

Evaluation of Genetic Variability and Correlation in Pod and Seed Traits of *Pongamia Pinnata (L.)* Pierre. Germplasm for Genetic Tree Improvement

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Abstract

Pongamia pinnata is a leguminous multipurpose tree species having enormous potential of producing high seed oil that could be as a source of biofuel. The collection of pods with higher seed quality characters is much important for Genetic tree improvement program for production of elite germplasm for nursery and plantation. A total of 24 candidate plus trees (RAKs) of *Pongamia pinnata* (L.) Pierre were selected to elucidate their variation and diversity based on twelve quantitative traits (4 pod traits, 5 seed traits of parent trees and 3 progeny traits) during 2004-2007. The results show that, RAK-5 had maximum for six traits viz pod length (65.6 mm), 100-pod weight (542.4 g), seed length (27.9 mm), seed breadth (17.4 mm), 100-seed weight (217.9 g) and plant height (164.3 cm). Lowest 100-pod and seed weight were recorded in RAK-7 (231.0 g) and RAK-24 (106.1 g). The maximum volume index was recorded in RAK-17. There was fair difference between genotypic coefficients of variation and phenotypic coefficients of variation for all traits except progeny traits. All the pod and seed traits showed high heritability and progeny growth traits had moderate heritability. The 100-pod weight exhibited highest heritability (more than 98.4%) followed by 100-seed weight (96.9%). The 100-pod weight and 100-seed weight expressed high heritability (98.4%, 96.9%), accompanied with high genetic advance (46.0%, 34.9%). Volume index expressed moderate heritability (47.4%), accompanied with high genetic advance (48.4%). It is revealed that the existence of substantial variation can be utilized for genetic resource conservation and further genetic tree improvement programmers of the species.

Keywords: *Pongamia pinnata*; Variability; Heritability; Genetic advance; Correlation; Path analysis

Introduction

Pongamia pinnata (L.) is an important species which have big potential for that and can be planted all over tropics. But there is very little information available about genetics, physiology and cultivation practices of Pongamia pinnata (L.) Pierre, synonymously known as Pongamia glabra Vent. Derris indica (Lam) Bennett. Millettia novoguineensis Kane & Hat and Cytisus pinnaus L. is an arboreal legume, belonging to the subfamily Papilionoideae and specifically the tribe Millettia. This medium-size tree, being indigenous to the Indian subcontinent and south-east Asia (Malaysia and Indonesia), have been successfully introduced to humid tropical regions of the world as well as parts of Australia, New Zealand, China and the USA [1]. Historically, this plant has been used in India and neighboring regions as a source of traditional medicines, green manure, timber, fish poison and fuel. The mature tree can withstand water logging and slight frost, and highly tolerant to salinity. Pongamia can help in restoration of fertility especially in degraded soils owing to its nitrogen fixing ability. Extracts from the plant are known to have the medicinal properties and effects on a wide array of organisms including insect and pests, mollusks and nematodes [2,3]. Pongamia seed oil resembling ground nut oil (Arachis hypogaea L.) with its fatty acid composition and high oleic acid content (45% - 70% w.t.) is a source for a number of bioactive compounds including flavonoids and furan-flavonoids, which has medicinal uses for rheumatism, skin diseases, etc. [4]. More importantly, P. pinnata has recently been recognized as a viable source of oil for the burgeoning biofuel industry [5]. Added to this, the low temperature operability of the corresponding methyl esters is superior to that of Jatropha oil because of the relatively high percentage of oleic acid in karanj oil [6]. P. pinnata contributes significantly as a source of nonedible oil feedstock and is capable of growing on marginal lands [7]. However, for meeting the future demands of feedstock for bio-diesel, it is important to establish extensive plantations from elite source. Although, it may look promising, it lacks the improved germplasm for large scale plantation. Seed polymorphism in *P. pinnata* has been found to play an important role in seed germination, seedling survival and growth [8]. The knowledge of genetic variability and correlation between pod and seed traits linked with progeny field performance at early stage among the collected germplasm is considered to provide necessary information for further genetic improvement of the species in maximizing the yield. The challenging task is to screen the naturally available genetic variation by evaluation of progeny traits for higher productivity. The progenies with better traits, not only have better adaptability to the study site, but also perform better for fruiting and seed oil yield, which consecutively provides opportunity for mass clonal propagation. Considering the present day scenario, an effort has been made to evaluate the extent of genetic variability, correlation among pod and seed traits with progeny traits as scope for further genetic improvement program.

