Field Evaluation of *Populus deltoides* Bartr. ex Marsh. at Two Sites in Indo-gangetic Plains of India

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Abstract

Results from clonal trials of *Populus deltoides* conducted in two distinct agroclimatic regions of Punjab in northwestern India are reported and discussed. Sixteen clones were evaluated at Hambran and Bathinda where commonly grown clone 'G-48' was considered as control. Significant differences among clones ($P < 0.001$) were observed for diameter at breast height (DBH), tree height and volume at the age of four and six years under both the site conditions. Clone 'L-48' ranked first for volume at six year age at both sites and was followed by clone 'Ranikhet'. The respective superiority for volume of these clones over control was 44.8 and 23.2 per cent at Hambran and 72.5 and 30.7 per cent at Bathinda. All growth traits registered significantly higher values at Hambran in comparison to those at Bathinda. Clone x site interaction was also significant ($P < 0.001$). The clones 'L-168', '154/86', 'Solan-z' and '170/88' experienced huge fluctuation in ranking between sites for volume at 6-year age. The DBH and height showed significant and positive correlation with each other and with tree volume at all the age combinations. The clonal mean heritability was quite high both at Hambran (0.73–0.86) and Bathinda (0.80–0.95). The genetic advance were the highest for volume (33.34–64.26%) and the lowest (10.65–22.79%) in case of height.

Key words: clonal heritability, clone-site interaction, genetic correlation, clonal selection.

Introduction

The natural forests of developing countries have been over-exploited since the middle of the last century for meeting the needs of burgeoning human and cattle population and for clearing of green land for farming. The gap between demand and supply for wood based products is widening in India, as the productivity of natural forests is very low (0.7 m^3/ha/yr) and the majority of the prevalent forests are degraded. The National Forest Policy of 1988 gave greater emphasis on the promotion of farm forestry to enhance wood productivity. Short rotation farm forestry tree species such as eucalypts, poplars, pines and subabul have drawn the attention of tree growers across India. Among these exotic tree species, *Populus deltoides* Bartr. ex Marsh., commonly known as 'poplar', is most extensively planted by farmers of north-western India. Its higher productivity (up to 48 m^3/ha/yr), short rotation (5–7 years), straight stem and deciduous nature make it more compatible in agroforestry systems (SIDHU and DHILLON, 2007). The soft, attractive, strong and easily workable wood of this species is suitable for manufacturing of matches, furniture, packing cases, plywood, sports goods, pulp and paper, rayon, fiberboard and pencils. After its introduction in 1950s in India (MATHUR and SHARMA, 1983), poplar was initially adopted by only a few innovative farmers of North-Western India (in eighties of the foregone century) for diversification from traditional rice-wheat crop rotation. However, its highly remunerative returns in comparison to rice-wheat rotation attracted large numbers of farmers towards poplar cultivation as a block plantation or on the farm boundaries. Poplar based agroforestry plantations in the states of Punjab, Haryana, Uttar Pradesh and Uttrakhand occupy an area equivalent to 60,000 ha of pure plantations of this species (CHANDRA, 2001). Commercial planting of *P. deltoides* in India has so far relied on the use of few clones of poplar viz. 'G-3', 'G-48', 'D-121', 'ST-67', 'S_7C_4' and 'S_7C_8' (CHATURVEDI, 1992). About 90 percent of the poplar plantations in India are based on clones 'G-48', 'G-3' and 'S_7C_{15}' (KUMAR et al., 1999). In the recent past, the highly narrow genetic base of these poplar plantations has resulted in the outbreak of leaf defoliators, bark eating caterpillar, stem borers, etc. in this region (SINGH et al., 2004).

