

# Juvenile-mature genetic correlations after simulated frost desiccation in seedlings of *Picea abies* (L.) Karst.

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To test a hypothesis that mimicking a limiting factor at the juvenile stage would improve juvenile-mature (J-M) relationships, genetic correlations were calculated between growth traits of 36 open-pollinated families of *Picea abies* after frost desiccation simulated in growth chambers and growth traits of progenies of the same maternal clones in 2 field trials in southern Sweden. Frost desiccation was simulated during 3 weeks at the later part of the rest period either after the 1st or the 2nd growth periods by exposing the above-ground part of the seedlings to 15°/5°C day/night and the roots to -3°C in a glycol bath. The light intensity was increased during 4 h in the middle of the day. Height growth, phenology, biomass traits and frost desiccation damage were assessed in growth chambers and height and diameter between age 10 and 17 were measured in the field trials. The traits with low heritabilities were not included in the analysis. The J-M genetic correlations were weak, only 14 of 266 correlation coefficients being significant for the treated material, and 5 of 126 for the control material. The damage scored after one of the frost desiccation treatments was significantly negatively correlated with field heights at age 10 and 14. Possible reasons for the weak J-M correlations were (1) different strength of selective effect of the simulated and natural frost desiccation, (2) effect of frost desiccation may have been reduced by the effect of a late spring frost in the field. Our study suggests that frost desiccation is not the main factor limiting growth of *Picea abies* seedlings in southern Sweden, however it might have some effect since the treated material tended to correlate more strongly than the control material with the field traits.

**Key words:** *Picea abies*, early tests, frost desiccation, juvenile-mature relationships, genetic correlation, growth chamber.

## Introduction

Reliable early testing is a valuable tool in shortening generation time in the breeding population to improve genetic gain per time unit. The juvenile-mature (J-M) correlations, especially between the traits from tests at the nursery and more mature stages under field conditions, are not always strong (e.g. Mikola 1985, Nanson 1987, Fries 1989, 1991, Jansson *et al.* 1998). Mature should not be taken literally rather it refers to material studied in field after the phase of establishment. The latter authors discussed various reasons for absence of strong J-M correlations such as:

1. low heritability at juvenile and/or mature stage,
2. different sets of genes expressed in juvenile and mature material,
3. genotype x environment (G x E) interaction.

If point 1 is valid it is meaningless to estimate any J-M correlations. If point 2 is the reason for the absence

of strong J-M correlations, it will not be possible to develop reliable early testing. The growth conditions usually differ considerably between field and nursery/greenhouse/growth chamber. This might give rise to a strong G x E interaction. If weak J-M correlations are due to the interaction (point 3 above) it might be possible to develop reliable early tests by simulation of key field conditions at the juvenile stage.

Nutrient availability, water availability and extreme temperatures are examples of factors affecting growth in the field. Water availability might be limiting throughout the year, even during winter leading to frost desiccation. Such a stress occurs when the ground is frozen and transpiration has started owing to high ambient air temperature (Tranquillini 1982, Sakai and Larcher 1987, Christersson and von Fircks 1988).

There is some support in the literature for improvement of the J-M correlations by simulations of limiting factors at the juvenile stage (Cannell *et al.* 1978, Wellen-

dorf 1979, Williams 1987, Jiang *et al.* 1989, Li *et al.* 1989, 1991, Lascoux *et al.* 1993). Acknowledging the importance of genotypic tolerance to water deficit for some American pines, Waxler and van Buijtenen (1981) for *Pinus taeda* families and Feret (1982) for *Pinus ponderosa* families have simulated different levels of water stress and related the family performance to the subsequent development in the field. According to Eriksson *et al.* (1993) the largest plants of *Pinus sylvestris* which were exposed to strong competition in growth chambers exhibited the strongest genetic correlations with the field data. In that case, competition for light might be the common stress in the growth chambers and the field trials. However, this was later rejected by Jansson *et al.* (1998). Larsen and Wellendorf (1990) found significant correlations for families of *Picea abies* between their performance in the field trial and water use efficiency and resistance to winter frost at the juvenile stage.

