

Genetic variation for growth and yield parameters in half-sib progenies of *Melia azedarach* (Linn.)

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Abstract: Fifty-four progenies of *Melia azedarach* selected from 11 geographical locations in India were evaluated for different growth parameters at the seed farm at Ladhawal, Punjab Agricultural University, Ludhiana, India. Significant differences were observed among and within progenies for all characters at the age of 8 years. Progeny number 1 exhibited superior growth for all traits except clear bole height and number of branches. High narrow-sense heritability (progeny basis, within-progeny basis, and individual plant basis) was higher for mean annual increments for total height and diameter at breast height than other recorded growth parameters. Genetic gain within progeny selection was higher than progeny selection for all traits. Fifty-four progenies clustered into 8 clusters on the basis of the Euclidean distance of the observed traits. Out of 54 progenies, progeny number 10 (Himachal Pradesh, Solan seed source) was found to be the best for the characters studied on the basis of adjusted treatment mean ranking for further multiplication.

Key words: *Melia azedarach*, progeny evaluation genetic gain, mean annual increment

1. Introduction

Melia azedarach (Linn.), commonly known as Persian lilac, white cedar, or dek (India), is a highly valuable species and is recognized as a multipurpose tree species. It is suitable for alkaline soils, waterlogging conditions, and acidic soil (Tomer et al., 2003). It has beautiful flowers and foliage; therefore, it is suitable for planting along roadsides, canal sides, and in gardens. It is also used for agroforestry, social forestry, and urban forestry plantations and has great potential for diversifying the most common poplar/eucalypt-based agroforestry systems in India in the years to come. Mature wood is used for furniture and agricultural implements, boxes, poles, and tool handles because of its resistance to termites, while immature wood and twigs are used as fuel wood. The species has been identified as a potential alternate pulpwood species (Chauhan et al., 2008). Its bark, fruits, leaves, and wood have insecticidal properties (Alché et al., 2003). This species with multifarious uses has gained only limited research attention, especially regarding tree improvement. As the species is of immense importance, a study to select and analyze potential open-pollinated progenies by assessing the existing variability was conducted so that the same is used in future improvement and plantation programs. The present study is a step towards selecting good genotypes for agroforestry plantations, which can be

multiplied to produce quality planting material that will be further available to farmers on selection.

2. Materials and methods

The study was conducted at University Seed Farm at Ladhawal, Punjab Agricultural University, Ludhiana, India, situated at 30°58'N, 75°44'E and at 247 m altitude with an average annual rainfall of 604.88 mm. Fifty-four open pollinated half-sib progenies of *M. azedarach* from 11 geographical locations (Table 1) within 8 states of India were raised in a randomized complete block design with 8 plants in 3 replications at the spacing of 4 × 4 m. Observations on tree height (m), clear bole height (CBH; m), basal diameter (cm), diameter at breast height (DBH; cm), and number of branches were recorded and mean annual increment (MAI) for total height and DBH were calculated at the age of 8 years.

Analysis of variance (ANOVA) was done according to Sukhatme and Amble (1989). The mean values of growth and yield traits were calculated and the coefficients of variation were established as variability indicators. The significance test was carried out by referring to the standard F table of Snedecor (1961). The calculated F-values were compared with the tabulated F-values. A calculated F-value higher than the tabulated value reflected significant differences. All the characters that showed significant differences among

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Table 1. Details of seed sources of 54 progenies of *Melia azedarach*.

S. no.	Name of institution/university and state (India)	Numbers
1	CCS Haryana Agricultural University, Hisar (Haryana)	4 (1–4)
2	CSK Himachal Pradesh Agricultural University, Palampur (Himachal Pradesh)	5 (5–9)
3	Dr. YS Parmar University of Horticulture and Forestry, Solan (Himachal Pradesh)	7 (10–16)
4	M.P.K.V. Rahuri, Ahemadnagar (Maharashtra)	5 (17–21)
5	Marathwada Agricultural University, Parbhani (Maharashtra)	4 (22–25)
6	Punjab Agricultural University, Ludhiana (Punjab)	15 (26–40)
7	Rajendra Agricultural University, Pusa, Samastipur (Bihar)	2 (41–42)
8	Sher-E-Kashmir University of Agriculture Science and Technology, Jammu (Jammu & Kashmir)	4 (43–46)
9	Tamil Nadu Agricultural University, Mettupalayam (Tamil Nadu)	2 (47–48)
10	UHF RHRS, Jacch, Nurpur, Kangra (Himachal Pradesh)	1 (49)
11	University of Agriculture Science, Dharwad (Karnataka)	4 (50–53)
12	Control (Bulk seed mixed general population)	1 (54)
Total		54