Punjab Agricultural University (PAU) Ludhiana initiated the introduction and evaluation of poplar clones in late 1980s, as poplar does not bear catkins in this region. Ninety seven clones were introduced during February 1996 from four institutes of India viz. WIMCO Seedling Ltd., Forest Research Institute, Dehra Dun, Uttrakhand State Forest Department and University of Horticulture & Forestry, Nauni. Based on initial screening for adaptability, 63 clones were tested under nursery conditions for two years and promising clones were short listed for the field evaluation. The selected clones were tested at two variable sites under field conditions to assess the variation in growth traits among clones at rotation age and to identify site specific clones for enhancing the productivity.

Materials and Methods

Study area

Clonal trials were conducted in two agroclimatic zones of the state. In the central-plain region, the study was conducted on a farmer's field at Village Hambran on the left bank of river Satluj which is 15 km from the main campus of Punjab Agricultural University (PAU), Ludhiana. The site suits well for the optimum growth of

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Table 1. – The location and climatic conditions of the study sites.

Climatic/edaphic feature		**Site 1** (Hambran)	**Site 2** (Bathinda)
Agro-climatic zone		Central-plain-region	Semi-arid region
Latitude, longitude and altitude		30°54'N, 75°52'E, and 240 m	30°17' N, 74°57' E and 211 m
Rainfall per annum		732 mm	400 mm
Soil Moisture Index (June-Sept. Weeks)	Wet humid	12	0
	Humid dry	1	6
	Dry arid	4	11
Underground water	Reservoir depth (ft)	20	100
	Quality	Good	Marginal
Irrigation Source		Tubewell	Canal
Soil pH		8.2	8.6
Soil texture		Sandy loam	Loamy sand to sandy loam

poplar with majority of agricultural fields in the vicinity having poplar plantations. The second trial was planted at the Experimental Farm of PAU at the Regional Research Station Bathinda. The climate in this region is semi-arid to arid with canal as the main source of irrigation. The climatic and edaphic conditions of sites are given in *Table 1*.

Treatments and experimental design

The clones used for the study were selected on basis of initial screening for two years at the nursery stage with respect to adaptability and tolerance to insects. At both the sites, 20 clones were planted and 16 clones were common. Seven clones (Ranikhet, Solan-1, 45, 200/85, 154/86, UFD-6400 and Solan-z) were introduced from University of Horticulture and Forestry, Nauni, India and another set of seven clones (L-127, L-17, L-47, L-168, L-57, L-170 and L-48) were procured from Uttrakhand State Forest Department Research Center, Lal Kuan (India). Clone '72/58' was obtained from Forest Research Institute, Dehra Dun. Clone 'G-48' (originated from Australia) which is most extensively planted in north-western India was used as a control at both sites. The ETP's (entire transplants, one year old rooted cuttings) of these clones, raised at nursery area of Department of Forestry & Natural Resources, PAU, Ludhiana, were transported to the study sites during January 1999. The experiments were conducted following complete randomized block design with four replications and plot size of five trees. A boundary row of non-experimental plants was planted to check the border effect. The clones were randomized independently in each of the four blocks/replications with plot shape of five plants as row. The ETP's were planted at 5 x 4 m spacing with planting depth of one meter. Uniform silvicultural practices of planting, fertilizer application, weeding and pruning (SIDHU et al., 1990) were applied to all trees of a trial throughout completion of the study. The frequency of irrigation at Bathinda was relatively less because of scanty canal supply for many weeks in a year, however the uniform life saving watering was applied to the trial during such periods.

Data recording and statistical analyses

The data on height and diameter at breast height (DBH), measured at 1.37 m from ground surface, were recorded from individual trees during December every year. The growth parameters recorded at the age of four and six years are given in this paper. Volume per plant was worked out on the basis of the following equation developed by DHANDA and VERMA (2001) for this region.

$$V = 0.00703 + 0.32223 * D_2H,$$

where V, D and H stands for volume (m^3), DBH (m) and tree height (m), respectively.