Since frost desiccation conditions occurred repeatedly during the eighties in southern Sweden it might have influenced the growth in progeny trials in this part of the country. If there is a genetic variation in tolerance to frost desiccation, this trait might be a good predictor of future growth under conditions of frost desiccation. In a previous study we have revealed genetic variation in frost desiccation tolerance. Our basic finding was that the family effect in growth traits and damage was significant for most of the traits affected by frost desiccation. We also noted that frost desiccation resulted in reduced seedling height growth. Thus frost desiccation may change family ranking in height growth and presumably would not result in significant loss of material in the field trials.

The objective of our study was to estimate genetic correlations between juvenile traits after frost desiccation treatment in growth chamber and field growth traits in two *Picea abies* progeny trials.

## Material and methods

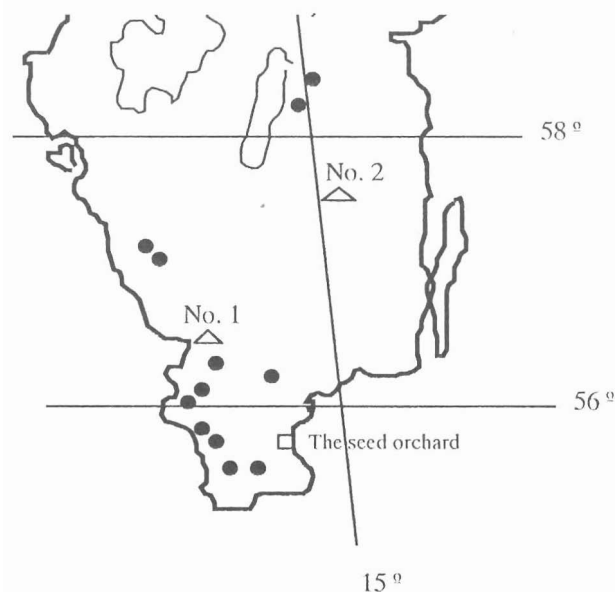
### Field trials

In the period 1971-73 partial diallel crossings (7 families per clone) for the field trials were performed among the 36 clones of *Picea abies* grown in Maglehem seed orchard located in southern Sweden (55°50' N, 14°07' E, 60 m a.s.l.). The clones were selected as plus trees in 12 southern Swedish stands (lat. 56°-59°) originating from continental Europe (Fig. 1).

The sowing for the field trials 1 and 2 was made in 1974 and the trials were established with 3-year-old seedlings spaced 2 x 2 m in 1977. The experimental de-

sign was 10 randomised complete blocks with single-tree-plots. Each full-sib family was represented by 40 seedlings in each of the trials. No thinning was performed.

The trials were established in different breeding zones (Wellendorf *et al.* 1986). The northerly trial 2 is located outside the area for which the seed orchard was recommended (Fig. 1).



**Figure 1.** Location of the Maglehem seed orchard from which the family seeds were collected (indicated by the square), the field trials (indicated by the triangles) and the original stands from which plus trees for the seed orchard were selected (indicated by the dots) in southern Sweden. Several plus trees within a stand were selected totalling 36 clones in the seed orchard.

Results from the field trials were reported earlier by Karlsson and Danell (1989). Height was measured on 12 trees per family and trial at age 9 (trial 2), 10 (trial 1), 14 and 17 (both the trials). The diameter of the same trees was measured at 1.3 m above ground at age 17. The variables are presented in Table 1.

### Growth chambers

In 1993 open-pollinated seeds were collected from the same 36 clones in Maglehem seed orchard which were used in the crosses for the field trials. Open-pollinated families were preferred since it allowed for studies of more parents which is required to get a satisfactory precision of the estimates of J-M relationships.

