Estimated Frequency of Natural Selfing in Lodgepole Pine (Pinus contorta var. murrayana) from Central Oregon

By F. C. Sorensen

U.S. Department of Agriculture, Forest Service,
Pacific Northwest Research Station,
Corvallis, Oregon 97331, USA

(Received 12th June 1986)

Summary

Frequency of natural selfing was estimated using recessive morphological marker traits in 27 wind-pollination progenies. Single-family estimates ranged from 0.4 to 41.0 percent self seedlings with mean value of 6.7 percent and median of 3.7 percent.

Key words: Inbreeding, selfing, mutant seedlings, lodgepole pine,
Pinus contorta var. murrayana.

Zusammenfassung

Es wurde die Häufigkeit von natürlicher Selbstung in 27 frci abgeblühten Nachkommenschaften unter Verwendung rezessiver morphologischer Merkmale geschätzt. Die Schätzwerte für Einzelfamilien lagen zwischen 0,4 und 41% für gesclbstete Sämlinge mit einem Mittel von 6,7% und einem Medianwert von 3,7%.

In 1982 and 1983, 272 families of lodgepole pine (*Pinus contorta* var. *murrayana* Grev. & Bale.) from the Cascade Range between the Columbia River and the Oregon-California border and from the Warner Mountains of southcentral Oregon were sown in a nursery test. Twenty-seven families were identified in the nursery as carrying morphological mutant markers that could be readily identified in the seedling progeny. Extra seeds from these families were germinated, mutant frequencies were determined, and the percentage of natural selfing at the germinant seedling level was estimated. This note summarizes the results.

Two types of mutants were observed: chlorophyll deficiencies (white seedling and various shades of yellow seedlings) and cotyledonary-lethal. The cotyledonary-lethal seedlings were nearly normal in appearance, but the cotyledons shriveled early in development (Franklin 1969). Three classes of cotyledonary-lethals were distinguished; before seedcoat shed (early), after seedcoat shed but before primary needle elongation, and when primary needles were 5 to 10 mm long (late).

The mutant markers observed in the wind-pollination progenies were used to estimate the frequency of seedlings that came from self-fertilization. The normal segregation ratio for a completely recessive, single-gene character is, after self-fertilization, 3 normal seedlings to 1 mutant (STURTEVANT and BEADLE 1962). Each mutant phenotype represents four individuals arising from self-fertilization. For a number of reasons (Sorensen 1967), this ratio is often different from 3 to 1. Based on counts from self-pollination families, average segregation ratios of 4.0 normal to 1 mutant and 4.2 to 1 have been reported for loblolly pine (Pinus taeda L.) (Franklin 1969) and Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) (Sorensen 1973), respectively. As part of another study (Sorensen and Adams, in preparation), an average ratio of 3.9 to 1 was observed in self-pollination families of lodgepole pine in central Oregon. In the present report, each mutant is assumed to represent 4.9 self-fertilization seedlings rather than the expected 4. For example, the percentage of selfing for family 1071 (*Table 1*, line 1) was estimated as:

 $(1 \text{ mutant} \times 4.9)/1342 \times 100 = 0.4.$

Mutant types and frequencies of self-seedlings are listed in *Table 1* for the 27 families. The mean frequency of self-seedlings was 6.7 percent, the median 3.7 percent, and the distribution strongly skewed to lower frequencies.

Of the four families with estimates greater than 10 percent for self-pollination seedlings, two families (1451 and 1452) came from the same stand that partially occupies a meadow of about 5 hectares, one (1042) came from a fringe stand around a mountain lake, and one (1442) came from an extensive lodgepole pine stand. Tree 1442 gave a very low percentage of filled seed — 94.6 percent of the round, normal-appearing seeds were empty. This suggests that its flowering phenology may be at an extreme end of the time distribution for its stand, thereby favoring selfing. Excluding these four families, the mean value for natural selfing was 3.4 percent.

All mutant phenoypes were treated as if they had resulted from self-fertilization, but some may represent matings between relatives. For this reason also, the true average level of self-fertilization is probably lower than that indicated in *Table 1*.

Table 1. — Mutant types, sample sizes, and calculated frequencies of self-seedlings for 27 lodgepole pine families from central Oregon. Frequency of selfing was calculated as [(number of mutants \times 4.9)/number of seddlings] \times 100. See text for further explanation.

