International Journal of Bio-resource and Stress Management https://pphouse.org/ijbsm.php

IJBSM June 2022, 13(6):578-585 Print ISSN 0976-3988 Online ISSN 0976-4038 Article AR2609

Research Article Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2022.2609

Estimation of Genetic Parameters of *Pinus wallichiana* Seedlings in the Nursery

Amanpreet Kaur[1], Rajesh Monga[3], D. R. Bhardwaj[1] and Jaipal Sharma[2]

[1]Dept. of Silviculture and Agroforestry, [2]Dept. of Tree Improvement and Genetic Resources, Dr. Yaswant Singh Parmar University of Horticulture and Forestry, Solan, Himachal Pardesh (173 230), India
[3]Research and Development, ITC-PSPD Unit Wimco Seedling, Rudrapur, Uttrakhand (263 153), India

Open Access

Corresponding rajeshmmonga@gmail.com

0000-0003-2486-0390

ABSTRACT

The present study was carried out at the Department of Silviculture and Agroforestry forest nursery, Dr. Y.S. Parmar UHF, Nauni, Solan, HP, India to estimate genetic parameters on seed germination and growth characters of Pinus wallichiana seedlings. Seeds were collected from different altitudinal ranges [1800–2100 (A_1), 2100–2400 (A_2), 2400–2700 (A_3), >2700 (A_4) m asl) of Himachal Pradesh in the year 2019–20. The seeds were sown under nursery using randomized block design with three replications. Data recorded for germination and growth character from 10 randomly selected seedlings of each replication and mean data were used for analysis. Analysis of variance revealed that the mean sum of squares were highly significant difference for most of the germination and growth traits. Irrespective of altitudes, the maximum environmental variance was reported in survival percentage (19.2%). The genotypic and phenotypic variance was recorded higher in germination capacity (76.3) and survival percentage (84.9), respectively. Along different altitudinal zones, the genotypic and phenotypic variance was higher at A_2 altitude in germination percentage (77.3, 81.3), respectively. Heritability in a broad sense along elevation was more in most of the germination parameters at A_2 and growth traits at A_1, representing characters are least influenced by environment and selection of character's is useful. Whereas, the genetic advance was more in germination capacity at A_2 altitude indicating the best selection of population from this altitude. So, it would be concluded that seedlings collected from lower (1800–2100m asl)and mid altitudes (2100–2400m asl) were found suitable for large scale plantations in this area.

KEYWORDS: Altitude, genetic gain, genotypic variance, heritability, phenotypic variation

***Citation* (VANCOUVER):** Kaur et al., Estimation of Genetic Parameters of *Pinus wallichiana* Seedlings in the Nursery . *International Journal of Bio-resource and Stress Management,* 2022; 13(6), 578-585. HTTPS://DOI.ORG/10.23910/1.2022.2609.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 05th September 2021 RECEIVED in revised form on 23rd May 2022 ACCEPTED in final form on 14th June 2022 PUBLISHED on 30th June 2022

1. INTRODUCTION

Coniferous forests are critical natural resources to sustain life in the Himalayas. The role of these forests lies in the maintenance of biodiversity, watershed protection as well as supplying timber, non–wood forest products, grazing land and habitat for threatened taxa (Ahmed et al., 2006). Blue pine (*Pinus wallichiana*), Chilgoza pine (*Pinus gerardiana*), fir (*Abies pindrow*), and spruce (*Picea smithiana*) dominate the Western Himalayan subalpine conifer forests, which cover an area of 39,700 km^2 in India, Nepal, Pakistan, and Afghanistan (Dar and Sundarapandian, 2016). This species, commonly known as Blue pine or Bhutan pine of the Pinaceae family, is a large evergreen conifer distributed across the Himalayas, spanning from northeast Pakistan to Yunnan in southwest China (Devkota, 2013). It generally grows at an elevation of 1500–3000 m.a.s.l up to 3400 m.a.s.l in Bhutan (Farjon, 2013). This species usually prefers to grow on deep moist soils, in pure as well as mixed stands with Cedrus deodara, Picea smithiana, Abies pindrow and Quercus sps. At the higher altitude above 3,000 m, it is associated with birch and juniper (Yadav and Bhattacharyya, 1997). Generally, pine trees are sensitive to moisture, and have strong common signals compared to other species (Thapa et al., 2017). It is useful for construction, furniture, cabinetry, light packing containers, paper production, planking, door, window frames, panels, furniture, drawing boards (Trotter, 1959).