The data from both the trials were pooled and analyzed according to the following model $Y_{ijkl} = \mu + S_i + B_{j(i)} + C_k + CS_{ik} + BC_{j(i)k} + e_{ijkl}$, where Y_{ijkl} is the performance of *l*th ramet of *k*th clone growing in *j*th block of *i*th site; μ is overall mean of the both sites; S_i is the effect of *i*th test site (i = 1,2); $B_{j(i)}$ is the effect of *j*th block within *i*th site (j = 1, … 4); C_k is the effect of the *k*th clone (k = 1, … 16); CS_{ik} is the interactive effect of *k*th clone and *i*th site; $BC_{j(i)k}$ is the interactive effect of *k*th clone and *j*th block (within *i*th site) and e_{ijkl} is the random error associated with ramets within plot (l = 1, … 5). All the factors were considered as random. The data from individual sites were also analyzed using the same model but without site and its interaction with clone.

Estimation of heritability and coefficients of variation

In case of the individual site analysis the broad sense heritability on individual tree basis was worked out as- $H^2_i = \sigma^2_c/\sigma^2_P$, where H^2_i denotes heritability on an individual tree basis which is relevant to estimation of gains from selection of best individual ramets from a particular clonal trial, σ^2_c variance due to clonal effects (i.e. including additive and non-additive genetic variances) for the particular trial and σ^2_P phenotypic variance among ramets in the trial. σ^2_P is calculated as $\sigma^2_P = \sigma^2_c + \sigma^2_{cb} + \sigma^2_w$, where σ^2_{cb} represents variance due to clone-block interaction and σ^2_w within-plot error.

The broad-sense heritability relevant to estimating genetic gain from selection of best clones is the "clonal heritability" (denoted H^2_c) which was calculated following equation suggested by LAMBETH et al. (1994).

$$H^2c = \frac{\sigma^2_c}{k_2\sigma^2_c/k_2 + (k_1\sigma^2_{bc}/k_1) + \sigma^2_e/k_2}$$

Where k_1 is coefficient associated with the variance due to block x clone interaction (σ^2_{bc}) and k_2 is the coeffi-

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cient associated with the variance due to clonal variation (σ^2_c).

Other genetic parameters like genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) was worked out following JOHNSON et al. (1955).

On basis of analysis across sites, clonal mean heritability (H^2c_P) was calculated using the following equation:

$$H^2c_P = \frac{\sigma^2_c}{k_5\sigma^2_c/k_5 + k_3\,\sigma^2_{cs}/k_5 + k_4\,\sigma^2_{bc}/k_5) + \sigma^2_e/k_5}$$

where σ^2_c, σ^2_{cs}, σ^2_{bc} and σ^2_e represents variance due to clones, clone-site interaction, clone-block interaction and within-plot error. k_3 is coefficient associated with the variance due to location x clone interaction (σ^2_{cs}), k_4 is the coefficient associated with the variance due to clone x block interaction and k_5 is the coefficient associated with the variance due to clonal variation (σ^2_c) and standard error for clonal repeatability was worked following BECKER (1992).

Estimation of genetic correlation among traits and Type B genetic correlations

Genetic correlation (r_{Gxy}) between traits x and y on same site was worked out using following expression

$$r_{Gxy} = COV_{Cxy}/\sqrt{(\sigma^2_{Cx}.\sigma^2_{Cy})},$$

where COV_{Cxy} is clonal covariance between traits x and y, σ^2_{Cx} and σ^2_{Cy} are variance due to clonal effects for traits x and y, respectively.

Type B genetic correlations (r_B) between same traits at different sites were worked out according to BURDON (1977).

$$r_B = r_{xy} / H_{c(x)}.H_{c(y)}$$

where r_{xy} is the phenotypic correlation of clonal means and $H_{c(x)}$ and $H_{c(y)}$ are square roots of clonal mean heritabilities at each environment estimated from within site data analysis.

