ORIGINAL PAPER

# Variation among poplar clones for growth and crown traits under field conditions at two sites of North-western India

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Received: 2010-07-22; Accepted: 2010-11-22 © Northeast Forestry University and Springer-Verlag Berlin Heidelberg 2011

Abstract: We evaluated the growth and crown traits of 36 poplar clones at two distinct agro-climatic regions of Punjab (Ludhiana and Bathinda) in northwestern India, following randomized block design with three replications and plot size of four trees. Significant differences among clones (p<0.001) were observed for diameter at breast height (DBH), tree height, volume, crown width and number of branches under both the site conditions. Clones 'G-3', '25-N' and '41-N' at Ludhiana and 'G-3', 'RD-01' and 'S<sub>7</sub>C<sub>8</sub>' at Bathinda were found to be superior for volume production. All growth and crown traits registered significantly higher values at Ludhiana in comparison to those at Bathinda. Clone × site interaction was also significant (p<0.001). For volume, clones 'L-62/84', '113520', '25-N' and 'S<sub>4</sub>C<sub>2</sub>' witnessed huge fluctuations in ranking between sites. The correlations between growth traits were positive and highly significant (p < 0.001) at both sites. The clonal mean heritability was moderate for DBH and volume both at Ludhiana (0.61-0.66) and Bathinda (0.61-0.62). Across sites, the genetic advance was the highest for volume (49.76%) and the lowest (6.50%) in case of height.

Keywords: clonal heritability; clonal selection; clone-site interaction; genetic correlation; *Populus deltoides* 

# Introduction

The Indo-Gangetic plain in the north-western India is a fertile tract of alluvial soils. It is known as the food bowl of India because of intensive cultivation of rice, wheat, cotton, and sugar-

The online version is available at http://link.springer.com

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cane, etc. Rich variety of flora and fauna was found in this region till the middle of the last century. The vegetative cover was cleared to meet the needs of wood based products and for cultivation of agricultural crops. The unplanned exploitation of natural resources i.e. forests, underground water and soil for the last three decades has caused several ecological problems like alarming rate of fall in underground water, deficiency of macro and micro nutrients, emergence of insects and disease epidemics. Global warming has further aggravated the problems for agroecosystem with fluctuations in temperature range, rainfall distribution and pest incidence. The decreasing productivity levels of food crops have forced the government to look for alternative cropping pattern and enhance the tree cover. The recent National Forest Policy of India had also emphasized 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. Populus deltoides Bartr. ex Marsh., commonly known as 'poplar', is one of such exotic tree species that are extensively planted by the farmers of India, Pakistan and China. In north-western India, poplar is widely adopted by farmers of Punjab, Haryana, Uttrakhand and Uttar Pradesh because of its higher productivity (up to 48 m<sup>3</sup>·ha<sup>-1</sup>·year<sup>-1</sup>), short rotation (5–7 years), straight stem and compatibility in agroforestry systems (Dhillon et al. 2010). Its wood is suitable for manufacturing of matches, furniture, packing cases, plywood, sports goods, pulp and paper, rayon, fiberboard and pencils. The innovative farmers of Punjab, Haryana and Uttar Pradesh started commercial cultivation of poplar on their farms in eighties of the foregone century for diversification of traditional rice-wheat crop rotation. Under well managed conditions, the economic returns of poplar plantations were quite high in comparison to rice-wheat cropping pattern (Jain and Singh 2000). This encouraged more farmers to adopt it under agroforestry conditions. As per an earlier estimate, poplar based agroforestry plantations in north-western India occupy an area equivalent to 60,000 ha of pure plantations of this species (Chandra 2001).

Considering the economic importance of poplar, the breeding programmes were initiated by many institutes of India. The exotic clones were introduced by Forest Research Institute (FRI), Dehradun and Uttrakhand State Forest Department, and controlled crossing work was also undertaken (Singh et al. 2001). WIMCO Seedling Ltd., and University of Horticulture & Forestry, Nauni are also involved in development of new clones. However, the commercial planting of P. deltoides in India has so far relied on the use of few clones of poplar (Chaturvedi 1992; Kumar et al. 1999). In the recent past, the highly narrow genetic base of these poplar plantations has resulted in the outbreak of various insects and diseases in this region (Singh et al. 2004). Punjab Agricultural University (PAU), Ludhiana initiated introduction and evaluation programme in early 1990s and recommended nine poplar clones for commercial cultivation. PAU was one of participating centers where the World Bank funded 'Poplar Improvement Project' of FRI Dehradun was undertaken from 1997 to 2001. Genetically superior clones (exotic and indigenous) were supplied by FRI for evaluation under diverse agro-climatic regions by all centers. This paper reports the performance of 36 poplar clones under two diverse agro-climatic zones of Punjab at rotation age with respect to growth and crown traits.

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

## 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 experimental farm of Department of Forestry & Natural Resources of PAU, Ludhiana (Site 1). The site suits well for the optimum growth of poplar with majority of agricultural fields in the vicinity having poplar plantations. Tubewell is the main source of irrigation. The soils are deep, well-drained, sandy loam in texture with low humus content.

