August 2007.

²⁾ Breeding values are standardized so the average of the 167 available clones (Table 2) is set to 0 and their standard deviation for breeding value to 1.

Contaminating pollen

The quite large loss of grafts from plus tree progenies (17%) may currently be a larger threat to the genetic quality of the orchard than changed clonal proportions, due to a larger influence from contaminating pollen from adjacent stands with unselected native Scots pines in combination with Västerhus being a rather young seed orchard. Pollen counts in 2006 show however higher pollen production per graft in Västerhus than in other developing seed orchards of the same age (Wennström, pers. communication). The pollen production in Västerhus 2006 has been estimated to the magnitude of 20 kg pollen per hectare, which traditionally is considered as sufficient to reduce pollen contamination. Contamination problems may thus be less serious in Västerhus. That almost one percent of the grafts are root-stocks reduces the gain from the seed orchard, in particular if seeds are harvested from these trees. That root-stocks may play a role in the genetic composition of seed orchard seeds is an argument to use root-stocks of a genetic material adapted to similar climate as the seed orchard clones.

Contamination rates have been studied with isozyme techniques on Scots pine seed orchards. In the studies, they varied between years and between clones, but high values were found: 53-58% (Lindgren 1994), 17-39% with differences between years (Harju & Muona 1994), and nearly 70% (Yazdani & Lindgren 1991). Undetected contamination caused by the occurrence of the same isozyme pattern in the contaminating pollen as in the seed orchard pollen is then included. Those figures become thus somewhat unsafe. New molecular techniques will however be used to study contamination in Västerhus. Then clonal differences in contamination rate and spatial differences in contamination within the seed orchard can be analyzed. The technique can in addition more effectively separate contaminating pollen from seed orchard pollen.

Conclusions from the present study of Västerhus

- Grafts which die and root stock which replace the grafts seem to cause rather small problems for the genetic quality of the seed orchard.
- Linear deployment increases the breeding value by approximately 5-6% compared to a traditional design with equal number of grafts from each clone at the same effective population size.

Acknowledgements

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References

Harju, A. & Muona, O. 1994. Background pollination in *Pinus sylvestris* seed orchards. Scand. J. For. Res. 4, 513-519.

Hannerz, M. & Ericsson, T. 2008. Planter's guide - a decision support system for the choice of reforestation material. In Lindgren, D. (editor). Proceedings of a Seed Orchard Conference, Umeå, 26-28 September 2007. In press.

Lindgren, D. 1994. Effect of tree cover on Scots pine pollination and seeds. Forest Genetics, 1, 73-80.

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

Prescher, F., Lindgren, D. & El-Kassaby, Y.A. 2006. Is linear deployment of clones optimal under different clonal outcrossing contributions? Tree Genetics & Genomes, 2, 25-29.

Prescher, F., Lindgren, D. & Karlsson, B. 2007. Genetic thinning of clonal seed orchards using linear deployment may improve both gain and diversity. For. Ecol. Managem. In print.

Yazdani, R. & Lindgren, D. 1991. Variation of pollen contamination in a Scots pine seed orchard. Silvae Genet. 40, 243-246.