Seeds are the species primary method of perpetuation, however, their seed germination characteristics are not only unpredictable, but also low and take longer to complete, resulting in delayed germination, uneven seedling development, and poor seedling quality. Natural regeneration in conifers is almost entirely dependent on seeds, which are dependent on production, dispersion germination capability, and seedling establishment success. Seeds, on the other hand, show a lot of variances, which may be related to differences in altitude that requires the gathering of seeds from various elevations (Barnett and Farmer, 1978). With the increase in demand of wood, there is a need to strengthen the tree improvement programme in the species with a view to find best altitude with improved growth characters for developing superior genotypes. Therefore, it is essential to understand the genetic architecture of this species which provides useful guidelines to determine the source population and from which it is possible to derive appropriate genotypes with desired characters. Effective tree breeding depends on an understanding of tree variation in nature and preserving such variation for future use.

Knowledge of variances and heritability within seeds from the different environments is important to develop strategies for breeding a particular trait. Heritability is important parameter in quantitative genetics to determine the response to selection (Piepho and Mohring, 2007). It helps to determine the degree of transmissibility of selected characters of interest to progenies during the breeding process (Sabesan et al., 2009). Further, the heritability at the early ages is usually higher than in later years because the environment is mostly homogenous in early tests. This means that the efficiency of early testing measured as genetic gain per unit of time may be higher than that of later testing (Eriksson et al., 1993). The heritability of the traits determines the extent of its transmission from one generation to the next. The response to selection will be higher if the heritability for the characters is higher (Sabu et al., 2009). But the estimates of heritability alone fail to indicate the amount of progress expected from selection. There is a strong relationship between heritability and genetic advance. Genetic advance describes the degree of gain acquired in a trait under a particular selection pressure (Ogunniyan and Olakojo, 2014). High genetic advance along with high heritability offers the most effective condition for selection of a specific traits (Islam et al., 2016). Dey et al. (2021) recorded high heritability and genetic advance for the traits viz., leaf length, number of tillers plant^{-1}, number of grains panicle^{-1}, 1000 seed weight, root length, root volume, root fresh weight plant^{-1}, root dry weight plant^{-1} etc of rice genotype. Genotypic and phenotypic correlations are important in determining the degree to which various characters are associated. A wide range of genetic variability has been reported for quality traits earlier. Zhao et al. (2012) reported remarkable differences for coefficients of phenotypic variation for growth and morphological traits measured among 30 white poplar hybrid clones and also found significant phenotypic correlation among stem height, diameter, diameter at breast height, and volume per plant. Zhao et al., 2014 reported extremely significant correlations between tree height and diameter at breast height in *Betula platyphylla*. Dhixya Deve and Parthiban (2014) studied the growth performance and variability of twenty *Dalbergia sissoo* clones. Among the traits studied height registered maximum heritability, followed by volume index. Heritability and genetic gain of all investigated traits were found to be high. Fakuta et al. (2015) evaluated twelve *Acacia senegal* provenances to estimate mean effects, genetic variability, heritability and genetic advance in *Acacia senegal* provenances. Genetic component analysis showed that both genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for all the traits except bark thickness. Keeping in view the above perspectives, The objectives of the present study are to compare the growth parameters of seedlings collected from different altitudes in the field conditions after nursery screening and to estimate the genetic parameters of *Pinus wallichiana.*

2. MATERIALS AND METHODS

The experiment was conducted at the Department of Silviculture and Agroforestry forest nursery, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India in the year 2020. Cones were collected from phenotypically superior trees (5 trees) at least 100 m away from each other from different zones of Himachal Pradesh. The nursery site is located at an elevation of 1200 m above mean sea level in the northwest of Himalaya and lies between 30°51'N latitude and 76°11'E longitude. The experimental area is hilly, marked with elevations, depressions and has a gentle slope towards the south-eastern aspect. The area experiences a wide range of temperatures with a minimum of 1°C in winters to a maximum of 33°C during May and June as the hottest months. The annual rainfall reaches up to 0–342 mm, with maximum downpour during the monsoon season (July – September).