the genotypes were subjected to estimation of genetic parameters. Parameters of variability were calculated as per the formula given by Burton (1952). All possible pairs of treatment means were compared with Duncan's multiple range test at the 5% probability level. The narrow-sense heritability and expected genetic gain resulting from the selection of 5% superior individuals were derived as suggested by Johnson et al. (1955).

3. Results

The data recorded for growth and yield parameters at the age of 8 years for 54 *Melia azedarach* progenies are shown in Table 2. All traits showed large differences, indicating a high level of morphological variation. ANOVA showed significant differences among the progenies with respect to all characters and indicated high genetic variability. In general, the highest levels of variations were recorded in the number of branches (35.63%), followed by DBH (26.89%), basal diameter (25.25%), and MAI for DBH (25.07%). Total height (16.01%) exhibited the lowest level of variation among the progenies.

Significant differences were found between and within progeny with respect to all characteristics under study at the 5% level of significance (Table 2). The highest total height was recorded in progenies 1 and 12 (11.50 m), which was on par with progenies 2, 13, 7, 14, 3, 11, and 54. The lowest total height was recorded in progeny 20 (4.48 m). Progeny 37 had the maximum value (3.15 m) for CBH, whereas the maximum basal diameter and DBH were both reported in progeny 1 (23.40 cm and 18.68 cm,

respectively), which shared the same level of significance with progenies 2 and 12. The lowest number of branches was observed in progeny 51, which was statistically similar to 14 other progenies. Maximum MAI for total height and for DBH were also recorded in progenies 12 and 1, respectively, whereas minimum MAI was recorded in progeny 20 for total height and in progeny 24 for DBH.

Maximum heritability on a progeny basis (h^2_f) and within-progeny basis (h^2_w) was observed in MAI for height and on an individual plant basis (h^2_i) in MAI for DBH. Minimum heritability was observed in total height, basal diameter, and DBH at the progeny level (Table 3). Genetic gain on a progeny and within-progeny basis reflected higher gains within progeny than in the progeny selection for all the characters. Maximum genetic gain on a progeny basis (G_f) for DBH and within-progeny basis (G_w) was higher for basal diameter, whereas minimum genetic gain was observed in the number of branches on a progeny basis and in total height on a within-progeny basis.

In general, the genotypic correlation coefficient values were higher than corresponding phenotypic values (Table 4). All traits showed positive relationships. The CBH, an important timber parameter, was positively and significantly correlated with basal diameters (0.201 and 0.229) and DBH (0.160 and 0.484) at the phenotypic and genotypic levels. MAI for total height and DBH were strongly correlated with total height and DBH, respectively. Both MAI for total height and DBH were strongly correlated with basal diameter.

Table 2. Variation in different growth and yield parameters in progenies of *Melia azedarach*. Values followed by different letters in a column are statistically significantly different.

