

Chapter

Quantifying: Genetic Traits in *Pinus wallichiana* Seedlings in the Northwestern Himalayan

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Abstract

Pinus wallichiana, commonly known as the Himalayan blue pine, holds significant ecological and economic importance in the northwestern Himalayan region. Understanding the genetic traits and variability within its seedling population is essential for sustainable forest management and conservation efforts. This study aimed to quantify and assess the genetic traits of *Pinus wallichiana* seedlings within a nursery environment situated in the northwestern Himalayas. Our research involved the collection and analysis of data from a representative sample of *Pinus wallichiana* seedlings from different sites in Himachal Pradesh in 2019–2020. Results revealed a diverse genetic pool with notable heritability for key traits, highlighting the potential for selective breeding and genetic improvement programs. Furthermore, our findings provide valuable insights into the adaptation and resilience of *Pinus wallichiana* to changing environmental conditions, which is crucial for addressing the challenges posed by climate change. The quantification of genetic traits in this study not only enhances our understanding of the species but also offers practical applications for forest managers and policymakers in the region. This research contributes to the broader context of forest genetics and underscores the importance of genetic conservation efforts for the sustainable management of *Pinus wallichiana* in the northwestern Himalayas.

Keywords: Kail, genetic diversity, heritability, nursery, germination, and growth traits

1. Introduction

The Himalayan coniferous forests hold great importance due to their contributions in terms of timber resources, non-wood forest products, grazing areas, and the provision of habitats for endangered species. The Western Himalayan subalpine conifer forests, which cover an approximate area of 39,700 km² across India, Nepal, Pakistan, and Afghanistan, are primarily characterized by the presence of four dominant tree species. These species include *Pinus wallichiana* (blue pine), *Pinus gerardiana* (Chilgoza pine), *Abies pindrow* (fir), and *Picea smithiana* (spruce) [1]. The blue pine, a large evergreen tree, is widely distributed throughout the Himalayan region. In the country of Bhutan, the growth of this particular entity occurs at an elevation of

3400 m.a.s.l. [2, 3]. Seeds play a crucial role in the perpetuation of a species, although the likelihood of seed germination is frequently unknown and challenging to predict. The natural regeneration of many coniferous tree species is mostly dependent on seed-based mechanisms. Seeds, however, exhibit considerable variations, potentially attributable to variations in altitudinal ranges, necessitating the collection of seeds from different elevations [4]. The process of evaluating genetic parameters for qualities in *Pinus wallichiana* seedlings within a nursery entails examining several genetic and environmental factors that contribute to the observed variations in traits.

Genetic parameters offer valuable insights into several aspects of genetic features, including their heritability, genetic connection, and potential for selective breeding. In the field of quantitative genetics, the idea of heritability is crucial because it enables us to determine how much selection influences traits and how likely it is that breeding will pass those traits down to subsequent generations. The heritability of qualities determines the degree to which they are transmitted through successive generations [5]. However, it is important to note that solely relying on heritability estimates does not offer a comprehensive understanding of the degree to which development might be influenced by selection. Estimates of heritability alone do not show how much growth can be expected from selection. High genetic advance along with high heritability offers the most effective condition for selection of specific traits [6]. To what extent a trait improves in response to a certain selection pressure can be thought of as a genetic advance [7]. Genotype-phenotype analyses are indispensable for estimating the strength of associations between traits. Researchers can gain a better understanding of the relationships between various traits and how selection may affect them by studying genotype and phenotype correlations [8]. This knowledge allows for a more comprehensive understanding of the factors that contribute to growth and the potential impact of breeding on future generations. Additionally, examining these correlations can help identify any potential limitations or constraints in breeding programs that may affect the transmission of desired traits. The objectives of the present study encompass a comprehensive investigation into several key aspects: Our objective is to conduct a rigorous comparative analysis of the growth parameters exhibited by *Pinus wallichiana* seedlings collected from diverse altitudinal zones. This analysis will be carried out under real-world field conditions following a thorough nursery screening process by examining factors such as height, diameter, and foliage characteristics and then estimating the genetic parameters of *Pinus wallichiana*; we seek to quantify and assess the genetic diversity within the studied population. This aspect of the study is pivotal for understanding the species' genetic makeup, heritability of important traits, and the potential for genetic improvement and conservation efforts.