Materials and Methods

Study site and sampling

An extensive wild germplasm exploration survey was conducted to identify the high yielding Candidate plus Trees RAKs (Rahuri Karanja Tree) of *P. pinnata* at fruiting stage from different predominant naturalized locations from 10 Districts of Western Maharashtra, India

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Received December 17, 2014; Accepted July 25, 2015; Published July 29, 2015

Citation: Gawali A, Wagh R, Sonawane C (2015) Evaluation of Genetic Variability and Correlation in Pod and Seed Traits of *Pongamia Pinnata (L.)* Pierre. Germplasm for Genetic Tree Improvement. Forest Res 4: 149. doi:10.4172/2168-9776.1000149

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viz Ahmednagar, Pune, Nasik, Sholapur, Sangli, Satara, Kolhapur, Dhule Nandurbar and Jalgaon. Since P. pinnata was grown as wild and had no definite geometry with neighboring trees for comparison, the selection was made by using single tree selection method based on phenotypic assessment of characters of economic importance viz. yield potential, crown spread, total height, girth at breast height, age of the tree, free from pest and diseases, seed size and seed weight. A total of 24 RAKs (Rahuri Karanja morphologically superior trees) covering a latitude and longitudinal range from N 16° 42' to 21° 23' and E 74° 16' to 74° 16' E, were selected. Three kilograms of mature pods from each RAK were collected following a random sampling procedure from all the four directions of the crown of each selected tree during fruiting season in April-June, 2004. The observations for 12 quantitative traits (4 pod traits, 5 seed traits of parent trees and 3 progeny traits) were recorded at AICRP on Agroforestry Department of Botany MPKV, Rahuri. 2004-2007. The area of field trial MPKV, Rahuri under (latitude: 19° 23'N, longitude: 74° 42 'E, and altitude: 715 m, m.s.l. approx.) is a Semi-Arid Tropics of climate receiving mean annual rainfall of 561.6 mm with 44 annual rainy days for, Annual minimum and maximum temperature is 12.7°C and 40.2°C, respectively, with lowest temperature in December and highest temperature in May every year. Soils of the study area are Vertisol. The pods were cleaned, dried and stored in muslin bags at ambient conditions. All pods were dried under similar temperature and humidity conditions to reach constant weight. A total of 300 healthy pods (hundred in each replication) were randomly selected and observations for four pod traits viz. pod length, pod width, pod thickness and 100-pod weight were measured. Samples of 300 seeds were randomly collected from each RAK to make three replications of each 100-seed. Measurement of morphometric traits viz seed length, seed breadth, 100 seed weight and aspect ratio. Pod and Seeds parameter were measured as mentioned in Table 1.

The progenies trials

Seeds of all the RAKs were uniformly pre-treated by soaking in cold water for 24 h. Three hundred pre-treated seeds of each RAK were directly sown in polythene bags of dimension of 30 cm \times 12 cm \times 10 cm filled with potting mixture of soil, sand and farmyard manure (2:1:1) in three replicates of each 100-seed during July 2004. Samples of 10 one-year-old seedlings were planted in the field (pit size 45 cm \times 45 cm \times 45 cm) in July 2005 in a randomized complete block design with 3 replications at spacing 6 m \times 6 m for field evaluation at AICRP on Agroforestry Farm field. At juvenile stage (24 months after planting (MAP)), observation were recorded on the trial for plant height (m), collar diameter (cm), at periodical bimonthly intervals viz., 2 months after planting (MAP), 4 MAP, 6 MAP, etc.

