Bordeaux, France. (Eds. IUFRO-AFOCEL). Association Forêt Cellulose, Nangis: (II) 73-86 (1992). — SAS Institute Inc.: SAS/STAT guide for personal computers. Version 6.03. (Ed. SAS Institute Inc.). Cary, N. C. (1988). — SIM, B. L.: Research on Acacia mangium in Sabah: a review. In: Australian Acacias in Developing Countries. Gympie, Australia. (Ed. Turnbull, J. W.). Australian Centre for International Agricultural Research, Canberra: 164-166 (1986). — SNEDECOR, G. W. and Cochran, W. G.: Méthodes statistiques. (Ed. A.C.T.A.). Paris, 649 pp. (1957). Tomassonf, R., Dervin, C. and Masson, J. P.: Biométrie, modélisation de phénomènes biologiques. (Ed. Masson). Paris, 553 pp. (1993).

— Wong, C. Y.: Vegetative propagation of Acacia mangium Wild. by cutting. In: Breeding Tropical Trees: Population Structure and Genetic Improvement Strategies in Clonal and Seedling Forestry. Pattaya, Thailand. (Eds. Gibson, G. L., Griffin, A. R. and Matheson, A. C.). Oxford Forestry Institute, Oxford, and Winrock International, Arlington: 451–453 (1989). — Wong, C. Y. and Haines, R. J.: Multiplication of families of Acacia mangium and Acacia auriculiformis by cuttings from young seedlings. In: Breeding Technologies for Tropical Acacias. Tawau, Malaysia. (Eds. Carron, L. T. and Aken, K. M.). Australian Centre for International Agricultural Research. Canberra: 112–114 (1991).

## Performance of Open-Pollinated Progenies of Blue Pine in Romania

By I. BLADA

Forestry Research Institute, Sos. Stefanesti 128. Bucharest 11, Romania

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#### Summary

Genetic variation in 8 traits, including height growth and resistance to blister rust (Cronartium ribicola Fisch ex. Rabenh.), was observed in 36 blue pine (Pinus wallichiana A. B. Jacks.) open-pollinated progenies. Results after 11 growing seasons were as follows: (1) Highly significant (p<0.001) genetic differences were observed among families for most traits; (2) The genetic components of variance accounted for 91%, 99%, 96%, 79%, 38%, 36% and 38% of the phenotypic variance for blister rust resistance, trees free of blister rust, survival, total height growth, diameter at 1/2 height, basal area at 1/2 height and stem volume, respectively; (3) The narrow-sense heritability estimates for the above traits were 0.909, 0.998, 0.960, 0.794, 0.379, 0.360 and 0.380, respectively; (4) No significant correlations were found for blister rust resistance and any growth traits; (5) The frequency distribution of blister rust resistance and height growth suggest a polygenic control; (6) Selecting the best 5, 10, 15 and 20 out of 36 families would result in genetic gain for blister rust resistance of 67%, 51%, 40% and 30%, and 18%, 14%, 11% and 8% for

Key words: Pinus wallichiana, Cronartium ribicola, open-pollinated progenies, rust resistance, growth traits, genetic variance, heritability, genetic gain.

FDC: 165.53; 443; 181.6; 232.12; 172.8 Cronartium ribicola; 174.7 Pinus wallichiana.

## Introduction

Blue pine grows throughout the Himalayan Mountains between latitudes 25 °N and 36 °N and longitudes 68 °E and 100 °E with a discontinuous pattern from eastern Afghanistan to Yunnan Province, China. It is an important component of middle and high elevation forests in this region (Critchfield and Little, 1966) and is found between 1320 m and 4125 m. The best growth occurs between 1980 m and 2970 m (Dogra, 1972).

Blue pine is a moderate to fast growing species and is one of the most important multipurpose timber species within its natural range. With its extensive range over a variety of habitats, and with its discontinuous distribution, genetic variation is a real possibility (Ahsan and Khan, 1972).

Using artificial inoculation techniques, blue pine was found to be moderate to highly resistant to blister rust

(Heimburger, 1962, 1972; Bingham, 1972a; Hoff et al., 1980; Delatour and Birot, 1982; Stephan, 1986; Blada, 1987).

