

Some final comments shall be devoted to one of the strongest assumptions of the previous theoretical investigations: the required proportionality between 'survival' and 'yielding ability'. This assumption may be due to vehement criticism.

All results and conclusions which have been obtained in this paper are only valid for populations where this assumption holds.

The survival-parameter describes the shifts of the initial composition of the clonal mixture and the yielding ability-parameter characterizes the different yielding potential of the clones (independent on the selective effects).

In our opinion, a proportionality between these two characters will be a very common situation in the field of practical applications. Many natural selection processes and the different non-systematic artificial thinning procedures too are in accordance with this simplifying assumption: In intimately mixed clonal mixtures lower-yielding individuals will be predominantly rejected if one applies non-systematic artificial thinning procedures. If this larger or lower yielding-capacity reflects a non-environmentally induced clone-specific genetic property, such a thinning approach will result in an increased frequency of the individuals of the higher-yielding clones in the final composition of the clonal mixture compared to the initial composition of the clonal mix. Correspondingly, a decrease

of the proportions of the lower-yielding clones will be observed.

Summarizing these facts, we may confirm and justify the required assumption of a proportionality between 'survival' and 'yielding ability'. Under the circumstances described above, this proportionality will be a common situation rather than a quite particular case. The results and conclusions of this paper, therefore, may be considered to be of significant practical relevance and interest.

But, nevertheless, there may be also situations where this assumption doesn't hold. For such cases the previous results and conclusions cannot be applied.

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Changes in Genetic Parameters and Ranks of Tree Height over Six Growth Years in *Tecomella undulata* (Sm.) Seem

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Abstract

Eleven half-sib plant progenies of *Tecomella undulata* (SM) SEEM were established during 1984. Tree height for six growth years was recorded. Progenies showing good growth in the initial stages were not necessarily performing the same in subsequent years. There were significant differences among the progenies over all the six growth years. Estimates of family heritability, single tree heritability and genetic gains from family and mass selection indicated that the gains were low with both the methods. As components of variance tend to stabilize after fourth year of growth, selection done in the earlier years may not be rewarding. Low values of heritability and genetic gains from family and single tree selection suggested that there is need for other selection procedures for higher genetic gains for tree height.

Key words: *Tecomella undulata*, height growth, half sib progeny trial, heritabilities, family vs. mass selection.

Introduction

Tecomella undulata (SM.) SEEM, an important multi-purpose tree of Indian arid zone has been widely exploited for carving, furniture and agricultural implements. As a result population of *T. undulata*, particularly the trees with desirable attributes is going down drastically. Till 1983, however, no effort had been made to understand the

variability *in situ* to collect the desirable types and use them in genetic improvement programme. Surveys were undertaken to assess the variability *in situ* for various morphological traits and foliage quality characters (JINDAL *et al.*, 1987a and b). Exploitation of germplasm collected during the surveys necessitated the study of between and within family variability and changes in genetic parameters over growth years. Hence eleven half-sib plant progenies trial was established in 1984 to predict the genetic gains from single trees and family selections.

Material and Methods

During May 1983 survey of *T. undulata* was conducted and 24 plus trees were identified from different parts of Rajasthan. Seeds from these trees were collected and the progenies were evaluated in nursery for many seedling characters. Eleven progenies were transplanted in the field in July 1984 in a randomised complete block design with three replications. Plot size was of two rows, each row accommodating 7 plants. Tree to tree distance within and between rows was 3 m x 3 m. Tree height on all the surviving plants was recorded every December from 1984 to 1989. Some plants which were apparently dead in first or second year showed regeneration. Data of such trees was not included in statistical analysis. Data were

Table 1. — Expectations of mean squares.

Source	d.f.	Expectations
Blocks	b — 1	$\sigma_e^2 + C\sigma_{bp}^2 + CP\sigma_b^2$
Progenies	p — 1	$\sigma_e^2 + C\sigma_{bp}^2 + CB\sigma_p^2$
B x P	(b — 1) (p — 1)	$\sigma_e^2 + C\sigma_{bp}^2$
Error	bp (c — 1)	σ_e^2

C = 12.9 ; number of plants/plot was not constant

Table 2. — Source, tree height and DBH of selected mother trees.