The data recorded at 24 MAP alone were considered for variability, correlation studies. Volume index was calculated as mentioned in Table

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Data analysis

The pod and seed parameters and progeny traits were analyzed using Analysis of variance (ANOVA) and Duncan Multiple Range Test (DMRT) to understand the significant difference among the pod, seed and progeny trait of RAKs under consideration [9]. The phenotypic variation for each trait was partitioned into components due to genetic (hereditary) and non-genetic (environmental) factors and estimated using the following formula [10]:

$$V_{p} = M_{SG} / r$$
⁽¹⁾

$$V_{g} = (M_{SG} - M_{SE}) / r$$
⁽²⁾

$$Ve = M_{SE}$$
(3)

Where, M_{sG} , M_{sE} and r are the mean squares of RAKs, mean squares of error and number of replications, respectively. The phenotypic variance (V_p) is the total variance among phenotypes. The genotypic variance (V_p) is the part of the phenotypic variance that can be attributed to genotypic differences among the phenotypes, and the error variance (V_e) is part of the phenotypic variance due to environmental effects. To compare the variation among traits, phenotypic (P_{CV}) and genotypic (G_{CV}) coefficients of variation were computed according to the method suggested by Burton [11]:

$$P_{\rm CV} = (\sqrt{V_{\rm p}}/X) \times 100 \tag{4}$$

$$G_{\rm CV} = (\sqrt{V_{\rm g}}/X) \times 100 \tag{5}$$

Where, V_p , V_g and X are the phenotypic variance, genotypic variance and grand mean for each pod and seed-related trait, respectively. Broad sense heritability (h^2B) was calculated according to Allen GS [12] as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p). Genetic advance (GA) was estimated in accordance with Johanson et al. [10] as follows:

$$G_{A} = K \times h^{2}B \times \sqrt{V_{p}}$$
(6)

$$G_{\rm A} = (G_{\rm A}/X) \times 100 \tag{7}$$

Where, *K* is the selection differential (2.06 for selecting 5% of the genotypes); GA is as % of the mean. Phenotypic (rp) and genotypic (rg) correlations were further computed to examine inter-character relationships among seed and seedling traits following Goulden [13] as:

$$V_{\rm p} = Co_{\rm vp} (x1, x2) / [V_{\rm p}(x1) \times V_{\rm p}(x2)]^{\frac{1}{2}}$$
(8)

S. No.	Traits	Methods
1	Pod length	Length of the pod at longest side measured using vernier caliper, average value was computed and expressed in mm.
2	Pod width	Length of the pod at shortest side measured using vernier caliper, average value was computed and expressed in mm.
3	Pod thickness	Thickness of the pod measured using vernier caliper, average value was computed and expressed in mm.
4	100 – pod weight	Weight of 100-pods weighed on electronic balance and average value was calculated and expressed in grams.
5	Seed length	Length of the seed at longest side, measured in mm.
6	Seed breadth	Length of the object at shortest side, measured in mm.
7	Aspect ratio	Ratio of length divided by breadth.
8	100 – seed weight	Weight of 100 seeds weighed on electronic balance, measured in grams.
9	Pod/seed ratio	Ratio of 100-pod weight divided by 100-seed weight.
10	Plant height	Length of the plant from ground level to tip in cm.
11.	Collar diameter	Stem diameter near the ground level in cm.
12.	Volume index	[Collar diameter (cm)] ² × Plant height (cm)]

Table 1: Methodology followed for measuring pod and seed traits of Pongamia pinnata

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$$r_{\rm g} = Co_{\rm vg} (x1, x2) / [V_{\rm g}(x1) \times V_{\rm g}(x2)]^{\frac{1}{2}}$$
(9)

Where, Co_{vp} and Co_{vg} are phenotypic and genotypic covariances for any two traits x1 and x2, respectively, and V_p and V_g are the respective phenotypic and genotypic variances for those traits. Path coefficient analysis was done using genotypic correlation coefficients following [14].

