

Estimation of Genetic Parameters for Resin Flow in Clonal Seed Orchards of Norway Spruce [*Picea abies* (L.) KARST.] in South Sweden

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1. Abstract

Observations of abnormal resin flow in Norway spruce [*Picea abies* (L.) KARST.] have been reported in Sweden. Assessments in 3 grafted clonal seed orchards containing clones of different provenances were carried out. Besides resin flow score, diameter of grafts was measured, and abnormal loss of needles was scored. Variation between provenances and genotypic variation between clones were estimated. Broad sense heritabilities for clones within provenances ranged between 0.18 and 0.39, which is considered high. Slightly significant differences in resin flow between provenances were found only in one seed orchard. There were no strong genotypic correlation estimates between resin flow and loss of needles.

Key words: provenance, clone, genotypic correlation, heritability.

FDC: 165.3; 165.5; 811.24; 232.11, 232.12; 165.441; 174.7 *Picea abies*; (485).

2. Introduction

Recently, observations of abnormal resin flow in Norway spruce have been reported from southern Sweden by ANDERSSON (cited in BARKLUND et al., 1995) and by BARKLUND et al. (1995). The first observations were made in the province of Halland, but SAMUELSSON (cited in BARKLUND et al., 1995) reports observations from both south and central Sweden. During 1994, the frequency of observations of resin flow increased (ANDERSSON, cited in BARKLUND et al., 1995), and the same symptoms have also been reported from Denmark (GUNDERSEN et al., 1995).

The symptoms are described by BARKLUND et al. (1995) as abnormal resin flow from spots with dead inner bark. In later stages, cracks may occur with continuous resin flow.

In 1994, a provenance trial with 37 different provenances of Norway spruce was analysed for resin flow by CLUER and PETERSSON (cited in BARKLUND et al., 1995). Differences were found between provenances. Investigations focusing on a more detailed genetic level have not been carried out.

Due to a large number of replications, which lack genetic variation (clones) and often even sites, clonal seed orchards are suitable for studies of genotypic variation. Both this and the lack of genetic field trials that are old enough to have developed the symptom of resin flow, made seed orchards suitable objects for this study.

This study was carried out in three clonal seed orchards of Norway spruce in south Sweden. They include plus tree clones from more than one provenance and are thus suitable objects to study between and within provenance variation of resin flow.

The aim of this study is to estimate genetic parameters for resin flow and the distribution of variation within and between provenances.

3. Material and Methods

Three clonal seed orchards, no. 31 Högseröd, no. 68 Slogstorp and no. 96 Skogsgård with observations of resin flow were selected for further studies. Data on the seed orchards are shown in *table 1*. The seed orchards are planted with grafts of the clones in a randomised block design. For this study, an area large enough to contain 15 replications/clone was selected in each seed orchard. Each selected area was divided into 8 to 9 blocks before analysis.

All 3 seed orchards contain clones from different provenances, although none of the seed orchards have clones in common. The distribution of clones within the different orchards is shown in *tables 2 to 4*.

Table 2. – Clones in seed orchard no. 31.

No. of clones (in this test)	Origin	Mean position (lat, long, altitude (m))
21 (21)	Province of Dalarna, Sweden	60°55' 14°22' 410
9 (8)	Province of Värmland, Sweden	60°51' 12°35' 372

Table 3. – Clones in seed orchard no. 68.

No. of clones	Origin	Mean position (lat, long, altitude (m))
30	South Sweden	57°13' 14°19' 213
5	Second generation west continental	56°27' 13°20' 78
10	Poland	51°45' 21°47' 347

Table 4. – Clones in seed orchard no. 96.