The detailed description of the methods used in the growth chamber experiment is presented in our previous paper on effects of frost desiccation on seedling

**Table 1.** Description of the variables

Variable	Description
<b>Traits from the field trials No. 1 and No. 2</b>	
I(9)10, I114, I117	Seedling heights at age 9 (TRIAL 2), 10 (TRIAL 1), 14, 17
INCR(9)10-14	Increment from age 9 (TRIAL 2), 10 (TRIAL 1) to 14
INCR14-17	Increment from age 14 to 17 years
INCR(9)10-17	Increment from age 9 (TRIAL 2), 10 (TRIAL 1) to 17
D17	Diameter at breast height at age 17
<b>Growth chamber traits</b>	
Frost desiccation damage	
DAMD1	Damage score in the treatment D1 at the later part of the rest period after the growth period (GP) 1
SURVD1	Survival after the treatment D1
HGP2*S	Final seedling height in GP2 multiplied by SURVD1
DAMD2	Damage score in the treatment D2 at the later part of the rest period after GP2
Height growth traits	
HGP1	Final height in GP1, mm
HGP2	Final height in GP2, mm
HGP3	Final height in GP3, mm
LEADHGP2	Final leader height in GP2, mm
LEADH	Final leader height in GP3, mm
SUN	Stem unit number on the leader in GP3
SUL	Stem unit length of the leader in GP3, mm
Phenology traits	
GP2LATNO	Total number of (alive and dead) laterals on GP2 stem
GP3FREE	Estimate of free growth in GP3
DAYHGP250	Day No. since the end of the treatment D1 to reach 50 % of the final leader height in GP2
DAYLIG50	Day No. since the end of the treatment D2 to lignify 75% of the final leader height in GP3
DAYS3	Day No. since the end of the treatment D2 to reach flushing stage 3 in GP3
Biomass traits	
GP2STEMDW	Dry weight of the stem of GP2 together with the needles attached to the stem, g
GP2LATDW	Dry weight of living laterals on GP2 stem, g
TOTALDW	Total seedling dry weight, g

development (Danusevičius *et al.* submitted). The methods are briefly described below.

The seedlings were grown in mineral wool in plastic tubes with 7 x 5 cm spacing in boxes. A nutrient solution was provided every or every second day depending on the growth rate of the seedlings. The frost desiccation was simulated during the later part of the rest period in the 1st (referred to treatment D1) and the 2nd (treatment D2) growth periods. A total of 540 seedlings (15 seedlings per family) were designated for each of the treatments and the control, altogether 1620 seedlings in the experiment. The experimental design was 5 blocks with 3 non-contiguous plots during the growth in the chambers and 4 blocks with 4 (3 in one block) non-contiguous plots during the frost desiccation treatment. To simulate a frost desiccation environment, the seedlings with sealed tubes were immersed in freezing baths filled with glycol providing -3°C for the roots. The baths were placed in a chamber with 15°/5°C day/night

temperature and 12/12 h day/night with light intensity of 300 mmol/m<sup>2</sup>/s and 4 h at noon with high light intensity (483 mmol/m<sup>2</sup>/s) for three weeks. During the frost desiccation treatment, the rest of the material was kept quiescent. After the treatment the seedlings were placed in the same chamber as the controls, and one week later a bud breaking treatment was started.

The damage caused by frost desiccation was scored during the following growth period:

- 0- no observable damage;
- 1- apical bud on the leader dead, laterals growing out;
- 2- dead leader, only the basal laterals flushing;
- 3- dead seedling;

The seedling survival was assessed as follows. For a dead seedling the survival was set at 0, if the leader was not flushing survival was set at 0.5 and for a seedling with flushing leader the survival was set at 1. The seedling final heights of the 1st, 2nd and 3rd growth periods were measured. The height growth was assessed at one week intervals to calculate the number of days to 50% of the final leader height. The assessments of phenology traits were made during the 3rd growth period. Apical bud flushing and bud set on the leader were scored at 2 day intervals (dynamic period) or weekly using a continuous scale, similar to the one developed by Krutzsch (1973). The length of the lignified part of the leader was measured weekly at 9 occasions. At the end of the 3rd growth period all the seedlings were harvested for assessment of the dry weight. The dry weight was assessed separately for the following parts of a seedling: (1) the leader, (2) stem of the 2nd growth period together with the needles attached to the stem, (3) living lateral shoots grown on the stem of the 2nd growth period (4) stem of the 1st growth period together with the laterals and the needles attached. The number of stem units on the leader was assessed by counting the needles during the harvest. The number of lateral buds on the leader and the number of laterals, including dead ones, grown on the stem of the 2nd growth period, were counted. The occurrence of free growth was estimated at the harvest as the ratio of the lateral buds on the leader which had flushed to the total number of lateral buds on the leader. More weight was given to the elongating buds as follows: the lateral buds on the leader which had flushed and elongated more than 1 cm were given a value of 1, the lateral buds on the leader which had flushed or elongated less than 1 cm were given a value of 0.5. The variables derived from the traits are summarised in Table 1.