Results and Discussion

Variability in pod and seed traits

Genetic improvement depends upon the nature and magnitude of existing variability and also on the degree of transmission of traits or heritability [15]. Seed size may vary due to both internal (maternal, hereditary) and external [environmental] conditions operating at the time of seed development [16]. This differential development might have an adaptive advantage in local edapho-climatic condition. Seed weight, depends on reserve food material, which is produced as a result of double fertilization (endosperm) and is dominated by the maternal traits, also influenced by the nutrient availability at the time of seed setting and environmental factors [12]. Embryo development and its physiological function are contributed by the maternal as well as by paternal (pollen grain) traits in the species. Analysis of variance for pod, seed and progeny traits reveled that there was significant variation among RAKs (Table 2). Seeds from different RAKs of P. pinnata varied significantly in respect of pod and seed traits at p= 0.05 level of significance. Variability of RAK-5 had maximum for six traits viz, pod length (65.6 mm), 100-pod weight (542.4 g), seed length (27.9 mm), seed breadth (17.4 mm), 100-seed weight (217.9 g) and plant height (164.3 cm). However, maximum volume index was recorded in RAK-17 (1 518.8 cm3), followed by RAK-3 (1 489.5 cm3), RAK-10 (1 486.8 cm3), RAK-19 (1 435.8 cm3) and RAK-14 (1 412.8 cm3). Lowest 100pod and 100-seed weight were recorded in RAK-7 (231.0 g) and RAK-24 (106.1 g) respectively. The difference recorded may be in response to different intensities of natural selection pressure acting upon these traits in their natural habitat. In a leguminous species the pod, seed and germination traits were considered largely under maternal influences but were strongly controlled by micro and macro habitats, besides the age and general health of the parent trees [17]. Such variations in relation to habitat have also been reported in *P. pinnata* by Kaushik, et al. [18] in Haryana, Srinivasan, et al. [3] in Tamil Nadu, and Mukta N et al., Murthy et al. [19,20] in Andhra Pradesh, India. P. pinnata being indigenous to Indian subcontinent with wide diversity form the basic resource for further improvement and breeding program at global level. The results of the present study will be valuable for seed zone delineations, strategies for conservation of genetic variation, prospects of improvement and assessment of the potential of locally adapted seed source. Hence, in the present study, various RAKs exhibiting significant variability in pod and seed traits could be attributed to fact that the species grows over a wide range of rainfall, temperature and soil type, indicating the marked difference in selection pressure. Habitat influences on pod and seed traits have also been reported in number of tree species like Jatropha curcas [21-23], Madhuca latifolia

