



## Identification of Seed Quality and Storability Traits in *Pongamia pinnata* (L.) Pierre

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### Authors' contributions

This work was carried out in collaboration between all authors. Author SP designed the study, wrote the protocol, recorded the data, performed the statistical analysis, interpreted the data, wrote the first draft of the manuscript and reviewed all drafts of the manuscript. Author KK reviewed the experimental design and first draft. Authors JS and SG identified the plants and supplied the seed material. Authors SN and TNVSRK managed the analysis of the study and first draft. All authors read and approved the final manuscript.

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### ABSTRACT

Twenty four *Pongamia pinnata* genotypes were screened out at the Department of Seed Science and Technology, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad during 2014 and 2015 to elucidate the relationship between seed physical and physiological traits on seed storability and to select best genotype with long storage life. Genotype TOIL 2 recorded maximum values for two traits viz., seed thickness (8.99 mm) and 3D seed volume (3057 mm<sup>3</sup>), TOIL 12 for seed storability (85% germination) and test weight (151.37 g) and

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TOIL 5 for initial seed germination (100%). Coefficients of variations observed were high for seed germination, moderate for seed width, thickness and 100 seed weight but seed length recorded with low variation. Broad sense heritability estimates ranged from 55.4% (for seed length) to 99.9% (100 seed weight), genetic advance as per cent of mean ranged between 8.91 (for seed length) to 126.42 (for seed germination after storage). Seed storability exhibited positive significant correlation with initial seed germination and 100 seed weight at both phenotypic and genotypic levels whereas, seed thickness exhibited positive significant correlation only at genotypic level. Path analysis revealed that initial seed germination ( $g=0.695$ ;  $p=0.667$ ) is contributing directly to seed storability followed by 100 seed weight ( $g=0.440$ ;  $p=0.266$ ) and seed length ( $g=0.048$ ;  $p=0.044$ ). Whereas, seed thickness showed directly negative effect ( $g= -0.304$ ;  $p= -0.143$ ) on seed storability. Out of five clusters, cluster-I and cluster-II showed more genotypes, 15 and 5, respectively. 100 seed weight contributed more towards genetic diversity of *Pongamia* followed by seed germination after storage. The cluster V recorded maximum cluster mean for four seed physical parameters, while cluster III for seed germination and crosses among them may result in substantial segregates and further selection for overall improvement of species and its seed storability.

**Keywords:** Divergence; *Pongamia pinnata*; variability; heritability; seed; storage.

## 1. INTRODUCTION

*Pongamia pinnata* (L.) Pierre or Indian Beech popularly known as Karanja is an indigenous, perennial, fast-growing leguminous tree. It is regarded as a sustainable biofuel feedstock of the future because of its abundant production of oil-rich seeds, tolerance to abiotic stress and ability to undergo biological nitrogen fixation [1,2,3]. *Pongamia* is propagated only through seed, hence storage behavior is very important for taking up of successful plantation programme. Variability with regard to seed storability can be exploited for the genetic improvement to evolve seeds with superior storage. Genetic differences associated with the place of origin have been several times as great as that among individual trees within the population. Hence it becomes necessary to conduct seed source testing prior to a more intensive breeding work. For a successful promotion of large scale plantations there is a need for carefully planned and well directed seed source research.

The success of any sustainable reforestation program, among other things, depends on the quality of seeds" [4]. Seed quality is also important for sustainable forestry and to transmit the current gene diversity to next generation by afforestation with suitable seed source" [5]. Moreover, genetic diversity is the richness of the hereditary information in the gene pool of one species. Over a long term, the ability of a species to respond adaptively to environmental changes depends on the level of its genetic variability [6]. The most important factor in basic selective breeding is genetic variation which is important

characteristic of interest. The genetic estimates can be very useful tools in predicting the amount of gains expected in a shorter period. Marginal difference between PCV (phenotypic coefficients of variation) and GCV (genotypic coefficients of variation) and high estimates of heritability (broad sense) for all 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 quantitative traits. To understand the causes of variation and apportioning of total phenotypic variance is of great utility as the heritable genetic variance could be exploited for future utility [7].

The level of genetic variation in a population is constantly changing and the gene pool of a population is always dynamic. The phenotype of a plant is determined by its genetic composition, the environment in which a plant is grown and the interaction of genotype with environment. The challenge that plant breeders face is to identify and select the plants that have genotypes conferring desirable phenotypes, rather than the plants with favourable phenotypes due to environmental effects. The traits with greater heritability can be modified more easily by selection and breeding than traits with lower heritability. Additive genetic variation makes proportionally a greater contribution to genetic variation than other types of gene action and is more easily captured by the commonly used methods of developing cultivars. Additive genetic variation is estimated by general combining ability. Traits can be classified as either qualitative, whereby variation occurs in discrete classes and often is controlled by one or

a few genes, or quantitative, where variation is continuous and often is controlled by several genes, each having a minor effect. Quantitative traits can be influenced greatly by environment and thus have lower heritability than qualitative traits. Keeping in view of the importance of *Pongamia* and its propagation by seeds, the present study was designed to identify variability among *Pongamia pinnata* genotypes for good seed storability.