Blue pine is useful in interspecific hybridization programs. When crossed with other white pine species it has produced hybrids that are both resistant to blister rust (Heimburger, 1958, 1962, 1972; Patton, 1964; Zsuffa, 1979b; Blada, 1987, 1992) and good growth (Righter and Duffield, 1951; Wright, 1959; Zsuffa, 1979a; Leandru, 1982; Kriebel, 1983; Blada, 1987, 1992; Kriebel and Dogra, 1992).

The IUFRO Committee on Resistance to White Pine Blister Rust selected blue pine as its first choice for immediate attention for the following reasons: good growth and relatively high level of rust resistance; an extensive natural range and, thus, a greater probability of genetic variability for important traits such as rust resistance, growth characteristics and hardiness (BINGHAM et al., 1972). Field trials in Ohio (USA) (KRIEBEL and DOGRA, in preparation) suggest that: (1) Most of the trees from the sources of blue pine tested at this location suffered annual injury from spring frosts that resulted in multistemmed trees and reduced growth; (2) Growth rate of blue pine varies widely with seed source; and (3) Pinus strobus x P. wallichiana hybrids were not damaged by frost and they have a higher specific gravidity than P. strobus. Garrett (1993) observed 56 half-sib families from 6 provenances in Pakistan and noted that survival was good to excellent for all sources (79% to 92%) after 9 growing seasons in southern Maine (USA) at latitude 43°30'N and longitute 70°45'W. There was no visible injury to buds or shoots that could be attributed to cold temperatures in spring or fall. Attacks by the white pine weevil (Pissodes strobi PECK.) that killed the terminal shoot ranged from 47% to 86% in blue pine and this level of attack severely retarded height growth. The variation within provenances suggested that more work is needed to properly evaluate the potential of this tree as a pure species or in hybrid combination with other white pines in North America.

The objective of this research in Romania was to test a limited number of open-pollinated families for rust resistance and growth traits.

Table 1. — Origin of the open-pollinated progenies from the Himalaya Mountains.

IUFR0 code	Our code	Origin	Latitude (N)	Longitude (E)	Altitude (m)
6136	16	Koh i Sufaid Bash i Lela (III)	33*55′	70°08′	2130
6148	24	Hindu Kush Mts.Kalkot (IV)	35° 16 ′	72°14′	2285
6149	25	Hindu Kush Mts. Kalkot (IV)	35°16′	72°14′	2285
6150	26	Hindu Kush Mts. Kalkot (IV)	35°16′	72°14′	2285
6152	28	Hindu Kush Mts. Kalkot (IV)	<b>35°16</b> ′	72°14′	2285
6156	31	Hindu Kush Mts. Kalkot (IV)	35°16′	72*14′	2285
6158	33	Hindu Kush Mts. Kumrat (V)	35°21′	72°10′	2438
6159	34	Hindu Kush Mts. Kumrat (V)	35° 21'	72*10′	2438
6162	37	Hindu Kush Mts. Kumrat (V)	35° 21′	72°10′	2438
6164	39	Hindu Kush Mts. Kumrat (V)	35°21′	72° 10′	2438
6168	43	Hindu Kush Mts. Usku (VII)	35°42′	72°44′	2133
6189	64	Himalayan Zone Zuzagli (XII)	33° 54′	73° 27′	2133
6193	68	Himalayan Zone Zuzagli (XII)	33° 54′	73° 27′	2133
6207	82	Hazara Shogran (XIV)	34° 44′	73°27′	2510
6222	97	Hazara Thandhiani (XV)	34° 13′	73° 21′	2438
6228	103	Azad Kashmir Davaryan (XVI)		73° 22′	1980
6230	105	Azad Kashmir Davaryan (XVI)		73° 22′	1980
6237	112	Azad Kashmir Dungian (XVII)	34° 05′	<b>74°</b> 15 ′	2346
6238	113	Azad Kashmir Dungian (XVII)	34° 05′	74° 15′	2346
6248	123	Azad Kashmir Kern (XVIII)	34° 47′	<b>74°</b> 05′	2133
6252	127	Azad Kashmir Kern (XVIII)	34° 47′	74° 05′	2133
6256	131	Azad Kashmir Sharda (XX)	34° 10′	73° 32′	2072
6258	133	Azad Kashmir Sharda (XX)	34° 10′	73* 32′	2072
6259	134	Azad Kashmir Sharda (XX)	34° 10′	73* 32′	2072
6272	147	Azad Kashmir Tararkal (XXI)	33° 35′	74° 11′	1828
6273	148	Azad Kashmir Tararkal (XXI)	33° 35′	74° 11′	1828
6277	150	Chitral Madaglas (XXII)	35° 37′	71° 45′	2500
6281	151	Rawalpindi Bhurban (XXIII)	33° 46′	73° 26′	2500
6286	153	Rawalpindi Patria (XXV)	33° 49′	73° 28′	2500
6299	161	Hazara Naran (XXXIII)	33° 45′	73° 38′	2650
?	654+	Himalaya (Pakistan range)			-
	657+	Himalaya (Pakistan range)			-
?	658 <sup>+</sup>	Himalaya (Pakistan range)			-
; ;	659 <sup>+</sup>	Himalaya (Pakistan range)			-
?	724+	Himalaya (Pakistan range)			-
?	725 <sup>+</sup>	Himalaya (Pakistan range)			-