Family	Mutant type	Total seedlings	Mutant seedlings	Self- seedling:
		(No.)	(No.)	(Percent
1071	White seedling	1342	1	0.4
942	Late cotyledonary-lethal	1250	1	. 4
1711	Late cotyledonary-lethal	3576	3	. 4
1721	Cotyledonary-lethal	1117	1	. 4
631	Yellow cotyledons	1312	2 2	.7
881	Cotyledonary-lethal	1150	2	. 8
391	White seedling	1158	2 2 3	. 9
941	Late cotyledonary-lethal	686	2	1.4
451	Pale yellow-green cotyledons	952	3	1.5
321	Early cotyledonary-lethal	870	3	1.7
1402	Yellow cotyledons	2521	12	2.3
682	Late cotyledonary-lethal	373	2	2.6
1921	Yellow cotyledons	145	1	3.4
1041	Pale yellow cotyledons	265	2	3.7
441	Yellow cotyledons	1345	11	4.0
152	Bright yellow cotyledons	347	3	4.2
1381	Cotyledonary-lethal	193	2	5.1
621	White seedling	€25	10	5.9
663	Cotyledonary-lethal	03	1	6.1
392	White seedling	502	7	6.8
1941	Cotyledonary-lethal	184	3	0.8
1121	Cotyledonary-lethal	334	7	8.9
1351	Pale yellow cotyledons	50	1	9.8
1451	Yellow cotyledonary	813	22	13.3
1042	Cotyledonary-lethal	2079	79	18.6
1442	Cotyledonary-lethal	35	2	28.0
1452	White seedling	1792	150	41.0
			Mean	6.7
			Median	3.7

Three of the four families with high frequencies of self-pollination seedlings came from small stands; the fourth from a tree which was contributing very few filled seeds to the regeneration seed pool. For widespread stands, the median appears to provide a better estimate of natural production of self-seedlings for central Oregon lodgepole pine than does the mean. Natural inbreeding appears to occur at relatively low frequency and should have negligible impact on natural or artificial regeneration of *P. contorta* var. *murrayana* in Oregon, except perhaps for a few stands or for a few individuals. The low level of natural self-fertilization is comparable to results reported for *P. contorta* var. *latifolia* in northeastern Washington (Epperson and Allard 1984) and British Columbia (Yeh and Layton 1979).

Acknowledgement

Seeds for some of the families were furnished by personnel of the Deschutes, Fremont, Mount Hood, and Winema National Forests, USDA Forest Service; the Bureau of Land Management, U.S. Department of the Interior; Diamond-International Corporation; and Weyerhaeuser Company.

References

EPPERSON, B. K., and Allard, R. W.: Allozyme analysis of the mating system in lodgepole pine populations. J. Hered. 75: 212-214 - Franklin, E. C.: Mutant forms found by self-pollination in loblolly pine. J. Hered. 60: 315-320 (1969). -- SORENSEN, F. C .: Linkage between marker genes and embryonic lethal factors may cause disturbed segregation ratios. Silvae Genet. 16: 132-134 (1967). Sorensen, F. C.: Frequency of seedlings from natural selffertilization in coastal Douglas-fir. Silvae Genet. 22: 20-24 (1973). Sorensen, F. C., and Adams, W. T.: Self-fertility and natural selfing in three contrasting stands of lodgepole pine (Pinus contorta var. murrayana) in the central Oregon Cascades (in preparation). -- Sturtevant, A. H., and Beadle, G. W.: An introduction to Genetics. Dover Publications, Inc., New York, N.Y. 391 p. (1962). YEH, F. C., and LAYTON, C.: The organization of genetic variability in central and marginal populations of lodgepole pine Pinus contorta spp. latifolia. Can. J. Genet. Cytol. 21: 487-503 (1979).

Genetic Variation in Juvenile Characters of Populus deltoides Bartr. from the Southern Great Plains 1)2)

By C. D. Nelson and C. G. Tauer3)

(Received 12th June 1986)

Summary

Genetic variation in first and second year characters of eastern cottonwood (*Populus deltoides* Barta.) from the southern Great Plains was assessed. Open-pollinated seed from four trees in each of 40 natural stands (159 families) was collected in June 1982 and sown in a greenhouse in July 1982. The seedlings were outplanted to two nursery locations in Oklahoma following seven weeks of greenhouse-growth.