Acc. No.	Source		Tree ht. (m)	DBH (cm)
	Village	District		
TU 3	Mogra	Jodhpur	6.0	16.8
JUF	Jodhpur	Jodhpur	—	—
TU 189	Haikhala	Jodhpur	8.6	33.1
TU 35	Kathari	Barmer	7.4	25.4
TU 60	Kaludi	Barmer	5.9	16.0
TU 74	Rawatsar	Barmer	6.6	22.6
TU 59	Kaludi	Barmer	7.8	25.4
TU 109	Chohtan	Barmer	11.0	60.0
TU 81	Rawatsar	Barmer	5.7	17.7
TU 95	Salonre ka Tla	Barmer	6.2	16.4
TU 106	Chohtan	Barmer	9.8	63.5

analysed tree wise and variance components were calculated as per expected mean squares given in table 1. Since number of trees living per plot was not uniform,

therefore C value was worked out. Family heritability with and without blocks were worked out as under.

$$\% \text{ Family heritability} = \frac{\sigma_p^2}{\sigma_e^2/CB + \sigma_{bp}^2/B + \sigma_p^2} \times 100$$

$$\% \text{ single tree heritability (without blocks)} = \frac{4 \sigma_p^2}{\sigma_e^2 + \sigma_{bp}^2 + \sigma_p^2} \times 100$$

$$\% \text{ single tree heritability (with blocks)} = \frac{4 \sigma_p^2}{\sigma_e^2 + \sigma_{bp}^2 + \sigma_p^2 + \sigma_b^2} \times 100$$

Genetic gain from half-sib progeny trial was calculated as below: —

$$\text{Genetic gain from family selection} = (\text{Selected families} - \text{average families}) \times \text{family heritability}$$

$$\text{Expected mass selection gain} = (\text{Selected trees} - \text{average trees}) \times \text{single tree heritability}$$

Genetic gain for family selection was calculated by using mean height of single family with highest mean, and for mass selection 39 best trees were used.

Results and Discussion

Tree height, DBH and location of eleven mother plants are given in table 2. Eight mother trees were from five villages of Barmer district and three mother trees were from three villages of Jodhpur district. Mother tree height and DBH ranged from 5.7 m to 11.0 m, and 16.0 cm to 63.5 cm respectively. These high ranges were due to differences in site, age and genotypes.

Table 3. — ANOVA for tree height in *T. undulata*.

Source of variation	df	Mean square					
		1984	1985	1986	1987	1988	1989
Blocks	2	1166*)	1013	5596	85800**)	8714	5646
Progenies	10	2028**)	3051*)	6476**)	20120**)	17109**)	15542**)
B x P	20	414	2257*)	3942**)	9565**)	9099**)	8351*)
Error	394	310	1397	2054	3999	4457	4422

*) P < 0.05 **) P < 0.01

Table 4. — Mean tree height of 11 half-sib progenies of *T. undulata* transplanted in July, 1984.

Acc. No.	Mean tree height (m)					
	1984	1985	1986	1987	1988	1989
TU 3	0.53	1.02	1.70	1.95	2.14	2.21
JU F	0.72	1.26	2.04	2.23	2.39	2.48
TU 189	0.55	1.03	1.73	1.86	1.99	1.99
TU 35	0.57	1.10	1.91	2.09	2.29	2.28
TU 60	0.47	1.06	1.85	2.03	2.32	2.33
TU 74	0.46	1.02	1.99	2.53	2.70	2.66
TU 59	0.61	1.09	1.95	2.34	2.43	2.46
TU 109	0.61	1.21	1.93	2.49	2.58	2.58
TU 81	0.53	0.99	1.92	2.11	2.23	2.32
TU 95	0.54	1.19	2.01	2.47	2.59	2.62
TU 106	0.54	1.05	1.67	2.12	2.21	2.21
Mean	0.56	1.09	1.88	2.20	2.35	2.38
Tree ht.						
CD 5%	0.08	0.17	0.20	0.28	0.30	0.30
CD 1%	0.10	0.22	0.26	0.37	0.39	0.39
SEm	0.03	0.06	0.07	0.10	0.11	0.11

Table 5. — Family and single tree heritability and percentage of variation due to different components in *T. undulata* for height in six years of growth.