*Statistical analyses*

The family variance components and predicted breeding values for the juvenile growth traits within each treatment in growth chambers were calculated according to the following model:

$$Y_{ijk} = m + B_i + F_j + e_{ijk},$$

where:  $Y_{ijk}$  is a  $k$ -th individual observation in  $i$ -th block of  $j$ -th family,  $m$  is the total mean,  $B_i$  is fixed effect of block  $i$ ,  $F_j$  is random effect of family  $j$ ,  $e_{ijk}$  is random error for  $ijk$ -th observation. For the frost desiccation damage scores in the growth chambers the analyses were made on family means per block, as this variable was measured on a non-linear scale.

The family variance components and predicted breeding values (BLUP) for the growth traits within a field trial were calculated with software VDIAL (Danell 1989) according to the following model:

$$Y_{ijkl} = m + B_i + (F_j + F_k) + F_{jk} + e_{ijkl},$$

where  $Y_{ijkl}$  is an  $l$ -th individual observation in  $i$ -th block of  $j$ -th and  $k$ -th parents,  $m$  is the total mean,  $B_i$  is fixed effect of block  $i$ ,  $F_j$  and  $F_k$  are random effects of the parents  $k$  and  $l$ ,  $F_{jk}$  is random interaction effect between parents  $j$  and  $k$ ,  $e_{ijkl}$  is random error of  $ijkl$ -th observation.

The Levene's variance homogeneity test (Levene 1960), W-test statistics on the model residual normality (Shapiro and Wilk 1965) and plot of residuals versus predicted values were used to test the validity of the assumptions for ANOVA. If the assumptions were not valid, a logarithmic transformation for continuous variables and arc sine square root transformation for the variables measured on a discontinuous scale were used.

The traits in the growth chambers and field trials were measured on the progenies of the same maternal clones but on different individuals. Thus, the genetic correlation coefficients were estimated essentially as suggested by Burdon (1977) and referred to type "B" genetic correlations. The following formula was used:

$$r_{gB} = r_{yy} / (r_{TPx} r_{TPy}),$$

where  $r_{yy}$  is the product-moment correlation among the predicted breeding values,  $r_{TP(x)}$  and  $r_{TP(y)}$  are the correlations between the true and predicted breeding values, which for the growth chamber data were estimated as follows:

$$r_{TP} = (k h_a^2) / (4 + (k-1) h_a^2)^{1/2},$$

where  $k$  is the harmonic mean of the number of observations per family and treatment in the growth chamber experiment and per family and trial in the field trial data,  $h_a^2$  is the individual tree (additive) heritability estimated as follows:

$$h_a^2 = s_a^2 / s_p^2,$$

where  $s_a^2$  is the additive variance estimated as four times the family variance component (half-sibs) or four times the parental variance component (full-sibs), and  $s_p^2$  is the phenotypic variance.

To illustrate the strength of the genetic relationships, the significance values of product-moment correlations among predicted breeding values are presented together with the coefficients of type "B" genetic correlation (cf. Burdon 1977).

Seedlings which did not flush their apical buds, i.e. were dead or had a dead leader, or which were classified as suppressed by competition, were excluded from all the analyses of the growth traits in growth chambers. During the measurements in the 3rd growth period, seedlings which visually seemed to be suppressed by competition were identified. To judge whether these seedlings (5% of the total number) were suppressed to such an extent that they should be classified as outliers, the screening was made separately for each family within each treatment. Trees with severe technical damage (e.g. stem break or windblown trees) were omitted from the analysis of the field data.

Owing to low survival, the precision of the estimates of genetic parameters for the juvenile traits was sometimes low. Therefore, if the standard error of the family variance component was larger than 1/2 of the family variance component, the trait was not included in the analyses.