Progenies	Total height (m)	Clear bole height (m)	Basal diameter (cm)	Diameter at breast height (cm)	Number of branches	MAI for total height	MAI for DBH
1	11.48 ^a	2.42 ^{abcdef}	23.40 ^a	18.68 ^a	7.00 ^{ab}	1.53 ^a	2.49 ^a
2	11.10 ^{ab}	2.16 ^{bcdefghi}	22.38 ^{ab}	17.46 ^{ab}	6.58 ^{abcd}	1.48 ^{ab}	2.33 ^{ab}
3	10.17 ^{abcde}	2.07 ^{bcdefghi}	12.67 ^{efghijklmnopq}	9.55 ^{defghijklmn}	5.00 ^{abcdefghi}	1.36 ^{abcde}	1.27 ^{fghijklmnop}
4	8.88 ^{cdefghijkl}	2.18 ^{bcdefghi}	14.28 ^{defghijklm}	10.91 ^{cdefghi}	6.25 ^{abcde}	1.18 ^{cdefghijk}	1.45 ^{efghijk}
5	7.33 ^{hijklm}	2.19 ^{bcdefgh}	11.43 ^{hijklmnopqr}	8.23 ^{fghijklmn}	6.08 ^{abcde}	0.98 ^{hijkl}	1.10 ^{ghijklmnopqr}
6	8.79 ^{defghijkl}	2.06 ^{bcdefghi}	12.88 ^{efghijklmnop}	10.42 ^{defghij}	6.75 ^{abcd}	1.17 ^{defghijk}	1.39 ^{efghijklm}
7	10.98 ^{abc}	2.16 ^{bcdefghi}	13.62 ^{defghijklmno}	10.51 ^{defghij}	4.83 ^{bcdefghi}	1.46 ^{abc}	1.40 ^{efghijkl}
8	7.54 ^{hijklm}	2.38 ^{abcdef}	16.08 ^{defghi}	11.64 ^{cdefgh}	6.83 ^{abc}	1.01 ^{hijkl}	1.55 ^{cdefghij}
9	9.33 ^{bcdefgh}	2.38 ^{abcdef}	13.11 ^{defghijklmnop}	11.24 ^{cdefghi}	6.75 ^{abcd}	1.24 ^{bcdefgh}	1.50 ^{cdefghijk}
10	7.88 ^{ghijklm}	2.23 ^{bcdefg}	18.17 ^{bcd}	14.98 ^{abc}	4.75 ^{bcdefghij}	1.05 ^{ghijkl}	2.00 ^{abc}
11	10.10 ^{abcdef}	2.55 ^{abc}	17.15 ^{cdef}	13.66 ^{bcd}	6.75 ^{abcd}	1.35 ^{abcdef}	1.82 ^{bcd}
12	11.50 ^a	1.48 ^{ghijkl}	21.56 ^{abc}	14.83 ^{abc}	6.83 ^{abc}	1.53 ^a	1.98 ^{bcd}
13	11.10 ^{ab}	2.76 ^{ab}	17.86 ^{bcde}	13.58 ^{bcd}	6.50 ^{abcd}	1.48 ^{ab}	1.81 ^{cde}
14	10.60 ^{abcd}	2.14 ^{bcdefghi}	11.78 ^{ghijklmnopqr}	7.86 ^{ghijklmn}	4.67 ^{bcdefghijk}	1.42 ^{abcd}	1.05 ^{ijklmnopqr}
15	6.88 ^{klmn}	2.46 ^{abcde}	11.93 ^{ghijklmnopqr}	10.43 ^{defghij}	5.42 ^{abcdefgh}	0.92 ^{ijklm}	1.26 ^{fghijklmnopq}
16	8.42 ^{efghijklm}	2.54 ^{abc}	12.82 ^{efghijklmnopq}	9.98 ^{defghijkl}	5.92 ^{abcdef}	1.12 ^{efghijkl}	1.33 ^{efghijklmno}
17	8.08 ^{efghijklm}	2.20 ^{bcdefgh}	10.42 ^{kmnopqr}	7.93 ^{fghijklmn}	4.42 ^{bcdefghijk}	1.08 ^{efghijkl}	1.06 ^{ijklmnopqr}
18	5.08 ^{no}	1.37 ^{hijk}	12.08 ^{fghijklmnopqr}	7.87 ^{fghijklmn}	7.75 ^a	0.68 ^{mn}	1.05 ^{ijklmnopqr}
19	6.94 ^{ijklmn}	1.68 ^{defghijk}	10.68 ^{ikmnopqr}	7.93 ^{fghijklmn}	6.67 ^{abcd}	0.93 ^{ijklm}	1.06 ^{ijklmnopqr}
20	4.48 ^o	1.08 ^k	11.41 ^{hijklmnopqr}	6.24 ^{ijklmn}	7.00 ^{ab}	0.60 ⁿ	0.83 ^{opqr}
21	7.25 ^{hijklm}	1.99 ^{bcdefghij}	10.86 ^{ikmnopqr}	8.2 ^{fghijklmn}	4.33 ^{bcdefghijk}	0.97 ^{hijkl}	1.07 ^{ijklmnopqr}
22	6.63 ^{mn}	1.90 ^{cdefghijk}	11.89 ^{ghijklmnopqr}	6.58 ^{ijklmn}	2.92 ^{ghijkl}	0.88 ^{lmn}	0.88 ^{mnopqr}
23	6.75 ^{lmn}	2.41 ^{abcdef}	9.66 ^{lmnopqr}	6.43 ^{ijklmn}	2.83 ^{ghijkl}	0.90 ^{klm}	0.86 ^{nopqr}
24	7.17 ^{ijklmn}	2.09 ^{bcdefghi}	7.41 ^r	4.80 ⁿ	3.17 ^{fghijkl}	0.95 ^{ijklm}	0.62 ^r
25	7.92 ^{ghijklm}	2.15 ^{bcdefghi}	11.59 ^{hijklmnopqr}	9.37 ^{efghijklm}	5.92 ^{abcdef}	1.06 ^{ghijkl}	1.25 ^{fghijklmnopq}
26	7.43 ^{hijklm}	2.03 ^{bcdefghij}	10.93 ^{ijklmnopqr}	8.8 ^{efghijklmn}	4.42 ^{bcdefghijk}	0.99 ^{hijkl}	1.17 ^{fghijklmnopq}
27	7.75 ^{ghijklm}	1.64 ^{defghijk}	10.71 ^{ikmnopqr}	8.08 ^{fghijklmn}	5.58 ^{abcdefgh}	1.03 ^{hijkl}	1.08 ^{hijklmnopqr}
28	7.61 ^{hijklm}	2.05 ^{bcdefghij}	13.84 ^{defghijklmn}	9.88 ^{defghijkl}	5.25 ^{abcdefgh}	1.01 ^{hijkl}	1.32 ^{efghijklmno}

