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ANALYSIS OF GENETIC DIVERGENCE IN SEED STANDS OF *BAUHINIA VARIEGATA* LINN.

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Studies were conducted to assess the magnitude of genetic divergence among 20 seed stands of *Bauhinia variegata* from different agroclimatic zones of Himachal Pradesh, Panjab and Uttar Pradesh at 12 months growth phase. These studies were also carried out to identify promising superior diverse stands for their utilization in future improvement programmes. Genetic divergence assessment by using Mahalanobis D^2 analysis led to grouping into nine clusters. Five seed sources fell in cluster I, one in II, two in III, one in IV, seven in V and one each in cluster VI, VII, VIII and IX. Maximum and minimum distances were observed between clusters VII and VIII and clusters V and VI, respectively.

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

Bauhinia variegata is a medium sized tree with elongated spreading crown and green foliage. It is characteristic to mixed dry deciduous forests and is useful for its lean winter fodder, fuel, fiber and small timber. The tree parts have diverse medicinal values. The bark is antiflamatory, astringent and used in skin diseases and ulcers. The dried buds are used as remedy for piles and dysentery. Flowers are light antidysenteric and cure diseases of bile, cough and menorrhagia (Kirtikar and Basu, 1933; Chopra *et al.*, 1956; Chunekar and Pandey, 1969). *Bauchinia variegata* is a unique tree used for agroforestry because of its multiple uses. In northern India it is planted in the agricultural field bunds and in pure culture system. A quantitative estimation of genetic diversity present among different seed stands/sources helps the breeder to attempt a cross between desirable but diverse genotypic stands for generating sufficient genetic diversity for a rapid progress in the improvement programmes. Multivariate analysis has been found to be a potential biometrical tool in quantifying the degree of divergence in the germplasm (Mahalanobis, 1936; Rao, 1952). It has been extensively used as an efficient tool to find out genetic divergence among agricultural Crops (Murthy and Pavte, 1962; Murthy and Arunachalam, 1966). Among tree crops, it has been used by Burley et al

