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Genetic divergence between half-sib families under different environments in *Kachnar* (*Bauhinia variegata* L.)

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Abstract

Thirty-two half sib progenies of *Kachnar* (*Bauhinia variegata* L.) belonging to different geographic regions of Himachal Pradesh, Haryana, and Jammu & Kashmir were sown in glasshouse and field condition during 2004 with a view to assess the impact of two different environments on the expression of genetic diversity using non-hierarchical Euclidean cluster analysis. Superior tree progenies were grouped into ten and eight clusters in glasshouse and field atmosphere, respectively. Families of plus tree T_5 and T_6 formed one cluster both under glasshouse and field back ground. Whereas, T_3 and T_9; T_{19} and T_2; T_{17} and T_{18}; T_{15} and T_{22}; T_{15} and T_{18}; T_{30} and T_{31}, formed same group but different clusters. Intra cluster distance only under glasshouse condition was zero for cluster II, VI and X. The highest inter cluster distance was found between cluster X and III (12.293, under glasshouse), cluster IV and I (7.325, under field situation). Seedling height contributed maximum to the total divergence and played a predominant role in creating the genetic diversity.

Key words: *Bauhinia variegata*, genetic divergence, Euclidean cluster, D^2 statistics

Introduction

Bauhinia variegata Linn. commonly known as *kachnar* belongs to family leguminosae and sub family caesalpiniodae. The species is generally prevalent in sub and outer Himalaya from the Indus river eastwards ascending to 1830m, right to Assam, Burma and other parts of Indian Peninsula. *Bauhinia variegata* is one of the important fodder tree species on which farmer bank upon during lean periods of December and January when green fodder is hardly available [1].

The knowledge of genetic divergence in tree species is of paramount importance for any breeding programme. The tree breeders are consistently emphasizing the use of diverse genotypes as a significant factor contributing towards higher yield. The major goal of genetic variation study is to classify different population into similar groups for the conservation purpose or to be used in future breeding and improvement programmes.

Such a classification is difficult to carry out on the basis of univerate analysis particularly when overlapping for one or more characters is frequent, but Euclidean cluster analysis can be very useful [2]. However, numerical data in terms of genetic distance (D^2 value) between genotypes showing the impact of environment in the expression of genetic diversity are lacking in forest trees in general and *Bauhinia variegata* in particular. Therefore, an effort was made to study the genetic differentiation in superior tree progenies under two different environments to identify the stable and diverse genotype to use further in hybridization programme.

Materials and methods

Mature pods from different parts of the crown of 32 phenotypically superior trees were collected during April and May, 2004 from Himachal Pradesh, Haryana, Uttranchal and Jammu & Kashmir on the basis of different morphological, fruit and seed characters mentioned below a) Tree Height, b) Tree diameter, c) Leaf area, d)Pod length, e) Pod width, f) Number of seeds per pod, and g) Seed weight per pod.

Candidate plus tree and four comparison trees almost of same size free from diseases and insect pests representing each stand were selected and the above observations recorded both for candidate and comparison trees. Out of these, the very best was selected as plus tree and marked with yellow paint after removing the bark. Uniform, healthy seeds were graded to constitute the seed lot of each tree family for experimental purposes for sowing in two experimental sites *viz.*, under glass house and field condition for the evaluation of the families of plus trees. Details of 32 plus trees are given in Table 1.

The experiments were conducted in the main campus of Dr. Y.S. Parmar University of Horticulture and Forestry in glass house and nursery of the Department of Tree Improvement and Genetic Resources in a Randomized Complete Block Design with three

Table 1. Details of 32 plus tree of *Bauhinia variegata* Linn.