Table 2. (Continued).

Progenies	Total height (m)	Clear bole height (m)	Basal diameter (cm)	Diameter at breast height (cm)	Number of branches	MAI for total height	MAI for DBH
29	8.75 ^{defghijklm}	2.61 ^{abc}	11.16 ^{hijkmnopqr}	7.83 ^{hijklmn}	3.92 ^{defghijkl}	1.17 ^{defghijk}	1.04 ^{ijklmnopqr}
30	8.96 ^{bcddefghijk}	1.58 ^{fghijk}	8.50 ^{opqr}	5.87 ^{lmn}	2.92 ^{ghijkl}	1.19 ^{cdefghij}	0.78 ^{pqr}
31	7.75 ^{ghijklm}	2.39 ^{abcdef}	12.65 ^{fghijkmnopq}	8.91 ^{efghijklmn}	4.67 ^{bcddefghijk}	1.03 ^{hijkl}	1.19 ^{fghijklmnopq}
32	7.96 ^{fghijklm}	1.20 ^{jk}	14.81 ^{defghijkl}	11.09 ^{cdefghi}	5.67 ^{abcdefg}	1.06 ^{ghijkl}	1.48 ^{defghijk}
33	7.83 ^{ghijklm}	1.64 ^{defghijk}	8.66 ^{mnopqr}	6.02 ^{lmn}	1.83 ^{kl}	1.04 ^{ghijkl}	0.80 ^{pqr}
34	9.00 ^{bcddefghijk}	2.41 ^{abcdef}	10.84 ^{ikmnopqr}	8.03 ^{fghijklmn}	2.75 ^{hijkl}	1.20 ^{bcddefghi}	1.06 ^{ijklmnopqr}
35	7.96 ^{fghijklm}	1.91 ^{bcddefghijk}	9.96 ^{lmnopqr}	7.42 ^{ijklmn}	2.83 ^{ghijkl}	1.06 ^{ghijkl}	0.99 ^{klmnopqr}
36	7.13 ^{ijklmn}	1.94 ^{bcddefghij}	9.79 ^{lmnopqr}	6.73 ^{ijklmn}	4.00 ^{cdefghijkl}	0.95 ^{ijklm}	0.90 ^{lmnopqr}
37	8.33 ^{efghijklm}	3.15 ^a	14.78 ^{defghijkl}	11.68 ^{cdefgh}	5.58 ^{abcdefgh}	1.11 ^{efghijkl}	1.56 ^{cdefghi}
38	9.29 ^{bcddefghi}	2.48 ^{abcd}	15.43 ^{defghijk}	12.53 ^{cde}	6.92 ^{ab}	1.24 ^{bcddefgh}	1.67 ^{cdef}
39	8.98 ^{bcddefghijk}	2.68 ^{abc}	12.10 ^{fghijkmnopqr}	9.68 ^{defghijklm}	6.83 ^{abc}	1.20 ^{bcddefghi}	1.29 ^{fghijklmnop}
40	8.04 ^{efghijklm}	2.21 ^{bcddefgh}	14.34 ^{defghijklm}	10.98 ^{cdefghi}	6.67 ^{abcd}	1.07 ^{fghijkl}	1.46 ^{efghijk}
41	8.38 ^{efghijklm}	1.83 ^{cdefghijk}	14.56 ^{defghijklm}	10.2 ^{defghijk}	6.08 ^{abcde}	1.12 ^{efghijkl}	1.36 ^{efghijklmn}