Type B genetic correlation (r_B) is the genetic correlation between the same trait expressed on two different sites and essentially is a measure of G x E interaction ($0 \le r_B \le 1$) and $r_B \approx 1$ indicates no G x E variance.

Working out genetic advance and correlated response

Genetic advance (Δ G) as per cent of mean from clonal selections in character y were estimated as

$$\Delta G = (i * H^2_c * \sigma_P/\bar{y}) * 100,$$

where i is selection intensity (1.80, selecting best 5 % clones), H^2_c is clonal mean heritability, σ_P is phenotypic standard deviation and $\bar{y}$ is general mean of the character.

The correlated response CR_y (% of mean) in desired character y brought about from the selection based on a secondary character x was calculated according to following expression FALCONER (1989)

$$CR_y = [(i.H_{Cx}.H_{Cy}.r_{Gxy}.\sigma_{Py})/\bar{y}] * 100,$$

where i is selection intensity (1.64, selecting best 10% clones), H_{Cx} and H_{Cy} are clonal heritabilities for trait x and y, r_{Gxy} is genetic correlation between trait x and y, σ_P is phenotypic standard deviation and $\bar{y}$ is general mean of the character.

Results

Clonal variation for growth traits

The analysis of variance indicated that clonal differences were found to be highly significant ($P < 0.001$) for diameter at breast height (DBH), tree height and volume per tree at both the sites at the age of 4 and 6 year (*Table 2* and *3*). The pooled analysis across sites also revealed significant differences ($P < 0.001$) among clones and between sites at both the ages for all the three traits (*Table 4*). At Hambran, Clone '154/86' registered the maximum DBH at age 4 and was statistically at par with clones 'L-48' and 'Ranikhet'. Clone 'L-57' was significantly superior to all others for tree height at age 4 at the same site. At age six, clone 'L-48' registered statistically superior DBH and was followed by clones 'Ranikhet' and 'L-47'. Five other clones recorded statistically higher values than control (G-48). For tree height, only 'L-48' was superior to control. Clone 'Solan-1' attained the bottom rank at Hambran for both the traits and ages. Clones 'L-48' attained top ranking for DBH and height at Bathinda at both ages, whereas, the lowest values were recorded for '72/58'.

The volume per tree at 4 year age ranged from 0.0907 to 0.1741 m^3 and 0.0217 to 0.0971 m^3 at Hambran and Bathinda, respectively (*Table 3*). At former site, the top ranking was attained by 'L-48' which was at par with four other clones. 'L-48' was significantly superior to all other clones at Bathinda and was followed by 'L-47', 'L-168' and 'Ranikhet'. 'L-48' maintained its top ranking at the both sites even at the age of 6-year and was statistically superior to others. Five other clones had higher volume than that of the control at Hambran. Like DBH and tree height, the lowest volume was recorded for 'Solan-1' at Hambran and '72/58' at Bathinda.

All the growth traits recorded at Hambran were significantly higher than their respective values at Bathinda at both the ages. The mean volume per tree after age 6 at Hambran (0.2506 m^3) was almost double than that (0.1319 m^3) at Bathinda. The clone x site interaction was also significant ($P < 0.001$) at both the ages for all three traits. Clones 'L-48', 'Ranikhet', '45', 'L-47', 'L-127' and 'L-17' remained almost stable across sites for all the traits, whereas, '154/86', 'L-168' and 'L-170' experienced huge changes in ranks between sites. Type B genetic correlation, another measure of g x e interaction, was the minimum (0.25) for DBH and the maximum value (0.51) was for height at four year age (*Table 4*). All the values increased at age 6 and ranged from 0.51 for DBH to 0.67 for volume. This indicated moderate clone-site interaction.

Genetic parameters and correlations

On the basis of individual site analysis, all genetic parameters were relatively higher at Bathinda than

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Table 2. – Mean diameter at breast height (DBH), tree height and genetic parameters of poplar clones planted at two sites.