+654, 657, 658, 659, 724, 725 = trees with lost identity.

## Materials and Methods

The material for this trial consisted of seed from 36 open pollinated families from 16 provenances in northern Pakistan (Table 1). Seed was collected under the guidelines established by the "IUFRO Program of Haploxylon Pine Gene Pool Exchange" coordinated by H. KRIEBEL (1976). Parent trees were apparently selected without regard for any trait-except abundance of cones on individual trees.

Seed was stratified according to standard procedures (Kriebel, 1973) and then sown in the spring of 1981 in in-

dividual polyethylene pots (12 cm  $\times$  18 cm  $\times$  18 cm) in a potting mixture consisting of 70% spruce humus and 30% sand. The seedlings remained in these pots for the first 6 growing seasons.

Inoculation and Experimental Design

Seedlings were artificially inoculated in 1982, 1983 and 1984, between August 20 to 30, when they were 2, 3 and 4 years old. During each inoculation period, pots with seedlings were placed in a polyethylene tent and arranged

Table 2. - Measured traits.

Traits	Units	Symbol
Blister rust resistance	Index 110	BR.1
Trees free of blister rust	%	BR.2
Tree survivers (free + cankered)	%	BR.3
Height increment in the 11-th year	dm	Hi
Total height	dm	Hŧ
Diameter at 1/2 height	cm	D
Basal area at 1/2 height	dm <sup>2</sup>	BA
Stem volume	dm <sup>3</sup>	V

Table 3. - Model for analysis of variance.

Source of	variation DF	MS	E (MS)
Total	JK -1		
Blocks (B)	K-1	MSB	$\sigma_e^2 + J\sigma_B^2$
Families (F)	J – 1	$MS_F$	$\sigma_e^2$ + $\kappa\sigma_F^2$
Error (E)	(J-1)(K-1)	MS <sub>E</sub>	$\sigma_{\rm e}^2$

in a complete block design. Each family was represented by a 12-seedling plot in each of 3 blocks.

Inoculum consisted of heavily infected leaves of Ribes nigrum L. harvested from a single population. Complete details of the inoculation procedure and tent are described by Bingham (1972b).

At age 6 the seedlings were outplanted on the Valiug Forest District (45°17'N latitude and 21°54'E longitude) in a randomized complete block design with 3 replications and 12 seedlings per plot. Space between rows and between trees within rows was 3 m.

The field test included one set of trees that was not inoculated with blister rust, as a control, to measure its performance against the general mean of the 36 inoculated families. The control group contained 36 seedlings and consisted of one seedling randomly selected from each of the 36 families in the test.

## Measurements

Eight traits (Table 2) were measured in the fall of 1991 when the trees were 11 years old. Blister rust resistance was assessed using 3 indices. The first index (BR.1) reflects both the economic and biological impact as well as the incidence of disease. This index takes into consideration both the number and the severity of the lesions. Numerical values were assigned as follows: 1 = tree dead or total susceptibility; 2 = 4 or more serious stem lesions; 3 = 3severe stem lesions; 4 = 3 less severe stem lesions; 5 = 2severe stem lesions; 6 = 2 less severe stem lesions; 7 = 1severe stem lesion; 8 = 1 less severe stem lesion; 9 = branch or very light stem lesions; 10 = no lesions or total resistance. The second and third indices (BR.2 and BR.3) were based on the BR.1 index data, i. e. all trees with a score of 10 were considered "trees free of blister rust (BR.2)", and trees that scored higher than 1 were considered "tree survivors (BR.3)". Before statistical analysis the percentages of BR.2 and BR.3 were transformed to arc  $\sin \sqrt{\%}$  values. The other traits listed in table 2 do not require additional explanation.