42	8.00 ^{fghijklm}	2.08 ^{bcddefghi}	15.84 ^{defghij}	11.62 ^{cdefgh}	7.08 ^{ab}	1.07 ^{fghijkl}	1.55 ^{cdefghij}
43	9.03 ^{bcddefghij}	2.08 ^{bcddefghi}	16.26 ^{defgh}	11.95 ^{cdefg}	4.75 ^{bcddefghij}	1.20 ^{bcddefghi}	1.59 ^{cdefgh}
44	7.08 ^{ijklmn}	2.03 ^{bcddefghij}	9.78 ^{lmnopqr}	8.08 ^{fghijklmn}	3.58 ^{efghijkl}	0.94 ^{ijklm}	1.08 ^{hijklmnopqr}
45	8.50 ^{defghijklm}	2.20 ^{bcddefgh}	10.06 ^{lmnopqr}	8.38 ^{fghijklmn}	5.67 ^{abcdefg}	1.13 ^{efghijkl}	1.12 ^{ghijklmnopqr}
46	9.00 ^{bcddefghijk}	2.03 ^{bcddefghij}	12.38 ^{fghijkmnopqr}	9.63 ^{defghijklm}	5.47 ^{abcdefgh}	1.20 ^{bcddefghi}	1.28 ^{fghijklmnop}
47	7.88 ^{ghijklm}	1.33 ^{ijk}	16.98 ^{cdefg}	11.98 ^{cdef}	6.50 ^{abcd}	1.05 ^{ghijkl}	1.60 ^{cdefg}
48	6.75 ^{lmn}	2.42 ^{abcdef}	9.38 ^{lmnopqr}	6.68 ^{ijklmn}	5.00 ^{abcdefghi}	0.90 ^{klm}	0.89 ^{lmnopqr}
49	6.50 ^{mno}	2.60 ^{abc}	8.65 ^{mnopqr}	6.65 ^{ijklmn}	2.33 ^{ijkl}	0.87 ^{lmn}	0.89 ^{lmnopqr}
50	8.17 ^{efghijklm}	2.39 ^{abcdef}	8.48 ^{opqr}	6.22 ^{ijklmn}	2.83 ^{ghijkl}	1.09 ^{efghijkl}	0.83 ^{opqr}
51	7.30 ^{hijklm}	2.22 ^{bcddefgh}	8.12 ^{pqr}	5.64 ^{mn}	1.42 ^l	0.97 ^{hijkl}	0.75 ^{qr}
52	6.79 ^{lmn}	2.26 ^{bcddefg}	7.67 ^{qr}	6.23 ^{ijklmn}	2.33 ^{ijkl}	0.91 ^{ijklm}	0.83 ^{opqr}
53	7.40 ^{hijklm}	1.61 ^{efghijk}	9.78 ^{lmnopqr}	5.95 ^{lmn}	1.92 ^{jkl}	0.99 ^{hijkl}	0.79 ^{pqr}
54	9.88 ^{abcdefg}	2.67 ^{abc}	13.26 ^{defghijklmnop}	9.62 ^{defghijklm}	4.67 ^{bcddefghijk}	1.32 ^{abcdefg}	1.28 ^{fghijklmnop}
Mean ± SE	8.26 ± 0.76	2.13 ± 0.30	12.72 ± 1.85	9.48 ± 1.47	5.03 ± 1.04	1.10 ± 0.10	1.26 ± 0.18
Max.	11.5	3.15	23.40	18.68	7.75	1.53	2.49
Min.	4.48	1.08	7.41	4.80	1.42	0.60	0.62

Table 3. Estimates of genetic parameters for 54 progenies of *M. azedarach*.

