*International Journal of Farm Sciences* **12(3):** 104-109, 2022; **doi: 10.5958/2250-0499.2022.00083.0**

# Evaluation of high resin yielding half sib families of *Pinus roxburghii* Sargent for growth traits

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***Received: 27.05.2022/Accepted: 21.06.2022***

## ABSTRACT

Field experiment was conducted for evaluation of high resin yielding half sib families of *Pinus roxburghii* Sargent for growth traits at Shilli Conservation Reserve, Solan, Himachal Pradesh during the year 2020-2021. Traits like height, diameter at breast height, bark thickness, crown height and crown length were studied. The study revealed that all the traits varied significantly, with mean values of diameter at breast height (31.10 cm), height (17.79 m), bark thickness (2.81 cm), crown length (10.75 m) and crown height (6.95 m). Variability estimates, genetic parameters, correlation studies, principal component analysis and divergence study exhibited high variability among all the half sib families. It may be concluded that evaluation of the chir pine diversity can be very useful in qualitative and quantitative improvement of different traits studied.

**Keywords:** Height; trait; chir pine; growth

## INTRODUCTION

*Pinus roxburghii* Sargent belongs to the Pinaceae family of the order Coniferale and is the most common of India's six native pine species. It can be found in the outer Himalayan monsoon belt which stretches from northeastern Pakistan to Arunachal Pradesh in India at elevations ranging from 450 to 2,300 m amsl over a 3,200 kilometer stretch between latitudes 26° to 36° N and longitudes 71° to 93° E from Afghanistan in the west to Bhutan in the east, at elevations ranging from 450 to 2,300 m amsl (Troup 1921). *P roxburghii* is the dominant tree species in forest subtypes 9/C1b (upper Himalayan chir pine forest) and 9/C1a (lower or Siwalik chir pine forest) of Himalayan subtropical pine forests. Winter buds are brown, thin, ovoid and non-resinous; bark becomes dark red-brown, dense, deeply and 2 longitudinally fissured and scaly. The three needle shaped leaves per bundle, which are slender, flabellate-triangular in cross section, distinguish chir pine from other pine species. Chir pine is a tall tree with a diameter of over 100 cm at breast height and a height of up to 55 meters (Ghildiyal et al 2010). Chir pine seed cones are pedunculate, ovoid and 10-20 cm x 6-9 cm in size. The seeds are 8-12 mm long with a 2.5 cm long wing and mature in October-November (Tiwari 1994). The present research work was carried out at Shilli Conservation Reserve, Solan, Himachal Pradesh where a block plantation of high resin yielders from 19 seed sources of Himachal Pradesh having high oleoresin properties was established in 1982. The half sib families from the plantation were evaluated for growth characteristics.

## MATERIAL and METHODS

The present research was carried out at Shilli Conservation Reserve, Solan, Himachal Pradesh where a block plantation of high resin yielders from 19 seed sources of Himachal Pradesh having high oleoresin properties was established in 1982. The half sib families from the plantation were evaluated for various growth traits like height, diameter, bark thickness, crown length and crown height. The block plantation comprised 190 trees (10 trees of 19 high resin yielding half sib families). Out of these 190 trees, 95 were evaluated in the field trials ie 5 genotypes from each family to study within family and between family variation. Statistical design employed was randomized block design (RBD).

**Growth traits**

Growth traits were observed for the different half sib chir pine progenies and the traits were measured according to standard procedures. Height was measured by Ravi altimeter in m, diameter at breast height (DBH) (1.37 m) in centimetres by tree calliper, bark thickness by Swedish bark gauge in centimeters, crown length by Ravi altimeter in meters and crown height by Ravi altimeter in meters. It was taken up to the point between lowest green branch and dead branch (Chatturvedi and Khanna 2011).

**Statistical analysis**

Different growth traits were analysed for estimation of variability and genetic parameters. The general linear model (GLM) procedure of SPSS-16 software was employed for analysis of variance (ANOVA). ANOVA for each trait was performed based on the following linear model (Singh et al 2013):

$$yij = \mu + Pi + eij$$

where yij= Trait of j$^{th}$ replication of the i$^{th}$ progeny, μ= Overall mean, Pi= Effect due to i$^{th}$ progeny (i= 1...21), eij= Error

Phenotypic (Vp), genotypic (Vg) and environmental (Ve) variances were calculated as (Singh and Chaudhary 1985):

$$Vp = Vg - Ve$$

$$Vg = \frac{MSG - MSE}{r}$$

$$Ve = \frac{MSE}{r}$$

where MSG, MSE and r= Mean squares of progenies, mean squares of error and number of replications respectively, Phenotypic variance (Vp)= Total variance among phenotypes when grown over the range of environments of interest, Genotypic variance (Vg)= Part of the phenotypic variance that can be attributed to genotypic differences among the phenotypes, Error variance (Ve)= Part of the phenotypic variance due to environmental effects