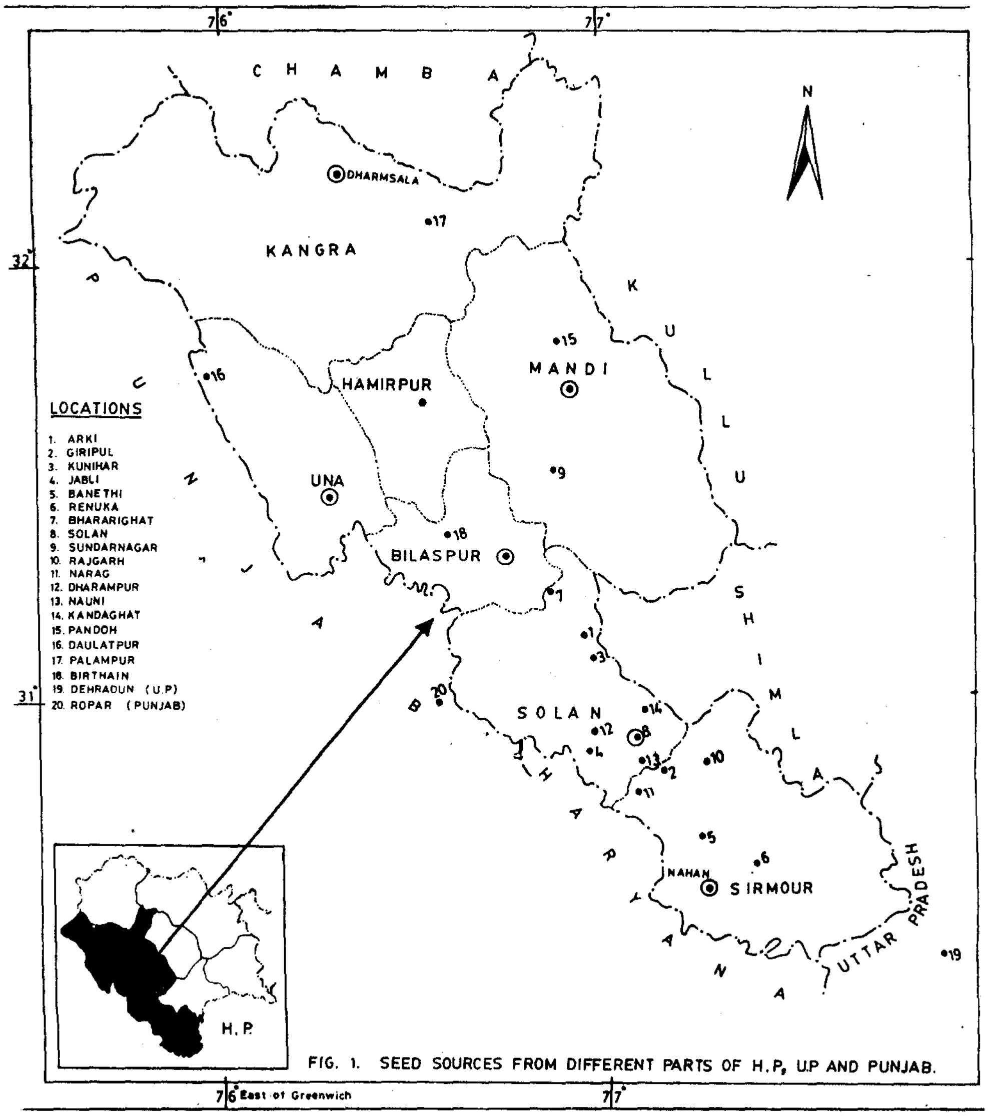

FIG. 1. SEED SOURCES FROM DIFFERENT PARTS OF H.P, U.P AND PUNJAB.

Fig. 1. Seed sources from different parts of H.P., U.P. and Punjab

(1971) in two year old trees of 25 provenances of *Eucalyptus camaldulensis,* Burley and Borrows (1972) in *Pinus kesiya,* Andrew (1973) in 16 provenances of *E. camaldulensis,* Khosla et al (1979) in *Populous ciliata* and Pandey et al (1995) in *Populus deltoidis.* The present studies were under taken, at 12 months growth period, to identify promising seed sources to be utilized in crossing programmes.

MATERIALS AND METHODS

Seeds were collected from twenty seed sources of *Bauhinia variegata* from different agroclimatic zones of HP, Panjab and UP (Fig. 1). The seeds were

Table 1. Mean data for different characters of *Bauhinia variegata* linn

Sr. No.	Seed sources	Height (cm)	Collar dia. (cm)	No. of Leaves	Internodal Length (cm)	No. of Nodes	Leaf area (cm^2)	No. of branches
1	Arki	44.86	7.08	29.00	3.07	14.53	48.15	3.50
2	Giripul	36.46	5.56	15.60	3.27	11.20	33.98	1.77
3	Kunihar	49.20	6.60	25.73	4.09	11.93	52.95	3.53
4	Jabali	52.80	7.38	21.80	3.41	14.40	52.61	2.67
5	Benathi	52.33	6.55	21.06	3.68	14.00	57.18	1.87
6	Renuka	50.96	5.82	17.63	3.62	14.00	55.36	1.50
7	Bararighat	51.16	7.32	25.73	3.32	15.86	56.20	3.50
8	Solan	61.70	7.95	33.70	4.12	14.93	69.78	3.73
9	Sundernagar	42.20	6.38	26.76	3.59	11.66	41.95	2.30
10	Rajgarh	54.06	6.98	23.23.	3.43	15.26	59.71	2.57
11	Narag	42.80	6.28	19.36	3.76	11.13	42.81	1.67
12	Dharampur	51.63	7.28	32.76	3.23	16.00	54.91	4.10
13	Nauni	44.50	6.90	17.40	3.20	13.93	39.96	2.00
14	Kandaghat	56.80	7.18	32.76	3.65	15.53	67.01	6.33
15	Pandah	51.61	7.50	30.96	4.26	12.13	57.86	2.33
16	Dharampur	50.06	6.67	27.20	3.56	14.00	56.73	4.10
17	Palampur	59.63	7.76	29.86	4.04	14.80	68.97	3.97
18	Birthian	53.66	7.01	24.56	3.58	14.60	61.25	2.30
19	Dehradun	54.46	7.50	20.63	7.39	14.33	63.76	2.37
20	Ropar	56.36	8.20	22.11	3.63	14.06	55.15	2.03
	Mean	50.56	7.03	24.89	3.61	13.91	52.41	2.96
	CD (0.05)	3.002	0.662	3.222	0.542	1.742	2.593	0.342

sown in randomized complete block design with three replications. An area of 2 m^2 per treatment per replication was taken to accommodate 24-25 seedlings at a distance of 25 cm from seedling to seedling and 50 cm from row to row. Ten seedlings other than the border ones were randomly selected in each treatment/stand replication wise and observations on seven different metric traits viz., seedling height, collar diameter, number of leaves, number of branches, internodal length, number of nodes and leaf area were recorded from individual seedlings at 12 months growth period. The data so collected was subjected to multivariate and canonical analysis (Rao, 1952).

RESULTS AND DISCUSSION

The mean data of different characters are given in Table 1. The seed sources showed significant variation for all quantitative characters. The variation ranges were observed for seedling height (36.46-61.70 cm), collar diameter (5.56-8.80 cm), number of leaves (15.60-33.70), number of branches (1.8-4.40), internodal length (3.07-4.26 cm), number of nodes (11.13-16.00) and leaf area (33.98-69.78 cm).