No. of clones (in this test)	Origin	Mean position (lat, long, altitude (m))
21 (20)	South Sweden	56°53' 14°09' 147
6 (6)	Second generation continental	56°56' 12°47' 170
16 (16)	Poland	49°49' 19°18' 579

In August-September 1995 assessments of the trees in the selected plots were carried out. The characters recorded are presented in *table 5*. RF1 (number of resin flows shorter than 20 cm), RF2 (number of resin flows 21 cm to 50 cm long), RF3 (number of resin flows longer than 50 cm) and TF (total number of resin flows/stem) were transformed to normal score values (ERICSSON, 1994) before analysis due to low frequencies for all sites. NL (needle loss), which is a scored character, was also transformed to normal scores.

Table 1. – Description of the seed orchards.

No. of clones (in this test)	Origin	Mean position (lat, long, altitude (m))
21 (21)	Province of Dalarna, Sweden	60°55' 14°22' 410
9 (8)	Province of Värmland, Sweden	60°51' 12°35' 372

Table 5. – Characters recorded and calculated in the orchards.

Name	Code	Unit	Description
Diameter	DIA	(mm)	Stem diameter measured at breast height.
Resin flow 1	RF1		Number of resin flows shorter than 20 cm on the surface of the first 4 meters of the trunk.
Resin flow 2	RF2		As RF1 but for resin flow 21-50 cm long.
Resin flow 3	RF3		As RF1 but for resin flow longer than 50 cm.
Total resin flows/stem	TF		RF1+RF2+RF3
Flows/area	TFM2	flows/m ²	TF/surface area of the observed part of the trunk.
Needle loss	NL	0-4	Abnormal loss of needles in the canopy where: 0 = No abnormal loss 1 = Some loss on the inner part of branches 2 = as 1 and some loss on the outer part of branches 3 = Remaining needles only on the outer parts of branches 4 = Extremely abnormal loss of needles

Analyses of variance and estimation of statistic and genotypic parameters were carried out with software by HARVEY (1990) using Mixed Model Equations (HENDERSON, 1975).

The model used for the statistical analysis was:

$$Y_{ijkl} = \mu + B_i + P_j + c_{jk} + e_{ijkl} \quad (1)$$

Where:

Y_{ijkl} = Value of the ijkl:th observation

μ = mean value of the population

B_i = fixed effect of block i

P_j = fixed effect of provenance j

c_{jk} = random effect of clone k in provenance j (N, σ_c^2)

e_{ijkl} = random error term (N, σ_e^2)

Genetic parameters were interpreted as:

$$\sigma_G^2 = \sigma_c^2$$

$$\sigma_E^2 = \sigma_e^2$$

where:

σ_G^2 = the genotypic variance

σ_E^2 = the environmental variance

The broad sense heritability (H^2) was calculated as the ratio between σ_G^2 and $\sigma_G^2 + \sigma_E^2$ (FALCONER, 1960).

Genetic correlation estimates and best linear unbiased predictors for clones (BLUP-values) were calculated with software by HARVEY (1990). BLUP values analysed with normal score were converted into percent (probability) breeding values using frequencies for each character in each seed orchard as reference value. For RF1, RF2, RF3 and TF the frequency of stems without resin flow was used and for loss of needles the frequency of grafts with score 0 and 1 was used as reference value.

4. Results

Experimental mean values, reference frequencies for the normal score conversion and probabilities from the statistical analysis are presented in tables 6 to 8 for the 3 seed orchards, respectively. Seed orchard no. 96 showed the highest occurrence with a mean value for total resin flow of 2.00. In seed orchard no. 31, all but 44% of all trees had resin flow and in nos. 68 and 96, all but 81% and 47% of the stems, respectively, had resin flow.

Table 6. – Mean values and results from the analysis of variance for seed orchard no. 31. For RF1, RF2, RF3 and TF "Freq." = frequency of stems without resin flow, and for NL "Freq." = frequency of grafts with light damage (score 0 to 1). Clone:prov = Clone within provenance.