	1984	1985	1986	1987	1988	1989
% Family heritability	79.6	52.9	39.1	52.5	46.8	46.3
% single tree h ² (without blocks)	46.4	5.5	11.6	23.2	16.5	15.1
% single tree h ² (with blocks)	45.7	—	11.5	20.82	—	—
% of variation due to:						
Blocks	1.45	—	0.51	10.25	—	—
Progenies	11.42	1.38	2.87	5.20	4.12	3.78
B x'P	2.21	4.49	6.43	8.23	7.16	6.20
Error	84.91	94.13	90.19	76.31	88.72	90.01

(—) Since σ_r^2 value was negative, therefore, it was taken as zero

Table 6. — Genetic gain for tree height by selecting one best family comprising 39 trees and by selecting 39 best trees in the progeny trial of *Tecomella undulata*.

Selection method	1984	1985	1986	1987	1988	1989
<i>Family selection.</i>						
Mean ht. of best family (m)	0.72	1.26	2.04	2.53	2.70	2.66
Genetic gain	0.127	0.089	0.062	0.173	0.164	0.130
Genetic gain as % of mean	22.7	8.2	3.3	7.9	7.0	5.5
<i>Mass selection</i>						
Mean ht. of 39 best trees (m)	0.90	1.81	2.68	3.32	3.40	3.45
Range (m)	0.82—	1.62—	2.50—	3.05—	3.20—	3.20—
	1.18	2.25	3.20	4.00	4.30	4.30
Genetic gain	0.159	0.040	0.093	0.260	0.173	0.162
Genetic gain as % of mean	28.5	3.6	4.9	11.8	7.4	6.8

The criteria of selection of plus trees were, however, straight, cylindrical, solid bole free from insect pests and diseases.

There were significant differences among the eleven progenies for tree height for all the six years (Table 3) though rate of growth was not same in all the progenies. The slowest growing progeny (TU 74) in the first year ranked first in the sixth year, whereas progeny (JUF) showing maximum height in first year ranked fourth in the sixth year of growth. Overall growth of the *T. undulata* population increased from 0.557 m in first year to 2.376 m in the sixth year, it being rapid in first three years (Table 4).

Family heritability and single tree heritability without blocks in different years is given in Table 5. Family heritability is more than single tree heritability. Family heritability is high in the first year, and tends to stabilize to moderate values from fourth year of growth. Single tree heritability was moderate in first year and low in subsequent years. The differences in values of family heritabilities and single tree heritabilities may not provide sufficient information for selection method to be followed for maximum genetic gains. The genetic gains for tree height by selecting one best family having an average of 39 trees and by selecting 39 best trees in the progeny trial comprising of 397 trees are presented in table 6. The

differences in gain by family selection over mass selection are not as high as appeared from differences in heritabilities. This has happened because the differences among family means are much less than those among individual trees. As a result selection differential is much less in family selection than in single tree selection. With 10% selection intensity gains were low with both the family selection and mass selection; the gains were slightly more with mass selection in most of the years. Like heritability gains from family and single tree selections were more in the first year of growth than that of subsequent years. High heritability in first year and its decrease with growth period upto first few years have been reported in *Picea sitchensis* (SAMUEL and JOHNSTONE, 1979), *Liquidambar styraciflua* and *Platanus occidentalis* (SCHULTZ, 1983) and black walnut (RINK, 1984). Components of variance as indicated by percentage of variation due to blocks, progenies, their interaction and error are fluctuating over years (Table 5). The fluctuations are more during first three years of growth and components appear to stabilize after fourth year of growth. Thus the selection based on genetic parameters derived from first three year growth data may not be effective. The values of heritability and genetic gains in the subsequent years are low and for gains in height it may be necessary to use other selection procedures.

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Untersuchungen zum Korrelationsmuster von Lärchenbeständen

1. Mitteilung: Problemstellung, Versuchsmaterial, Auswertungsmethodik sowie theoretische Nachbarschaftskorrelationen

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Zusammenfassung

In der Reihe "Untersuchungen zum Korrelationsmuster von Lärchenbeständen" werden auf der Grundlage eines umfangreichen Lärchendatenmaterials bestehend aus europäischen und japanischen Lärchen sowie deren Hybriden experimentelle Ergebnisse zur Korrelationsstruktur von Beständen (Nachbarschaftskorrelationen) sowie zur zeitlichen Veränderung dieses Korrelationsmusters während der Bestandsentwicklung diskutiert. Die herangezogenen Merkmale sind "Höhe" und "Durchmesser".