Based on D^2 value, 20 seed sources were grouped into nine clusters as per the method described by Tocher and reported by Rao (1952). The criterion used for clustering was that any two genotypes/seed sources belonging to the same cluster should, at least on an average, show a smaller D^2 value than those belonging to different clusters. The clustering pattern of these twenty seed sources is depicted in table 2. Cluster I contained five seed sources, cluster II one, cluster III two, cluster IV one, cluster V seven, cluster VI to IX contained only one seed source each. The intra cluster distances ranged from 0.00 to 92.43 (Table 3) with the maximum value of 92.43 in cluster III followed by 49.59 in cluster V, 32.40 in cluster I and 0.00 in clusters II, IV,

Table 2. Clustering pattern of 20 genotypes on the basis of genetic divergence in *Bauhinia variegata* Linn.

Clusters	Seed stands
1	1, 3, 7, 4, 12
2	9
3	16; 20
4	13
5	10, 11, 5, 18, 6, 19, 15
6	17
7	2
8	8
9	14

VI, VII, VIII and IX as they possessed only one seed source. The intra cluster distance was less than the corresponding D^2 values indicating more divergence of genotypes between the clusters. Surendran and Chandrasekharan (1988) also reported similar results in 35 half sib progenies of *Eucalyptus tereticornis* Sin.

Table 3. Average intra and inter cluster D^2 values in *Bauhinia variegata*

	1	2	3	4	5	6	7	8	9
1	32.40	64.81	46.25	77.73	65.11	76.14	194.55	187.27	151.18
2		0	121.45	49.76	89.86	234.66	71.13	275.46	66.94
3			92.43	98.98	91.72	91.88	151.65	142.28	145.93
4				0	73.10	213.50	75.36	267.79	359.83
5					49.59	108.17	212.09	126.72	280.04
6						0	435.79	10.51	106.34
7							0	526.80	156.53
8								0	154.50
9									0

The pattern of distribution in these nine clusters showed that there was considerable amount of genetic divergence in these seed sources. Calculation of inter cluster distances revealed the maximum value of 526.80 between cluster VII and VIII, indicating that Giripul and Solan were most divergent seed sources followed by VI and VII cluster i.e. Palampur and Giripul and minimum divergence was available for clusters VI and VIII (Palampur and Solan) indicating their close relationship with each other. The importance of different seedling characters in intercluster divergence was further studied by comparing cluster means for different characters. Significant differences between these two clusters were observed for seedling height, collar diameter, number of leaves, internodal length and leaf area (Table 4). Higher cluster means were

Table 4. Character means for 9 clusters of 20 *Bauhinia* genotypes

Character	I	II	III	IV	V	VI	VII	VIII	IC	VD	% contri
Seedling height	49.93	42.10	50.21	44.50	51.33	59.63	34.46	61.70	56.80	3.002	10.94
Collar diameter	7.13	6.38	7.74	6.90	6.77	7.76	5.56	7.95	7.18	0.662	18.42
No. of leaves	27.00	26.76	24.64	17.40	22.87	29.86	15.60	33.70	32.76	3.222	13.16
No. of branches	3.46	2.30	3.58	2.67	2.63	3.97	3.50	3.73	6.33	0.413	11.62
Internodal length	3.40	3.59	3.65	3.20	3.72	4.04	3.27	4.12	3.65	0.542	11.24
No. of nodes/ seedling	14.54	11.66	14.03	13.90	13.55	14.80	11.20	14.93	15.53	1.742	19.49
Leaf area 52.90	41.95	55.94	29.96	56.20	68.97	33.98	69.78	67.01	2.593	15.11	

obtained in cluster IX for number of branches and number of nodes/seedling. The contribution of individual character towards divergence indicated higher magnitude (19.47%) for number of nodes/seedling and collar diameter (18.42%), leaf area (15.11%), number of leaves (13.16%), number of branches (11.62%) and internodal length (11.24%). However, contribution due to seedling height was observed to be much lower (10.94%). Martin et al (1981) also examined variation in okra genotypes and distinguished 5 out of 29 characters.

While selecting the seed sources as parents, in addition to genetic divergence, other practical considerations such as disease and insect reaction and quality index should also be taken into account. The estimation of genetic divergence has a wide scope in tree improvement as it helps in identifying the diverse genotypes for a crossing programme. Thus on the basis of present findings it is suggested that crossing between clusters from Solan and Giripul and Palampur and Giripul will result in wide spectrum of variability with transgressive segregates for increased seedling height and collar diameter in the subsequent generations and the selection for these traits will be effective with high heterotic response.

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