To compare the variation among traits, phenotypic (PCV) and genotypic (GCV) coefficients of variation were computed as per Burton and DeVane (1953).

$$PCV\ (\%) = \sqrt{Vp/\bar{x}}\ \text{x}\ 100$$

$$GCV\ (\%) = \sqrt{V/\bar{x}}\ \text{x}\ 100$$

where Vp and Vg= Phenotypic and genotypic variances respectively and the population mean of the character

Broad sense heritability ($H^2$) was calculated as suggested by Johnson et al (1955) and Singh and Chaudhary (1985).

$$H^2 = \frac{Vg}{Vp}\ \text{x}\ 100$$

where $H^2$, Vp and Vg= Broad sense heritability, phenotypic variance and genotypic variances respectively

Genetic advance (GA) expected and GA as per cent of the mean (genetic gain) assuming selection of the superior 5 per cent of the progenies were estimated in accordance with Johnson et al (1955) as:

Genetic advance= (Vg/Vp) x K

Genetic gain (%)= (Genetic advance/x) x 100

where K= Selection differential at 5 per cent selection intensity, K= 2.06 at 5 per cent selection intensity

Phenotypic (rp) and genotypic (rg) correlations were further computed to examine inter-character relationships among growth traits following Warghese et al (1976) as:

Phenotypic correlation coefficient between character x and y, rp (xy):

$$r_p\ (xy) = V_p\ (xy)/\sqrt{Vx(g) * Vy\ (g)}$$

Genotypic correlation coefficient between character x and y, rg (xy):

$$r_g\ (xy) = V_g\ (xy)/\sqrt{Vx(g) * Vy\ (g)}$$

where Vp (xy) and Vg (xy)= Phenotypic and genotypic variance between x and y respectively

The significance of correlation coefficients was tested against 'r' values as given by Fisher and Yates (1963) at n-2 degrees of freedom.

Principal component analysis or canonical (vector) analysis was carried out to study the amount of variation along different axis of differentiation. It is a multivariate statistical technique to reduce the data with large number of correlated variables into a substantially smaller set of new variables through linear combinations of variables that account most the variation present in the original variables. PCA is a function of Eigen values and Eigen vectors covariance matrix. The factors having Eigen values less than one were not taken for further consideration. Since the aim of principal component analysis was to replace the original set of variables with few variables as possible, so some information contained in the original variables had to be sacrificed, but this lost information was minimum (Lawley and Maxwell 1963).

Genetic divergence was estimated by Mahalanobis $D^2$ statistics (Mahalanobis 1936) and the half sib families were grouped on the basis of minimum generalized distances using Tocher's method as described by Rao (1952). Using SPSS.16 software which grouped the diverse families into different clusters, based the mean of the growth traits.

## RESULTS and DISCUSSION

All the chir pine families were examined for different growth traits viz height, bark thickness diameter at breast height, crown length and crown height. The differences in growth features between the different half sib families of *P roxburghii* were analysed (Table 1) and were found to be significant.

It was found that diameter at breast height (DBH) varied from 22.60 [Hamirpur (T10)] to 40.20 cm [Hamirpur (T14)]. Height varied from 22.42 m [Majhin (T9)] to 13.67 m [Surami (T4)]. Bark thickness varied from 3.22 cm [Majhin (T15)] to 2.33 cm [Hamirpur (T10), Mahasu (T1)]. Crown length varied from 13.46 meters [Majhin (T15)] to 7.40 meters [Surami (T4)]. Crown height varied from 8.13 meters [Chanina (T2)] to 6.08 meters [Mahasu (T1)].

### Genetic analysis

Genetic parameters were evaluated for the growth characteristics and the results are presented in Table 2. The diameter at breast height had the largest coefficient of variation at both the phenotypic (9.66%) and genotypic (7.55%) levels. These traits were found to be moderately heritable. Bark thickness (80.46% heredity) had the highest heritability whereas crown length had the lowest (59.46%). The most genetic progress was found in the diameter at breast height (3.78) whereas the most genetic gain was seen in bark thickness (48.17). The genotypic and phenotypic variances as well as their accompanying coefficients of variation determine the degree of variability in a trait (Thakur et al 2014).

In terms of selection, the realized genetic gain over the other families evaluated was 12.16 per cent for DBH, 17.71 per cent for height and 29.13 per cent for crown height. This clearly demonstrates that selection followed by clonal seed orchard establishment can be highly profitable which is consistent with Matziris (2000) in *Pinus halepensis*, Han et al (1985) in *P koraiensis* and Kant et al (2006) in *P halepensis*. Heritability and other genetic characteristics highlight the value of variation in modern breeding programmes. Because of the environment's modifying effect on the strong genetic connection of features, the genotypic coefficient of variation was lower than the phenotypic values (Gwaze et al 2000, Singh et al 2013).