The following data were collected during the first two years of growth: greenhouse height (GHT); first year height (HT1) and date of leaf fall (LF1); second year height (HT2), date of leaf fall (LF2), *Melampsora* spp. leaf rust score (MLR), number of branches per decimeter of tree height (BRPD) and survival (SURV). Analyses of variance were performed for each character, to test for significance of differences among stand and among family within-stand means. Geographic variation (among stand) was quantified and characterized. Family mean heritabilities and genetic correlation coefficients were estimated for each character and selected pairs, respectively.

Significant (P < .05) differences among stand means were found for all characters except SURV and among family means for GHT, HT1, DIA, LF1, LF2, MLR and BRPD. Significant location by stand interactions were found for all characters, while location by family interactions were significant for LF1 only. Continuous northwest-to-southeast patterns of variation were found for all characters except BRPD. Heritability estimates were zero for SURV (.00 \pm .14) ;moderate for HT2 (.19 \pm .15) and DIA (.30 \pm .13); and high for GHT (.49 \pm .07). HT1 (.35 \pm .10),

LF1 (.39 \pm .11), LF2 (.61 \pm .07), MLR (.38 \pm .11) and BRPD (.69 \pm .06). Genetic correlation coefficients between characters showed second year diameter (DIA) to be the most useful character on which to base selections at age two.

Key words: Genetic variation, geographic variation, juvenile characters, heritability, genetic correlation, Populus deltoides.

Zusammenfassung

Bei Populus deltoides BARTR. aus den südlichen Great Plains wurde die genetische Variation von Merkmalen im ersten und zweiten Jahr geschätzt. Frei abgeblühte Samen von vier Bäumen in jedem der 40 natürlichen Bestände (159 Familien) wurden im Juni 1982 gesammelt und im Juli 1982 in einem Gewächshaus ausgesät. Die Sämlinge wurden sieben Wochen später in zwei Baumschulen in Oklahoma ausgepflanzt, und in den ersten zwei Jahren wurden folgende Daten erhoben: Gewächshaushöhe (GHT), Einjahreshöhe (HT1), Datum des Laubabfalles (LF1), Zweijahreshöhe (HT2), Datum des Laubabfalles (LF2), Melampsora spp. Blattrostbefall (MLR), Anzahl Äste pro dm Baumhöhe (BRPD) und Überlebensfähigkeit (SURV). Für jedes Merkmal wurden Varianzanalysen durchgeführt, um die Signifikanzen der Unterschiede zwischen Beständen und Familien innerhalb der Bestände zu testen. Die geographische Variation (zwischen Beständen) wurde quantifiziert und charakterisiert. Familienheritabilitäten im engeren Sinne und genetische Korrelationskoeffizienten wurden für jedes Merkmal und selektierte Paarungen geschätzt. Signifikante Unterschiede für P < 0,05 zwischen Bestandesmittelwerten wurden für alle Merkmale außer SURV und zwischen Familien für GHT, HT1, DIA, LF1, LF2, MLR und BRPD gefunden. Signifikante Standort imes Bestand-Interaktionen wurden für alle Merkmale gefunden, während Standort imes Familien-Interaktionen nur für LF1 festzustellen waren. Kontinuierliche Nordwest/Südost-Variationsmuster wurden für alle Merkmale außer BRPD gefunden. Heritabilitäts-Schätzwerte waren für SURV null (0,00 \pm 0,14), für HT2 (0,19 \pm 0,15) und DIA (0,30 \pm 0,13) gemä-

216 Silvae Genetica 36, 5—6 (1987)

¹) Journal article No. J-4777 of the Oklahoma Agricultural Experiment Station, Oklahoma State University, Stillwater, OK 74078.

²) This study was funded in part by United States Forest Service, Cooperative agreement No. 19-84-64, Southern Forest Experiment Station.

³⁾ Research Assistant, Department of Forest Resources, University of Minnesota, St. Paul, MN 55108 and Professor, Department of Forestry, Oklahoma State University, Stillwater, OK 74078.