Parameters	Total height (m)	Clear bole height (m)	Basal diameter (cm)	Diameter at breast height (cm)	No. of branches	MAI for height	MAI for DBH
PCV	3.36	0.35	19.69	13.12	4.92	0.23	0.06
GCV	1.62	0.08	9.37	6.66	1.71	0.13	0.03
h ² f	28.12	42.69	28.35	28.49	41.52	67.94	53.52
h ² w	36.62	51.84	34.41	42.53	49.09	54.12	46.61
h ² i	31.45	49.16	36.63	37.62	52.49	47.22	63.42
Gf	13.20	9.00	21.59	22.87	4.92	13.11	20.65
Gw	21.44	29.11	56.89	49.63	24.18	34.15	47.62
Gt	34.64	38.11	78.48	72.50	29.10	47.26	68.27

PCV = phenotypic coefficient of variability, GCV = genotypic coefficient of variability, h²f = heritability on a progeny basis, Gf = genetic gain of progeny selection, h²w = heritability on a within-progeny basis, Gw = genetic gain of within-progeny, h²i = heritability on an individual basis, Gt = total genetic gain (Gf + Gw).

Table 4. Genotypic and phenotypic correlation among different traits of *Melia azedarach*.

Characters		Total height (m)	Clear bole height (m)	Basal diameter (cm)	Diameter at breast height (cm)	Number of branches	MAI for total height (m)
Clear bole height	p	0.114					
	g	0.146					
Basal diameter	p	0.290**	0.201**				
	g	0.682**	0.229**				
Diameter at breast height	P	0.263**	0.160**	0.928**			
	g	0.643**	0.484**	0.989**			
Number of branches	p	0.040	0.125	0.390**	0.337**		
	g	0.325**	0.231**	0.126	0.135**		
MAI (total height)	p	0.569**	0.114	0.288**	0.262**	0.04	
	g	0.798**	0.147	0.683**	0.645**	0.263	
MAI (DBH)	p	0.228**	0.08	0.686**	0.730**	0.282**	0.227**
	g	0.049	0.492**	0.874**	0.986**	0.356**	0.110

Critical value of r at 5% = 0.1536 and at 1% = 0.2002. **: Significant at 1% level. P = phenotype; g = genotype.

Fifty-four accessions of *M. azedarach* were grouped into 8 clusters on the basis of nonhierarchical Euclidian cluster analysis (Table 5). The maximum numbers of accessions (14) were grouped in cluster VI, followed by 13 accessions each in clusters VII and VIII. Cluster I had 1 accession, II had 2 accessions, III had 3 accessions, and VI and V had 4 accessions. The analysis showed that the Euclidean distances between clusters were 1.73 (I and II),

2.27 (II and III), 2.50 (III and IV), 2.53 (IV and V), 3.53 (V and VI), 3.61 (VI and VII), and 4.14 (VII and VIII). The analysis further exhibited that clusters I, II, III, IV, and V were more closely related, whereas clusters V, VI, VII, and VIII were distant from each other.

According to the adjusted treatment mean ranking for all recorded characters, the best performance was recorded in progeny number 10 (Himachal Pradesh, Solan seed

Table 5. Agglomerative hierarchical clustering and Euclidean distance.

Cluster	Similar groups and distance	Cluster	Similar groups and distance
Cluster I	1	Cluster V	27, 28, 29, 9
Distance	1.73	Distance	3.525
Cluster II	2, 12	Cluster VI	4, 6, 7, 8, 20, 16, 25, 19, 32, 37, 40, 41, 43, 47
Distance	2.271	Distance	3.612
Cluster III	42, 39, 3	Cluster VII	14, 15, 17, 23, 5, 18, 30, 31, 34, 35, 45, 46, 48
Distance	2.502	Distance	4.137
Cluster IV	10, 11, 13, 38	Cluster VIII	21, 22, 24, 26, 33, 36, 44, 49, 50, 51, 52, 53, 54
Distance	2.533		

Agglomerative coefficient = 0.861.

source), followed by 1, 38, 39, 28, 37, 9, 11, 29, and 13. The poorest performance was recorded in progeny number 33, which belonged to Ludhiana seed sources. Out of the top

10 progenies, 5 progenies represented Punjab seed sources (Table 6). The Figure depicts the adjusted mean ranking for 4 important growth traits (total height, CBH, basal

Table 6. Adjusted treatments means and ranks for all recorded characters.