The variance components and the predicted breeding values for the growth chamber data were estimated using the REML (Restricted Maximum Likelihood) method in the MIXED procedure and the product-moment correlations were obtained using the CORR procedure in the SAS statistical package for personal computers (SAS Institute 1987). The genetic parameters for the field trial material were estimated with the package for personal computers VDIAL, which is specially designated for analysis of genetic experiments by Danell (1989). This package is based on Henderson's Mixed Model Equations (Henderson 1975) and REML variance and covariance estimation method. For each trait from the field data, the grand mean of the trial was added to the BLUP.

**Results**

As seen from Table 2, there were only a few strong genetic correlations between the juvenile traits in growth chambers and the traits in the field trials. Thus,

18 of 140 correlation coefficients (13%) were larger than 0.5 in treatment D1, 12 of 126 (10%) were larger than 0.5 in treatment D2 and in the controls 7 from 126 (6%) were larger than 0.5.

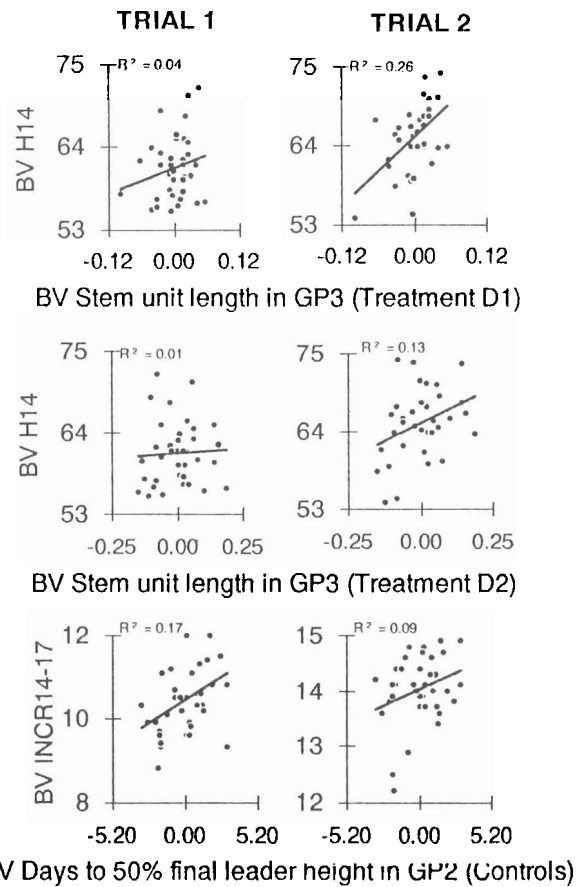
**Table 2.** Number of significant and moderately strong genetic correlation coefficients between the traits in the growth chambers and field traits. The traits are pooled into categories. The presentation is the following: number of significant correlations\* / number of correlations larger than 0.5, including the significant ones / total number of correlations calculated.

Growth chamber	Height (field)		Diameter (field)	
	Trial 1	Trial 2	Trial 1	Trial 2
<b>Treatment D1</b>				
Height	0/1/36	5/7/36	0/1/6	1/1/6
Phenology	0/0/6	0/0/6	0/0/1	0/0/1
Biomass	0/0/12	0/0/12	0/0/2	0/0/2
Damage	2/3/6	0/4/6	0/1/1	0/0/1
<b>Treatment D2</b>				
Height	0/1/24	6/7/24	0/0/4	0/1/4
Phenology	0/0/18	0/2/18	0/0/3	0/0/3
Biomass	0/0/6	0/0/6	0/0/1	0/1/1
Damage	0/0/6	0/0/6	0/0/1	0/0/1
<b>Controls</b>				
Height	0/0/24	0/0/24	0/0/4	0/0/4
Phenology	5/5/12	0/2/12	0/0/2	0/0/2
Biomass	0/0/18	0/0/18	0/0/3	0/0/3

\*- least significant genetic correlation with d.f.=35 was 0.57

The juvenile height of the frost desiccated seedlings was significantly correlated with the heights in the field trial 2 in 11 of 60 cases, though none of the 60 correlation coefficients with trial 1 was significant. Juvenile phenology traits of the controls were significantly correlated with heights in field trial 1. No significant correlations between the juvenile biomass traits and field traits were obtained. Some of the significant relationships are illustrated for each of the field trials in Figure. 2. Stem unit length of the treated seedlings was more strongly correlated with the traits assessed in the northerly field trial 2 than with trial 1. Day number to 50% of the final leader height of the control material in the growth chambers was more strongly correlated with height increments in trial 1 than in trial 2.