The second trial was planted at the Experimental Farm of PAU at the Regional Research Station Bathinda (Site 2). The climate in this region is semi-arid to arid and soils are mainly sandy to loamy sand. The irrigation source is mainly canal with limited use of tube-well irrigation during drought periods or when canal irrigation was not available. The details of climatic and edaphic conditions at both sites are given in Table 1.

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

#### Clones used and experimental design

The clones used for the study were supplied by Forest Research Institute Dehradun under 'Poplar Improvement Project'. Out of 36 common clones at both sites, 32 clones (3167, S7C20, S7C2, S<sub>7</sub>C<sub>8</sub>, 82-26-5, S<sub>4</sub>C<sub>2</sub>, 3324, 421-2, S<sub>7</sub>C<sub>1</sub>, S<sub>7</sub>C<sub>4</sub>, S<sub>13</sub>C<sub>11</sub>, 82-35-4-1, ST-124, 2502, A-194, 113520, D-121, 22-N, 23-N, 25-N, 26-N, 34-N, 37-N, 38-N, 39-N, 40-N, 41-N, 42-N, 43-N, 63-N, UD-88 and RD-01) had origin of America and two clones (G-48 and G-3) were Australian. Two clones (L-34/82 and L-62/84) were developed by Uttrakhand State Forest Department. For comparison, 'PL-2' and PL-3 were used as control (check) clones at Ludhiana and Bathinda, respectively. The ETP's (entire transplants, one year old rooted cuttings) of these clones were raised at nursery area of Department of Forestry & Natural Resources, PAU, Ludhiana, and were transported to the study sites during first week of February 2000. The experiments were conducted following complete randomized block design with three replications and plot size of four trees. A boundary row of nonexperimental plants was planted to check the border effect. The clones were randomized independently in each of the three blocks/replications with plot shape of four plants as row. The ETP's were planted at 5 m  $\times$  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.

## Data recording and statistical analyses

The data on total height (ground level to tip of the tree) and diameter at breast height (DBH) were recorded from individual trees during December every year. The tree height was measured with the help of 'Ravi's Multimeter' and observer height was added in the reading. The DBH, measured at 1.37 m from ground surface, was measured with the help of tree caliper. The crown width was calculated by taking average of two readings taken in NS and EW directions from the centre of the bole. Observations on crown width and number of branches were recorded at age four years. The growth parameters recorded at the age of five years are given in this paper. Volume per plant was worked out on the basis of the volume equation developed by Dhanda and Verma (2001) for this region.

The data from both the trials were pooled and analyzed according to the following model:

$$Y_{ijkl} = \mu + S_i + B_{j(i)} + C_k + CS_{ik} + BC_{j(i)k} + e_{ijkl}$$
(1)

where  $Y_{ijkl}$  is the performance of  $l_{th}$  ramet of  $k_{th}$  clone growing in  $j_{th}$  block of  $i_{th}$  site;  $\mu$  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,...3);  $C_k$  is the effect of the  $k_{th}$  clone (k=1,...36);  $CS_{ik}$  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,...4).

All the factors were considered as random. The data of 37 clones from individual sites were also analyzed using the same model but without site and its interaction with clone.

#### Estimation of heritabilities and coefficients of variation

In case of the individual site analysis the broad sense heritability on individual tree basis was worked out as:

$$H^{2}_{i} = \sigma^{2}_{c} / \sigma^{2}_{P}$$
<sup>(2)</sup>

where  $H_i^2$  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,  $\sigma_c^2$  variance due to clonal effects (i.e. including additive and non-additive genetic variances) for the particular trial and  $\sigma_P^2$  phenotypic variance among ramets in the trial.  $\sigma_P^2$  is calculated as

$$\sigma^2_{\rm P} = \sigma^2_{\rm c} + \sigma^2_{\rm cb} + \sigma^2_{\rm w} \tag{3}$$

where  $\sigma_{cb}^2$  represents variance due to clone-block interaction and  $\sigma_w^2$  within-plot error.

The broad-sense heritability relevant to estimating genetic gain from selection of best clones is the "clonal heritability" (denoted  $H^2c$ ), which was calculated following Lambeth et al. (1994). On the basis of analysis across sites, clonal mean heritability ( $H^2c_P$ ) and its standard was worked following Becker (1992). Other genetic parameters like genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) were worked out following Johnson et al. (1955).

# Estimation of genetic and phenotypic correlation among traits

Genetic correlation  $(r_{Gxy})$  and phenotypic correlation  $(r_{Pxy})$  between traits x and y on the same site was worked out using following expressions:

$$\mathbf{r}_{\mathrm{Gxy}} = \mathrm{COV}_{\mathrm{Cxy}} / \sqrt{(\sigma^{2}_{\mathrm{Cx}} . \sigma^{2}_{\mathrm{Cy}})}$$
(4)

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

$$\mathbf{r}_{\mathrm{Pxy}} = \mathrm{COV}_{\mathrm{Pxy}} / \sqrt{(\sigma^{2}_{\mathrm{Px}} . \sigma^{2}_{\mathrm{Cy}})}$$
(5)

where  $COV_{Pxy}$  is phenotypic covariance between traits x and y,  $\sigma^2_{Px}$  and  $\sigma^2_{Py}$  are phenotypic variances for traits x and y, respectively.