Source of variation (df)	DIA	RF1	RF2	RF3	TF	TFM2	NL
Mean value	220	1.37	0.37	0.27	2.00	0.72	1.89
Freq. (%)		53.0	81.0	85.0	44.0		20.0
Provenance (1) Prob <	0.7157	0.3721	0.3562	0.4943	0.4524	0.6341	0.6743
Clone:prov (27) Prob <	0.0000	0.0000	0.0266	0.0000	0.0000	0.0000	0.0000

Table 7. – Mean values and results from the analysis of variance for seed orchard no. 68. For RF1, RF2, RF3 and TF "Freq." = frequency of stems without resin flow, and for NL "Freq." = frequency of grafts with light damage (score 0 to 1). Clone:prov = Clone within provenance.

Source of variation (df)	DIA	RF1	RF2	RF3	TF	TFM2	NL
Mean value	274	0.49	0.18	0.33	0.99	0.29	1.86
Freq. (%)		81.0	92.0	87.0	81.0		30.0
Provenance (2) Prob <	0.1501	0.0538	0.0083	0.4153	0.0225	0.0466	0.0008
Clone:prov (42) Prob <	0.0000	0.0000	0.2525	0.0000	0.0000	0.0000	0.0000

Table 8. – Mean values and results from the analysis of variance for seed orchard no. 96. For RF1, RF2, RF3 and TF "Freq." = frequency of stems without resin flow, and for NL "Freq." = frequency of grafts with light damage (score 0 to 1). Clone:prov = Clone within provenance.

Source of variation (df)	DIA	RF1	RF2	RF3	TF	TFM2	NL
Mean value	236	1.39	0.16	0.03	1.58	0.51	1.50
Freq. (%)		51.0	87.0	98.0	47.0		59.0
Provenance (2) Prob <	0.0094	0.0593	0.1295	0.5631	0.0788	0.1059	0.0433
Clone:prov (39) Prob <	0.0000	0.0000	0.0000	0.2109	0.0000	0.0000	0.0000

Significant differences between clones within provenances are found for all characters except RF2 in orchard no. 68 and for RF3 in orchard no. 96.

Significant differences between provenances for total resin flow are found only in seed orchard no. 68. For loss of needles, significant differences between provenances are found in both nos. 68 and 96.

Tables 9 to 11 show estimated coefficients of genotypic correlation and broad sense heritabilities for traits in each seed orchard. H^2 is rather high for total resin flow in seed orchard nos. 31 ($H^2=0.19$) and 68 ($H^2=0.18$) and high in no. 96 ($H^2=0.39$). For loss of needles, H^2 is high for all seed orchards. There are significant correlations between diameter and loss of needles in seed orchard nos. 31 ($r_g=0.35$) and 96 ($r_g=0.68$), and between total resin flow and loss of needles and NL in nos. 31 and 68 ($r_g=0.47$ and 0.31).

Table 9. – Estimated genotypic correlations and broad sense heritabilities (H^2) for traits in seed orchard no. 31. Df=28.

	RF1	RF2	RF3	TF	TFM2	NL	H^2
DIA	-0.08	0.73	0.42	0.19	-0.05	0.35	0.53
RF1	.	0.46	0.13	0.89	0.82	0.27	0.16
RF2	.	.	1.00	0.83	0.72	0.46	0.03
RF3	.	.	.	0.60	0.58	0.55	0.18
TF	0.93	0.47	0.19
TFM2	0.35	0.17
NL	0.24

Table 10. – Estimated genotypic correlations and broad sense heritabilities (H^2) for traits in seed orchard no. 68. Df=43.

	RF1	RF2	RF3	TF	TFM2	NL	H^2
DIA	0.22	0.09	0.01	0.19	0.11	-0.10	0.43
RF1	.	1.00	0.22	0.89	0.87	0.32	0.25
RF2	.	.	1.00	1.00	1.00	0.32	0.01
RF3	.	.	.	0.64	0.64	0.19	0.08
TF	0.99	0.31	0.18
TFM2	0.33	0.18
NL	0.14

Table 11. – Estimated genotypic correlations and broad sense heritabilities (H^2) for traits in seed orchard no. 96. Df=40.