The maturing cones of *P. wallichiana* were collected from vigorous, middle–aged and excellent form of trees. 8–10 cones were collected from each selected tree from mid-October to mid-November, 2019. The cones were dried in the sun, and seeds were extracted by shaking and manually twisting of cones. Before sowing, seeds were stratified by pit method with different strata of sand and moss for about 60 days for breaking of dormancy. After completion of the stratification period, the seeds were directly sown in root trainers filled with deodar forest soil: FYM in a proportion of 2:1 then placed under nursery condition. Sown seeds were managed by providing required management practices of irrigation, weeding, etc.

2.1. *Assessment of the Traits*

The observations were recorded in 12 months old seedlings i.e. in the last week of December. Germination parameters (germination percent, germination capacity, germination energy, germination speed and value) and growth parameters (seedling height, collar diameter, needle area, number of roots, root length, etc.) were recorded at the end of the trial.

2.2. *Statistical analysis*

The field experiment data was analyzed according to the procedure of analysis of variance for two factors Randomized Block Design in accordance with the procedure outlined by Gomez and Gomez (1984) with three replications for each seed source of *Pinus wallichiana.* Genotypic, phenotypic, environmental variances and coefficients of variability, expected genetic advance at 5 per cent of selection intensity was calculated by the formula as per Johnson et al. (1955).

Environmental variance (Ve)=Me

Genotypic variance (Vg)= $\frac{Mt-Me}{r}$

Phenotypic variance (Vp)=Vg+Ve

Where, Mt=Mean sum of square due to treatment, Me=Mean sum of square due to error, and r=Number o Genotypic, Phenotypic and environmental variances were calculated as

Environmental coefficient of variability (%)= $\frac{\sqrt{Ve}}{X}\times 100$

Phenotypic coefficient of variability (%)= $\frac{\sqrt{Vp}}{\bar{X}}\times 100$

Genotypic coefficient of variability (%)= $\frac{\sqrt{Vg}}{\bar{X}}\times 100$

$\bar{X}$=Population mean of character

Heritability in the broad sense, genetic advance at 5 percent intensity and genetic gain was calculated as suggested by Johnson et al. (1955).

$$h^2_{b.s}=\frac{Vg}{Vp}\times 100$$

Where,

$h^2_{b.s}$ = Heritability (broad sense)

Genetic Advance (GA) $=\left[\frac{Vg}{Vp}\right]\times(\sqrt{Vp})\times K$

K=Selection differential at 5 per cent selection intensity. The value of K=2.06 (Allard 1960).

The genetic gain was worked out following the method suggested by Johnson et al. (1955) as under:

Genetic advance as percentage of the mean (%) $=\frac{GA}{X}\times 100$

3. RESULTS AND DISCUSSION

The genetic parameters furnished in Figures 1 and 2 revealed variability among the *Pinus wallichiana* germination and growth traits. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all growth parameters. In the present findings, the heritability estimates (broad sense) were used to estimate the heritable portion of the variation. The genotypic and phenotypic variance was found to be higher in germination capacity (76.3) and survival percentage (84.9), respectively. Roy et al., 2004 also reported the phenotypic, genotypic and environmental variance was exhibited highest for germination in *Pinus roxburgii* seedlings. However, the minimum value for environmental, genotypic and phenotypic variance was observed in the dry weight of seedlings, seedling height and diameter. The difference between phenotypic and genotypic coefficients of variation (PCV and GCV) suggested that the traits were influenced by the environment as also reported by Sivasubramanian and Madhavamenon (1973). Weber et al. (1984) found a large range of variation in 15 leaf, branch and phonological characters in *Populus trichocarpa* and its hybrids due to regional climatic gradient, riparian environment and the life history characteristics of the species. Significant difference