By pursuing these objectives, our research aims to provide a comprehensive understanding of how altitude influences the growth patterns of *Pinus wallichiana* seedlings while also shedding light on the genetic underpinnings of this ecologically and economically significant tree species.

2. Material and methods

Experimental site: The experiment was carried out during the years 2019–2020 at the forest nursery, Department of Silviculture and Agroforestry, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India. In 2019–2020, a study in Himachal Pradesh to gather seeds from various altitudinal ranges 1800–2100 (A₁), 2100–2400 (A₂), 2400–2700 (A₃), and > 2700 (A₄) m.a.s.l. [9].

The nursery location is situated at a height of 1200 m.a.s.l. in the northwestern region of the Himalayas, between the latitudes of 30°51' N and longitudes of 76°11' E. The experimental site exhibits topographical variations, including elevations, depressions, and a gradual incline in the southeastern direction. The region has a diverse range of temperatures, spanning from a minimum of 1°C during the winter season to a maximum of 33°C in the months of May and June, which are characterized as the peak of summer. The yearly precipitation ranges from 0 to 342 mm, with the highest amount occurring during the monsoon season, which typically spans from July to September.

Sample collection: Cones were collected from five phenotypically superior trees located in different sites of Himachal Pradesh (**Figure 1**). These trees displayed exceptional esthetic qualities and were selected based on a minimum distance of 100 m between each other. The mature cones of *Pinus wallichiana* were obtained from phenotypical superior trees in the intermediate stage of their life cycle and exhibited overall good health.

Prior to being sown, the seeds underwent a 60-day period of storage in a trench that consisted of discrete layers of sand and moss, which facilitated the process of breaking dormancy. Then, the 75 seeds per replication were subsequently seeded directly into root trainers that were filled with deodar forest soil mixed with FYM (Farmyard manure) at a ratio of 2:1. These root trainers were placed in polyhouse for 6 months and then in open nursery for hardening of the seedlings.

Design followed: Randomized Block Design.

Number of Replication: Three.

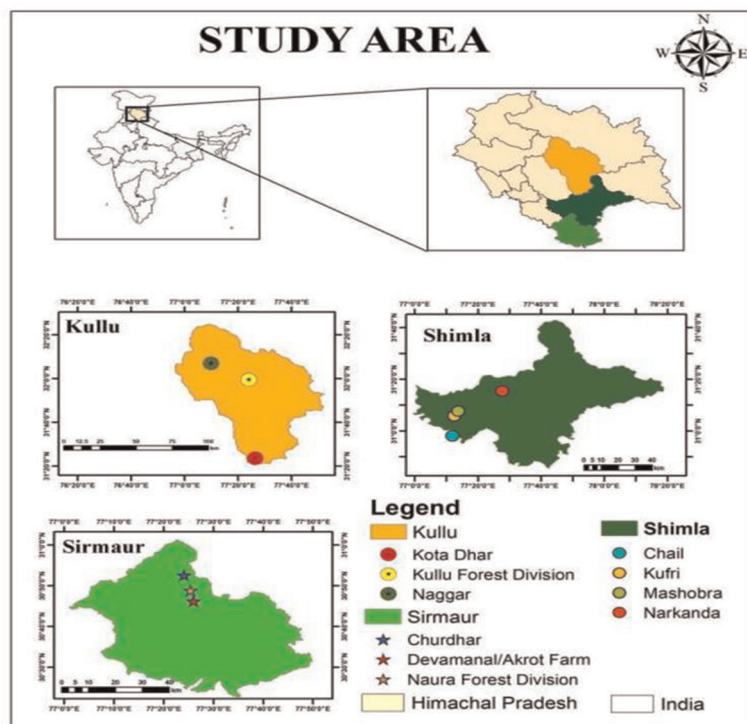


Figure 1.
Study area map.

Parameters: The observations (**Table 1**) were documented in seedlings that were 12 months old (final week of December). For calculation of genetic parameter irrespective of altitude, 60 plants were selected 5 plants per treatment, and for altitudinal effect, 15 plants per altitude were selected for data calculation.

Selecting individuals with optimal phenotypic expression is essential in the process of improving a trait. The developmental traits are the result of a combination of genetic and environmental variables. The computation of variability estimates and genetic parameters was performed for a range of seedling characteristics. The statistical measures of coefficient of variation and analysis of variance were computed for the phenotypic, genotypic, and environmental variations (**Table 2**). The study also involved the calculation of heritability estimates (in the broad sense), genetic advance (at a selection intensity of 5%), and genetic gain (expressed as a percentage of the mean). GCV and PCV can be categorized into three groups based on their magnitudes: low (less than 10%), moderate (10–20%), and high (more than 20%).