S.No.	Place name of seed sources	Code	Altitude (m)	Latitude*	Longitude*	Annual rainfall (mm)
1.	Nalagarh	T_1	500	31°02'N	76°42'E	1352
2.	Paonta Sahib	T_2	320	30°26'N	77°36'E	1936
3.	Pinjore	T_3	540	30°47'N	76°54'E	580
4.	Subathu	T_4	1380	30°59'N	76°58'E	1435
5.	Solan	T_5	1300	31°55'N	77°06'E	1372
6.	Kunihar	T_6	960	31°03'N	77°55'E	1354
7.	Nahan	T_7	760	30°35'N	77°18'E	1428
8.	Mandi	T_8	800	31°44'N	76°56'E	1938
9.	Sundernagar	T_9	740	31°35'N	76°53'E	1115
10.	Kandaghat	T_{10}	1180	30°59'N	77°06'E	1412
11.	Rajgarh	T_{11}	1760	30°51'N	77°18'E	1021
12.	Giripul	T_{12}	1120	30°50'N	77°12'E	939
13.	Nauni	T_{13}	1200	30°54'N	76°10'E	934
14.	Una	T_{14}	740	31°28'N	76°16'E	2300
15.	Jabli	T_{15}	620	30°51'N	76°59'E	1926
16.	Kalka	T_{16}	470	30°50'N	76°56'E	1897
17.	Arki	T_{17}	1280	31°09'N	76°57'E	1527
18.	Bilaspur	T_{18}	660	31°19'N	76°46'E	1032
19.	Hamirpur	T_{19}	780	31°40'N	76°31'E	1173
20.	Jawalajee	T_{20}	520	31°88'N	76°00'E	2532
21.	Palampur	T_{21}	1280	32°07'N	76°31'E	3148
22.	Narag	T_{22}	1060	31°15'N	77°28'E	1972
23.	Sarahan	T_{23}	1480	31°33'N	77°47'E	1358
24.	Renuka	T_{24}	1060	30°37'N	77°25'E	1620
25.	Dhaulakuan	T_{25}	380	30°29'N	77°31'E	756
26.	Dehradun	T_{26}	620	30°20'N	78°02'E	1500
27.	Chandrabani	T_{27}	660	30°19'N	77°59'E	1381
28.	Sahastradhara	T_{28}	740	30°22'N	78°05'E	2073
29.	Jammu	T_{29}	440	32°42'N	74°51'E	1115
30.	Kathua	T_{30}	380	32°22'N	75°31'E	1678
31.	Udhampur	T_{31}	680	32°55'N	75°07'E	1129
32.	Jhajjer Kotti	T_{32}	540	32°53'N	74°57'E	1121

*Encarta U.S. Geological Survey

replications. The experimental area is situated at 30°50' N latitude and 76°11'E longitude at an elevation of 1200 meters above mean sea level on North Eastern aspect. Fifty seeds of each families of plus trees/replication were sown in poly bags of size 10 × 20 cm with 1:1:1 (Sand, Soil, FYM) and in field at a distance of 10 cm from seed to seed and 30 cm row to row.

After six months growth fifteen seedlings of each families of plus trees/replication were randomly selected and tagged excluding the border ones during last week of November. The data were recorded on eleven morphological and biomass traits *viz.*, seedling height, collar diameter, internodal length, number of leaves, leaf area, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight, shoot/root ratio, and seedling biomass. Analysis of variance was done as per Panse and Sukhatme [3] and genetic divergence by using non-hierarchical Euclidean cluster analysis [4].

Results and discussion

Seedling characteristic can be used as a quantitative character defining genotype in measuring genetic distance between populations and differentiating population at early stages in variability studies. As tree characters measured in natural population are amenable to geographical and environmental interactions, seedling characters measured in different environment are more useful in differentiating population at preliminary stage [5].

The analysis of variance revealed the existence of significant difference among 32 plus tree progenies for all the traits, indicating the existence of huge genetic variability. The highest D^2 value 855.11 and 248.73 was observed between T_{27} and T_9; T_{15} and T_6 under glass house and field conditions, respectively. However, minimum D^2 distance 15.23 and 1.57 was observed between T_{21} and T_4; T_{29} and T_{17} under both the environments, correspondingly.