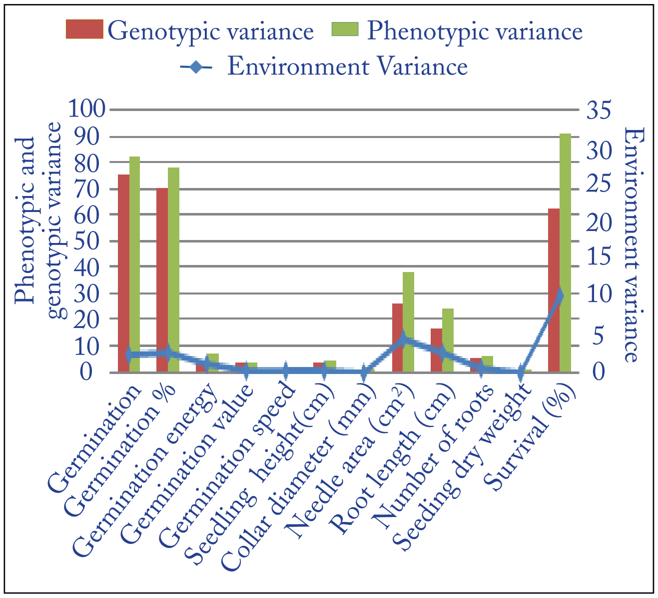

Figure 1: Environment, genotypic and phenotypic variance for germination and growth traits of *Pinus wallichiana* 12 month old seedlings

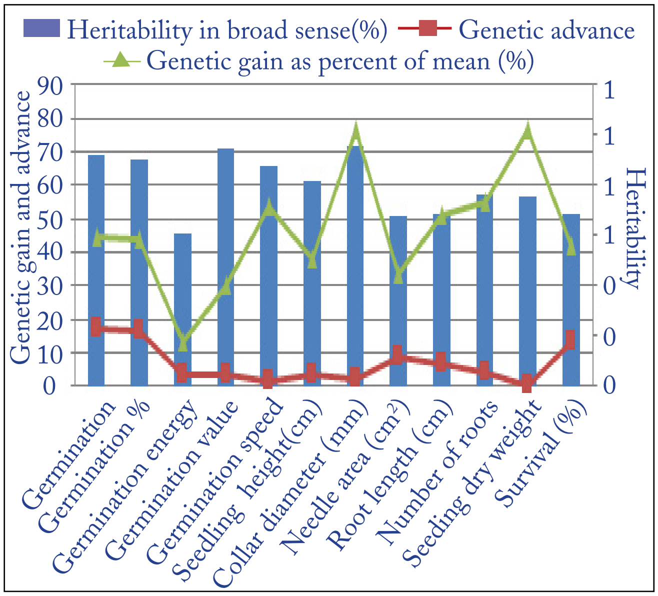

Figure 2: Heritability and genetic gain analysis for germination and growth traits of *Pinus wallichiana* 12 month old seedlings

among leaf characters in nursery growth of willow was obtained by Singh et al. (2012b).

However, broad sense heritability was maximum in collar diameter (0.92%) followed by germination value (0.90%) and germination capacity (0.79%) indicating they are least influenced by the environment. As far as the genetic advance was concerned it was maximum in germination capacity and germination percent (19.0) while, genetic advance as percent of mean was maximum in collar diameter and seedling dry weight. The high value of genetic advance indicates characters are governed by additive genes and selection will be beneficial for such traits. Heritability estimates in the broad sense are reliable if accompanied by the high genetic gain (Burton and De Vane, 1953). Johnson et al. (1955) reported that heritability estimates along with expected genetic gain are more useful and realistic than the heritability alone predicting the resultant effect for selecting the best genotype. The findings reported are in agreement with Zeps et al. (2010) on poplar hybrids; Singh et al. (2001) on *Populus deltoides* and Callister et al. (2007) in *Eucalyptus cladocalyx.*

Altitudinal variation effect on genetic parameters of *P. wallichiana* seedlings

In the present study seeds obtained from different altitudinal zones were evaluated for genetic parameters estimation. Since the seeds were collected from different locations, differences observed in seed parameters may be attributed to the different genetic architectures developed as a result of adaptation to diverse environmental conditions prevailing throughout their distributional range (Salazar and Quesda, 1987). Seedlings of different seed sources when grown under common nursery environmental conditions often display different patterns of shoot growth (Dormling, 1979; Rehfeldt and Wycoff, 1981 and Sorensen, 1979). In the present investigation, where all seed sources were raised under identical nursery conditions, the environmental influences are expected to have been reduced to minimal, therefore, variation among seed sources in nursery emergence and growth could be interpreted as genetic. Selection plays a major role in tree improvement where testing of a large number of genotypes is not possible due to the testing area and other resource constraints.