### Correlation studies

Correlation study was performed on growth parameters such as DBH, height, bark thickness, crown height and crown length with one another (Table 3). Height was significant with DBH (0.572) at 5 per cent level of significance, bark thickness was significant with DBH (0.670) at 1 per cent level of significance, crown height was highly significant with DBH (0.750) and bark thickness (0.589) at 1 per cent level of significance and crown length was associated with height (0.911) (at 1% level of significance). Similar work has been reported by Bhat S (2015) in *P roxburghii*.

### Principal component analysis (PCA)

PCA is a dimensionality-reduction method for reducing the dimensionality of large data sets by transforming a large collection of variables into a smaller set that nevertheless contains the majority of the information in the large set. The growth data (Table 4) show the factor pattern and a summary of PCA. Only two components were found to have Eigen values greater than one and these components were kept for

Table 1. Variation in mean performance of growth traits among different half sib families of chir pine

| Family | Growth trait | | | | |
|---|---|---|---|---|---|
| | DBH (cm) | Height (m) | Bark thickness (cm) | Crown height (m) | Crown length (m) |
| Mahasu (T1) | 26.60 | 18.31 | 2.33 | 6.08 | 11.67 |
| Chanina (T2) | 38.40 | 19.61 | 3.20 | 8.13 | 11.43 |
| Soigni (T3) | 28.80 | 19.13 | 2.48 | 7.04 | 12.04 |
| Surami (T4) | 26.40 | 13.67 | 3.17 | 6.09 | 7.40 |
| Jassi (T5) | 23.80 | 17.56 | 2.39 | 6.86 | 10.89 |
| Bitroli (T6) | 28.20 | 15.32 | 2.48 | 6.50 | 8.47 |
| Surami (T7) | 32.40 | 16.55 | 3.18 | 8.03 | 8.48 |
| Bijhri (T8) | 27.60 | 17.40 | 2.63 | 6.60 | 10.63 |
| Majhin (T9) | 32.80 | 22.42 | 2.69 | 6.58 | 12.69 |
| Hamirpur (T10) | 22.60 | 14.56 | 2.33 | 6.53 | 7.72 |
| Hamirpur (T11) | 34.40 | 19.06 | 3.21 | 7.84 | 11.60 |
| Dharamshala (T12) | 27.60 | 18.66 | 2.72 | 6.46 | 12.08 |
| Bijhri (T13) | 36.40 | 19.05 | 3.14 | 7.95 | 11.42 |
| Hamirpur (T14) | 40.20 | 18.75 | 3.05 | 7.58 | 11.19 |
| Majhin (T15) | 36.20 | 20.03 | 3.22 | 7.30 | 13.46 |
| Chabhitra (T16) | 31.90 | 17.07 | 2.73 | 6.26 | 10.76 |
| Bharwain (T17) | 39.40 | 18.70 | 2.73 | 7.70 | 11.00 |
| Mahasu (T18) | 26.20 | 16.84 | 2.46 | 6.07 | 10.46 |
| Habroi (T19) | 31.00 | 17.40 | 3.16 | 6.47 | 10.93 |
| Mean | 31.10 | 17.79 | 2.81 | 6.95 | 10.75 |
| CD | 9.93 | 3.78 | 0.36 | 1.27 | N/S |
| SE(m) | 3.51 | 1.34 | 0.13 | 0.45 | 1.29 |
| P | 0.01 | 0.03 | 0.00 | 0.00 | 0.08 |

Table 2. Estimates of variability and genetic parameters for growth traits among different half sib families of chir pine

| Trait | Mean | Variance | | | Coefficient of variation | | | Heritability [$H^2$ (%)] | Genetic advance | Genetic gain (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Env | Gen | Phen | Gen | Env | Phen | | | |
| DBH (cm) | 31.10 | 3.51 | 5.52 | 9.03 | 7.55 | 6.02 | 9.66 | 61.12 | 3.78 | 12.16 |
| Height (m) | 17.79 | 1.34 | 3.29 | 4.63 | 5.83 | 3.72 | 6.92 | 71.06 | 3.15 | 17.71 |
| Bark thickness (cm) | 2.81 | 0.13 | 0.54 | 0.67 | 2.35 | 1.16 | 2.62 | 80.46 | 1.35 | 48.17 |
| Crown height (m) | 6.95 | 0.45 | 1.30 | 1.75 | 3.67 | 2.16 | 4.25 | 74.29 | 2.02 | 29.13 |
| Crown length (m) | 10.75 | 1.29 | 1.89 | 3.18 | 4.42 | 3.65 | 5.74 | 59.46 | 2.18 | 20.32 |