The damage scored after desiccation treatment D1 (DAMD1) was significantly negatively correlated with the family heights at ages 10 and 14 years in trial 1 (the type "B" genetic correlations were -0.75 and -0.67, and the product-moment correlations among the predicted breeding values were significant at the 5% level). The genetic correlations between DAMD1 and height at age 17 in trial 1 as well as the heights in trial 2 were close to significance. In contrast to the damage after treatment D1, the damage scored after treatment D2 was not significantly correlated with the field traits (Table 2).



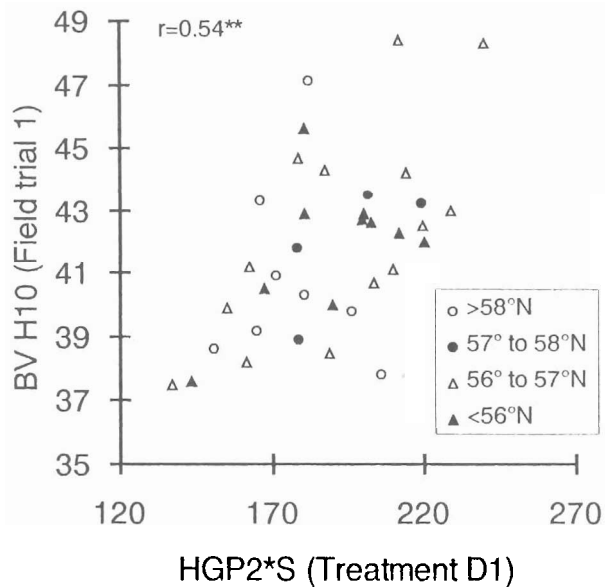
**Figure 2.** Relationships between the family breeding values (BV) in the field trials 1 (the column of plots to the left) and 2 (the column of plots to the right) and growth traits of the material in growth chambers (plotted on the X axis).

When the final height in the 2nd growth period of the seedlings in treatment D1 was weighed with their survival after the frost desiccation, this variable was more strongly correlated with the field heights than the unweighed height (the product-moment correlations among the family means were 0.54\*\* and 0.32 respectively, Fig. 3). Figure 3 also shows that variation within the latitudinal intervals of the family origin was greater than the variation among the latitudinal intervals for both traits in the field and in the growth chambers.

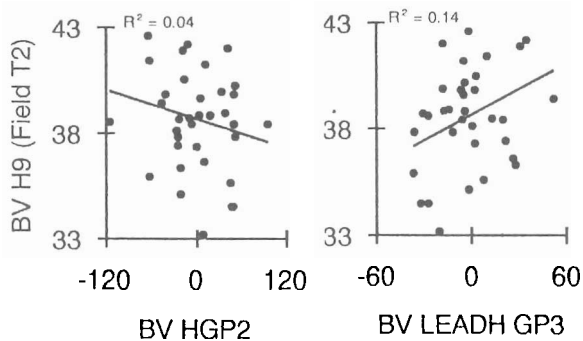
The correlation between the final height of the families before treatment D2 and height at age 9 in field trial 2 was weaker than that between the leader height of the same families after treatment D2 and height at age 9 in field trial 2 (Fig. 4).

**Discussion**

In general, the genetic correlations between the juvenile traits of the treated material in growth cham-



**Figure 3.** Relationship between the family mean height x survival after frost desiccation treatment D1 in growth chambers (plotted on X axis) and breeding values (BV) for the family height at age 10 in the southerly field trial 1. The legend shows latitudinal intervals within which the families originated. The product-moment correlation coefficient and the significance level are shown in the upper left corner of the plot.