The estimates of variability with regard to genetic parameters studied at the nursery stage. It is observed from Table 1 along with different altitudinal ranges and between different germination and growth parameters maximum value of environment variance was observed in survival percentage at A_4 altitude (34.49) and maximum value of genotypic and phenotypic variance was observed in germination percentage at A_2 (77.28 and 81.34, respectively). However, environmental, genotypic and phenotypic coefficient of variance was higher in the dry weight of seedlings at A_3 (27.05, 50.10, and 56.74 respectively). Broad sense heritability was maximum in germination parameter at A_2 altitude as compared to other while growth parameters at A_1 altitude. The genetic advance was reported maximum in germination percentage (17.65) at A_2 altitude compared to others. Genetic advance as per percent of mean was observed maximum in dry weight of seedlings at A_1 (93.2) altitudinal range. Variation in seed and seedling traits among and within sources suggests that selection among sources might result in a rapid genetic gain for the traits.

Table 1: Genetic parameters analysis of germination and growth parameters of *Pinus wallichiana* along different altitude

Traits	ALT	GC	GP	GE	GV	GS	SH	CD	NA	RL	NOR	SDB	SP
Environment variance	A_1	5.12	3.28	0.59	0.07	0.05	0.87	0.04	0.47	13.87	0.92	0.01	14.36
	A_2	5.48	4.06	0.80	0.22	0.12	0.35	0.07	12.9	4.87	1.24	0.01	13.19
	A_3	4.04	3.48	3.27	0.14	0.07	0.39	0.07	9.83	3.20	3.11	0.02	31.39
	A_4	2.49	0.85	2.46	0.32	0.08	0.35	0.01	1.97	2.95	0.99	0.01	34.49
Phenotypic variance	A_1	14.06	17.47	1.20	0.35	0.17	0.87	0.15	43.7	22.35	3.35	0.05	20.78
	A_2	79.08	81.34	8.18	4.23	0.69	4.86	1.03	43.7	12.62	3.39	0.04	14.79
	A_3	22.47	15.10	4.98	1.07	0.99	1.25	0.73	17.8	4.17	4.98	0.08	58.01
	A_4	13.07	6.96	5.89	7.57	1.45	3.00	2.85	13.80	9.18	1.15	0.03	58.93
Genotypic variance	A_1	8.94	14.19	0.61	0.27	0.12	NA	0.11	43.22	8.48	2.43	0.04	6.42
	A_2	73.61	77.28	7.38	4.01	0.57	4.50	0.96	30.80	7.75	2.15	0.03	1.60
	A_3	18.43	11.63	1.71	0.93	0.92	0.86	0.67	7.95	0.97	1.87	0.06	26.63
	A_4	10.59	6.11	3.43	7.25	1.37	2.64	2.83	11.82	6.23	0.16	0.02	24.44
Environment coefficient of variance	A_1	3.12	2.61	2.20	1.87	6.37	7.92	7.56	1.82	17.59	10.63	18.70	6.56
	A_2	3.66	3.26	2.48	3.30	10.9	6.67	10.1	10.10	13.81	12.53	23.80	7.27
	A_3	3.51	3.38	5.45	2.60	8.84	6.34	8.15	9.97	12.76	20.00	27.05	13.38
	A_4	2.90	1.77	4.75	4.46	9.50	6.81	3.52	4.23	14.28	21.33	25.73	14.67
Phenotypic coefficient of variance	A_1	5.17	6.01	3.14	4.06	12.1	7.90	14.5	17.56	22.32	20.34	51.97	7.89
	A_2	13.89	14.62	7.92	14.6	25.7	24.7	38.9	18.62	22.23	20.72	42.43	7.70
	A_3	8.28	7.05	6.73	7.28	33.2	11.3	27.2	13.40	14.56	25.29	56.94	18.18
	A_4	6.66	5.06	7.35	21.6	40.9	19.9	52.5	11.19	25.19	23.00	40.34	19.18
Genotypic coefficient of variance	A_1	4.12	5.42	2.23	3.61	10.2	NA	12.3	17.46	13.75	17.34	48.49	4.38
	A_2	13.40	14.25	7.52	14.2	23.3	23.8	37.6	15.64	17.42	16.50	35.13	2.53
	A_3	7.50	6.18	3.94	6.79	31.9	9.38	25.9	8.96	7.02	15.48	50.10	12.32
	A_4	5.99	4.74	5.61	21.1	39.	18.6	52.4	10.36	20.75	8.62	31.07	12.35
Heritability in broad sense	A_1	0.64	0.81	0.51	0.79	0.72	NA	0.73	0.99	0.38	0.73	0.87	0.31
	A_2	0.93	0.95	0.90	0.95	0.82	0.93	0.93	0.71	0.61	0.63	0.69	0.11
	A_3	0.82	0.77	0.34	0.87	0.93	0.69	0.91	0.45	0.23	0.37	0.77	0.46
	A_4	0.81	0.88	0.58	0.96	0.95	0.88	1.00	0.86	0.68	0.14	0.59	0.41
Genetic advance	A_1	4.91	6.99	1.14	0.96	0.62	NA	0.57	13.47	3.69	2.74	0.40	2.90
	A_2	17.05	17.65	5.31	4.02	1.40	4.21	1.95	9.60	4.50	2.41	0.28	0.86
	A_3	8.01	6.16	1.58	1.86	1.91	1.58	1.60	3.88	0.98	1.72	0.46	7.20
	A_4	6.03	4.77	2.91	5.43	2.34	3.15	3.46	6.56	4.24	0.31	0.20	6.56
Genetic advance as percent of mean	A_1	6.77	10.05	3.28	6.59	17.9	NA	21.7	35.78	17.44	30.45	93.20	5.02
	A_2	26.64	28.61	14.7	28.6	43.5	47.3	74.7	27.05	28.13	27.08	59.92	1.72
	A_3	13.99	11.18	4.76	13.1	63.4	16.0	50.9	12.34	6.97	19.52	90.82	17.19
	A_4	11.10	9.16	8.82	42.5	79.8	36.1	107	19.76	35.21	6.66	49.30	16.39