## Data Analysis

Analysis of variance was carried out on plot means. The statistical model is as follows:

$$x_{ik} = m + a_i + b_k + e_{ik} \tag{1}$$

 $x_{jk} = m + a_j + b_k + e_{jk} \eqno(1)$  where:  $x_{jk}$  = an individual tree observation from the j-th open-pollinated family in the k-th block; m = the overal mean of the experiment;  $a_j = the$  effect of the j-th open pollinated family (j = 1, 2, ... J);  $b_k = the$  effect of the k-th block (k = 1, 2, ... K);  $e_{jk}$  = the random error.

The model for analysis of variance with expectations of mean squares and formulas for estimating the variance components are presented in table 3.

Standard errors (SE) of the variance components were calculated according to Anderson and Bancroft's (1952) formula (2):

$$SE = \sqrt{\frac{2}{\frac{2}{K_1^2}} \frac{(MS_g)^2}{f_g + 2}}$$
 (2)

where:  $K_1$  = coefficient of the variance components;  $MS_g$ = the g-th mean square; fg = the degrees of freedom of the g-th mean square.

Narrow-sense heritability (h2) estimates at family level were calculated using the formula suggested by Johnson, ROBINSON and COMSTOCK (1955), as follows:

$$h^2 = \sigma^2_F / (\sigma^2_F + \sigma^2_e)$$
 (3)

Table 4. — Analysis of variance (MS), variance components ( $\sigma^2$ ), standard errors (SE|, narrow-sense heritabilities ( $h^2$ ) and trait means ( $\overline{\chi}$ ).

Source of	1	Mean squares of the traits								
variation	DF	BR.1	BR.2	BR.3	Hi	Hŧ	D	BA	V	
Blocks (B) Families (F) Error (E)	2 35 70	0 .100 6 .622 *** 0 .215	0 .021 193 .496** 0 .105	5.951 * 957.447*** 12.965	0.480 0.394 0.296	0 . 108 4 · 214*** 0 · 336	0.025 0.101*** 0.036	0 .028 0 .130*** 0 .048	10 ,774 37 ,502** 13 ,193	
Components										
σ <sub>F</sub> ± SE		2 .136 ± 0 .513	64.464 ± 14.988	314.830 ± 74.171	0.033 ± 0.035	1.292 ± 0.327	0.022 ± 0.008	0.027 ± 0.010	8.103 ± 3.210	
$\sigma_{\mathbf{e}}^2 \pm SE$		0.215 ±0.036	0.105 ± 0.017	12.965 ± 2.161	0.296 ± 0.049	0.336 ± 0.056	0.036 ± 0.006	0.048 ± 0.008	13,193 ± 2,199	
$\sigma_{P}^{2}$		2.351	64.569	327.795	0.329	1,628	0.058	0.075	21.296	
h² ≅		0.909 3.2	0.998 9.7	0.960 49.0	0.100 2.5	0.794 10.4	0. <i>37</i> 9 2.5	0.360 0.043	0.380 0.458	

<sup>\*\*\*</sup> p < 0.001;

where:  $\sigma^2_F$  and  $\sigma^2_e$  = the family and error variance, respectively.

Genetic gain ( $\Delta G$ ) was estimated using Falconer's (1960) formula (4):

$$\Delta G = ih^2 \sigma_P \tag{4}$$

where: i = intensity of selection;  $\sigma_{\rm P}$  = phenotypic standard deviation.

## Results

## Genetic variation

Highly significant differences (p<0.01) were observed among open pollinated families for all traits except height increment in the 11-th year ( $Table\ 4$ ). This suggests that differences were attributable to genetic causes and that selection within the population of blue pine included in this test is possible.

The families were ranked and distributed into homogeneous groups using Duncan's test (Table 5), where:

- Blister rust resistance averaged 3.2 points. The most susceptible family scored only 1.1 points while the most resistant family scored 5.7 points, i. e. 418% more resistant.
- Blister rust resistance was distributed into 13 undifferentiated groups. The first 2 groups encompass the 8 most resistant families originating in 4 natural populations.
- Total height growth averaged 10.4 dm. The slowest growing family was 8.4 dm while the fastest growing family was 13.9 dm, i. e. 65% taller.
- Total height growth was distributed into 16 homogeneous groups. The first 2 groups contain the best 7 families from 7 populations.
- Stem volume growth rate averaged 0.458 dm<sup>3</sup>. The slowest growing family averaged 0.239 dm<sup>3</sup> and the fastest growing family averaged 0.695 dm<sup>3</sup>. A 191 % difference. Of course, we cannot expect such great differences at the end of rotation, as stem volume at young ages is normally less correlated with total production in whole rotation than height.
- Stem volume was distributed into 8 homogeneous groups. The first group contained 3 families of unknown origin and 14 families from 11 populations with known origin.