Statistical analysis: The data obtained from the field experiment was subjected to analysis using the analysis of variance (ANOVA) approach using OPSTAT software (<http://opstat.pythonanywhere.com/>) and MS Excel, which is commonly employed for examining the effects of two factors at p-value (0.05). The analysis of variance (ANOVA) procedures were used to test for significant effect of treatments (**Table 3**).

Traits	Method used
Germination (%)	$GP = \frac{\text{Number of healthy seeds germinated}}{\text{Number of seeds sown}} \times 100$
Germination Capacity (%)	The cumulative number of seeds that germinated during the 28 days of test period plus the number of viable seeds at the end of the test expressed in percentage.
Germination Energy (%)	$GE = \frac{\text{Number of healthy seeds germinated upto the time of peak germination}}{\text{Number of seeds sown}} \times 100$
Germination Speed	$GV = \sum \frac{DGS}{N} \times (GP \times 10)$ Where DGS = Daily germination speed = Cumulative germination per cent/Number of test days. N = Frequency or number of DGS during the test GP = Germination per cent at the end of the test
Germination Value	$GS = \sum_{i=1}^n \frac{\text{number of newly germinated seeds}}{\text{number of days since sowing}}$
Seedling Height (cm)	It was measured with the help of a meter scale in centimeter from leading shoot tip to the collar region of the seedling at the ground surface.
Collar Diameter (mm)	The diameter of seedling was recorded in millimeters with the help of a digital Vernier caliper.
Needle Area (cm ²)	The projected leaf area was determined on CI-202 Leaf Area Meter.
Root Length (cm)	The root length was measured with the help of using a digital caliper (Mitutoyo Absolute) from the cut base to the tip of the taproot.
Seedling Dry Weight (gm)	Total seedling dry weight was obtained by summing up root and shoot dry weight in gram.
Survival (%)	$SP = \frac{\text{Total percent germination}}{\text{Number of seeds germinated in the that seed source}} \times 100$

Table 1.
Germination and growth parameters measured in the nursery.

Sr. No.	Parameter name	Symbol	Calculation	Description
1.	Genotypic variance	Vg	$\frac{Mt-Me}{R} \times 100$	Mt = Mean sum of square due to treatment Me = Mean sum of square due to error R = Number of replications. X = Mean of the character K = Selection intensity at 5 percent, which is equal to 2.06
2.	Phenotypic variance	Vp	$Vg + Ve$	
3.	Environmental variance	Ve	Me	
4.	Phenotypic coefficient of variation	PCV (%)	$\frac{\sqrt{Vp}}{X} \times 100$	
5.	Genotypic coefficient of variance	GCV (%)	$\frac{\sqrt{Vg}}{X} \times 100$	
6.	Environmental coefficient of variance	ECV (%)	$\frac{\sqrt{Ve}}{X} \times 100$	
7.	Heritability in broad sense	h^2 (%)	$\frac{Vg}{Vp}$	
8.	Genetic advance	GA	$K. \sqrt{VP} \cdot h^2$	
9.	Genetic gain/Genetic advance as percent of mean	GG	$\frac{GA}{X} \times 100$	

Table 2.
Genetic parameters calculation methods.

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F. Cal.
Replications	(r-1)	S_r	$\frac{S_r}{(r-1)} = Mr$	M_r/M_e
Genotype	(g-1)	S_g	$\frac{S_g}{(g-1)} = Mt$	M_g/M_e
Error	(r-1) (g-1)	S_{rg}	$\frac{S_e}{(r-1)(g-1)} = Me$	
Total	(rg-1)	$S_{(rg-1)}$		

Where r = Number of replications, g = Number of genotypes/Plant number, and M = Mean sum of square. The calculated "F" values were compared with the tabulated "F" values at 5 percent level of significance. If the calculated value is higher than the tabulated value, it will be considered significant. Critical difference (CD) for comparing the means of any two treatments will be calculated as: $SE(d) = \pm (2Me/r)^{1/2}$
 Critical Difference (CD) = $SE(d) \times t(5\%)$ value at error degrees of freedom. The calculation of predicted genetic advance at a selection intensity of 5 percent was performed using the formulas discussed in Table 2 [10], taking into account genotypic and phenotypic variances, environmental variances, and coefficients of variability.