Where, ALT: Altitude; GC: Germination capacity; GP: Germination percentage; GE: Germination energy; GV: Germination value; GS: Germination speed; SH: Seedling height; CD: Collar diameter; NA: Needle area; RL: Root length; NOR: Number of roots; SDB: Shoot dry biomass; SP: Survival percentage

Related finding by Dhanai (2002) in *Albiziza chinesis*; Singh (2004) in *Celtis australis*, and Rawat and Bakshi (2011) in *Pinus wallichiana*. There was a close match between the phenotypic and genotypic coefficients of variation, indicating that the genotypes had enough variance in their characteristics. As a result, these characteristics have a chance for improvement. These results are in general accordance with the findings of Yadav (2007), Showkat and Tyagi (2010). The results are also in agreement with the findings of Fakuta et al. (2015) where they found PCV was higher in proportion than GCV with respect to all the traits studied in *Acacia senegal.* Volker et al. (1990) has shown that heritability estimates along with genetic gain were more useful than the heritability alone in predicting the resultant effect for selecting the best genotypes for a given trait. Sharma et al. (2011) found high heritability in Indian willows collected from 20 sites, as well as high genetic advance as percentage mean for root length, internodal length, plant height, root to shoot ratio, leaf area, lamina breadth and petiole length, and biomass characters, indicating that selection for these characters could be more effective due to additive gene action. The latest study was conducted Anand and Dwivedi (2014) in *Bauhinia variegata* a strong simple, the genotypic and phenotypic correlation was observed between biomass traits and some morphological traits especially collar diameter, plant height and leaf area.

4. CONCLUSION

High genetic variability in the genotypes of *Pinus wallichiana* was observed. Survival percentage was more influenced by the environment while germination capacity and germination percentage have higher genotypic and phenotypic variance. Germination percentage has maximum genotypic variance; heritability was more at A_1 and A_2 altitude for most of the germination and growth traits, indicates characters are least influenced by environment and selection for improvement of characters might beuseful from the lower (1800–2100 m asl) and mid–altitudinal (2100–2400 m asl) ranges.

5. ACKNOWLEDGMENT

The authors are thankful to the head of the department of Silviculture and Agroforestry, Dr. YS Parmar University of Horticulture and Forestry; Department of Science and Technology, Government of India, New Delhi, India for providing the financial support for the present study.

6. REFERENCES

Ahmed, M., Hussain, T., Sheikh, A.H., Siddiqui, M.F., 2006. Phytosociology and structure of Himalayan forests from different climatic zones of Pakistan. Pakistan Journal of Botany 38, 361–383.

Anand, R.K., Dwivedi, S.V., 2014. Association studies for morphological and biomass traits of Bauhinia variegata Linn. International Journal of Agricultural Sciences 10, 61–65.