Progeny number	Adjusted treatment rank	Ranking (seed sources)	Progeny number	Adjusted treatment rank	Ranking (seed sources)	Progeny number	Adjusted treatment rank	Ranking (seed sources)
1	13.18	2 (HH)	19	8.16	41 (MHA)	37	12.16	6 (L)
2	9.35	22 (HH)	20	7.08	49 (MHA)	38	12.68	3 (L)
3	10.48	15 (HH)	21	6.92	52 (MHA)	39	12.49	4 (L)
4	9.63	21 (HH)	22	7.05	50 (MHP)	40	8.75	3 (L)
5	8.91	31 (HPP)	23	10.87	12 (MHP)	41	8.02	45 (B)
6	10.60	14 (HPP)	24	6.59	53 (MHP)	42	10.92	11 (B)
7	9.95	18 (HPP)	25	10.47	16 (MHP)	43	6.96	51 (J)
8	8.40	38 (HPP)	26	8.62	37 (L)	44	8.86	32 (J)
9	11.97	(HPP)	27	8.08	44 (L)	45	8.76	34 (J)
10	14.21	1 (HPS)	28	12.48	5 (L)	46	10.40	17 (J)
11	11.97	8 (HPS)	29	11.52	9 (L)	47	7.64	46 (TN)
12	9.25	23 (HPS)	30	8.09	43 (L)	48	10.78	13 (TN)
13	11.28	10 (HPS)	31	8.70	36 (L)	49	9.73	20 (HPK)
14	8.26	40 (MHA)	32	9.23	24 (L)	50	9.86	19 (K)
15	9.07	26 (MHA)	33	6.29	54 (L)	51	7.23	48 (K)
16	8.78	33 (MHA)	34	8.14	42 (L)	52	8.98	27 (K)
17	8.98	28 (MHA)	35	9.22	25 (L)	53	8.92	30 (K)
18	7.50	47 (MHA)	36	8.93	29 (L)	54	8.33	39 (C)

Approximate CD at 5% level of significance for adjacent treatments = 1.11

B = Bihar seed sources, C = control, HH= Haryana Hisar seed sources, HPP = Himachal Pradesh Palampur seed sources, HPS = Himachal Pradesh Solan seed sources, HPK = Himachal Pradesh Kangra seed sources, J = Jammu seed sources, K = Karnataka seed sources, L = Ludhiana seed sources, MHA = Maharastra Ahmednagar seed sources, MHP = Maharastra Prabhani seed sources, TN = Tamil Nadu seed sources.

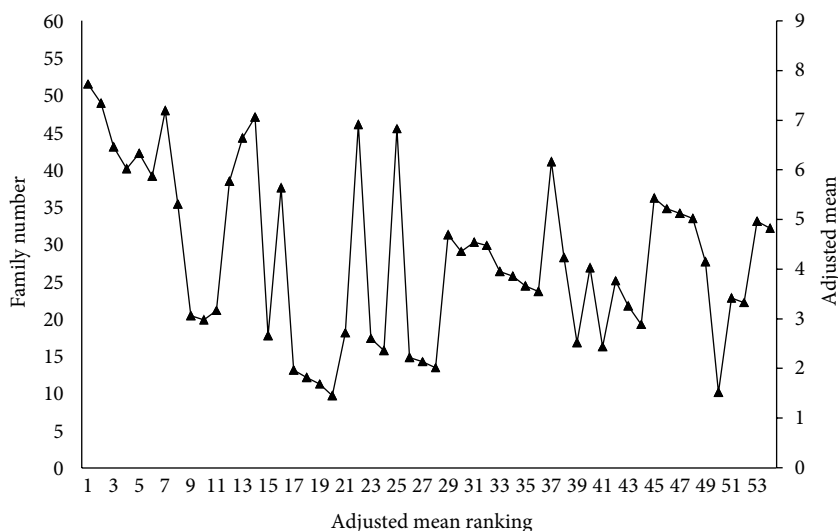


Figure. Adjusted mean and rank for 4 important growth parameters (total height, clear bole height, basal diameter, and diameter at breast height).

diameter, and DBH), where the trend was very different than that depicted in Table 6. Even highly ranked progeny number 10 was not included in the top 10 progenies. Progeny number 1 received the highest adjusted mean ranking out of the 4 characters under study, followed by 2, 7, 14, 22, 25, 13, 3, 5, and 37. These top 10 progenies can be selected for timber production under the irrigated agroecosystem in Punjab, India.