## Results

#### Clonal variation for growth traits

The analysis of variance indicated that clonal differences were found to be highly significant for diameter at breast height (DBH), tree height and volume per tree at both the sites (Table 2). The pooled analysis across sites also revealed significant differences among clones and between sites for all the three growth traits (Table 3). The DBH at Site 1 varied from 13.11 cm to 18.95 cm, tree height from 14.44 m to 19.07 m and wood volume per tree from 0.0879 m<sup>3</sup> to 0.2330 m<sup>3</sup>. Clone 'G-3' recorded the highest DBH and was statistically at par with clones '25-N' and '41-N'. Thirteen other clones had also significantly higher values than the control (PL-2). For tree height clone 'G-3' was significantly superior to all others except clones 'L-62/84', '25-N' and '41-N'. Like DBH, clone 'G-3' registered the highest volume and was statistically superior to all clones except clones '25-N' and '41-N'. Overall 15 clones recorded significantly higher volume over the control. The bottom rank for all the three growth traits was attained by clone '2502'.

At Bathinda (Site 2), the DBH varied from 10.40 cm to 18.82 cm (Table 2). The top ranking was attained by clone 'G-3' and was statistically at par with three clones ' $S_7C_8$ ', 'RD-01' and '22-N'. Clone 'G-3' was superior for tree height, followed by clones 'RD-01', ' $S_7C_8$ ', '22-N', 'UD-88' and 'G-48'. The volume per tree ranged from 0.0603 m<sup>3</sup> to 0.2140 m<sup>3</sup>. The highest value was registered by clone 'G-3', which was superior to all others except clone 'RD-01'. Overall, 18 clones recorded higher volume than the control (PL-3). Clone 'A-194' had the lowest values for DBH and volume in all the clones, whereas the minimum height was recorded by clone 'S4C<sub>2</sub>'.

All the growth traits recorded at Site 1 were significantly higher than their respective values at Site 2. The clone × site interaction was also significant (p<0.001) for all three traits (Table 3). Clones 'S<sub>7</sub>C<sub>8</sub>', '82-26-5', '421-1', 'S<sub>7</sub>C<sub>1</sub>', 'G-3', '2502', 'A-194', '22-N', '26-N' and '41-N' remained almost stable across sites for wood volume, whereas clones 'L-62/84', '113520', '25-N', '39-N', 'S<sub>4</sub>C<sub>2</sub>', '82-35-4-1', 'ST-124' and '42-N' experienced huge changes in ranks between sites.

#### Clonal variation in crown traits

The differences in crown width and number of branches were statistically significant among clones both at Ludhiana and Bathinda. The crown width varied from 3.41 to 5.02 m at Site 1 and number of branches from 41.30 to 65.73 (Table 4). Clone ' $S_7C_2$ ' and '23-N' recorded the maximum value for crown width which was statistically at par with 'G-3' and 'RD-01'. The number of branches was the highest in case of '41-N'and was superior to all others except that of clone G-3. Clone 'G-3' was significantly superior to others for crown width at Site 2, followed by six clones i.e. 'RD-01', '63-N', ' $S_7C_8$ ', 'G-48', '23-N' and 'UD-88'.



For number of branches, the top rank was in case of  ${}^{\circ}S_{7}C_{8}{}^{\circ}$  and was at par with

was at par with 'ST-124', 'G-48', 'G-3' and '41-N'.