Barnett, P.E., Farmer, R.E., 1978. Altitudinal variation in germination characteristics of yellow poplar in the Southern Appalachians. Silvae Genetica 27, 101–04.

Burton, G.W., Devane, E.W., 1953. Estimating hereditary in fall Festuca arrundinuca Gomenticatged clonal material. Agriculture Journal 78–81.

Callister, A., Bush, D., Collins, S., Davis, W., 2007. Prospects for genetic improvement of *Eucalyptus cladocalyx* in Western Australia. Paper presented in Australasian forest genetics conference − breeding for wood quality − incorporating meetings of the Australasian Forestry Research Working Group 1 (Genetics) and the IUFRO Southern pine working group (2.02.20) 11–14 April 2007, The Old Woolstore, Hobart, Tasmania, Australia.

Dar, J.A., Sundarapandian, P., 2016. Patterns of plant diversity in seven temperate forest types of Western Himalaya, India. Journal of Asia–Pacific Biodiversity 9, 280–292.

Devkota, A., 2013. Biodiversity : Gymnosperms. In : Jha, P.K., Neupane, F.P., Shrestha, M.L., Khanal, I.P., (Eds.), Biological diversity and conservation. Nepal Academy of Science and Technology, Kathmandu, 127–134.

Dey, S., Kumar, R., Battan, K.R., Chhabra, A.K., Lokeshwar, A.R., 2021. Study of coefficient of variation, heritability and genetic advance for different traits of rice genotypes grown under aerobic condition. International Journal of Bio-resource and Stress Management 12, 426–430.

Dhanai, C.S., 2002. Provenance variation in seed and seedling of Albizia chinensis (Osbeck). Ph.D Thesis work. H.N.B.G.U. Srinagar Garhwal, Uttarakhand, 1–50.

Dhixya Deve, K.R., Parthiban, K.T., 2014. Growth performance and variability of Dalbergia sissoo Roxb. clones. Electronic Journal of Plant Breeding 5, 317–321.

Dormling, I., 1979. Influence of light and temperature on photoperiodic response of Norway spruce provenances. I: Proc. IUFRO Norway spruce Meeting Bucharest, 398–408.

Eriksson, G.A., Jonsson, I., Dormling, L., Norell, Stener, L.G., 1993. Retrospective early tests of *Pinus sylvestris* L. seedlings grown under five nutrient regimes. Forest Science 39, 95–117.

Fakuta, N.M., Ojiekpon, I.F., Gashua, I.B., Ogunremi, O.C., 2015. Quantitative genetic variation in gum arabic (*Acacia senegal* (L) Willd.) provenances. American Journal of Plant Sciences 6, 2826–2831.

Farjon A., 2013. *Pinus wallichiana*. The IUCN Red List of Threatened Species 2013: e. T42427A2979371. doi:10.2305/IUCN.UK.2013-1.RLTS.T42427A2979371.en.

Gomez, K.A., Gomez, A.A., 1984. Statistical procedure for agricultural research. 2nd edition, John Wiley and Sons, New York, 357–427.

Islam, M., Khalequzzaman, M., Bashar, M., Ivy, N., Haque, M.M., Mian, M.A.K., 2016. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. The Scientific World Journal, 1–14.

Johnson, H.W., Robinson, H.F., Comstock, R.F., 1955. Estimates of genetic and environmental variability in soyabean. Agronomy Journal 47, 314–318.

Ogunniyan, D.J., Olakojo, S.A., 2014. Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). Nigerian Journal of Genetics 28, 24–28.

Piepho, H.P., Mohring, J., 2007. Computing heritability and selection response from unbalanced plant breeding trials. Genetics 177, 1881–1888.

Rawat, K., Bakshi, K., 2011. Provenance variation in cone, seed and seedling characteristics in natural populations of *Pinus wallichiana* A.B. Jacks (Blue Pine) in India. Annnals Forest Research 54, 39–55.

Rehfeldt, G.E., Wycoff, W.R., 1981. Periodicity in shoot elongation among populations of Pinus contorta from the northern Rocky Mountain. Annals of Botany 48, 371–377.

Roy, M., Thapliyal, R.C., Phartyal, S.S., 2004. Seed source variation in cone, seed and seedling characteristic across the natural distribution of Himalayan Low Level Pine *Pinus roxburghii* Sarg. Silvae Genetica 53, 116–123.

