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Genetic divergence in *Acacia catechu* Willd.

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Abstract

Nine tree attributes were used to evaluate the performance of forty seed sources of *Acacia catechu* in a selection trial. On the basis of D^2 analysis, all the seed sources were grouped into fifteen clusters. The pattern of distribution of seed sources in different clusters indicated that genetic divergence did not agree to the geographical differentiation. Seed source S38 of cluster X recorded higher cluster mean values and therefore was recommended for selection. Seed sources from cluster XIV and XV may be utilized as parents in the hybridization program to release greater variability and/or to get heterosis in the following generation. D^2 analysis served as a useful tool to understand the nature of genetic distribution of population within the species.

Key words : *Acacia catechu*, seed source, genetic divergenc, D^2 statistic.

Introduction

Acacia catechu Willd., locally known as *Khair*, is a multipurpose tree species suitable for both agroforestry and commercial forestry. It is widely distributed through out the greater part of India except the most humid and driest regions. It is common in sub-Himalayan tract and outer Himalayas ascending upto 900 to 1200m altitude. The species belongs to the family leguminoseae and sub family mimisoideae. It is a medium sized deciduous tree of 12 to 15m height. The heartwood is brownish red to nearly black in color, extremely hard, strong and durable,. Thus, it is one of the most valued raw material for cartwheel, boat making, gun carriage and building construction [1]. *Katha* an extract of the heartwood is used in many pharmaceutical formulations. It was reported to be digestive, aphrodisiac and cooling agent. The species is considered as an important lean season fodder tree as the leaves are palatable and contain about 13.03 to 18.75 per cent crude protein [2]. Because of its multifarious economic uses and wider adaptability to varying agroclimatic conditions, it is gaining attention of progressive farmers and entrepreneurs for commercial plantation. Furthermore, there is now rising interest in developing sustainable farm tree plantation resources to diversify farm incomes, to supply raw material to local industries and to stimulate the regional rural economy.

Presence of wide genetic variation within a species provides a greater scope for it's genetic improvement. Study of genetic diversity and it's significance had been emphasized in many tree crops such as *Acacia nilotica* [3] and *Pinus gerardiana* [4]. The species having wide geographic distribution is generally expected to be composed of geographical clines and fairly distinct ecotypes[5]. Genetic differentiation and the resulting genetic distance in such cases may be due to geographical isolation and stratification. As no pertinent information was available in the above discussed aspect, multivariate analysis was carried out to find out the nature and degree of divergence present in the species so that desirable parents could be selected to develop the stock population for operational planting out vis-a-vis hybridization of diverse seed sources to obtain wide variability and maximum possible heterotic vigor in the hybrid progenies.

Materials and methods

The experimental material consisted of forty seed sources of *Acacia catechu* collected from randomly selected phenotypically superior trees with mature pods. These sources were located at edapho-climatically different and geographically isolated locations in India except the only seed source which was from Nepal (Table 1). The representative seed samples were sown in the nursery of Department of Tree Improvement and Genetic Resources, Dr Y S Parmar University of Horticulture and Forestry, Solan, situated at 30° 50'N latitude and 76° 11'E longitude at an elevation of 1100 m above mean sea level in a Completely Randomized Block Design with three replications during May 1995. Twelve months after seed sowing, 5 seedlings in each replication were selected randomly and were assessed for nine quantitative traits such as seedling height, collar diameter, internodal length, number of leaves, leaf area, fresh and dry weight of shoot as well as

Table 1. Geographical location and habitat data of various seed sources under study