		Po	d traits				Seed traits	5	Progeny traits			
	Length (mm)	Width (mm)	Thickness (mm)	100-Pod weight (g)	Length (mm)	Breadth (mm)	Aspect ratio	100-seed weight (g)	Pod/ seed ratio	Height (cm)	Collar diameter (cm)	Volume index (cm³)
RAK-1	56.7	26.4	11.5	357.8	24.5	16.9	1.5	151.5	2.4	125.5	2.7	929.9
RAI-2	49.1	23.2	9.8	276.3	20.3	16.2	1.3	146.1	1.9	148.7	3.0	1386.1
RAK3	55.9	20.4	12.0	358.1	23.4	15.2	1.5	123.0	2.9	140.2	3.2	1489.5
RAK-4	51.0	26.6	11.5	407.5	25.6	17.6	1.5	171.5	2.4	147.0	2.8	1166.4
RAK-5	65.6	23.7	11.7	542.4	27.9	17.4	1.6	217.9	2.5	164.3	2.9	1435.8
RAK-6	58.2	25.0	12.7	474.4	26.6	17.5	1.5	165.8	2.9	125.7	2.4	698.9
RAK-7	56.7	26.4	11.5	357.8	24.5	16.9	1.5	151.5	2.4	125.5	2.7	929.9
RAK-8	47.7	19.8	12.3	284.6	23.5	16.2	1.5	135.3	2.1	146.5	2.9	1230.0
RAK-9	50.0	23.7	12.0	352.4	24.1	17.3	1.4	154.0	2.3	135.2	2.9	1128.2
RAK-10	65.7	23.6	11.0	451.8	26.8	15.2	1.8	174.8	2.6	149.0	3.2	1486.8
RAK-11	57.7	23.1	12.1	358.9	25.6	14.4	1.8	183.7	2.0	145.2	3.0	1352.3
RAK-12	58.5	26.0	10.5	337.3	24.9	15.1	1.7	156.1	2.2	126.2	2.6	882.2
RAK-13	50.3	23.4	9.7	274.8	24.0	14.6	1.6	128.9	2.1	112.0	1.9	445.9
RAK-14	44.7	18.7	10.3	233.3	23.6	15.0	1.6	125.9	1.9	123.0	2.3	703.4
RAK-15	48.5	21.3	11.8	303.1	23.7	15.2	1.6	135.7	2.2	125.2	1.9	482.4
RAK-16	45.1	18.7	11.0	257.6	23.6	14.4	1.6	121.6	2.1	134.3	2.6	973.9
RAK-17	48.8	27.1	10.1	329.2	22.2	17.5	1.3	148.5	2.2	150.3	3.2	1518.7
RAK-18	47.4	21.1	11.6	366.5	25.6	14.6	1.8	137.2	2.7	122.5	2.5	795.3
RAK-19	50.0	20.3	12.0	356.4	24.1	16.6	1.5	161.5	2.2	128.8	2.4	837.2
RAK-20	43.2	20.4	10.7	333.3	23.7	14.2	1.7	185.0	1.8	141.5	3.0	1298.3
RAK-21	48.2	22.8	10.7	343.5	24.3	14.5	1.8	144.7	2.4	136.8	2.7	1049.4
RAK-22	51.5	24.9	11.7	423.1	24.4	16.6	1.5	176.9	2.4	146.0	3.1	1412.8
RAK-23	44.4	24.3	11.3	296.7	22.7	15.3	1.5	144.7	2.1	116.2	2.2	629.9
RAK-24	49.1	23.2	9.8	276.3	20.3	16.2	1.3	146.1	1.9	148.7	3.0	1386.1
mean	51.4	22.9	11.2	341.8	24.2	15.7	1.6	150.5	2.3	132.6	2.6	994.5
SEM	0.7	0.4	0.2	5.7	0.4	0.1	0.03	2.7	0.1	7.3	0.3	206.0
CD 5 %	2.1	1.1	0.5	16.7	1.2	0.4	0.08	7.8	0.2	21.3	0.7	599.5

Table 2: Mean performance of selected genotypes for pod and seed traits in Pongamia pinnata.

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[24] and Pongamia pinnata [23].

Genetic variability and correlation studies

The success of tree breeding programme depends largely on the type and extent of genetic variability present in the base population, which is measured by different population parameters including genotypic and phenotypic variations and genotypic and phenotypic coefficient of variation [25]. The genetic estimates of pod, seed and progeny growth performance are shown in Table 3. There were fair difference between genotypic coefficients of variation and phenotypic coefficients of variation for all traits except progeny traits. All the pod and seed traits showed high heritability and progeny growth traits had moderate heritability. The 100-pod weight exhibited highest heritability (more than 98.4%) followed by 100-seed weight (96.9%). The 100-pod

weight and 100-seed weight expressed high heritability (98.4%, 96.9%), accompanied with high genetic advance (46.0%, 34.9%). Volume index expressed moderate heritability (47.4%), accompanied with high genetic advance (48.4%). In general, the genotypic correlation coefficient values were higher than corresponding phenotypic values (Table 4). The variation among genotypes is commonly used as an estimate of total genetic variation to calculate the degree of genetic control for a particular trait [26]. Marginal difference between PCV (phenotypic coefficients of variation) and GCV (genotypic coefficients of variation) and high estimates of heritability (broad sense) for all pod and seed traits revealed the heritable nature of variability present. Relatively high value of genotypic variance resulted in high estimates of heritability, contributing to the high genetic gains in twelve quantitative traits (4 pod traits, 5 seed traits and 3 progeny traits). Gains from tree breeding programs depend on the type and extent of genetic variability. The trait