— Family distribution in many homogeneous groups suggest a polygenic mode of inheritance for both blister rust resistance and growth traits.

The results demonstrate that considerable genetic variation exists at the family level for the most economically important traits. This high genetic diversity could be used in an operational program or as the base for future breeding activities.

### Variance components

Separate analysis for the traits have yielded the variance components and their standard errors listed in the lower part of *table 4*.

The variance component for height increment measured at age 11, was only 10% of the phenotypic variance. This insignificant amount of variation was attributable to a high intensity of blister rust that occured by age 11. Due to such heavy attacks, the height increment in the 11-th year was extremly low for all families.

Genetic component estimates of variance accounted for 91%, 99%, 96%, 79%, 38%, 36% and 38%, respectively, of the phenotypic variance for rust resistance, trees free of rust, tree survival, total height growth, diameter, basal area and stem volume. It is evident that the estimates of family genetic variance for the 3 rust resistance traits (BR.1, BR.2, BR.3) were substantially higher than those for growth traits, with the exception of total height growth.

With the exception of height increment in the 11-th year, all genetic variance component estimates were associated with approximately 2 to 4 times smaller standard errors, indicating their reliability.

These results demonstrated that there is a highly significant amount of genetic variance to be used in a blue pine breeding program.

## Heritability

Estimates of heritability of traits on a family basis are given in the lower part of table 4.

Narrow-sense heritability estimates for rust resistance, trees free of rust, tree survival and total height growth were very high, i. e. 0.909, 0.998, 0.960 and 0.794, respectively. Heritability of other traits such as diameter, basal

The mean square, variance and standard error values for BA and V were multiplied by 1000.

Table~5.~- Distribution of the families into homogeneous groups for several traits according to Duncan's test (p < 0.05).

area and stem volume growth were relatively low, i. e. 0.379, 0.360 and 0.380, respectively.

These significant heritability estimates, coupled with the large amount of variation observed within blue pine, suggests that an effort to increase both rust resistance and height growth through family selection would be rewarding.

## Correlations

Phenotypic correlations between traits are presented in table 6.

Table 6. — Phenotypic correlation among tested traits (DF = 34).

	BR.2	BR.3	Hi	Ht	D	BA	٧	Latit 1)
BR.1 BR.2	0.893 ***	0.890 *** 0.763 ***	0.076 - 0.033	- 0.079 - 0.111	0,172 0.093	0.172 0.086	0.067 - 0.003	0.663 <sup>+++</sup>
BR.3		0.763	- 0.059	- 0,165	0,155	0.141	- 0.001	0.639***
Hi Ht				0,756***	0.510*** 0.700***	0.505**	0.652***	- 0.018
D BA						0.996***	0.927*** 0.934***	0.116 0.221
V								0.044

 $<sup>^{1}</sup>$ ) Only 30 families (with known identity) were taken into consideration;  $^{++}p=0.01$ ;  $^{+++}p=0.001$ .

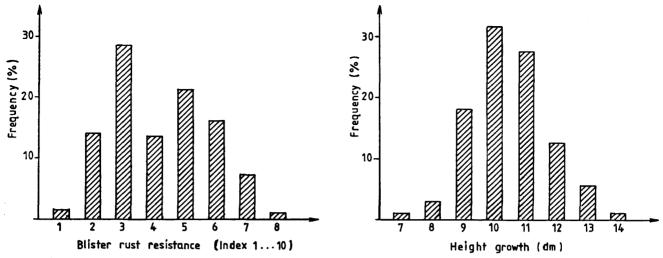


Figure 1. — Frequency distribution in the P. wallichiana tested population evaluated for blister rust resistance and height growth.