Source No.	Name of seed source	District	State/ Country	Latitude	Longitude	Altitude (m)	Rainfall (cm)
1	Arki	Solan	HP	31°09’ N	76°57’ E	1260	120.1
2	Awadevi	Hamirpur	HP	31°40’ N	76°39’ E	996	131.0
3	Badrama	Sambalpur	Orissa	21°09’ N	83°10’ E	300	160.1
4	Badsar	Hamirpur	HP	31°32’ N	76°28’ E	717	145.3
5	Bagar	Solan	HP	30°51’ N	76°15’ E	1190	139.6
6	Balera	Solan	HP	31°08’ N	76°54’ E	1100	141.3
7	Bhanjal	Una	HP	31°46’ N	76°07’ E	730	100.8
8	Bharighat	Solan	HP	31°15’ N	76°50’ E	1150	124.4
9	Bharmour	Chamba	HP	31°54’ N	76°39’ E	1100	110.6
10	Bhota	Hamirpur	HP	31°37’ N	76°33’ E	900	144.8
11	Bilaspur sadar	Bilaspur	HP	31°19’ N	76°48’ E	825	131.5
12	Dalautpur chowk	Una	HP	31°49’ N	75°57’ E	650	108.6
13	Dharja	Solan	HP	30°48’ N	77°13’ E	1124	142.1
14	Dhameta	Kangra	HP	31°50’ N	75°55’ E	700	121.3
15	Kothi	Solan	HP	30°58’ N	77°03’ E	1100	139.2
16	Gagret	Una	HP	31°40’ N	76°05’ E	500	110.4
17	Gandhal	Sirmour	HP	30°48’ N	70°15’ E	1009	121.4
18	Ghumarwin	Bilaspur	HP	31°25’ N	76°45’ E	1050	122.9
19	Gadchiroli	Gadchiroli	Maharashtra	20°03’ N	80°01’ E	250	160.0
20	Jabalpur	Jabalpur	MP	23°05’ N	79°58’ E	400	140.5
21	Kalah	Jammu	J&K	32°35’ N	74°40’ E	621	92.3
22	Khadpanjawar	Una	HP	31°32’ N	76°09’ E	512	112.8
23	Kharah	Jammu	J&K	33°10’ N	74°12’ E	950	89.5
24	Kheri	Sirmour	HP	30°50°’N	77°08’ E	1106	121.6
25	Kothipura	Bilaspur	HP	31°17’ N	76°47’ E	1076	107.2
26	Kotlabarog	Sirmour	HP	30°50’ N	77°14’ E	1101	122.7
27	Kwangdhar	Sirmour	HP	30°51’ N	76°19’ E	1253	132.5
28	Manlogkala	Solan	HP	30°56’ N	77°04’ E	1200	138.1
29	Naglahar	Kangra	HP	31°37’ N	76°41’ E	750	121.2
30	Naintatikkar	Sirmour	HP	30°48’ N	77°07’ E	1100	124.7
31	Nakroh	Una	HP	31°46’ N	76°05’ E	702	112.2
32	Narag	Sirmour	HP	30°49’ N	77°11’ E	1150	121.9
33	Oel	Una	HP	31°38’ N	76°05’ E	500	117.6
34	Pasha river	Bara	Nepal	27°18’ N	86°03’ E	280	200.0
35	Rewa	Rewa	MP	24°32’ N	81°11’ E	300	116.8
36	Salohberi	Una	HP	31°53’ N	75°55’ E	600	102.9
37	Sithu	Solan	HP	31°10’ N	76°54’ E	1090	123.5
38	Swarghat	Bilaspur	HP	31°14’ N	76°42’ E	850	121.6
39	Talwara	Una	HP	31°51’ N	75°49’ E	622	109.2
40	Taunidevi	Hamirpur	HP	31°42’ N	76°36’ E	1024	131.5

root. Plot means for these traits were estimated and analysis of variance was performed on plot mean data. Wilk's criterion and Mahalanobis D^2 statistic [6] were estimated using computer package SPAR1. Based on the D^2 values, the seed sources were grouped into individual clusters with the help of Tocher's method [6].

Results and discussion

The analysis of variance revealed significant differences among the seed sources for all the nine characters studied. Utilising Wilk's criterion to test the significance of the dispersion of seed sources in the multidimensional space, the estimated V-statistic was found to be highly significant (2004 at 351 d.f.). The D^2 values ranged from 3.65 to 4009.1 (Table 2) among the seed sources. Applying Tocher's method, all the forty seed sources were grouped into fifteen clusters (Table 3). Cluster I had 13 seed sources followed by cluster II and III with 4 and 5 seed sources, respectively. Cluster IV and V contained 2 seed sources each. In rest of the clusters single seed source was included.

Table 2. Inter and intra cluster distances (D^2) in *Acacia catechu* seed sources

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	**32.9**	100.4	121.0	69.6	234.1	103.6	97.95	50.8	116.3	219.8	152.4	61.5	583.6	1387.9	2808.7
II		**23.2**	118.8	72.8	139.2	116.3	72.8	95.6	91.1	67.4	158.2	168.5	366.5	1265.8	2408.5
III			**40.0**	83.5	316.5	72.4	111.1	101.5	142.6	140.2	287.8	228.4	282.6	1394.9	1977.9
IV				**38.3**	206.2	69.2	109.8	63.7	57.1	160.5	207.2	110.8	419.5	1143.2	2464.6
V					**34.4**	358.0	160.0	236.4	260.6	148.9	78.2	196.5	576.0	984.6	3001.8
VI						**37.6**	132.5	117.1	82.7	119.1	336.5	179.7	347.7	1425.6	2171.7
VII							**47.6**	118.0	155.6	102.9	147.2	158.8	373.1	1352.7	2433.6
VIII								**0**	11.1	167.9	139.4	106.6	550.9	1290.6	2711.8
IX									**0**	208.0	279.8	176.9	467.2	1185.0	2674.8
X										**0**	184.0	308.3	233.9	1265.0	2038.9
XI											**0**	51.8	523.4	1337.9	2738.9
XII												**0**	750.6	1225.3	3235.5
XIII													**0**	1324.3	1109.2
XIV														**0**	4009.1