## 2. MATERIALS AND METHODS

An extensive survey was conducted across the forest areas of Adilabad and Ranga Reddy districts of Telangana during the year 2002. About 8700 genotypes of *Pongamia* were collected. These genotypes were planted during August, 2003 in the nursery and fields of Tree Oils India limited, Zaheerabad, Telangana (India). From these 8700 genotypes 110 genotypes were selected based on characters like early maturity, seed oil content, crop canopy with less branching, less height and girth and good yield potential. From these 110 genotypes, finally 24 genotypes were screened based on their phenotypical characteristics, efficiency and performance. *Pongamia* seeds were collected from these candidate plus trees which were identified at farm of Tree Oils India Limited, Zaheerabad during February, 2014. Seed physiological and storability studies were carried out in the Department of Seed Science and Technology, Seed Research and Technology Centre, PJTSAU, Rajendranagar, Hyderabad (India) during 2014 and 2015 to study the existence of variation among 24 genotypes of *Pongamiapinnata* and the performance of seed quality parameters during seed storage.

The laboratory experiment was laid out in completely randomized design with four replications by storing 2 kilograms of each genotype in cloth bags. Seed physical parameters were studied immediately after harvesting and seed physiological parameters were studied after harvesting and also after six months of storage. Measurement of morphometric characters such as seed length, seed width and thickness were taken from 100 randomly selected seeds using a digital verniercaliper (Indosaw) with 0.01 mm accuracy and expressed in mm. Seed length: seed width ratio was the seed length divided by seed width. The 100-seed weight was obtained by weighting 100 randomly selected pure seed with precision

balance (Radwag) having 0.01 g accuracy and was expressed in grams. Seed size was measured as a product of three physical dimensions. Standard germination test was employed as per ISTA, 2007 [8] using sand method [9] by placing hundred seeds in large germination trays in four replications and germination per cent was expressed using below formula at 21 days after sowing.

$$\text{Germination per cent} = \frac{\text{Number of seeds germinated}}{\text{Number of seeds sown}} \times 100$$

Data were analyzed statistically by adopting CRD (Completely Randomized Design) techniques, as described by Panse and Sukhatme, 1985 [10]. Variability and genetic divergence studies for seed physical and storability parameters were carried out during the reported period under study by following standard procedures [8,11]. The data recorded as percentage were transformed to the respective angular (arc sine) values before subjecting them to statistical analysis by using WINDOSTAT package of 8.5 version. The traits were analyzed using Analysis of variance (ANOVA) and verified ANOVA assumptions to understand the significant difference among the traits of TOILs under consideration [12]. After testing the differences between genotypes for each of the characters, a simultaneous test for significance for differences in mean values of a number of correlated variations with regard to the pooled effect of characters was carried out by using V statistics which in turn utilizes Wilk's  $\Lambda$  criterion. The sum of squares and sum of product of error + genotype were used for this purpose. The components of variance were used to estimate genetic parameters like genotypic and phenotypic coefficients of variation (PCV and GCV) were calculated according to the formula given by Falconer, 1981 [13]. Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon, 1973 [14]. Heritability ( $h^2$ ) in the broad sense was calculated according to the formula given by Allard, 1960 [15] and heritability estimates were categorized as suggested by Johnson et al., 1955 [16]. From the heritability estimates the genetic advance was estimated by following the formula given by Burton, 1952 [17]. In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent of mean was computed and range of

genetic advance of mean was classified as suggested by Johnson et al. [16]. To test the significance of correlation coefficients, the estimated values were compared with the table value as statistical table by Fisher and Yates, 1967 [18] at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5% and 1% level of significance, respectively. Path coefficient analysis was done using genotypic correlation coefficients following Dewey and Lu, 1959 [19]. A measure of group distance based on multiple characters was given by Mahalanobis, 1936 [20] using  $D^2$  statistic by which, genetic divergence between genotypes was estimated.

### 3. RESULTS AND DISCUSSION

#### 3.1 Seed and Seedling Traits

Analysis of variance for six characters revealed that the mean sums of squares were highly significant for all characters indicating the greater diversity among the *Pongamia* genotypes for seed physical and storability characteristics (Table 1 and Table 2). Variability studies for seed physical and physiological traits revealed that genotype TOIL 12 recorded highest test weight (151.37 g) and maximum seed germination (85%) after storage with no reduction in seed germination over a period of storage. TOIL 5 recorded maximum value for initial seed germination (100%) but it is recorded comparatively higher reduction (23%) over a period of six months of storage when compared to TOIL 12. TOIL 2 recorded maximum values for two traits viz., seed thickness (8.99 mm) and 3D seed volume (3057 mm<sup>3</sup>) and TOIL 17 for seed length (24.78 mm), TOIL 10 for seed width (17.03 mm) and TOIL 22 for 100 seed weight (184.45 g). However lowest values were recorded with TOIL 18 for five traits (seed length, seed thickness, 100 seed weight, seed size and high reduction in seed germination after storage) followed by TOIL 15 for two traits (initial seed germination and germination after storage) and TOIL 11 for one trait (seed thickness). All these characters were differed significantly among the genotypes.