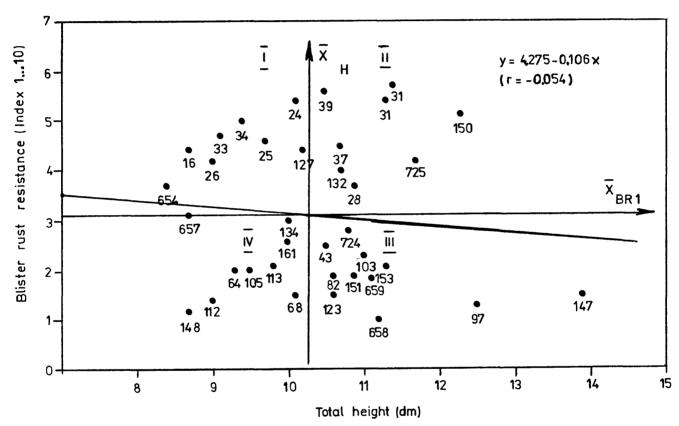


Figure 2. — Regression between blister rust resistance (BR.1) and height growth (Ht).

A highly significant (p<0.001) positive phenotypic correlation was found between blister rust resistance and latitude. Families from northern latitudes exhibited a higher resistance to rust. For example, all 8 families, with the exception of 6256, placed in Duncan's homogeneous groups 1 and 2 have their origin above  $35^{\circ}$ N latitude (*Tables 1* and 5).

There were strong (p<0.001) correlations among growth traits, such as: height increment in the 11-th year, diameter at 1/2 height and total height. Significant positive correlations among these traits imply genetic gain in all of these traits even if selection is undertaken on only 1 trait.

No significant correlations were found between growth traits and latitude and between growth traits and blister rust resistance. Therefore, growth and blister rust resistance are independent traits, which suggests that improvement using indirect selection is not possible in this case. However, indirect selection can be used for improvement in growth traits.

## Type of Distribution

Frequency histograms illustrate the range of blister rust resistance and total height growth of the tested blue pine population (Figure 1). The histograms have a fairly normal distribution although the rust resistance data show a degree of bimodality, suggesting that the tested families

Table 7. — Expected genetic gain ( $\triangle G$ ) for the main traits.

Trait	ΔG(%) if selected the best families					
	5	10	15	20		
BR.1	67	51	40	30		
BR.3	54	41	32	24		
Hŧ	15	11	9	7		
D	6	5	4	3		
ВА	11	9	7	5		
V	18	14	11	8		

could belong to 2 different populations. However, these patterns of variation are specific to quantitative traits that are polygenically controlled. This type of control is extremly important for rust resistance because it provides horizontal resistance which is effective against all races of *C. ribicola* (Vanderplank, 1968).

## Expected Genetic Gain

Table 7 presents the gains which might be expected in tested traits at different levels of selection intensity. If the best 5, 10, 15 or 20 of the 36 families were selected and planted on sites similar to that used in this trial, a genetic gain in blister rust resistance (BR.1) and stem volume growth rate of about 67%, 51%, 40%, 30% and 18%, 14%, 11% and 8%, respectively, could be achieved. Even smaller increases than these would result in appreciable improvement if the planting area is large enough. Therefore, breeding blue pine for blister rust resistance and growth traits would be both possible and profitable.

Differences Between Inoculated and Uninoculated Progenies

A comparison of overall means at age 11 indicates that uninoculated trees perform 213%, 60%, 26%, 9%, 14% and 40% better in rust resistance (BR.1), height increment in the 11-th year, total height growth, diameter, basal area and stem volume growth rate, respectively (*Table 8*). It is

obvious that blister rust caused significant losses in the main economically important traits of blue pine.

### Breeding Strategy

Using the results of this test one can develop a program for blue pine improvement. According to Zobel and Talbert (1984), the "family plus within-family selection" method is the predominant form of selection used in most advanced generation tree improvement programs. This method consists of selecting the best families along with the best individuals within those families. Consequently, this method will be adopted for improving blister rust resistance and total height growth. Since there is no significant positive correlation between the 2 traits, indirect selection is not applicable in this instance. For our purposes "tandem selection" will be employed, e. g. the blister rust resistance will be improved first. When a desired level has been obtained, breeding efforts will be concentrated on growth traits. However, if one intends to improve blister rust resistance and height growth simultaneously, then an "independent culling" method would be recommendable.

#### Discussions and Conclusions

The results of this study confirmed that the economically important traits, such as height growth, volume growth rate and blister rust resistance vary widely with seed source. It should be mentioned that though the degree of variation in blister rust resistance was extremly high, the general mean of this trait was unexpectedly low. Perhaps the artificial inoculation was too heavy and the tested biological material was not resistant enough.