Clone	Hambran				Bathinda			
	DBH 4 yr	Height 4 yr	DBH 6 yr	Height 6 yr	DBH 4 yr	Height 4 yr	DBH 6 yr	Height 6 yr
Ranikhet	18.23^{ab}	15.46^{b}	21.70^{b}	19.26^{bc}	12.53^{cd}	11.67^{ef}	17.80^{b}	16.05^{c}
Solan-1	14.18^{g}	12.69^{j}	17.28^{k}	16.23^{j}	11.24^{gh}	10.99^{g}	14.48^{j}	14.54^{g}
45	15.55^{f}	14.53^{h}	18.48^{j}	18.09^{g}	10.86^{i}	10.85^{gh}	14.70^{ij}	14.02^{i}
200/85	18.13^{b}	14.83^{fg}	20.15^{cde}	19.06^{cd}	11.87^{ef}	11.52^{f}	16.30^{f}	14.98^{f}
154/86	18.50^{a}	15.03^{e}	20.47^{c}	18.88^{de}	10.90^{hi}	10.63^{h}	14.05^{k}	14.43^{gh}
UFD-6400	16.88^{d}	14.27^{i}	19.80^{efg}	18.46^{f}	12.22^{de}	11.51^{f}	16.75^{de}	15.65^{d}
Solan-z	17.10^{cd}	14.73^{g}	19.80^{efg}	17.60^{h}	12.18^{de}	11.58^{f}	16.28^{f}	15.37^{e}
72/58	17.00^{d}	14.45^{h}	19.89^{ef}	17.67^{h}	7.43^{k}	7.51^{l}	9.70^{m}	10.06^{j}
L-127	17.30^{c}	15.23^{cd}	19.98^{de}	18.49^{f}	10.98^{hi}	12.68^{bc}	15.73^{g}	15.74^{d}
L-17	16.85^{de}	14.86^{fg}	19.55^{fgh}	17.98^{g}	10.86^{i}	11.08^{g}	15.00^{h}	14.30^{gh}
L-47	18.20^{b}	15.22^{d}	21.35^{b}	18.49^{f}	12.70^{bc}	12.98^{b}	17.10^{c}	17.13^{b}
L-168	17.05^{cd}	14.92^{ef}	18.98^{i}	18.78^{e}	12.91^{b}	11.51^{f}	16.93^{cd}	15.48^{de}
L-57	16.58^{e}	16.08^{a}	19.23^{hi}	19.38^{b}	11.57^{fg}	12.33^{cd}	14.85^{hi}	15.64^{de}
L-170	18.08^{b}	15.50^{b}	20.30^{cd}	19.48^{b}	9.82^{j}	10.98^{gh}	13.03^{l}	14.20^{hi}
L-48	18.25^{ab}	15.42^{b}	22.83^{a}	20.53^{a}	13.93^{a}	13.90^{a}	19.28^{a}	17.68^{a}
G-48 (control)	17.28^{c}	15.37^{bc}	19.48^{gh}	19.24^{bc}	11.99^{c}	11.98^{de}	16.53^{ef}	16.29^{c}
Mean ± S.E.	17.20±0.17	14.91±0.07	19.95±0.12	18.60±0.08	11.50±0.21	11.50±0.21	15.53±0.15	15.09±0.11
$M.S._c$	25.39***	11.24***	33.25***	19.25***	43.55***	37.47***	98.79***	56.75***
$M.S._e$	1.84	1.01	2.66	0.953	1.67	1.10	3.79	1.30
H^2_i	0.33	0.23	0.26	0.33	0.42	0.41	0.54	0.56
H^2_c	0.85	0.73	0.76	0.79	0.85	0.83	0.95	0.92
PCV (%)	10.58	9.05	11.19	8.19	18.39	16.83	18.96	14.32
GCV(%)	6.05	4.31	5.65	4.70	11.86	10.84	13.99	10.75
GA (% of mean)	14.77	10.89	14.01	10.65	25.75	22.79	29.68	21.49

Means followed by same letter do not differ (P < 0.05) by LSD test. *** indicate significance at P< 0.001.
$M.S._c$ is mean sum of squares for clones; $M.S._e$ is mean sum of squares for error; H^2_i is individual tree heritability; H^2_c is clonal heritability and GA is genetic advance as per cent of mean.