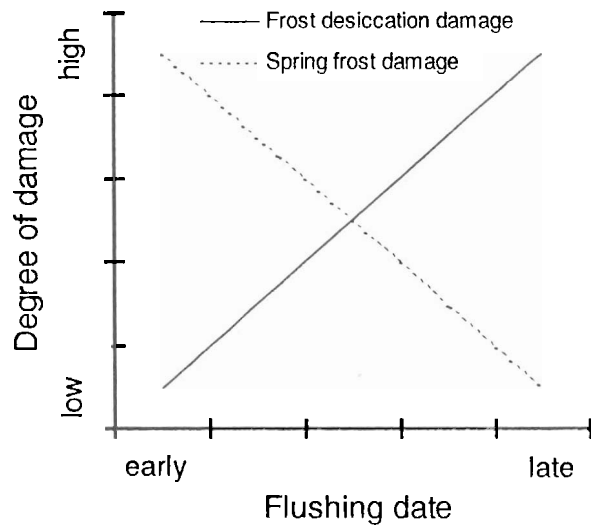
**Figure 4.** Relationship between the family breeding values (BV) for final height in the 2nd growth period, i.e. before the treatment D2 (left), leader height of the same seedlings after the treatment D2 (right) in growth chambers and breeding value for height in the field trial 2 at 9 years of age

bers and traits in the field trials were weak, only 12 of 266 correlation coefficients being significant. A reason for this may be that the effect of treatment D1 was too weak to differentiate among the families to the same degree as under the natural conditions in the field trials, whereas the effect of treatment D2 was too strong

which in turn reduced the precision of the estimates of true family mean values of the juvenile growth traits (Danusevicius *et al.* submitted). However, we culled the traits with low precision of their estimates to avoid calculation of correlations between such traits.

The genetic correlations between the damage score in treatment D1 and field height at age 10 and 14 were significant and negative. Thus, severely damaged families had low breeding values for the field height. The same tendency was present in the relationship between height weighed with survival after treatment D1 and the field heights (Fig. 3). The relationship between field height at age 9 and the leader height after treatment D2 was somewhat better than the corresponding relationship with height at the end of the 2nd growth period of the same seedlings before the treatment (Fig. 4). In general, there was only a minor difference between the controls and treatments as regards the number of significant correlations. The J-M relationships between traits assessed in treatments D1 and D2 and in field trial 2 resulted in 12 significant correlations out of 133. This is somewhat above the expectation of the number of significant correlations for random reasons only. Only 2 significant correlations out of the 12 significant ones were associated with field trial 1 (Table 2). A possible explanation is that winter damage including desiccation was more severe in trial 2 which is located at 1° higher latitude and 140 m higher altitude than trial 1.

In our previous study (Danusevičius *et al.* submitted) we showed that late flushing families were less tolerant to frost desiccation than early flushing families. In the field trials, on the other hand, survival and good growth of a progeny were dependent on avoidance of late spring frosts (cf. Karlsson and Danell 1989). This means that late flushers have been more likely to perform well in the field trials. Thus, there might be two opposing factors influencing field performance - occurrence of severe late spring frosts or severe frost desiccation periods (Fig. 5). Depending on the strength of these two factors, either of them might be the most important for field performance. In our material, families which tolerate frost desiccation might have been damaged by late spring frost and, thus, selective effect of late spring frost dominated over frost desiccation, resulting in weak J-M correlations with the phenology traits of the seedlings treated with frost desiccation. In contrast to the situation with the treated materials, there ought to be a positive relationship between flushing time and field performance in the control material. Some



**Figure 5.** Schematic illustration of the contrasting relationship between date of flushing and degree of damage by frost desiccation and late spring frost respectively in *Picea abies*. The families which tolerate frost desiccation may be damaged by late spring frost.

support for this is found in the five significant J-M phenology - field performance correlations.

The absence of strong J-M correlations between field performance and growth traits in the control material suggests that different sets of genes were active during the two ontogenic stages. However, the growth conditions at the juvenile stage of the control material were by far more favourable than in the field which might have provoked a G x E interaction. Therefore, we cannot distinguish which explanation is correct. Nor was this the purpose of our study.