Table 3.
Statistical analysis of the measured germination and growth traits.

3. Results

3.1 Assessment of genotypic and phenotypic variability in nursery seedlings

The study aimed to assess the variability in germination and seedling growth characteristics among different seed sources, taking into account both genetic and environmental factors. A sample of five mother trees was used for cone and seed collection, and the results are presented in Table 4.

The data in Table 4 indicate significant variation (p -value ≤ 0.05) in various characteristics among the seed sources. Notably, the survival rate, needle area, root length, and germination rate exhibited the highest levels of environmental diversity. This suggests that these traits are particularly influenced by environmental conditions.

Traits	Variance			Coefficient of variance			HBS	GA	GAPM	CD _(0.05)
	EV	GV	PV	ECV	PCV	GCV				
GC	6.29	75.6	81.9	4.04	14.6	14.0	0.92	17.1	27.6	1.96
GP	7.56	70.1	77.6	4.61	14.8	14.0	0.90	16.3	27.3	2.15
GE	2.80	4.37	7.18	4.88	7.81	6.10	0.61	3.35	9.76	1.31
GV	0.20	3.41	3.61	3.20	13.7	13.3	0.95	3.68	26.5	0.35
GS	0.10	0.74	0.84	10.3	29.1	27.2	0.88	1.65	52.3	0.25
SH	0.73	3.31	4.04	8.72	20.5	18.5	0.82	3.37	34.4	0.67
CD	0.06	1.16	1.21	8.13	37.9	37.0	0.95	2.15	74.2	0.18
NA	12.4	25.7	38.1	10.2	17.9	14.7	0.67	8.52	24.8	2.15
RL	7.59	16.8	24.4	17.4	31.2	25.9	0.69	6.97	44.1	2.75
SDW	0.01	0.04	0.05	24.3	49.1	42.6	0.75	0.34	75.9	0.09
SP	28.9	62.5	91.4	11.3	20.2	16.7	0.68	13.4	28.3	4.20

p-value (0.05) = <0.0001.

EV, Environment variance; PV, Phenotypic variance; GV, Genotypic variance; ECV, Environment coefficient of variance; PCV, Phenotypic coefficient of variance; GCV, Genotypic coefficient of variance, HBS, Broad-sense heritability; GA, Genetic advance; GAPM, Genetic advance as percent of mean; GC, Germination capacity; GP, Germination percent; GE, Germination energy; GS, Germination speed; GV, Germination value; SH, Seedling height; CD, Collar Diameter; NA, Needle area; RL, Root length; SDW, Seedling Dry weight; SP, Survival percentage.

Table 4.

Genetic parameters analysis of the *Pinus wallichiana* seedlings, irrespective of altitudinal ranges.

The study also revealed substantial variability in both genotypic and phenotypic characteristics, with germination capacity and plant survival showing the most significant variation. Additionally, the coefficient of variation for environmental, phenotypic, and genotypic components showed higher values for the dry weight of seedlings, indicating that this trait is influenced by a combination of genetic and environmental factors. On the other hand, collar diameter and germination value displayed the highest levels of broad-sense heritability, indicating a strong genetic component in these traits. Genetic advance and genetic gain were most prominent in germination capacity and germination percentage, whereas dry weight of seedlings and collar diameter showed the greatest potential for genetic improvement.

3.2 Assessment of genotypic and phenotypic variability across altitudinal gradients in nursery seedlings

Table 5 presents data illustrating significant variations (p -value ≤ 0.05) in germination and growth parameters across different altitudinal ranges. Environmental variance was notably high in survival percentage at altitude A₄, highlighting the influence of altitude on this particular trait. Altitude A₂ exhibited the highest genotypic and phenotypic variations in germination percentage, indicating the significance of altitude in shaping these characteristics. Furthermore, the coefficients of variance for environmental, genotypic, and phenotypic components were highest for the dry