Table 3. – Mean volume per tree and genetic parameters at two ages for poplar clones planted at two sites.

Clone	Age 4 years				Age 6 years			
	Hambran		Bathinda		Hambran		Bathinda	
	Mean (m^3)	Rank	Mean (m^3)	Rank	Mean (m^3)	Rank	Mean (m^3)	Rank
Ranikhet	0.1728^{a}	3	0.0681^{cd}	4	0.3012^{b}	2	0.1724^{b}	2
Solan-1	0.0907^{i}	16	0.0539^{hi}	11	0.1658^{k}	16	0.1089^{i}	13
45	0.1210^{h}	15	0.0533^{hi}	14	0.2084^{j}	15	0.1081^{i}	12
200/85	0.1653^{b}	6	0.0599^{fg}	9	0.2583^{c}	6	0.1367^{fg}	8
154/86	0.1740^{a}	2	0.0499^{i}	13	0.2688^{de}	5	0.1020^{j}	14
UFD-6400	0.1391^{g}	14	0.0634^{ef}	7	0.2426^{fg}	10	0.1448^{de}	6
Solan-z	0.1470^{cf}	11	0.0641^{def}	6	0.2320^{ghi}	12	0.1413^{ef}	7
72/58	0.1431^{fg}	13	0.0217^{k}	16	0.2371^{fghi}	11	0.0400^{l}	16
L-127	0.1545^{cd}	8	0.0566^{gh}	10	0.2465^{f}	7	0.1343^{g}	9
L-17	0.1439^{fg}	12	0.0509^{i}	12	0.2302^{hi}	13	0.1123^{i}	11
L-47	0.1701^{ab}	5	0.0760^{b}	2	0.2827^{c}	3	0.1720^{b}	3
L-168	0.1502^{de}	10	0.0702^{c}	3	0.2274^{i}	14	0.1526^{c}	5
L-57	0.1510^{de}	9	0.0616^{ef}	8	0.2393^{fgh}	9	0.1208^{h}	10
L-170	0.1738^{a}	4	0.0421^{j}	15	0.2715^{cd}	4	0.0876^{k}	15
L-48	0.1741^{a}	1	0.0971^{a}	1	0.3540^{a}	1	0.2275^{a}	1
G-48 (control)	0.1569^{c}	7	0.0655^{de}	5	0.2444^{f}	8	0.1484^{cd}	4
Mean±S.E.	0.1517±0.0020		0.0596±0.0014		0.2506±0.0037		0.1319±0.0030	
$M.S._c$	0.00996***		0.0052***		0.03441***		0.0359***	
$M.S._e$	0.00074		0.00025		0.0022		0.00111	
H^2_i	0.33		0.35		0.31		0.58	
H^2_c	0.86		0.81		0.80		0.95	
PCV (%)	23.75		41.21		26.75		41.25	
GCV(%)	13.63		24.42		14.79		31.34	
Genetic advance (% of mean)	33.34		54.88		35.09		64.26	

Means followed by same letter do not differ (P < 0.05) by LSD test. *** indicate significance at P < 0.001.
$M.S._c$ is mean sum of squares for clones, $M.S._e$ is mean sum of squares for error. H^2_i is individual tree heritability, H^2_c is clonal heritability.

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Table 4. – Analysis of variance, variance components and genetic parameters for various growth traits of poplar clones based on pooled analysis across sites.