The clustering pattern of 32 plus trees for glass house and field atmosphere is given in Table 2. Under glass house and field context they were grouped into ten and eight clusters, respectively. The variation under glass house and field situation for total number of cluster could be attributed mainly due to the environmental differences as the range of day and night temperature and humidity are wide in glass house and field conditions. The present result substantiates the findings in linseed [6] Prasad and Singh in maize

Table 2. Distribution of 32 superior tree progenies of *Bauhinia variegata* Linn in different clusters (glass house and field environment 2004)

Cluster	No. of superior trees in each cluster		Notation of superior trees	
	(Glass house)	(Field)	(Glass house)	(Field)
I	3	5	T_5, T_6, T_{20}	T_3, T_5, T_6, T_9, T_{14}
II	1	6	T_{29}	T_{17}, T_{27}, T_{28}, T_{29}, T_{30}, T_{31}
III	2	3	T_3, T_9	T_{19}, T_{21}, T_{23}
IV	3	3	T_{24}, T_{25}, T_{26}	T_{11}, T_{22}, T_{24}
V	6	2	T_2, T_{10}, T_{11}, T_{17}, T_{22}, T_{28}	T_{15}, T_{18}
VI	6	2	T_4, T_{19}, T_{21}, T_{30}, T_{31}, T_{32}	T_1, T_{10}
VII	5	6	T_1, T_{14}, T_{15}, T_{16}, T_{18}	T_2, T_4, T_7, T_8, T_{20}, T_{32}
VIII	3	5	T_7, T_{13}, T_{27}	T_{12}, T_{13}, T_{16}, T_{25}, T_{26}
IX	2		T_8, T_{23}	
X	1		T_{12}	

[7]. Cluster V and VI exhibited the highest number of six families (T_2; T_{10}; T_{11}; T_{17}; T_{22} and T_{28}) and (T_4; T_{19}; T_{21}; T_{30} and T_{32}) under glass house situation. Whereas, under field background maximum number of progenies occurred in cluster II and VII (T_{17}; T_{27}; T_{28}; T_{29}; T_{30} and T_{31}) and (T_2; T_4; T_7; T_8; and T_{32}).

Families of plus tree T_3 and T_9; T_{19} and T_{21}; T_{15} and T_{18}; T_{11} and T_{22}; T_{25} and T_{26}; T_{30} and T_{31} formed same groups in different clusters indicating that, even though the genotypes (parents) were selected form different ecogeographic areas, the genetic make up along with breeding system, heterogeneity, natural and unidirectional selection pressure may be the cause of genetic diversity among different families of plus tree besides geographic variation to some extent. The cluster pattern proved that geographical variation need not necessarily be related to genetic diversity [8, 9].

Intercrossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage. Progeny derived from such diverse crosses are expected to show wide spectrum of genetic variability provided a greater scope for isolating transgressive segregants in the advance generation. Hence, these genotypes might be used in multiple crossing programme to recover transgressive segregants [10].

Inter cluster distance was found to be highest between cluster X and III (12.293) under glass house (Table 3). Whereas, under field condition cluster IV and I showed maximum (7.325) inter cluster distance. However, 32 families within a cluster showed low intra-cluster distance (<1.681), under both the environments, revealing their genetic closeness. The higher inter cluster distance under glasshouse condition may be due to the more homogeneous environmental conditions in the glasshouse than under field back ground [11, 12].

Contribution of different characters to total divergence is illustrated in Table 4. Seedling height contributed maximum (59.67% and 55.92%) followed by seedling diameter (14.77% and 17.90%) and internodal length (7.50% and 14.70%). Minimum contribution was observed for seedling biomass (0.04% and 0.05%) under both backgrounds.