The main conclusions of this study are as follows:

- (1) The blue pine sources used in this trial exhibited only a low to moderate level of blister rust resistance.
- (2) Highly significant genetic variation in both rust resistance and growth traits was found within open pollinated blue pine populations from the Himalayan Mountains of Pakistan.
- (3) The high amount of genetic variance observed in this trial could be exploited in an operational program or as a base for future breeding activities.
- (4) The very high estimated heritability value for blister rust resistance and the moderate values for some growth

Table~8.- Differences (d) in some traits between blue pine open-pollinated families, artificially inoculated (I) with blister-rust and uninoculated (U).

Genotype/	Traits					
<sup>/</sup> Difference	BR	Hi	Ht	D	BA	٧
Inoculated (1) Uninoculated (U) Difference (%) (d)	3.2 10.0 +213	2.5 4.0 +60	10.4 13.1 +26	2.3 2.5 +9	0.043 0.049 + 14	0.458 0.643 + 40

$$d = \frac{U - I}{I} \times 100$$

traits, along with a highly significant variation ensures the success of blue pine improvement.

- (5) A lack of significant correlation between blister rust resistance and growth traits suggests that indirect selection is not applicable. A tandem selection, starting with blister rust resistance as the most important trait, appears to be a suitable improvement method.
- (6) Both blister rust resistance and growth traits seem to be polygenically controlled. Such control confers a "horizontal" resistance which is equally effective against all races of *C. ribicola*.
- (7) A significant genetic gain could be achieved by planting the best families on suitable sites.

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#### Literature

Ahsan, J. and Khan, M. I. R.: Pinus wallichiana A. B. Jackson in Pakistan, In: Bingham, R. T. et al. (Eds): Biology of rust resistance in forest trees. USDA For. Serv., Misc. Publ., 1221, pp. 151-162 - Anderson, R. L. and Bancroft, T. A.: Statistical theory in research. Mc Graw-Hill Book Co., New-York, 399 p., (1958). BINGHAM, R. T.: Taxonomy, crossability, and relative blister rust resistance of 5-needled white pines. In: BINGHAM, R. T. et al. (Eds.): Biology of rust resistance in forest trees. USDA For. Serv., Misc. Publ., 1221, pp. 271-280 (1972a). - BINGHAM, R. T.: Artificial inoculation of a large number of Pinus monticola seedlings with Cronartium ribicola. In: BINGHAM, R. T. et al. (Eds): Biology of rust resistance in forest trees. USDA For. Serv., Misc. Publ., 1221, pp. 357—372 (1972b). — BINGHAM, R. T., KRIEBEL, H. B. and GREMMEN, J.: Report of the 1969 organizational meeting of the working party for resistance of white pines to blister rust. In: BINGHAM, R. T. et al. (Eds.): Biology of rust resistance in forest trees. USDA For. Serv., Misc. Publ., 1221, pp. 645-656 (1972). -I.: Genetic resistance to Cronartium ribicola and height growth in some five needle pines and of some interspecific hybrids. Ph. D. Thesis, Academy of Agric. and Forestry Sci., Bucharest. 146 p. - BLADA, I.: Analysis of genetic variation in a Pinus strobus x P. griffithii F, hybrid population. Silvae Genetica 41 (4-5): 282-289 (1992). - CRITCHFIELD, W. B. and LITTLE, E. L.: Geographic distribution of the pines of the world. USDA For. Serv., Misc. Publ., 991, 97 p. (1966). — Delatour, C. and Birot, Y.: The international IUFRO experiment on resistance of white pines to blister rust. In: HEYBROEK, H. et al. (Eds.): Resistance to diseases and pests in forest trees. PUDOC, Wageningen, The Netherlands. - Dogra, P. D.: Intrinsic qualities, growth and pp. 412-414 (1982). adaptation potential of Pinus wallichiana. In: BINGHAM, R. T. et al. (Eds): Biology of rust resistance in forest trees. USDA For. Serv., Misc. Publ., 1221. pp. 163-178 (1972). -- FALCONER, D. S.: Introduction to quantitative genetics. Ronald Press, New-York. 365 p. (1960). — Heimburger, C.: Forest tree breeding and genetics in Canada.. In: Proc. Genetics Soc. Canada, Vol. 3, pp. 41-49 - Heimburger, C.: Breeding for disease resistance in forest trees. For. Chron. 38: 356-362 (1962). --- Heimburger, C.: Relative blister rust resistance of native and introduced white pines in eastern North America. In: BINGHAM, R. T. et al. (Eds.): Biology of rust resistance in forest trees. USDA For. Serv., Misc. Publ., 1221, pp. 257-269 (1972). --- Hoff, R. J., Bingham, R. T. and McDonald, G. I.: Relative blister rust resistance of pines. Eur. J. For. Path 10(5): 307-316 (1980). - Johnson, H. W., Robinson, H. F. and Comstock, R. E.: Estimates of genetic and environmental variability in soybean. Agron. Journal 47: 314—318 (1955). KRIEBEL, H. B.: Methods for germinating seed of five needle pines. IUFRO Instructions, 2 p. (1973). --- KRIEBEL, H. B.: The IUFRO program for haploxylon pine gene pool exchange, selection and breeding. In: Proc. 16-th IUFRO World Congress, Oslo, pp. 239-- Kriebel, H. B.: Breeding eastern white pine: a 245 (1976). world-wide perspective. Forest Ecology and Management 6: 263-279 (1983). -- KRIEBEL, H. B and Dogra, P. D.: Adaptability and growth of blue pine of documented seed origin in northern Ohio. U.S.A. (In preparation, 1993). - LEANDRU, L.: Hibrizi interspecifici la pini. Buletin ICAS, Seria 2-a, 78 p. (1982). -R. F.: Interspecific hybridization in breeding for white pine blister rust resistance. In: GERHOL, H. D. et al. (Eds.): Breeding pest resistance trees. Pergamon Press, Oxford, pp. 367-376 (1964). RIGHTER, F. I. and DUFFIELD, J. W.: Interspecies hybrids in pines. J. Hered. 42: 75-80 (1951). - STEPHAN, B. R.: The IUFRO experiment on resistance of white pines to blister rust in northern Germany. Proc. 18th IUFRO World Congress, Ljubliant, Division 2, Vol. I, 80-89 (1986). — Vanderplank, J. E.: Disease resistance in plants. Academic Press, New York. 201 p. (1968). — Wright, J: Species hybridization in the white pines. Forest Sci. 5: 210-222 - ZOBEL, B. and TALBERT, J.: Applied forest tree improvement. John Wiley and Sons, New York. 505 p. (1984). -L.: Poplar, white pine and ornamental tree breeding at Ontario For. Res. Centre, Maple. In: Proc. 17th Meet. Canad. Tree Improv. Assoc., Chalk River, pp. 133-138 (1979a). - Zsuffa, L.: The genetic improvement of eastern white pine in Ontario. In: SCARRAT, J. B. (Ed.): Proc. Tree Improv. Symp., Toronto, Can. For. Serv. Publ., 0-P-7, pp. 153-160 (1979b).