	ALT	GC	GP	GE	GV	GS	SH	CD	NA	RL	SDW	SP
EV	A ₁	5.12	3.28	0.59	0.07	0.05	0.87	0.04	0.47	13.9	0.01	14.4
	A ₂	5.48	4.06	0.80	0.22	0.12	0.35	0.07	12.9	4.87	0.01	13.2
	A ₃	4.04	3.48	3.27	0.14	0.07	0.39	0.07	9.83	3.20	0.02	31.4
	A ₄	2.49	0.85	2.46	0.32	0.08	0.35	0.01	1.97	2.95	0.01	34.5
PV	A ₁	14.1	17.5	1.20	0.35	0.17	0.87	0.15	43.7	22.3	0.05	20.8
	A ₂	79.1	81.3	8.18	4.23	0.69	4.86	1.03	43.7	12.6	0.04	14.8
	A ₃	22.5	15.1	4.98	1.07	0.99	1.25	0.73	17.8	4.17	0.08	58.0
	A ₄	13.1	6.96	5.89	7.57	1.45	3.00	2.85	13.8	9.18	0.03	58.9
GV	A ₁	8.94	14.2	0.61	0.27	0.12	NA	0.11	43.2	8.48	0.04	6.42
	A ₂	73.6	77.3	7.38	4.01	0.57	4.50	0.96	30.8	7.75	0.03	1.60
	A ₃	18.4	11.6	1.71	0.93	0.92	0.86	0.67	7.95	0.97	0.06	26.6
	A ₄	10.6	6.11	3.43	7.25	1.37	2.64	2.83	11.8	6.23	0.02	24.4
ECV	A ₁	3.12	2.61	2.20	1.87	6.37	7.92	7.56	1.82	17.6	18.7	6.56
	A ₂	3.66	3.26	2.48	3.30	10.9	6.67	10.1	10.1	13.8	23.8	7.27
	A ₃	3.51	3.38	5.45	2.60	8.84	6.34	8.15	9.97	12.8	27.0	13.4
	A ₄	2.90	1.77	4.75	4.46	9.50	6.81	3.52	4.23	14.3	25.7	14.7
PCV	A ₁	5.17	6.01	3.14	4.06	12.1	7.90	14.5	17.6	22.3	52.0	7.89
	A ₂	13.9	14.6	7.92	14.61	25.7	24.7	38.9	18.6	22.2	42.4	7.70
	A ₃	8.28	7.05	6.73	7.28	33.2	11.3	27.2	13.4	14.6	56.9	18.2
	A ₄	6.66	5.06	7.35	21.57	41.0	19.9	52.5	11.2	25.2	40.3	19.2
GCV	A ₁	4.12	5.42	2.23	3.61	10.2	NA	12.3	17.5	13.8	48.5	4.38
	A ₂	13.4	14.2	7.52	14.2	23.3	23.8	37.6	15.6	17.4	35.1	2.53
	A ₃	7.50	6.18	3.94	6.79	32.0	9.38	25.9	8.96	7.02	50.1	12.3
	A ₄	5.99	4.74	5.61	21.10	39.8	18.6	52.4	10.4	20.8	31.1	12.3