	RF1	RF2	RF3	TF	TFM2	NL	H^2
DIA	0.29	0.53	0.24	0.34	0.21	0.68	0.48
RF1	.	0.75	0.79	1.00	0.98	-0.12	0.39
RF2	.	.	0.71	0.82	0.76	-0.03	0.09
RF3	.	.	.	0.78	0.83	-0.78	0.01
TF	0.97	-0.11	0.39
TFM2	-0.20	0.35
NL	0.26

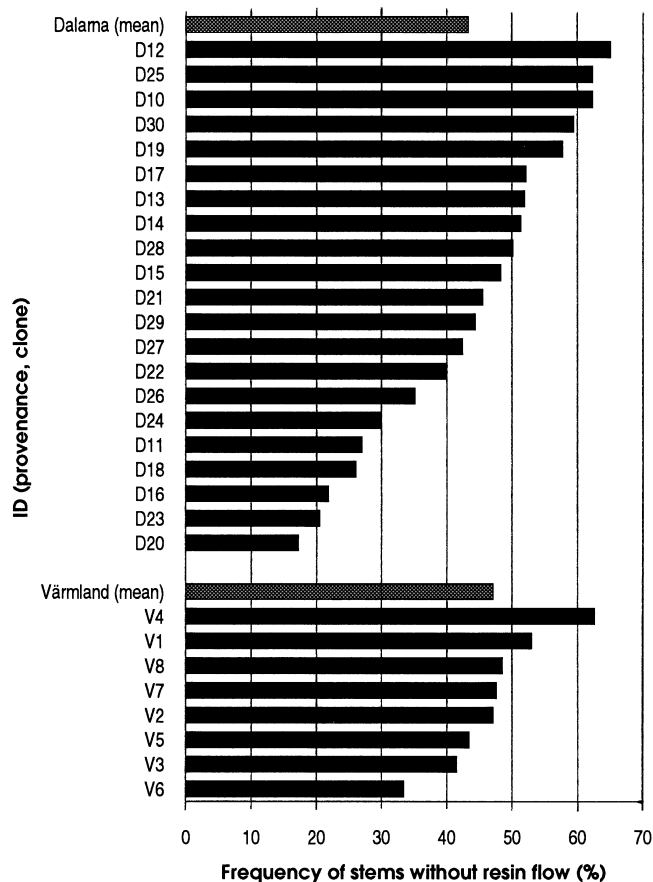


Figure 1. – Blup values for the clones in seed orchard no. 31. The least square means of each provenance group are shown above the individual clone BLUP values. Identities starting with D are from Dalarna and V indicates Värmland clones.

The distribution of BLUP values in total resin flow expressed as the frequency of stems/clone without any resin flow is shown in figures 1 to 3. The largest differences between clones within provenance are found for the Polish provenance in seed orchard no. 96, where BLUP values vary from 4.4 to 71.8% without any flows (Fig. 3).

Block effects were found to be significant for total resin flow but not for diameter in orchard no. 68. In the other 2 orchards, block effects were significant for diameter but not for total resin flow.

5. Discussion

The most interesting result in this study is the great variation of resin flow between clones within provenances. Broad sense heritabilities ranging between 0.18 and 0.39 are high and indicate that clones within provenance explain a large part of the variation in resin flow.