Trait	Source	Mean Sum of squares	H^2_C	Genetic Advance (% of mean)	r_B
DBH 4 yr	Site	5194.24***	0.27±0.08	6.59	0.25
	clone	41.41***			
	Site x clone	27.53***			
	error	1.91			
Height 4 yr	Site	1883.76***	0.39±0.09	8.84	0.51
	clone	32.54***			
	Site x clone	16.18***			
	error	1.25			
Volume 4 yr	Site	1.356***	0.33±0.08	13.11	0.35
	clone	0.00972***			
	Site x clone	0.00547***			
	error	0.000414			
DBH 6 yr	Site	3181.99***	0.45±0.09	8.36	0.51
	clone	87.03***			
	Site x clone	43.68***			
	error	3.35			
Height 6 yr	Site	2131.24***	0.44±0.09	8.66	0.56
	clone	49.55***			
	Site x clone	23.37***			
	error	1.301			
Volume 6 yr	Site	2.275***	0.62±0.09	23.94	0.67
	clone	0.0533***			
	Site x clone	0.0158***			
	error	0.00173			

H^2_c is clonal mean heritability, r_B is Type B genetic correlation. *** indicate significance at $P < 0.001$.

those at Hambran for both the ages and all the growth traits (*Table 3*). For any age, the phenotypic coefficients of variation (10.57 to 40.85%) and genotypic coefficients of variation (6.05 to 30.89%) were relatively higher for volume and the lowest values were for tree height. The genetic advance also followed similar trend with relatively higher values for volume both at Hambran (33.34 to 35.09%) and Bathinda (54.88 to 64.26%). The clonal mean heritability (on the basis of pooled analysis) was low for DBH and Height, and relatively higher values were observed for volume at both the ages (*Table 4*). It ranged from 0.27 for DBH at 4 year age to 0.62 for volume at age 6. The heritability increased at higher age for all the growth traits. Genetic correlations between traits within each site are shown in *Table 5*. All the trait combination had significantly ($P < 0.001$) positive correlation with one another. The correlated response (% of mean) for volume at age 6 was quite high both at Hambran (26.3–32.6) and Bathinda (54.7–61.3) (*Table 6*).

Discussion

This study clearly indicated the potential for considerable improvement in growth traits of *P. deltoides* under Punjab conditions, as huge amount of variation among clones ($P < 0.001$) exists at the two sites. Clones 'L-48', 'Ranikhet' and 'L-47' were found to be superior with respective volume superiority over check (G-48) of 44.8, 23.2 and 15.7 per cent at Hambran and 72.5, 30.7 and 30.4 per cent at Bathinda. The significant variation

Table 5. – Genetic correlation coefficients between various growth traits of poplar clones at two sites.

	DBH 4	DBH 6	Height 4	Height 6	Volume 4	Volume 6
DBH 4		0.995***	0.889***	0.858***	0.996***	0.992***
DBH 6	0.999***		0.804***	0.807***	0.965***	0.989***
Height 4	0.890***	0.930***		0.963***	0.916***	0.858***
Height 6	0.994***	0.940***	0.999**		0.772***	0.872***
Volume 4	0.972***	0.998***	0.908***	0.981***		0.998***
Volume 6	0.998***	0.980***	0.948***	0.933***	0.999***	

*** denotes the significant at 0.1 per cent, respectively. Figures in above diagonal are for 'Hambran" and in lower diagonal are for Bathinda.

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Table 6. – Correlated genetic advance (% of mean) of height, DBH and volume at age 6 at two sites in responses to indirect selection.