Env= Environmental, Gen= Genotypic, Phen= Phenotypic

Table 3. Correlation for the growth traits among different families of chir pine

| Trait | DBH (cm) | Height (m) | Bark thickness (cm) | Crown height (m) | Crown length (m) |
|---|---|---|---|---|---|
| DBH (cm) | 1 | | | | |
| Height (m) | 0.572* | 1 | | | |
| Bark thickness (cm) | 0.670** | 0.182 | 1 | | |
| Crown height (m) | 0.750** | 0.399 | 0.589** | 1 | |
| Crown length (m) | 0.44 | 0.911** | 0.112 | 0.213 | 1 |

*Significant at 5% LoS, **Significant at 1% LoS additional genetic study. Eigen values less than one were not taken into account any further. These variables accounted for 86.9 per cent of the variation. For component I ($\lambda 1= 2.969$) explaining 59.4 per cent variation, DBH was attached with maximum loading value (0.905) followed by height (0.801) while bark thickness had lowest value (0.652). Component II ($\lambda 2= 1.378$) explained 27.6 per cent of variation with maximum loading value attached to crown length (0.684) followed by height (0.566).

Singh (2006) studied *Populus* sp, Rodríguez-Banderas et al (2009) studied *P leiophylla*, Huang et al (2015) studied *P yunnanensis* and Bhat (2015) studied *P roxburghii*. They also discovered that different Eigen values larger than one explained varying percentage of variance for certain attributes.

## Genetic divergence studies

The 19 half sib families were divided into three clusters based on their growth features (Table 5). Cluster I had the most families (8) with families numbered 1, 4, 5, 6, 8, 10, 12 and 18 whereas cluster II had the fewest (5) with families numbered 2, 13, 14, 15, and 17. Cluster III had 6 half sib families (3, 7, 9, 11, 16 and 19).

According to divergence studies for growth traits of different half sib families of chir pine (Table 6) included in clusters revealed that mean maximum DBH 38.12 cm, height 19.22 m, bark thickness 3.07 cm, crown height 7.73 and crown length 11.7 m were maximum in cluster II followed by cluster III and least in cluster I. The families came from a variety of eco-geographical zones around the state therefore they had

Table 4. Principal component analysis for growth traits among different half sib families of chir pine

| Trait | Component | | | | | Communalities |
|---|---|---|---|---|---|---|
| | I | II | III | IV | V | |
| DBH (cm) | 0.905 | -0.235 | 0.029 | -0.353 | 0.021 | 0.874 |
| Height (m) | 0.801 | 0.566 | 0.029 | 0.046 | -0.186 | 0.962 |
| Bark thickness (cm) | 0.652 | -0.6 | -0.443 | 0.137 | -0.024 | 0.784 |
| Crown height (m) | 0.777 | -0.418 | 0.432 | 0.184 | 0.04 | 0.778 |
| Crown length (m) | 0.693 | 0.684 | -0.139 | 0.073 | 0.165 | 0.948 |
| Eigen values (λ) | 2.969 | 1.378 | 0.404 | 0.184 | 0.064 | |
| Percentage of variance | 59.4 | 27.6 | 8.1 | 3.7 | 1.3 | |
| Cumulative percentage of variance | 59.4 | 86.9 | 95 | 98.7 | 100 | |

Table 5. Cluster for genetic divergence in growth traits among different half sib families of chir pine

| Cluster | Number of progenies | Progenies |
|---|---|---|
| 1 | 8 | 1, 4, 5, 6, 8, 10, 12, 18 |
| 2 | 5 | 2, 13, 14, 15, 17 |
| 3 | 6 | 3, 7, 9, 11, 16, 19 |

Table 6. Means of growth traits for different half sib families of chir pine included in clusters

| Trait | Cluster | | |
|---|---|---|---|
| | I | II | III |
| DBH (cm) | 26.13 | 38.12 | 31.88 |
| Height (m) | 16.54 | 19.22 | 18.61 |
| Bark thickness (cm) | 2.56 | 3.07 | 2.91 |
| Crown height (m) | 6.399 | 7.73 | 7.04 |
| Crown length (m) | 9.92 | 11.7 | 11.08 |

a wide range of differences. Aside from that, significant variation in these attributes must be related to the genetic makeup of the species. As the pattern of group constellations demonstrates, geographic diversity does not have to be connected to genetic diversity. Aslam et al (2011) discovered similar results in *P wallichiana*, Huang et al (2015) in *P yunnanensis*, and Bhat (2015) in *Pinus roxburghii*.

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