Clone		Ludhiana			Bathinda			
	DBH	Height	Volume per tree	DBH	Height	Volume per tree		
	(cm)	(m)	(m <sup>3</sup> )	(cm)	(m)	(m <sup>3</sup> )		
3167	17.05 <sup>fghi</sup>	18.23 <sup>cde</sup>	0.1958 <sup>cdef</sup>	14.91 <sup>gh</sup>	14.83 <sup>ijklm</sup>	0.1253 <sup>gh</sup>		
S7C20	17.25 <sup>efgh</sup>	17.68 <sup>fghijk</sup>	0.1801 <sup>fghi</sup>	13.59 <sup>ijklm</sup>	14.10 <sup>lmnopq</sup>	0.0991 <sup>ij</sup>		
$S_7C_2$	15.99 <sup>klmnop</sup>	17.25 <sup>ijklm</sup>	0.1524 <sup>klmnop</sup>	15.53 <sup>efg</sup>	15.78 <sup>defghi</sup>	0.1353 <sup>efgh</sup>		
S <sub>7</sub> C <sub>8</sub>	17.85 <sup>cde</sup>	18.07 <sup>defg</sup>	0.2027 <sup>cde</sup>	17.81 <sup>ab</sup>	17.15 <sup>ab</sup>	0.1892 <sup>bc</sup>		
82-26-5	13.93 <sup>t</sup>	15.30 <sup>s</sup>	0.1041 <sup>uv</sup>	12.83 <sup>lmno</sup>	13.35 <sup>opqrs</sup>	0.0812 <sup>jklmn</sup>		
S <sub>4</sub> C <sub>2</sub>	16.55 <sup>hijkl</sup>	17.73 <sup>efghij</sup>	0.1640 <sup>ijklm</sup>	11.50 <sup>pqr</sup>	11.27 <sup>t</sup>	0.0733 <sup>klmn</sup>		
G-48	17.74 <sup>def</sup>	17.21 <sup>jklm</sup>	0.1859 <sup>efgh</sup>	17.63 <sup>bc</sup>	16.55 <sup>abcde</sup>	0.1804 <sup>bc</sup>		
3324	13.84 <sup>tu</sup>	16.94 <sup>mn</sup>	$0.1142^{tu}$	12.65 <sup>mnop</sup>	14.50 <sup>ijklmn</sup>	$0.0876^{jkl}$		
421-2	15.58 <sup>nopq</sup>	17.73 <sup>efghij</sup>	0.1526 <sup>klmnop</sup>	12.95 <sup>jklmn</sup>	12.75 <sup>s</sup>	0.0873 <sup>jklm</sup>		
$S_7C_1$	15.30 <sup>pqr</sup>	17.56 <sup>ghijkl</sup>	0.1479 <sup>mnop</sup>	12.79 <sup>lmno</sup>	13.72 <sup>nopqrs</sup>	0.0812 <sup>jklmn</sup>		
$S_7C_4$	16.43 <sup>ijklm</sup>	17.82 <sup>efgh</sup>	0.1686 <sup>hijk</sup>	11.94 <sup>nopq</sup>	12.82 <sup>s</sup>	0.0698 <sup>lmn</sup>		
S <sub>13</sub> C <sub>11</sub>	14.41 <sup>st</sup>	15.60 <sup>qrs</sup>	0.1172 <sup>stu</sup>	14.05 <sup>hij</sup>	13.92 <sup>mnopqr</sup>	0.0972 <sup>ij</sup>		
82-35-4-1	16.66 <sup>hijk</sup>	17.77 <sup>efghi</sup>	0.1755 <sup>ghij</sup>	13.62 <sup>ijklm</sup>	13.22 <sup>opqrs</sup>	0.0954 <sup>ijk</sup>		
ST-124	15.22 <sup>qr</sup>	15.55 <sup>r</sup>	0.1287 <sup>qrst</sup>	13.85 <sup>hijkl</sup>	14.38 <sup>jklmno</sup>	0.1155 <sup>hi</sup>		
G-3	18.95 <sup>a</sup>	19.07 <sup>a</sup>	0.2330 <sup>a</sup>	18.82 <sup>a</sup>	17.55 <sup>a</sup>	$0.2140^{a}$		
2502	13.11 <sup>u</sup>	14.44 <sup>t</sup>	$0.0879^{v}$	10.80 <sup>qr</sup>	12.88 <sup>rd</sup>	$0.0644^{mn}$		
A-194	14.38 <sup>st</sup>	16.12 <sup>opq</sup>	0.1190 <sup>stu</sup>	10.40 <sup>r</sup>	11.42 <sup>t</sup>	0.0603 <sup>n</sup>		
113520	13.73 <sup>tu</sup>	15.50 <sup>rs</sup>	0.1082 <sup>u</sup>	15.25 <sup>fg</sup>	15.32 <sup>ghijk</sup>	0.1290 <sup>efgh</sup>		
D-121	15.98 <sup>klmnop</sup>	17.78 <sup>efghi</sup>	0.1577 <sup>jklmno</sup>	15.53 <sup>efg</sup>	15.73 <sup>defghi</sup>	0.1437 <sup>efg</sup>		