Selection aimed at	Hambran			Bathinda		
	Height 6	DBH 6	Vol 6	Height 6	DBH 6	Vol 6
Ht 4	9.9	11.1	28.7	19.0	24.2	54.7
Ht 6	10.8	11.6	30.7	20.3	25.5	57.6
DBH4	9.5	14.7	35.7	17.2	26.3	58.2
DBH 6	8.4	13.9	26.3	19.0	27.7	60.5
Vol 4	8.6	14.8	36.2	18.5	25.6	56.9
Vol 6	10.0	14.1	35.0	19.0	27.0	61.3

among clones for all growth traits at both the site conditions in the present study may be attributed to their different genetic constitution. Similar significant clonal variation for diameter, height and volume under field conditions in *P. deltoides* was reported by earlier studies conducted under field conditions in India (TOKY et al., 1996; SINGH et al., 2001; PURI et al., 2002; SIDHU and DHILLON, 2007) and abroad (RANDALL and COOPER, 1973, NELSON and TAUER, 1987).

The pooled analysis across sites indicated that the site means of all growth traits recorded at Hambran were significantly higher than respective values at Bathinda at both ages. The mean DBH, height and volume superiority at Hambran after 6 year age was 28.5, 23.2 and 89.7 per cent. This may be attributed to favourable conditions at the former site like higher rainfall, better intensity and quality of irrigation and nearly neutral soils as described in *Table 1*. Similarly, significantly ($P < 0.05$) higher growth of *P. deltoides* in central-plain region of Punjab was noticed by DHILLON (2004), than those in semi-arid region, while evaluating another set of clones.

The clone x site interaction was also significant ($P < 0.001$) for all traits at both ages. The volume growth of clones '154/86' and 'L-170) was comparatively better at Hambran, whereas clones 'UFD-6400' and 'L-168' were relatively superior at Bathinda. On the other hand, many clones ('Ranikhet', 'L-17', 'L-47', 'L-57' and 'L-48') were relatively stable clones after 6 year age at both sites with rank changes of ≤ 2. The type B genetic correlations also indicated the moderate to high clone x site interaction for growth traits. The significance of clone x site interaction might be due to differential response of clones to the environments. Significant genotype x site interaction has been reported in young cottonwoods by RANDALL and COOPER (1973) for growth traits. RIEMENSCHNEIDER et al. (2001) also found that clone x location interaction in poplar was significant at age 3 year or higher. Many other findings on *P. deltoides* (RANDALL and MOHN, 1969; ARES, 2002), *Populus* hybrid (KHALIL, 1984; ZHANG et al., 2003), and *P. tomentosa* (GU et al., 1998) have also found significant clone-site interaction. Type B genetic correlations are commonly used to quantify the family/clone by site interactions in tree breeding programs (JOHNSON and BURDON, 1990; HODGE and WHITE, 1992).

The success or failure of any tree breeding program depends largely on extent of variability in the breeding population which is measured by different population parameters including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability. In the present study, the genotypic coefficients were considerably lower than respective phenotypic coefficients. The PCV, GCV and genetic advance were relatively high for wood volume. The clonal mean heritability based on individual site analysis was quite high for all the traits (0.73–0.95). SINGH et al. (2001) while evaluating 50 clones of *P. deltoides* in Indo-gangetic plains of India reported the heritability for height, diameter and single tree volume to be 46.0, 54.7 and 70.4 per cent, respectively. However, low heritability for growth traits in the same species was found by WILCOX and FARMER (1967) and NELSON and TAUER (1987). Such variation may be due to the fact that heritability values are the estimates which often vary with age, population and site conditions.

Significant and positive correlation exists between all trait combinations in the present study which indicates that possible simultaneous improvement could be obtained while selecting for one or the other trait. Such relationships are useful as they provide a huge advantage to the breeder for improvement of these traits. Other studies (FOSTER, 1986; TEWARI et al., 1994) have also found positive and significant correlation between various growth traits of *P. deltoides*.

Conclusion

The study involving testing of 16 poplar clones at two sites revealed highly significant differences among clones which offer great scope for selection. Genetic correlations were significant between all trait combinations including those measured at four year age, therefore evaluation at an early age (4 yr) may be accurate. The clone-site interaction was moderate to high and all future genetic testing should be conducted over a range of sites.

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