Highest mean values for different traits under glass house condition was shown by cluster X for seedling height (65.56), seedling biomass (12.65), internodal length (6.12), number of leaves (10.27), leaf area (46.91), shoot fresh weight (0.37), root fresh weight (4.27), shoot dry weight (3.19), root dry weight (1.36). Seedling diameter (3.64) and shoot/root ratio (4.41) were highest for cluster IV and III, respectively (Table 4). However under field environment cluster IV possessed the maximum mean value for seedling height (26.49), seedling diameter (3.96), internodal length (2.60), leaf area (29.73) and shoot dry weight (2.09) whereas, cluster VIII exhibited maximum mean value for shoot fresh weight (15.19), root fresh weight (11.05), root dry weight (3.75) and seedling biomass (16.64). Maximum number of leaves (13.20) and shoot/root ratio (1.13) were noticed for cluster V. The present result supports the findings in *Leucaena latisiliqua* and *Prosopis cineraria* [13, 14].

Table 3. Inter- and intra-cluster distances of 32 superior tree progenies of *Bauhinia variegata* Linn (glass house and field environment 2004)

Cluster No.		I	II	III	IV	V	VI	VII	VIII	IX	X
I	G*	**1.665**									
	F**	**1.688**									
II	G	3.952	**0.000**								
	F	5.548	**1.385**								
III	G	4.750	7.594	**0.885**							
	F	2.968	4.747	**1.441**							
IV	G	3.490	2.956	7.125	**1.543**						
	F	7.325	2.575	5.762	**1.147**						
V	G	2.415	3.132	5.357	3.161	**1.131**					
	F	4.121	4.911	5.622	6.870	**1.096**					
VI	G	3.584	2.086	7.205	2.635	2.188	**1.479**				
	F	4.546	3.686	4.759	4.822	4.748	**1.009**				
VII	G	2.908	4.766	4.500	3.263	2.761	3.799	**1.681**			
	F	3.052	4.013	2.716	5.354	5.379	2.734	**1.213**			
VIII	G	5.195	3.810	8.902	3.088	4.166	2.479	4.704	**1.386**		
	F	6.931	2.433	6.043	2.488	6.341	3.344	4.658	**1.207**		
IX	G	2.590	4.576	4.123	5.338	3.453	4.909	4.392	6.959	**1.371**	
X	G	8.539	6.445	12.293	5.821	7.664	5.832	8.316	4.614	10.405	**0.000**

*G - Glass house environment; **F - Field environment.

Table 4. Mean values for various characters in different clusters for 32 superior tree progenies of *Bauhinia variegata* Linn, (glass house and field environment 2004)

Characters		I	II	III	IV	V	VI	VII	VIII	IX	X	Per cent contribution
Seedling height (cm)	G*	51.05	50.44	35.76	55.20	52.34	52.12	43.51	56.04	46.96	65.56	59.67
	F**	17.41	23.98	20.29	26.49	18.46	17.37	18.74	23.95	-	-	55.91
Seedling diameter (cm)	G	2.86	3.03	2.47	3.64	2.81	2.93	3.26	3.37	2.37	3.50	14.77
	F	2.68	3.75	3.20	3.96	3.68	3.04	2.69	3.58	-	-	17.98
Internodal length (cm)	G	4.75	5.91	4.37	5.18	5.00	5.33	4.28	4.67	4.94	6.12	7.50
	F	1.78	2.00	2.66	2.68	1.36	1.77	1.99	2.03	-	-	14.76
Number of leaves	G	9.31	9.40	8.10	8.90	9.56	9.97	8.87	10.12	8.63	10.27	5.88
	F	9.91	12.39	9.47	10.93	13.20	9.77	9.13	11.59	-	-	5.14
Leaf area (cm^2)	G	39.02	31.75	32.94	39.13	30.72	34.24	36.61	37.09	30.60	46.91	4.59
	F	17.59	27.87	20.27	29.73	18.53	15.55	19.23	22.49	-	-	2.80
Shoot fresh weight (g)	G	3.34	4.35	2.39	5.17	4.56	5.06	4.47	6.05	2.75	8.37	4.06
	F	3.11	4.70	2.67	5.10	4.35	4.80	3.71	5.19	-	-	1.19
Root fresh weight (g)	G	1.85	3.32	0.67	2.62	1.95	2.61	1.92	3.31	1.34	4.27	1.80
	F	3.33	8.25	4.57	1.12	3.89	8.87	6.59	11.05	-	-	0.80
Shoot dry weight (g)	G	1.44	1.82	1.31	2.17	2.06	2.42	2.18	2.84	1.16	3.19	0.90
	F	1.21	1.80	1.28	2.09	2.00	2.01	1.40	2.05	-	-	0.72
Root dry weight (g)	G	0.62	1.07	0.30	0.90	0.70	1.06	0.69	1.29	0.59	1.36	0.69
	F	1.50	2.84	1.95	3.39	1.79	2.91	2.53	3.75	-	-	0.48
Shoot/root ratio	G	2.47	1.69	4.41	2.45	2.86	2.31	3.49	2.22	1.99	2.35	0.18
	F	0.87	0.64	0.67	0.62	1.13	0.70	0.57	0.55	-	-	0.15
Seedling biomass (g)	G	5.19	7.67	3.06	7.79	6.42	7.67	6.39	9.01	4.09	12.65	0.04
	F	6.44	12.95	7.24	15.21	8.24	13.67	10.18	16.64	-	-	0.05