Sabesan, T., Suresh, R., Saravanan, K., 2009. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. Electronic Journal of Plant Breeding 1, 56–59.

Sabu, K.K., Abdullah, M.Z., Lim, L.S., Wickneswari, R., 2009. Analysis of heritability and genetic variability of agronomically important traits in *Oryza sativa*x *Oryza rufipogon* crosses. Agronomy Research Journal 7, 97–102.

Salazar, R., Quesada, M., 1987. Provenance variation in *Guazuma ulmifolia* L. in Costa Rica. Common wealth Forest Review 66, 317–324.

Sharma, J.P., Singh, N.B., Sankhyan, H.P., Chaudhary, P., Huse, S.K., 2011. Estimation of genetic parameters of newly introduced tree willow clones in Himachal Pradesh, India. Genetika 43, 487–501.

Showkat, M., Tyagi, S.D., 2010. Genetic variability in soybean (*Glycine max* L. Merrill). Research Journal of Agricultural Science 1, 102–106.

Singh, B., Bhatt, B.P., Prasad, P., 2004. Effect of seed source and temperature on seed germination of *Celtis australis* (L.): A promising agroforestry tree crop of Central Himalaya, India. Forests Trees and Livelihood 14, 53–60.

Singh, N.B., Kumar, D., Rawat, G.S., Gupta, R.K., Singh, K., Negi, SS., 2001. Clonal evaluation on poplar (*Populus deltoides* Bartr.) in eastern Uttar Pradesh. II–estimates of genetic parameters in field testing. Indian Forester 127, 163–172.

Singh, N.B., Sharma, J.P., Huse, S.K., Thakur, I.K., Gupta, R.K., Sankhyan, H.P., 2012. Heritability, genetic gain, correlation and principal component analysis in introduced willow (*Salix* species) clones. Indian Forester 138, 1100–1109.

Sivasubramanian, J., Madhavamenon, P., 1973. Genotypic and phenotypic variability in rice. Madras Agricultural Journal 12, 15–16.

Sorensen, F.C., 1979. Provenance variation in *Pseudotsuga menziesii* seedlings from the var. menziesii and var. glauca transition zone in Oregon. Silvae Genetica 28, 96–103.

Thapa, U.K., George, S.S., Kharal, D.K., Gaire, N.P., 2017. Tree growth across the Nepal Himalaya during the last four centuries. Progress in Physical Geography 41, 478-495.

Trotter, K., 1959. (Reprinted 1960). The common commercial timber of India and their uses. Manager of Publications, Delhi. 296 p.

Volker, P.W., Dean, C.A., Tibbits, W.N., Ravenwood, I.C., 1990. Genetic parameters and gain expected from selection in *Eucalyptus globulus* in Tasmania. Silvae Genetica 39, 18–21.

Weber, J.C., Stettler, R.F., Heilman, P.E., 1985. Genetic variation and productivity of Populus trichocarpa and its hybrids. I. Morphology and phenology of 50 native clones. Canadian Journal of Forest Research 15, 376–383.

Yadav, R.K., 2007. Genetic variability and coheritability estimates in soybean (*Glycine max* (L.) Merrill). International Journal of Plant Sciences 2, 9–11.

Yadav, R.R., Bhattacharyya, A., 1997. Climate and growth relationship in blue Pine (*Pinus wallichiana*) from the western Himalaya India. The Korean Journal of Ecology 20, 95-102.

Zeps, M., Lazdina, D., Auzenbaha, D., Gailis, A., Lazdins, A., 2010. Fast growing willow family tree clones and hybrids–experience and research in Latvia. Fifth International Poplar Symposium on Poplars and willows: from research models to multipurpose trees for a bio–based society 20– 25 September 2010 Palazzo dei Congressi Orvieto (Italy) Book of Abstracts pp .4

Zhao, X., Bian, X., Liu, M., Li, Z., Li, Y., Zheng, M., 2014. Analysis of genetic effects on a complete diallel cross test of Betula platyphylla. Euphytica 200, 221–229.

Zhao, X.Y., Ma, K.F., Shen, Y.B., Zhang, M., Li, K.Y., Wu, R., 2012. Characteristic variation and selection of forepart hybrid clones of Sect. Populus. Journal of Beijing Forestry University 34, 45–51.