4. Discussion

Genetic variability in tree species is a gift to mankind, as it forms the basis for selection and further improvement of species. The information on the genetic structure and diversity relationship of a candidate plus tree provides a basis for planning future efficient utilization of genetic resources to realize the potentiality for maximizing growth and yield. The results clearly indicated that for a majority of traits there is much scope for selection for improvement in *Melia*. Variations among progenies are commonly used as an estimate of total genetic variation and to calculate the degree of genetic control for a particular trait. In the present study, for all traits the genotypic coefficient of variation (GCV) was found to be of a lower magnitude than the phenotypic coefficient of variation. This indicates that these traits are influenced by local environmental factors, as evidenced in *Azadirachta indica* (Dhillon et al., 2003) and also in progenies of *Dalbergia sissoo* (Dogra et al., 2005). Similarly, significant differences were found for growth parameters among 34 genotypes of *M. azedarach* (Atwal, 2004) and *M. volkensii* (Runo et al., 2004).

A high heritability indicated that much of the variation for a given characteristic observed in the population

is genetic in origin. Therefore, there is a high probability of selecting parents that have desirable phenotypes. High heritability coupled with high genetic advance for basal diameter, DBH, and MAI for DBH suggests the potential of source material for improvement through selection for these traits. High heritability accompanied by high genetic advance for several growth parameters has been reported in *D. sissoo* (Devagiri et al., 2004), *Jatropha curcas* (Ginwal et al., 2004; Rao et al., 2008), *E. tereticornis* (Kumar et al., 2007, 2010), and 11 progenies in *M. azedarach* (Dhillon et al., 2009).

In all characters, genetic gain was higher within progeny than in the progeny selection. In the present study, the selection intensity was 5%. Better results can be achieved through the genetic base with more intensive progeny selection, though the genetic base will narrow down. The results are in agreement with the studies carried out in *E. globulus* and *E. nitens* (Raymond, 2002) for different genetic parameters. Genetic gain of progeny selection contributes less to total genetic gain because of the high selection intensity. Burton (1952) suggested that the study of GCV together with heritability estimates could give the best picture of the success to be achieved through selection. High values of genetic gain are indicative of additive gene action involved in the expression of various polygenic traits; low values are indicative of nonadditive gene action. The heritability and genetic gain revealed that satisfactory genetic gains could be obtained by phenotypic selection in *M. azedarach*; however, heritability estimates indicated only the effectiveness of selection of genotype on phenotypic performance. They failed to explain the real genetic progress.

Correlation shows the extent of association between traits, which may be the criteria for selection in breeding program. Correlated quantitative traits are of major interest in an improvement program, as the improvement of one character may cause simultaneous related changes in the other associated characters. In the present study, genotypic and phenotypic correlation coefficients between various characters revealed that magnitudes of correlation coefficients at the genotypic level were higher than their corresponding phenotypic coefficients of correlation, thus indicating the minimal effect of the environment and the true representation of genotype through phenotype selection (Parthiban, 2001; Kumar et al., 2013). The genotypic correlation is an estimated value, whereas phenotypic correlation is a derived value from the genotype and environmental interaction (Chaturvedi and Pandey, 2004).

The clustering pattern in this study revealed that geographical diversity was not necessarily related to genetic diversity. This kind of genetic diversity might be due to differential adoption methods, selection criteria, natural selection pressure, or environmental factors (Vivekananda and Subramanian, 1993). This indicated that genetic drift produced greater diversity than the

geographic diversity (Singh et al., 1996). The trees that originated in one region were distributed into different clusters, indicating that trees with same geographic origin could have undergone changes for different characters under selection. Observations on cluster formation show that the progenies within a cluster do not group together because of geographical affinities but rather due to the presence of common growth traits, e.g., CBH, total height, basal diameter, DBH, number of branches, MAI for DBH, and total height. However, clustering patterns did not indicate any relationship between genetic diversity and geographical distribution (Kaushik et al., 2007).

From the present study, it is clear that considerable differences exist among seed sources for growth and yield characters in *M. azedarach* and appreciable improvement in growth parameters can be achieved by collecting seeds from selected plus trees on a short-term basis. These seed sources show promise in their further exploitation for plantation, improvement, and multiplication. High genotypic correlation coefficients among the various characters indicated that the traits under study were genetically controlled and selection can be a very effective tool in the improvement of this economically and ecologically important tree species.

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