G* - Glass house environment; F** - Field environment.

Reference

1. **Chauhan K. C. and Hosalli R.** 2003. Proximate composition of *Leucaena* species/varieties under mid-hill conditions of Himachal Pradesh. J. Hill Res., **16**: 74-76.
2. **Kant A ., Dutt V. and Sharma D. R.** 2006. Genetic variability in phenotypic characters of *Pinus gerardiana*. Indian J. For., **132**: 681-690.
3. **Panse V. G. and Sukhatme P. V.** 1967. Statistical methods for agricultural research workers. ICAR. New Delhi, p 610.
4. **Spark D. N.** 1973. Euclidean cluster analysis Algorithm. Applied Statistic, 58. **22**: 126-130.
5. **Hedge M., Ramtete P. K. and Subramanian K.** 2004. Genetic variation and intense genetic correlation of seedling characteristics in teak. Indian J. For., **27**: 19-24.
6. **Murthy B. R., Aurchananlum V. and Anand I. J.** 1973. Effect of Environment on the genetic divergence among linseed. Indian J. Genet., **33**: 305-314.
7. **Prasad S. K. and Singh T. P.** 1990. Genetic diversity under different Environments in maize. Indian J. Genet., **50**: 407-411.
8. **Chaturvedi O. P. and Pandey N.** 2001. Genetic divergence in *Bombax ceiba* L. germplasm. Silvea Genetica, **50**: 99-102.
9. **Surendran C. and Chandrasekharan P.** 1984. Heritability, variation and genetic gain estimates in half sib progenies of *Eucalyptus tereticornis.* J. Tree Sci., **3**: 1-4.
10. **Thoday J. M.** 1960. Effect of disruptive selection III - Couping and repulsion. Heredity, **14**: 35-39.
11. **Chauhan K. C., Srivastava A. and Thakur R. C.** 1997. Analysis of genetic divergence in seed stands of *Bauhinia variegata* Linn. Indian J. Plant Genet. Resources, **10**: 115-121.
12. **Pandey D., Tewari S. K. and Tripathy S.** 1995. Genetic divergence in *Populus deltoides*, Bart. Indian J. Genet., **55**: 129-131.
13. **Gupta V. K. and Patil B. D.** 1988. Genetic variability and path analysis in white popiral (*Leucaena latisiliqua*). Indian J. Agri. Sci., **58**: 483-484.
14. **Manga V. K. and Sen D. N.** 2000. Genetic diversity among different genotypes of *Prosopis cineraria* Druce. Indian J. For., **23**: 291-295.