	Traits	Genotypic Variation	Phenotypic Variation	Heritability (%)	GA (%) of mean
	Length (mm)	12.1	12.3	96.2	24.4
Pod traits	Width (mm)	11.5	11.8	94.6	22.9
Poulialts	Thickness (mm)	7.8	8.2	89.4	15.2
	100-pod weight (g)	22.5	22.7	98.4	46.0
	Length (mm)	6.6	7.2	82.6	12.3
	Breadth (mm)	8.2	8.4	96.8	16.7
Seed traits	Aspect ratio	10.4	11.0	90.4	20.4
	100 -seed weight (g)	17.2	17.5	96.9	34.9
	Pod – seed ratio	12.7	13.4	89.9	24.7
	Plant height (cm)	11.5	14.9	58.9	18.1
Progeny traits	Collar diameter (cm)	15.9	23.3	46.7	22.4
	Volume index (cm ³)	34.1	49.5	47.4	48.4

Table 3: Genetic estimates of pod, seed and progeny traits in Pongamia pinnata.

Traits		Pod width	Pod thickness	100-Pod weight	Seed length	Seed breadth	Aspect ratio	100-seed weight	Pod–Seed ratio	Plant Height	Collar Diameter	Volume index
Pod length	Р	0.44 [*]	0.22	0.74**	0.64**	0.36	0.09	0.57**	0.49*	0.43 [*]	0.38	0.43 [*]
	G	0.45 [*]	0.21	0.73**	0.61 ^{**}	0.35	0.11	0.55**	0.48 [*]	0.32	0.27	0.29
Pod width	Р		-0.19	0.37	0.05	0.61**	-0.46*	0.36	0.11	0.11	0.13	0.15
	G		-0.18	0.37	0.07	0.58**	-0.41 [*]	0.35	0.12	0.11	0.12	0.12
Pod thickness	Р			0.51**	0.54**	0.20	0.19	0.29	0.55**	0.21	0.21	0.16
	G			0.49	0.50 [*]	0.18	0.20	0.27	0.51**	0.20	0.15	0.13
100-Pod weight	Р				0.79**	0.52**	0.07	0.82**	0.63**	0.66**	0.59**	0.60**
	G				0.73**	0.50**	0.08	0.81**	0.62**	0.51**	0.40*	0.41 [*]
Seed length	Р				0.61 ^{**}	0.74**	-0.24	0.65**	0.52**	0.53**	0.38	0.40*
	G				0.58**	0.71**	-0.18	0.60**	0.46*	0.38	0.26	0.28
Seed breadth	Р					0.08	0.56**	0.59**	0.57**	0.24	0.09	0.09
	G					0.07	0.61**	0.53**	0.51**	0.22	0.18	0.16
Aspect ratio	Р						0.08	0.45*	0.23	0.51 [™]	0.41 [*]	0.42 [*]
	G						0.07	0.45 [*]	0.20	0.38	0.28	0.29
100-seed weight	Р							-0.01*	0.18	-0.28	-0.29	-0.30
	G							-0.01 [*]	0.19	-0.17	-0.11	-0.12
Pod-Seed ratio	Р								0.09	0.78**	0.67**	0.69**
	G								0.04	0.60**	0.47 [*]	0.49 [*]
Plant Height	Р									0.11	0.18	0.16
	G									0.08	0.11	0.09
Collar Diameter	Р										0.96**	0.97**
	G										0.84**	0.89**
												0.99**
	Р											0.97**

Notes: *significant at p=0.05, **significant at p=0.01

Table 4: Genotypic (G) and phenotypic (P) correlation matrix of pod, seed and progeny traits in Pongamia pinnata.