	ALT	GC	GP	GE	GV	GS	SH	CD	NA	RL	SDW	SP
HBS	A ₁	0.64	0.81	0.51	0.79	0.72	NA	0.73	0.99	0.38	0.87	0.31
	A ₂	0.93	0.95	0.90	0.95	0.82	0.93	0.93	0.71	0.61	0.69	0.11
	A ₃	0.82	0.77	0.34	0.87	0.93	0.69	0.91	0.45	0.23	0.77	0.46
	A ₄	0.81	0.88	0.58	0.96	0.95	0.88	1.00	0.86	0.68	0.59	0.41
GA	A ₁	4.91	6.99	1.14	0.96	0.62	NA	0.57	13.5	3.69	0.40	2.90
	A ₂	17.1	17.7	5.31	4.02	1.40	4.21	1.95	9.60	4.50	0.28	0.86
	A ₃	8.01	6.16	1.58	1.86	1.91	1.58	1.60	3.88	0.98	0.46	7.20
	A ₄	6.03	4.77	2.91	5.43	2.34	3.15	3.46	6.56	4.24	0.20	6.56
GAPM	A ₁	6.77	10.1	3.28	6.59	17.9	NA	21.7	35.8	17.4	93.2	5.02
	A ₂	26.6	28.6	14.7	28.6	43.5	47.3	74.7	27.1	28.1	59.9	1.72
	A ₃	14.0	11.18	4.76	13.1	63.5	16.0	50.9	12.3	6.97	90.8	17.2
	A ₄	11.1	9.16	8.82	42.5	79.8	36.1	107	19.8	35.2	49.3	16.4
p-value (0.05)	A ₁	<0.0001	<0.0001	0.0008	<0.0001	<0.0001	0.4957	<0.0001	<0.0001	0.0092	<0.0001	0.0269
	A ₂	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.2344
	A ₃	<0.0001	<0.0001	0.0163	<0.0001	<0.0001	<0.0001	<0.0001	0.0027	0.0709	0.05	0.0021
	A ₄	<0.0001	<0.0001	0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.005
CD (0.05)	A ₁	3.14	2.52	1.07	0.38	0.31	1.30	0.28	5.18	0.95	0.11	5.27
	A ₂	3.25	2.80	1.25	0.65	0.49	0.83	0.37	3.07	4.98	0.15	5.05
	A ₃	1.61	1.50	1.45	0.30	0.21	0.50	0.21	1.44	2.52	0.11	4.49
	A ₄	2.19	1.28	2.18	0.79	0.39	0.82	0.16	2.39	1.95	0.14	8.16
EV, Environment variance; PV, Phenotypic variance; GV, Genotypic variance; ECV, Environment coefficient of variance; PCV, Phenotypic coefficient of variance; GCV, Genotypic coefficient of variance; HBS, Broad-sense heritability; GA, Genetic advance; GAPM, Genetic advance as percent of mean; ALT, Altitude; GC, Germination capacity; GP, Germination percent; GC, Germination capacity; GE, Germination energy; GS, Germination speed; GV, Germination value; SH, Seedling height; CD, Collar diameter; NA, Needle area; RL, Root length; SDW, Seedling dry weight; SP, Survival percentage												

Table 5. Genetic parameter analysis of germination and growth traits of *Pinus wallichiana* along different altitudinal ranges.

weight of seedlings at altitude A_3 , suggesting that this trait is influenced by both genetic and environmental factors, particularly at this altitude. Collar diameter at altitude A_4 displayed the greatest degree of heritability, emphasizing the strong genetic influence on this trait. Needle area at altitude A_1 also showed a high level of heredity. The study revealed that altitude A_2 had the most significant genetic enhancement in germination percentage compared to other altitudes, while the most substantial genetic improvement was observed in the dry weight of seedlings at altitude A_1 . The disparity between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) across all traits underscores the interplay between genetic and environmental factors in shaping these characteristics. This study highlights the pronounced influence of environmental factors in the A_1 altitudinal range on seedling growth and development, emphasizing the importance of considering both genetic and environmental elements in the analysis of these traits.

4. Discussion

The findings of this study suggest that root length, survival percentage, and germination percentage were predominantly influenced by site-specific and environmental factors. While heredity plays a significant role, it is clear that site conditions exerted a greater influence on these traits. To gain a comprehensive understanding of the potential for selection in the studied material, it is essential to examine heritability and expected genetic gain together, as these factors collectively provide a more reliable and credible assessment [10]. Relying solely on heredity can be limiting, and incorporating both heritability estimates and genetic gain into predictions for the future selection of optimal genotypes offers a more advantageous approach [11].

Previous research on *Grewia optiva* [12] and *Celtis australis* [13] has documented higher heritability estimates and statistically significant genetic effects on seed weight increase. Furthermore, significant findings in *Albizia chinensis* [14], *Celtis australis* [13], and *Pinus wallichiana* [15] align with the outcome of our study, supporting the influence of genetics on these traits.

Our investigation revealed that genotypic coefficients of variance (GCV) were consistently higher than their corresponding phenotypic coefficients of variance (PCV), indicating that the genetic component played a more substantial role in trait variation at the genotypic level. This finding is in agreement with other studies, such as [16], who observed inter- and intraspecific genetic variation in seedling drought tolerance in different pine species. Similarly, [17] identified distinct patterns in loci associated with phenotypic traits in loblolly pine, suggesting a genetic basis for these traits. Genetic correlations tended to be higher than phenotypic correlations, indicating that phenotypic correlations can serve as fair estimates of their genetic counterparts in many scenarios [18]. Additionally, a negative genetic correlation between height growth and other traits in jack pine, emphasizing the importance of considering multiple traits in selection approaches [1]. GCV is a superior indicator of the genetic relationships among traits in pines [19].