L-34/82	15.88 <sup>lmnopq</sup>	17.15 <sup>klm</sup>	0.1601 <sup>jklmn</sup>	12.87 <sup>klmno</sup>	13.11 <sup>qrs</sup>	0.0963 <sup>ij</sup>		
L-62/84	17.49 <sup>defg</sup>	18.92 <sup>ab</sup>	0.1990 <sup>cde</sup>	12.89 <sup>jklmno</sup>	14.10 <sup>lmnopq</sup>	0.0831 <sup>jklm</sup>		
22-N	17.89 <sup>cde</sup>	18.13 <sup>cdef</sup>	0.2124 <sup>bc</sup>	17.78 <sup>ab</sup>	17.14 <sup>abc</sup>	0.1882 <sup>bc</sup>		
23-N	17.88 <sup>cde</sup>	18.05 <sup>defg</sup>	0.1956 <sup>cdef</sup>	15.23 <sup>fg</sup>	15.10 <sup>ghijkl</sup>	0.1279 <sup>fgh</sup>		
25-N	18.63 <sup>ab</sup>	18.90 <sup>ab</sup>	0.2231 <sup>ab</sup>	14.02 <sup>hijk</sup>	14.29 <sup>klmno</sup>	0.1128 <sup>hi</sup>		
26-N	14.29 <sup>st</sup>	16.58 <sup>no</sup>	0.1222 <sup>rstu</sup>	11.75 <sup>opq</sup>	11.63 <sup>t</sup>	$0.0769^{jklmn}$		
34-N	18.12 <sup>bcd</sup>	18.50 <sup>bcd</sup>	0.2081 <sup>bcd</sup>	15.22 <sup>fg</sup>	14.94 <sup>ghijklm</sup>	0.1412 <sup>efg</sup>		
37-N	14.84 <sup>rs</sup>	15.90 <sup>pqr</sup>	0.1335 <sup>pqrs</sup>	13.78 <sup>hijklm</sup>	14.23 <sup>lmno</sup>	0.0989 <sup>ij</sup>		
38-N	16.29 <sup>jklmn</sup>	17.38 <sup>hijklm</sup>	0.1633 <sup>ijklm</sup>	16.23 <sup>def</sup>	15.95 <sup>defgh</sup>	0.1496 <sup>ef</sup>		
39-N	15.73 <sup>mnopq</sup>	16.59 <sup>no</sup>	0.1441 <sup>nopq</sup>	16.50 <sup>bcde</sup>	15.60 <sup>efgh</sup>	0.1469 <sup>efg</sup>		
40-N	16.06 <sup>klmno</sup>	16.56 <sup>no</sup>	0.1551 <sup>klmnop</sup>	14.75 <sup>ghi</sup>	14.18 <sup>lmnop</sup>	0.1468 <sup>efg</sup>		
41-N	18.52 <sup>ab</sup>	18.64 <sup>abc</sup>	0.2223 <sup>ab</sup>	16.36 <sup>def</sup>	16.08 <sup>cdefg</sup>	0.1515 <sup>de</sup>		
42-N	15.35 <sup>opqr</sup>	16.30 <sup>op</sup>	0.1402 <sup>opqr</sup>	14.40 <sup>ghi</sup>	13.44 <sup>nopqrs</sup>	$0.1277^{\text{fgh}}$		
43-N	15.66 <sup>nopq</sup>	17.23 <sup>jklm</sup>	0.1540 <sup>klnop</sup>	13.61 <sup>ijklm</sup>	14.11 <sup>lmnopq</sup>	0.0994 <sup>hij</sup>		
63-N	16.60 <sup>hijkl</sup>	17.05 <sup>1mn</sup>	0.1670 <sup>hijklm</sup>	16.99 <sup>bcd</sup>	16.41 <sup>bcde</sup>	0.1732 <sup>cd</sup>		
UD-88	16.86 <sup>ghij</sup>	17.25 <sup>ijklm</sup>	$0.1904^{defg}$	16.94 <sup>bcd</sup>	16.77 <sup>abcd</sup>	0.1785 <sup>c</sup>		
RD-01	17.64 <sup>def</sup>	18.00 <sup>defg</sup>	$0.1904^{defg}$	17.80 <sup>ab</sup>	17.20 <sup>ab</sup>	0.2023 <sup>ab</sup>		
PL-2/PL-3 (Control) <sup>+</sup>	15.72 <sup>mnopq</sup>	17.08 <sup>lmn</sup>	0.1488 <sup>lmnop</sup>	12.95 <sup>jklmn</sup>	15.41 <sup>fghij</sup>	$0.0942^{ijk}$		
Mean $\pm$ SE	16.27±0.15	17.28±0.10	$0.1644 \pm 0.0036$	14.63±0.19	14.72±0.16	0.1245±0.0039		
M.S.c	24.515***	12.72***	0.01438***	46.1382***	27.629***	0.01814***		
M.S.e	4.8266	0.9179	0.003144	5.4197	2.7596	0.002624		
$H^2_i$	0.21	0.28	0.18	0.24	0.17	0.22		
H <sup>2</sup> <sub>c</sub>	0.66	0.64	0.61	0.62	0.46	0.61		
PCV (%)	16.56	9.44	41.31	23.55	18.74	56.94		
GCV(%)	7.51	5.01	17.29	11.47	7.64	26.64		
GA (% of mean)	19.81	10.93	45.65	26.44	15.63	62.85		