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and 100-pod weight expressed positive significant correlation at both genotypic and phenotypic levels with plant height (rg= 0.66, rp= 0.51), collar diameter (0.59, 0.40) and volume index (0.60, 0.41) at 24 MAP (Months after sowing) respectively. However, pod length (0.43) and seed breadth (0.42) expressed positive significant correlation only at genotypic level with volume index at 24 MAP. Path analysis of pod, seed and progeny growth traits was carried out to unlock the direct and indirect contributions of pod, seed and progeny growth characters on volume index at 24 MAP. The seed breadth had the highest direct (2.18) and indirect effect on volume index through pod width (1.32) and 2D surface area (1.62). Though 100-seed weight was highly significantly correlated with volume index at 24 MAP, the direct effects were less.

In the present study, the genotypic coefficients of variation and the genetic gain were found to be comparatively higher for important traits such as volume index, 100-pod and 100-seed weight. The trait for volume index may be changed considerably by selecting the superior 5% of the genotypes. High heritability's accompanied by high genetic advance for growth parameters have been reported in other tree species like Jatropha curcas [21,22]; indicating possibility of genetic improvement in growth parameters. The ultimate goal of the tree improvement is to improve growth and yield traits of tree species. Growth and yield traits are complex and the product depends on the interplay of many physiological and morphological attributes, hence improvement based on performance of tree species alone might prove to have less effective. In genetic improvement of growth and yield traits of P. Pinnata, clear understanding of the relationships among different pod, seed and growth traits is very essential. As variation among clones is used for estimation of genetic variation and genetic gain, co-variance estimates between traits can be used to estimate genetic correlations between the traits [27]. Correlation shows the extent of association between seed traits, which may form additional criteria for selection in breeding program. Correlated quantitative traits are of a major interest in an improvement program, as the improvement of one character may cause simultaneous correlated changes in the other characters. Genotypic and phenotypic correlation coefficients between various characters revealed that magnitude of correlation coefficient at genotypic level was higher than their corresponding phenotypic coefficient of correlations. The genotypic correlation is an estimated value, whereas, phenotypic correlation is a derived value from the genotype and environmental interaction [28]. The genotypic correlation indicates genotypic association among the traits and is, therefore, a more reliable estimate value for examining the degree of relationship between character pairs. Path analysis of pod, seed and progeny growth traits revealed that, even though seed breadth has slightly low (0.42) correlation coefficients, it has highest direct (2.18) and indirect effect on volume index through pod width (1.32). Hence seeds with good breadth may be selected for producing better progenies in addition to 100-pod and seed weight. Though 100-seed weight is highly significantly correlated with volume index at 24 MAP, the direct effect is less. Positive correlation between seed weight and seedling height was found in Pinus spp. but it disappeared with the growing age of the seedlings [29]. However correlation between seed weight and plant height was observed in Pinus taeda till 15 years [30]. Khalil [31] stated that, 1000-seed weight and plant height in Picea glauca at four years appeared significant positive correlation. Hence, seed weight may be an index among the criteria for selection of plus trees. Among different seed traits, viz., seed coat, gametophyte and embryo weight, the embryo weight had strong relation with seedling growth traits in Pinus elliotti [32]. n Douglas fir, similar contribution of seed weight to seedling height was reported.

Conclusion

This results of investigation revealed that significant differences exist among RAKs on basis of pod, seed and progeny traits. The traits like 100-pod and seed weight were highly correlated with growth traits of tree. In addition, pod length and seed breadth expressed correlation with volume index at 24 MAP. Hence identification of good RAKs may be advantageous based on seed weight, size and shape traits. Since traits viz. 100-pod weight, 100-seed weight and volume index have high heritability and genetic advance, these traits may be considered for further improvement by breeding. RAK-5 is found to be superior on the basis of these traits, viz., 100-pod weight, 100-seed weight, seed breadth and volume index, hence seeds of these RAK may be importance for massive production of elite germplasm for nursery and afforestation program. The present study can however serve as a pointer at later stages of study especially on seed, and oil yield and agroforestry models.

Acknowledgements

The authors are grateful to National Oilseed and Vegetable Oils Development Board (NOVOD), Ministry of Agriculture, New Delhi, Govt. of India for financial assistance in the form of Research and Development grants and fellowship.

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