This phenomenon may be attributed to genotype–environment interaction or the influence of environmental elements on trait expression. Our findings align with similar observations in full-sibling offspring of specifically chosen clones of *Populus deltoides* [20] and the outcomes of studies on willow clones [21],

collectively suggesting that GCV provides a more accurate representation of genetic relationships among traits than PCV. The results of studies conducted by various scientists [11, 22, 23] are consistent with these findings. The observation of a notable level of agreement between phenotypic and genotypic coefficients of variation suggests substantial diversity in genotypes, indicating the potential for improvement in these specific characteristics. This underscores the importance of considering genotypic values when studying trait inheritance and selection in plant populations.

5. Conclusion

In conclusion, our research uncovers substantial genetic diversity within *Pinus wallichiana* genotypes. While environmental factors predominantly dictate survival rates, our study underscores the influential role of genetic and phenotypic variance, particularly in shaping germination capacity and, notably, germination percentage. Among these traits, germination percentage emerges as the most genetically diverse, suggesting its potential as a prime target for selective breeding initiatives. Furthermore, our findings highlight altitudes A_1 and A_2 as regions where heritability plays a prominent role in governing germination and growth traits, indicating their relative resilience to environmental influences within these altitudinal ranges. Consequently, focusing on trait improvement within the lower (1800–2100 m.a.s.l.) and mid-altitudinal (2100–2400 m.a.s.l.) zones appears strategically advantageous. The application of these insights in selective breeding holds promise for bolstering the adaptability and vitality of *Pinus wallichiana* populations. As we look ahead, our findings offer valuable guidance for sustainable forest management, conservation, and breeding programs, particularly in diverse altitudinal contexts, fostering the long-term resilience of this important species.

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Conflict of interest

A researcher has a significant financial interest (publication fee).

A. Appendix

See **Table 6.**

See **Table 7.**

See **Table 8.**

SOV	Df	Germination capacity			Germination percent			Germination energy			Germination value			Germination speed		
		SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal
Genotype	59.00	13750.1	233.05	37.0	12849.0	217.78	28.81	939.70	15.93	5.68	616.00	10.44	52.91	136.70	2.32	22.19
Replication	2.00	167.98	83.99	13.34	742.84	371.42	49.14	932.70	466.35	166.37	14.52	7.26	36.80	0.35	0.17	1.65
Error	118.00	742.73	6.29		891.85	7.56		330.77	2.80		23.29	0.20		12.32	0.10	
Total	179.0	14660.8			14483.7			2203.2			653.82			149.37		
SOV	Df	Seedling height			Collar diameter			Root length			Needle area			Seedling dry weight		
		SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal
Genotype	59.00	7.15	0.12	10.21	208.30	3.53	63.28	3416.31	57.90	7.63	5274.71	89.40	7.20	7.15	0.12	10.21
Replication	2.00	0.04	0.02	1.68	0.72	0.36	6.43	755.97	377.98	49.80	78.41	39.20	3.16	0.04	0.02	1.68
Error	118.00	1.40	0.01		6.58	0.06		895.61	7.59		1465.84	12.42		1.40	0.01	
Total	179.0	8.59			215.60			5067.9			6818.9			8.59		
Survival Percentage																
SOV	Df	SS	MSS	F cal												
Genotype	59.00	12766.6	216.38	7.49												
Replication	2.00	1101.90	550.95	19.07												
Error	118.0	3409.73	28.90													
Total	179.0	17278.2														

Table 6.
 ANOVA for nursery traits in *Pinus wallichiana* seedling.