Table 2. Mean grov	vth traits of popla	r clones planted at tw	o sites of Punjab.

Means followed by the same letter do not differ (p<0.05) by LSD test. \*\*\* indicate significance at p<0.001. M.S.<sub>c</sub> is mean sum of squares for clones; M.S.<sub>e</sub>, mean sum of squares for error; H<sup>2</sup><sub>i</sub>, individual tree heritability; H<sup>2</sup><sub>c</sub>, clonal heritability and GA, genetic advance as per cent of mean.  $\clubsuit$  Clone PL-2 and PL-3 were control at Ludhiana and Bathinda, respectively.

Table 3. Analysis of variance, variance components and genetic parameters for various growth and crown traits of poplar clones based on pooled analysis across sites

Trait	Source	df	Mean Sum of squares	H <sup>2</sup> <sub>C</sub> ±S.E.	Genetic Ad- vance (% of mean)
	Site	1	443.37***	0.60±0.060	20.67
DBH	clone	35	59.41***		
Лри	$\operatorname{Site} \times \operatorname{clone}$	35	17.724***		
	error	681	6.8330		
	Site	1	1240.93***	$0.30{\pm}0.054$	6.50
Height	clone	35	26.12***		
riegiit	$\text{Site} \times \text{clone}$	35	15.01***		
	error	681	3.1949		
	Site	1	0.25981***	$0.60{\pm}0.059$	49.76
Volume	clone	35	0.02746***		
volume	$\text{Site} \times \text{clone}$	35	0.007954***		
	error	681	0.003627		
	Site	1	39431.83***	$0.25{\pm}0.049$	9.97
Number of	clone	35	673.28***		
branches	$\text{Site} \times \text{clone}$	35	439.029***		
	error	681	100.6953		
	Site	1	203.486***	$0.76 \pm 0.045$	27.17
Crown width	clone	35	6.118***		
	$\text{Site} \times \text{clone}$	35	0.7959*		
	error	681	0.3406		

 $H_c^2$  is clonal mean heritability. \* and \*\*\* indicate significance at p < 0.05 and p < 0.001, respectively.

#### Genetic parameters and correlations

On the basis of individual site analysis, the individual tree heritability was generally low (Table 2 and 4) for all growth and crown traits at both sites with comparatively higher values for crown width (0.29-0.30). The clonal mean heritability was medium for growth traits (0.46-0.66), crown width (0.62-0.64) and was comparatively low for number of branches (0.38-0.52). The phenotypic coefficients (41.31-56.94%) and genotypic coefficients of the variations (17.29%-26.64%) were relatively higher for volume and the lower values were for tree height and crown width. The genetic advance also followed similar trend with relatively higher values for volume both at Site 1 (45.65%) and Site 2 (62.85%).

The clonal mean heritability (on the basis of pooled analysis) was medium for DBH, volume and crown width and comparatively lower value was for height and number of branches (Table 3). The genetic advance as percent of mean was the highest (49.76%) for volume and the minimum value (6.50%) was for height. Genetic and phenotypic correlations between growth traits are shown in Table 5 (Ludhiana) and Table 6 (Bathinda). All growth traits had significantly positive phenotypic correlations with one another at both the sites. The correlation coefficients of number of branches with other growth traits were relatively lower. Similarly genetic correlations between growth traits were also high and positive.

Table 4. Mean crown traits of poplar clones planted at two sites of Punjab.