Eriksson *et al.* (1993) reported that J-M correlations in *Pinus sylvestris* full-sib families did not become strong until age 23. The *Pinus sylvestris* trials were established at a denser spacing than the *Picea abies* trials in our study which means that competition and thereby genetic resolution among the entries would be considerably larger than in our field material. Therefore, it cannot be excluded that J-M relationships might become stronger once the same competitive environment is reached in the *Picea abies* trials. Moreover, non-genetic effects are important during the phase of establishment and such effects are expected to be reduced by time.

It was reported that J-M correlations at the family level were stronger if the families originated from more provenances than one (Mikola 1988, Ekberg *et al.* 1994).

In our previous paper (Danusevicius *et al.* submitted), we reported that the families behaved as representatives of one population rather than of several. This might have contributed to the low number of significant J-M correlations.

In conclusion, our study suggests that frost desiccation is not the main factor limiting growth of *Picea abies* seedlings in southern Sweden. Frost desiccation might have some effect since the growth chamber data from treatments D1 and D2 tended to correlate more strongly than data from the controls with field data.

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## ГЕНЕТИЧЕСКАЯ КОРРЕЛЯЦИЯ МЕЖДУ ПОВРЕЖДЕНИЯМИ СЕЯНЦЕВ ЕЛИ ОБЫКНОВЕННОЙ (*PICEA ABIES* (L.) KARST.) ИСКУССТВЕННОЙ МОРОЗНОЙ ЗАСУХОЙ И РОСТОМ САЖЕНЦЕВ СТАРШЕГО ВОЗРАСТА В ЛЕСНЫХ КУЛЬТУРАХ

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### Резюме

Существует гипотеза, что на основе оценки повреждений сеянцев искусственной морозной засухой в климатических камерах можно определить критические факторы для саженцев старшего возраста в лесных культурах. С целью проверки этой гипотезы были вычислены коэффициенты генетической корреляции между повреждениями сеянцев 36-ти полусибсовых семей ели обыкновенной в климатических камерах под воздействием искусственной морозной засухи и ростом семейного потомства этих же самых материнских деревьев, которые произрастают в 2-х опытных культурах Южной Швеции. Оценка устойчивости сеянцев против морозной засухи произведена в конце стадии покоя влиянием на надземную часть сеянцев температуры +15°С в течение дня и +5°С в почное время. В то время корни сеянцев находились при температуре -3°С. Они были помещены в емкости заполненные незамерзающим гликолем. Причем, днем в течение 4-х часов было увеличено освещение.

Для сеянцев, выращиваемых в климатических камерах, определен прирост в высоту, фенологические признаки и биомаса, а также повреждения морозной засухой. В опытных лесных культурах в возрасте 10, 14 и 17 лет определялась высота деревьев, а в 17-летнем возрасте - и диаметр стволиков. Признаки, которые показали степень низкой наследуемости, в анализ не включены. Генетическая корреляция у признаков между сеянцами и деревьями в лесных культурах была низкой. Так, только у 14-ти признаков из 266 корреляционные коэффициенты были существенными, а у контрольных сеянцев были существенными 5 признаков из 126-ти. Степень повреждений, которая определена после одного из опыта морозной засухи, оказалась существенной, но отрицательной по отношению с высотой деревьев в 10-ти и 14-летнем возрасте.

Низкие корреляционные связи между повреждением сеянцев и ростом саженцев в культурах могли оказаться из-за токовых причин: (1) силы влияния искусственной и натуральной морозной засухи на рост растений могли быть различными; (2) поздние весенние заморозки могли уменьшить отборный эффект морозной засухи в лесных культурах.

Опыты показали, что морозная засуха не является основным фактором, лимитирующим рост саженцев в Южной Швеции. Но она все-таки может иметь некоторое влияние на рост саженцев в лесных культурах, так как показатели поврежденных сеянцев искусственной морозной засухой имели более тесные связи с показателями лесных культур, нежели контрольные опытные сеянцы.

**Ключевые слова:** *Picea abies*, ранний тест, морозная засуха, ювенильное-взрослое соотношение, генетическая корреляция, климатическая камера.