Altitudes	SOV	Df	Germination capacity			Germination percent			Germination energy			Germination value			Germination speed		
			SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal
1800-2100 masl (A1)	Genotype	14	447.07	31.933	6.24	641.97	45.855	13.963	33.83	2.416	4.082	12.566	0.898	12.107	5.886	0.420	8.745
		2	100.005	50.00	9.771	578.7	289.03	88.01	163.84	81.918	138.390	8.664	4.332	58.434	0.262	0.131	2.724
	Error	28	143.293	5.118		91.956	3.284		16.574	0.592		2.076	0.074		1.346	0.048	
	Total		690.363			1311.9			214.23			23.306			7.493		
Germination capacity																	
2100-2400 masl (A2)	Genotype	14	3168.167	226.29	41.328	3302.642	235.90	58.155	321.148	22.939	28.567	171.455	12.247	56.812	25.487	1.820	14.783
		2	43.318	21.659	3.956	210.356	105.178	25.929	613.53	306.76	382.030	1.626	0.813	3.772	0.039	0.019	0.157
	Error	28	153.319	5.476		113.580	4.056		22.484	0.803		6.036	0.216		3.448	0.123	
	Total		3364.80			3626.578			957.162			179.117			28.973		
Germination capacity																	
2400-2700 masl (A3)	Genotype	14	830.703	59.336	14.676	536.968	38.355	11.029	117.691	8.407	2.569	41.060	2.933	21.419	39.764	2.840	40.207
		2	168.076	84.038	20.785	230.559	115.279	33.148	100.70	50.350	15.384	2.659	1.330	9.711	0.241	0.121	1.709
	Error	28	113.209	4.043		97.376	3.478		91.641	3.273		3.834	0.137		1.978	0.071	
	Total		1111.988			864.902			310.031			47.553			41.984		
Germination capacity %																	
>2700masl (A4)	Genotype	14	479.44	34.245	13.761	268.412	19.172	22.572	178.622	12.759	5.186	308.98	22.070	68.139	58.514	4.180	53.766
		2	119.810	59.905	24.072	289.016	144.51	170.135	185.821	92.911	37.764	3.847	1.923	5.938	3.177	1.588	20.431
	Error	28	69.681	2.489		23.782	0.849		68.888	2.460		9.069	0.324		2.177	0.078	
	Total		668.93			581.210			433.331			321.899			63.867		

Table 7.
ANOVA for germination traits in *Pinus wallichiana* Seedlings among different altitudinal ranges.

Altitudes	SOV	Df	Root length			Seedling height			Collar diameter			Seedling dry weight			Needle area			Survival Percent		
			SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal	SS	MSS	F cal
1800-2100m asl (A1)	Genotype	14	550.219	39.301	2.833	11.968	0.855	0.981	5.042	0.36	8.988	1.879	0.134	21.17	1821.78	130.13	277.78	470.796	33.628	2.342
	Replication	2	75.204	37.602	2.710	23.941	11.971	13.74	0.134	0.07	1.676	0.02	0.01	1.877	20.833	10.417	22.23	182.221	91.110	6.345
	Error	28	388.470	13.874		24.402	0.872		1.122	0.04		0.178	0.01		13.117	0.468		402.05	14.359	
	Total		1013.89			60.312			6.298			2.08			1855.73			1055.07		
2100-2400m asl (A2)	Genotype	14	393.850	28.132	5.777	194.09	13.86	39.32	41.49	2.96	42.294	1.283	0.09	7.539	1473.56	105.25	8.183	251.848	17.989	1.364
	Replication	2	523.209	261.60	53.72	54.299	27.15	76.99	0.589	0.29	4.201	0.01	0.01	0.142	172.800	86.40	6.717	264.662	132.33	10.03
	Error	28	136.347	4.870		9.873	0.353		1.962	0.07		0.34	0.01		360.150	12.863		369.289	13.189	
	Total		1053.41			258.27			44.04			1.627			2006.51			885.799		
2400-2700m asl (A3)	Genotype	14	85.570	6.112	1.908	41.432	2.959	7.551	28.917	2.07	31.364	2.921	0.21	11.29	471.486	33.678	3.426	1557.76	111.269	3.545
	Replication	2	75.881	37.941	11.84	15.569	7.784	19.86	1.242	0.62	9.428	0.08	0.04	2.248	323.408	161.70	16.448	599.384	299.69	9.549
	Error	28	89.696	3.203		10.974	0.392		1.844	0.07		0.517	0.02		275.267	9.831		878.787	31.385	
	Total		251.148			67.975			32.00			3.521			1070.16			3035.93		
>2700m asl (A4)	Genotype	14	302.950	21.639	7.331	115.94	8.281	23.52	119.16	8.512	664.86	0.79	0.06	5.375	524.156	37.440	18.968	1509.37	107.81	3.126
	Replication	2	280.123	140.06	47.45	53.846	26.92	76.5	0.049	0.02	1.933	0.00	0.00	0.02	323.408	161.70	81.925	849.636	424.82	12.32
	Error	28	82.647	2.952		9.857	0.352		0.358	0.01		0.29	0.011		55.267	1.974		965.595	34.486	
	Total		665.720			179.64			119.57			1.09			902.831			3324.60		

Table 8.
ANOVA for growth traits in *Pinus wallichiana* Seedlings among different altitudinal range.

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