*Values in bold faces are intra cluster distances

Table 3. Composition of D^2 clusters in *Acacia catechu* seed sources

Clusters	No. of seed sources	Code of seed* sources
I	13	S2, S3, S4, S9, S11, S16, S19, S20, S23, S24, S29, S33, S39
II	4	S13, S22, S27, S30
III	5	S6, S26, S31, S36, S40
IV	3	S7, S25, S28
V	3	S8, S35, S37
VI	2	S32, S14
VII	2	S1, S34
VIII	1	S10
IX	1	S15
X	1	S17
XI	1	S18
XII	1	S21
XIII	1	S5
XIV	1	S12
XV	1	S38

*Symbols as per Table 1

The pattern of distribution of seed sources in different clusters indicated that genetic divergence was not related to geographical differentiation. Many seed sources of close geographic proximity fell in different clusters and vice-versa. Tendency to form such type of clustering ignoring the geographical boundaries showed that regional isolation was not the only factor contributing to diversity in the natural population [7]. Clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the possibility of free exchange of breeding material. But in the natural range of a forest tree species like *Acacia catechu*, this possibility seems to be very less. However, unidirectional selection practiced for a particular trait or a group of linked traits in several places may produce similar phenotype which can aggregate into one cluster irrespective of their geographic origin [8]. This may be true in *Acacia catechu* as the heartwood of the species is primarily exploited for *katha* extraction through out the country. On the other hand, seed sources of many spatially closer habitat were scattered over different clusters. Such genetic diversity among the seed sources of common geographic origin may be due to their parentage, developmental traits, past history of selection, different amount of inbreeding in the adjacent stands, different out crossing rates of parent trees contributing to the seed lots and year to year variation in the out crossing ratios [9]. Genetic drift and selection forces under diverse environments might have caused greater diversity than geographical distances [10].

The maximum inter-cluster D^2 value was obtained between cluster XIV and XV (Table 3). These two clusters may be utilized in the hybridization programme as hybridization between divergent seed parents is likely to produce wide variability and transgressive segregants with high heterotic effects. Such recommendation had also been made in *Eucalyptus tereticarnis* [11]. The minimum distance between cluster I and VIII revealed that the seed sources belonging to these clusters are relatively closer. Such analysis was meant to avoid selection of parents from genetically closer clusters which may in turn result narrow genetic base and inbreeding depression.

Comparison of cluster means revealed that XV gave exceptionally high values for eight characters followed by cluster X (Table 4). Cluster mean for leaf area was highest for cluster IX. Therefore, these seed sources can be involved in hybridization programme to get recombinants with higher values for all the traits under study. However, selection in the cluster XV can be practiced as it contains only one seed source and has mean values higher for eight traits. Success of selection in this cluster could be fairly successful. The reason may be that the species is insect pollinated, more predominantly by bees [12]. The populations were fragmented and discrete without any definite clinal

Table 4. Cluster mean values for different traits among the seed sources of *Acacia catechu*

Cluster Trait	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
Seedling height (cm)	47.74	58.19	75.83	67.84	67.58	63.86	66.62	74.67	66.58	81.86	60.13	48.03	74.85	65.45	114.7
Collar diameter (mm)	6.05	7.44	10.03	8.76	9.82	8.99	9.82	6.94	8.90	10.03	6.98	6.72	11.95	7.30	17.60
Internodal length (mm)	14.57	15.23	20.10	16.02	19.84	14.71	20.05	18.22	14.30	21.03	19.99	14.26	19.91	15.00	25.21
No. of leaves	72.97	88.32	136.2	99.41	126.1	127.4	117.0	110.3	84.80	167.0	133.0	104.8	180.7	91.73	289.6
Leaf area (cm^2)	12.69	15.96	18.57	16.41	16.54	16.69	16.05	17.89	20.94	20.63	16.02	10.77	20.35	16.83	19.44
Fresh shoot weight (g)	20.32	40.12	66.95	44.03	44.49	47.70	45.06	36.67	27.33	74.73	28.73	15.73	117.1	69.13	253.8
Fresh root weight (g)	11.48	25.60	29.93	25.40	40.46	20.30	26.33	21.13	19.80	43.93	28.73	14.80	55.47	69.33	90.67
Dry shoot weight (g)	9.37	20.90	26.77	16.87	22.89	21.60	24.83	16.40	13.13	37.73	17.47	7.47	50.53	16.40	98.40
Dry root weight (g)	4.96	12.31	12.06	9.68	19.71	7.50	12.26	8.33	7.73	20.87	14.73	6.13	21.07	15.40	34.60

pattern for any character studied. The pollination behaviour and population structure suggest that the chance of flux of breeding material among the different populations is remote. Therefore, it may be hypothesized that, such isolated, distinct populations are free to differentiate with regard to any character and there could be fixation of different alleles at the same locus in the species when there is geographic isolation [13].

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