# Inheritance of Initial Survival and Rooting Ability in Eucalyptus Globulus Labill. Stem Cuttings

By N. M. G. Borralho<sup>1</sup>) and Ph. J. Wilson<sup>2</sup>)

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## Summary

Additive genetic variances and covariances and their corresponding heritabilities and genetic correlations were estimated for the initial survival of *Eucalyptus globulus* Labill. stem cuttings (in the propagation environment) and the rooting ability of the survivors. Cuttings were harvested on four occasions from 494 clones of 10 full-sib

families. Percentage survival of cuttings was moderately heritable, with an estimated overall heritability of  $\mbox{$\hat{n}^2$=0.20}$ , whereas the percentage of survivors which rooted had a higher estimated heritability ( $\mbox{$\hat{r}^2$=0.41}$ ). There were no genetic or phenotypic correlations between these traits ( $\mbox{$\hat{r}_g$=$-0.12}$  and  $\mbox{$\hat{r}_p$=$-0.02}$ , respectively). The magnitude of the genotype-occasion interaction was marked for survival (P<2%) but small and not significant for rooting (P>50%). These results indicate that genetic improvements of propagation characteristics in E. globulus could be made, and that survival and rooting ability of the survivors should be assessed separately. Selection accuracy appeared to increase with higher overall levels of survival and rooting.

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Cooperative Research Centre for Temperate Hardwood Forestry, Plant Science Dept., University of Tasmania, GPO Box 252C, Hobart, Tasmania 7001, Australia.

<sup>&</sup>lt;sup>3</sup>) Departamento de Engenharia Florestal, Inst. Superior de Agronomia, Tapada da Ajuda, P-1399 Lisboa, Portugal.