Results from an analysis of resin flow in a provenance experiment by CLUER and PETERSSON (cited in BARKLUND et al., 1995) indicate significant differences between provenances. The frequency of trees with resin flow in that study varies between 7% and 67% depending on provenance and time of assessment. That corresponds rather well with this study even if the comparison might be somewhat biased since the study by CLUER and PETERSSON excludes resin flow shorter than 3 cm. In this study, differences between provenances for total resin flow, are only significant in one of the orchards. In CLUER and PETERSSON (cited in BARKLUND et al., 1995), a group of Swedish provenances had the most resin flow while west continental Alp provenances were the least damaged. In this study, the group of west continental clones showed more resin flow than the Swedish and Polish clones, which were at almost the same level in seed orchard no. 68. In no. 96, however, the Polish clones had more resin flow than the Swedish clones. The sites do not differ and are not far apart so there is no good explanation of why there are such large differences between Polish and Swedish clones in one orchard but not in the other. The clones in the 2 groups are not the same in the different orchards and rather few in each group, which means that a few Polish clones with a high degree of resin flow in seed orchard no. 96 may explain some of the difference.

The cause of resin flow cannot be determined in this study. However, one may discuss whether drought might be the reason, as is suggested by BARKLUND et al. (1995) and GUNDERSEN et al. (1995). In this study however, lack of block effects, which also may be interpreted as drought effects, in 2 of the orchards, contradicts the hypothesis that drought is a strong causal factor. In seed orchard no. 68, where block effects exist, the highest frequency of resin flow was found in the least dry part of the orchard. Of course, the even sites of the seed orchards do not provide great differences in drought level. If drought is a relevant cause of resin flow, there should be good correlation to flowering and cone production, which are also promoted by drought stress (PHILIPSON, 1983). If good cone production indicates a low stress threshold, it would be very unfortunate and defeat much of the idea of seed orchards, since less stress-tolerant parent trees would occur in higher frequencies in the seed crop than more tolerant clones. That would be a good argument for using vegetatively propagated plants from sparsely flowering parents.

The positive correlation between resin flow and diameter indicates that large trees have more resin flow than smaller ones. The correlation between TFM2 and diameter is strong enough to support such a hypothesis in 2 orchards but not in no. 31 where the correlation is close to zero.

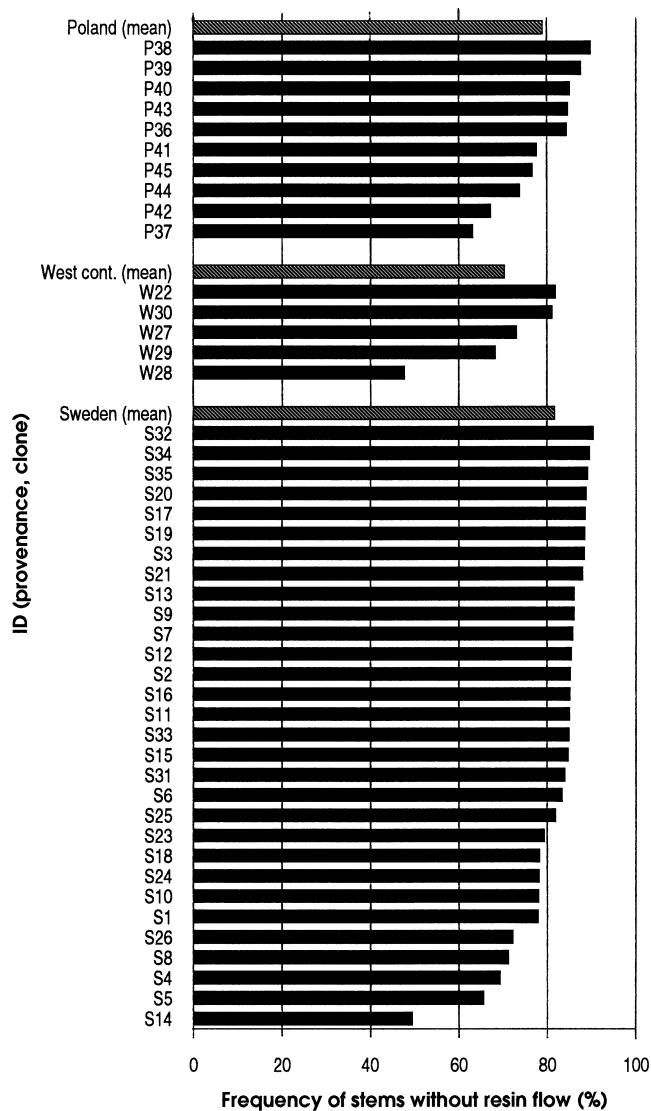


Figure 2. – Blup values for the clones in seed orchard no. 68. The least square means of each provenance group are shown above the individual clone BLUP values. Identities starting with P are from Poland, W are West continental and S indicates Swedish clones.