Die vorliegende 1. Mitteilung umfaßt zunächst eine Einführung in die Problemstellung sowie eine Darstellung der Gesamtkonzeption. Daneben erfolgt eine Beschreibung der zehn verwendeten Lärchenversuchsflächen (Standort, Sorten, Anlagdatum, Wiederholungen, Parzellengrößen, Verband, Messungen, Populationsumfänge) sowie eine Diskussion der verschiedenen herangezogenen Auswertungsmethoden, wie z. B.: 1. Definition der unterschiedlichen Korrelationskoeffizienten zur Untersuchung der Nachbarschaftskorrelationsstruktur der Bestände und 2. Konstruktion von Thiessen-Polygonen zur Analyse von Beständen mit unregelmäßigen Pflanzenverteilungen.

Daneben werden noch einige mehr am Rande liegende Fragestellungen mit angesprochen, wie z.B.: 1. Beiträge derartiger Korrelationsuntersuchungen zum Problem der Beständigkeit der überlegenen Leistung der Hybriden bzw. zur zeitlichen Dauer einer Hybridenüberlegenheit und 2. Beziehungen zwischen den realisierten Merkmalswerten und den zur Verfügung stehenden Standräumen der einzelnen Bestandesindividuen, wenn diese Standräume über die Flächen der zugehörigen Thiessen-Polygone quantifiziert werden. Diese Untersuchungen sollen anhand einer langjährig (bis zum Alter 50) einzelbaumweise vermessenen Versuchsfläche durchgeführt werden.

Unter einer Reihe von vereinfachenden Annahmen (regelmäßiger quadratischer Pflanzverband ohne Fehlstellen; gleiches Alter der Bestandesindividuen; statische Betrachtungsweise, d. h. Beschreibung der Konkurrenzverhältnisse in einer ganz bestimmten Altersstufe; Konkurrenzbeeinflussung einer Pflanze nur durch die 4 'direkten' Nachbarn; Verwendung von 2 verschiedenen Merkmalen zur Analyse von Konkurrenzigenschaften: Konkurrenzfähigkeit F und Konkurrenzwirkung W ; Effekte der Nachbarn auf eine Pflanze sind unabhängig von Stellung und

Richtung der Konkurrenten; Wirkungen der 4 Nachbarn sind additiv und linear; ausreichend großer Bestand; zufällige Verteilung der Pflanzen über die Fläche) wird sodann noch das Korrelationsmuster eines Bestandes theoretisch untersucht. Dabei werden die folgenden Nachbarschaftskorrelationen behandelt: 1. Korrelation zwischen 'direkten' Nachbarn; 2. Korrelation zwischen 'diagonalen' Nachbarn; 3. Korrelation zum übernächsten Nachbarn, d. h. Korrelation zwischen Pflanzen mit einem gemeinsamen Konkurrenten; 4. Korrelation zur Summe der 'direkten' Nachbarn; 5. Korrelation zur Summe der 'diagonalen' Nachbarn und 6. Korrelation zur Summe aller Nachbarn ('direkt' und 'diagonal').

Alle diese Nachbarschaftskorrelationen lassen sich mit Hilfe von nur 2 Parametern (Verhältnis der Standardabweichungen von F und W und Korrelationskoeffizient zwischen F und W) explizit ausdrücken. Diese Formeln werden abgeleitet und diskutiert.

Schlagwörter: Korrelationsmuster, Lärche: *Larix europaea*, *Larix leptolepis* und ihre Hybriden, Nachbarschaftskorrelationen, Veränderung des Korrelationsmusters während der Bestandsentwicklung, Höhe, Durchmesser, Thiessen-Polygone, Konkurrenz.

Summary

Investigations on the Correlation Pattern in Stands of Larch. First Communication: Problems, Material, Methodology of Analysis and Theoretical Correlations between Neighbours.

In the series "Investigations on the correlation pattern in stands of larch" experimental results on the correlation structure of stands (neighbourhood correlations) and, additionally, on the temporal changes and trends of these correlation patterns during stand development are discussed. These studies are based on quite extensive data sets of measurements on larch where the plant material consists of *Larix europaea*, *Larix leptolepis* and their hybrids. The characters used are 'height' and 'diameter'.

This first communication covers a general introduction into the problems involved in the series on correlation patterns and a representation of the underlying concepts.

Furthermore, descriptions of the ten field trials with *Larix europaea*, *Larix leptolepis* and their hybrids are presented (sites, entries, dates of establishment of the plantations, replications, plot sizes, plant distances, measurements, population sizes).

Explanations of the different methods of analysis are included, for example: 1. Definition of the different cor-

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