	Lud	hiana	Bath	ninda
Clone	Crown width	Number of	Crown width	Number of
	(m)	branches	(m)	branches
3167	$4.27^{jkl}$	52.64 <sup>jkl</sup>	3.40 <sup>hijkl</sup>	38.92 <sup>hi</sup>
S7C20	4.36 <sup>ghijk</sup>	54.18 <sup>hijk</sup>	3.15 <sup>nopq</sup>	44.22 <sup>de</sup>
$S_7C_2$	4.24 <sup>klm</sup>	51.67 <sup>klm</sup>	3.49 <sup>fghij</sup>	39.00 <sup>hi</sup>
$S_7C_8$	4.56 <sup>def</sup>	59.75 <sup>cd</sup>	3.83 <sup>b</sup>	51.92 <sup>a</sup>
82-26-5	4.16 <sup>lmn</sup>	53.80 <sup>ijkl</sup>	3.32 <sup>jklmn</sup>	39.80 <sup>fgh</sup>
$S_4C_2$	5.02 <sup>a</sup>	$56.36^{\text{defghi}}$	3.22 <sup>Imnop</sup>	28.09 <sup>op</sup>
G-48	4.73 <sup>bcd</sup>	59.08 <sup>cdef</sup>	3.81 <sup>bc</sup>	51.10 <sup>a</sup>
3324	3.86 <sup>pq</sup>	44.56 <sup>op</sup>	3.38 <sup>ijklm</sup>	41.00 <sup>efgh</sup>
421-2	3.79 <sup>q</sup>	53.27 <sup>ijkl</sup>	3.01 <sup>qr</sup>	31.00 <sup>nop</sup>
$S_7C_1$	3.92 <sup>opq</sup>	50.50 <sup>lmn</sup>	2.94 <sup>rs</sup>	43.22 <sup>defg</sup>
$S_7C_4$	4.72 <sup>cde</sup>	47.70 <sup>no</sup>	3.38 <sup>ijklm</sup>	37.91 <sup>hijk</sup>
S <sub>13</sub> C <sub>11</sub>	4.15 <sup>1mn</sup>	55.20 <sup>ghijk</sup>	3.64 <sup>cdef</sup>	41.00 <sup>efgh</sup>
82-35-4-1	4.46 <sup>fghi</sup>	50.45 <sup>lmn</sup>	3.43 <sup>ghij</sup>	34.70 <sup>klmn</sup>
ST-124	4.32 <sup>ijkl</sup>	41.30 <sup>p</sup>	3.09 <sup>opqr</sup>	51.33 <sup>a</sup>
G-3	4.95 <sup>a</sup>	$64.08^{ab}$	4.06 <sup>a</sup>	49.73 <sup>ab</sup>
2502	3.41 <sup>r</sup>	53.11 <sup>ijkl</sup>	2.71 <sup>t</sup>	31.43 <sup>mno</sup>
A-194	4.26 <sup>kl</sup>	43.18 <sup>p</sup>	2.94 <sup>rs</sup>	35.00 <sup>jklm</sup>
113520	4.04 <sup>nop</sup>	$48.42^{mn}$	3.21 <sup>mnop</sup>	38.55 <sup>hij</sup>
D-121	4.15 <sup>lmn</sup>	48.33 <sup>mn</sup>	3.57 <sup>efgh</sup>	42.80 <sup>defg</sup>
L-34/82	3.92 <sup>opq</sup>	52.90 <sup>ijkl</sup>	2.63 <sup>t</sup>	39.75 <sup>ghi</sup>
L-62/84	4.50 <sup>fghi</sup>	53.92 <sup>ijkl</sup>	2.92 <sup>rs</sup>	27.40 <sup>p</sup>
22-N	4.33 <sup>hijkl</sup>	54.50 <sup>hijk</sup>	3.35 <sup>jklm</sup>	45.82 <sup>cd</sup>
23-N	5.02 <sup>a</sup>	58.18 <sup>cdefg</sup>	3.77 <sup>bcd</sup>	41.00 <sup>efgh</sup>
25-N	4.91 <sup>ab</sup>	59.40 <sup>cde</sup>	3.56 <sup>efghi</sup>	41.27 <sup>efgh</sup>
26-N	3.88 <sup>op</sup>	50.33 <sup>lmn</sup>	3.63 <sup>cdef</sup>	36.00 <sup>ijkl</sup>
34-N	4.33 <sup>hijkl</sup>	52.92 <sup>ijkl</sup>	3.04 <sup>pqr</sup>	40.90 <sup>efgh</sup>
37-N	4.06 <sup>mnop</sup>	53.50 <sup>ijkl</sup>	2.80 <sup>st</sup>	33.10 <sup>lmn</sup>
38-N	4.24 <sup>klm</sup>	57.75 <sup>cdefgh</sup>	3.54 <sup>fghi</sup>	43.50 <sup>defg</sup>
39-N	4.45 <sup>fghij</sup>	55.91 <sup>efghi</sup> j	3.08 <sup>opqr</sup>	35.00 <sup>jklm</sup>
40-N	4.24 <sup>klm</sup>	52.63 <sup>jkl</sup>	3.22 <sup>lmnop</sup>	37.56 <sup>hijk</sup>
41-N	4.42 <sup>fgijk</sup>	65.73 <sup>a</sup>	3.61 <sup>defg</sup>	48.42 <sup>abc</sup>
42-N	3.98 <sup>noq</sup>	55.70 <sup>fghij</sup>	3.42 <sup>hijk</sup>	31.71 <sup>mno</sup>
43-N	4.54 <sup>efg</sup>	55.91 <sup>efghij</sup>	3.24 <sup>klmno</sup>	46.29 <sup>bcd</sup>
63-N	4.51 <sup>fgh</sup>	48.91 <sup>mn</sup>	3.84 <sup>b</sup>	45.30 <sup>cd</sup>
UD-88	$4.50^{\text{fghi}}$	60.75 <sup>bc</sup>	3.74 <sup>bcde</sup>	43.56 <sup>def</sup>
RD-01	4.86 <sup>abc</sup>	42.17 <sup>p</sup>	3.85 <sup>b</sup>	38.20 <sup>hijk</sup>
PL-2/PL-3				
(Control) <sup>♠</sup>	4.27 <sup>jkl</sup>	54.83 <sup>ghijk</sup>	3.14 <sup>nopq</sup>	34.80 <sup>jklm</sup>
$Mean \pm SE$	4.35±0.03	$5346 \pm 0.57$	$3.36 \pm 0.03$	40.21±0.66
M.S.c	1.40***	335.62***	1.149***	392.17***
M.S.e	0.075	41.5245	0.069	38.59
$H_{i}^{2}$	0.30	0.12	0.29	0.20
$H^2_{c}$	0.64	0.38	0.62	0.52
PCV (%)	12.08	18.61	15.09	25.67
GCV(%)	6.58	6.43	8.14	11.52
GA (%	of 1385	12.83	16.97	24.20
mean)				

Means followed by the same letter do not differ (p < 0.05) by LSD test. \*\*\* indicate significance at p < 0.001. M.S.<sub>c</sub> is mean sum of squares for clones, M.S.<sub>e</sub> is mean sum of squares for error. H<sup>2</sup><sub>i</sub> is individual tree heritability, H<sup>2</sup><sub>c</sub> is clonal heritability. \*Clone PL-2 and PL-3 were control at Ludhiana and Bathinda, respectively.



# Discussion

This study found the considerable potential for an 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. 'G-3', '25-N' and '41-N' were promising clones at Site 1 (Ludhiana) with respective volume superiority over control (PL-2) of 56.6%, 49.9% and 49.4%. The promising clones at Bathinda (Site 2) were 'G-3' and 'RD-01'. The significant variation among clones for all growth traits at both the site conditions in the present study may be attributed to their different genetic constitution. The significant variation for diameter, height and volume among poplar clones under field conditions was reported by earlier studies conducted in India (Toky et al. 1996; Singh et al. 2001; Puri et al. 2002; Sidhu and Dhillon 2007; Dhillon et al. 2010) and abroad (Randall and Cooper 1973; Nelson and Tauer 1987).