The highly significant correlation between diameter and loss of needles in seed orchard no. 96 may be explained by a top removal which was carried out in the winter of 1993/1994. The trees were cut at 6 metres to 7 metres height during the cone harvest in order to lower the cost of the harvest and to avoid excessively tall trees for the next harvest. That might have caused greater loss of the vigorous part of the green canopy in tall trees that also have a big diameter. The higher degree of lost needles for thick trees may also be due to a later growth termination for these trees. The climate is mild enough to favour trees with late growth cessation, but it might cause needle damage in certain years. HANNERZ (1994) found a tendency for more needle damage to occur on clones with a late cessation of growth.

Further studies to investigate the cause of resin flow and the mechanism in the tree that causes the symptoms need to be carried out. For tree breeding it is urgent to find juvenile

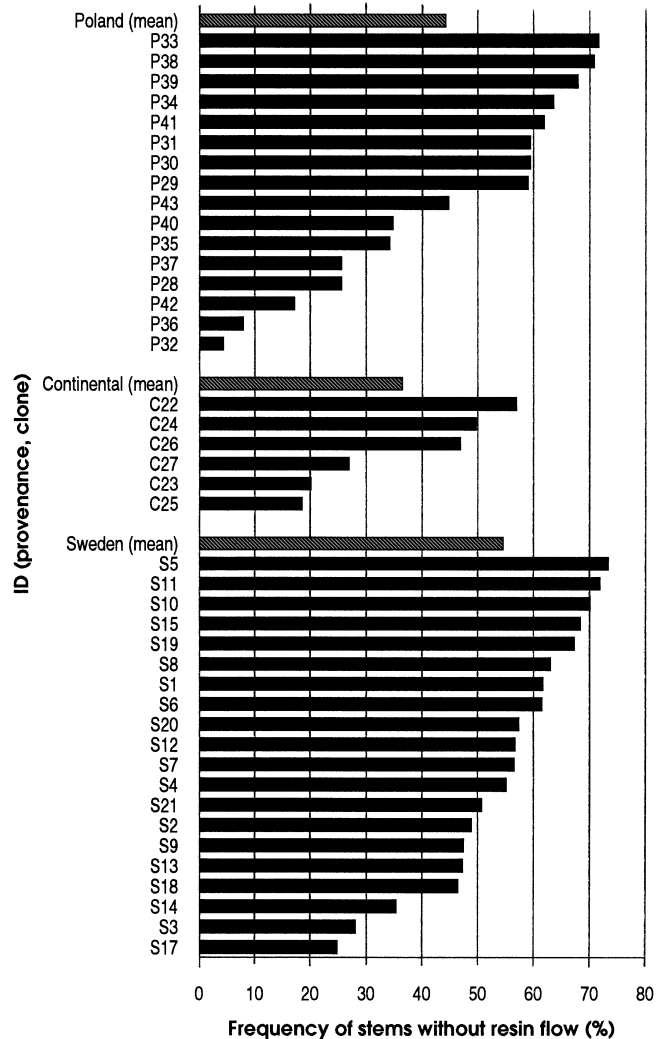


Figure 3. – Blup values for the clones in seed orchard no. 96. The least square means of each provenance group are shown above the individual clone BLUP values. Identities starting with P are from Poland, C are Continental and S indicates Swedish clones.

measurable traits in order to avoid these genotypes in breeding and mass propagation.

6. References

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