Table 5. Genetic correlation coefficients (above diagonal) and phenotypic correlation coefficients (lower diagonal) between various traits of poplar clones at Ludhiana

	DBH	Height	Crown width	Number of branches	Volume
DBH		0.969	0.852	0.385	0.995
Height	0.996***		0.795	0.411	0.987
Crown width	0.592***	0.484**		0.054	0.779
Number of branches	0.224*	0.441*	0.224*		0.448
Volume	0.997***	0.996***	0.542**	0.211*	

\*, \*\* and \*\*\* denote the significant levels of 0.05, 0.01 and 0.001, respectively.

 

 Table 6. Genetic correlation coefficients (above diagonal) and phenotypic correlation coefficients (lower diagonal) between various growth traits of poplar clones at Bathinda

	DBH	Height	Crown width	Number of branches	Volume
DBH		0.995	0.642	0.731	0.993
Height	0.968***		0.617	0.863	0.980
Crown width	0.829***	0.744***		0.629	0.648
Number of branches	0.521**	0.318*	0.448**		0.696
Volume	0.994***	0.935***	0.801***	0.520**	

\*, \*\* and \*\*\* denote the significant levels of 0.05, 0.01 and 0.001, respectively.

The pooled analysis across sites indicated that the means of all growth traits recorded at Site 1 were significantly higher than respective values at Site 2. The mean DBH, height and volume at Site 1 was higher by 11.2%, 17.4% and 32.0% than that at Site 2, respectively. This may be attributed to higher rainfall, ensured and better irrigation facilities and better edaphic conditions (Table 1) at Site 1. Poplar growth in general is adversely affected in the soils having high pH values (as was the case in this study, at

Site 2). Similarly, earlier studies in this region (Dhillon 2004; Dhillon et al. 2010) had also concluded that the poplar growth in central-plain region of Punjab is significantly higher than those in semi-arid region.

The clone × site interaction was also significant (p<0.001) for all growth traits. Clones 'L-62/84', '113520', '25-N', 'S<sub>4</sub>C<sub>2</sub>', '39-N', '82-35-4-1', 'ST-124' and '42-N' were unstable clones with huge changes in ranking (>10). On the other hand, many clones ('S<sub>7</sub>C<sub>8</sub>', '82-26-5', '421-1', 'S<sub>7</sub>C<sub>1</sub>', 'G-3', '2502', 'A-194', '22-N', '26-N' and '41-N') were relatively stable clones at both sites. Randall and Cooper (1973) reported significant genotype × site interaction in young cottonwoods for growth traits. Riemenschneider et al. (2001) also found that clone × location interaction in poplar was significant at age 3 year or higher. Significant clone-site interaction was also found in *P. deltoides* (Randall and Mohn 1969; Ares 2002; Dhillon et al. 2010), *Populus* hybrid (Khalil 1984; Zhang et al. 2003), and *P. tomentosa* (Gu et al. 1998).

The extent of variability in the breeding population was estimated by measuring different population parameters including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability. In this study, the genotypic coefficients were considerably lower than respective phenotypic coefficients of variation. The PCV, GCV and genetic advance were comparatively higher for wood volume. The clonal mean heritability based on individual site analysis was relatively higher for volume and lower for number of branches. Dhillon et al. (2010) found that clonal mean heritability was high for DBH (0.73-0.95), height (0.73-0.92) and wood volume (0.80-0.95). Singh et al. (2001) reported the heritability for height, diameter and single tree volume to be 46.0%, 54.7% and 70.4%, respectively after evaluating 50 clones of P. deltoides in Indo-gangetic plains of India. However, low heritability for growth traits in the same species was found by Wilcox and Farmer (1967) and Nelson and Tauer (1987). Such variation in heritability values may be due to the fact that these values are the estimates that vary with age, population and site conditions.

Significant and positive correlation exists between all trait combinations in the present study, indicating 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; Dhillon et al. 2010) have also found positive and significant correlation between various growth traits of *P. deltoides*.

### Conclusion

The study involving testing of 36 poplar clones at two sites revealed highly significant differences in growth traits among clones, which offer great scope for selection. On basis of evaluation at individual site, the clones 'G-3', '25-N' and '41-N' may be used for commercial cultivation at Ludhiana. The promising clones for Site 2 were 'G-3', 'RD-01' and 'S<sub>7</sub>C<sub>8</sub>'. The clone-site interaction was moderate, indicating that the future genetic test-

ing should be conducted over a range of sites. The site-specific clones may be used for commercial cultivation. The correlations between all growth traits were highly significant; therefore the evaluation may be aimed at any growth trait.

## Acknowledgements

We thank the funding agency 'Forest Research Institute, Dehradun for providing necessary funds and supplying the clones used in the study. The sincere thanks are also due to the Head, Department of Forestry & Natural Resources, PAU Ludhiana for providing the necessary facilities for the study. The support given by the field staff is also acknowledged.

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