Resultant of double fertilization, endosperm, contributes to the seed weight which determines the seed size and supports seed germination by providing food material for developing seedling during seed germination. These characters along with embryo development and its physiological functions were influenced by the maternal traits

and environmental factors [21]. In most plant species, seeds vary in their degree of germinability between and within populations and between and within individuals [22,23] due to maternal and/or environmental factors. Similar findings were revealed by Sudhir Kumar, 2003 [24] in *Jatropha curcas* and Vasanth Reddy et al. 2007 [25] in *Pongamia pinnata*. This could be attributed to the fact that more seed weight of TOIL 12 might have contributed to more seed storability by making reserved food material availability to the newly developing seedlings even after seed storage. Conversely, reverse trend was recorded with regard to TOIL 18 in which less seed size and seed physical parameters might have contribute to very high reduction in seed germination during storage. In the present study, seeds of twenty four genotypes exhibited significant variability in seed physical and storability traits which could be attributed to gene flow in genotypes. This type of variability in seed morphology and seed germination is attributed to the out-breeding nature. Genetic control of seed size traits has been observed in several tree species like *Tectona grandis* by Sivakumar et al., 2002 [22], *Strychnos cocculoides* by Mkonda et al., 2003 [23] and *Juniperus procera* by Mamo et al., 2006 [26]. Hence, in the present study, various TOILs exhibiting significant variability in seed and seedling 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* [27-29], *Madhuca latifolia* [30] and *Pongamia pinnata* [31].

#### 3.2 Genetic Variability Assessment

Genetic estimates of seed physical and storability characters are presented in Table 3. The phenotypic and genotypic coefficients of variations were close to each other in all traits except seed germination which is exhibited higher variations compared to other traits. Coefficients of variations observed were high for seed germination, moderate for seed width, thickness and 100 seed weight but seed length recorded low variation. Broad sense heritability estimates ranged from 55.4% (for seed length) to 99.9% (100 seed weight), genetic advance as per cent of mean ranged between 8.91 (for seed length) to 126.42 (for seed germination after storage). Higher estimates of phenotypic

coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and high heritability values accompanied by high genetic advance estimates were also reported for seed thickness and 100-seed weight indicated additive gene action [7,32-40]. The genetic variance which is heritable could be exploited for future utility [7]. The variability in seed source is largely attributed to the heterogeneity of the genotypes and the genotype X environment interactions [41]. In the present study, the phenotypic and genotypic variances were close to each other and indicating genotypic component as major contributor to the total variance for all the traits under study i.e., most of the variability observed in the phenotype for traits has more of a genetic than a non-genetic basis. This variability due to genotypic variance further indicates considerable scope for selection. Higher GCV indicates that worthwhile improvement could be achieved for these traits through simple selection while higher genetic advance value suggests that population means for these traits may be changed considerably by selecting the superior 5% of the genotypes.

### 3.3 Correlation Studies

In general, the genotypic correlation coefficient values were higher than corresponding phenotypic values (Table 4). Seed germination after storage exhibited high positive significant correlation with initial seed germination at genotypic (0.638) and phenotypic (0.623) levels and it exhibited positive significant correlation with seed width at genotypic level (0.197). However, 100 seed weight with seed length, seed width and seed thickness and seed length with seed thickness also expressed positive significant correlations at both the levels.

The genotypic correlation is an estimated value, whereas, phenotypic correlation is a derived value from the genotype and environmental interaction. The genotypic correlation is, therefore, a more reliable estimate for examining the degree of relationship between characters. Both phenotypic and genotypic correlations between seed width, initial seed germination and germination after storage and between 100 seed weight with seed length, seed thickness and seed width and seed thickness with seed length were strong. This offers an opportunity to select phenotypes based on these traits. Correlated quantitative traits are major interest in an improvement program, as the improvement of

one character may cause simultaneous changes in the other character. Here seed width, seed thickness, 100 seed weight, initial seed germination and germination after storage are under strong genetic control [with high GCV, PCV,  $h^2_B$  and GA (as % of the mean)], hence improvement in these character can lead to improved seed storability. The results agree with the findings in *Santalum album* [42], which also exhibited positive correlation between 100-seed weight and germination percentage. The results agree with the findings in *Jatropha curcas* [40], which also exhibited positive correlation between 100 seed weight and germination percentage.

Similarly, high level of genotypic correlations than the corresponding phenotypic correlations indicated the presence of strong inherent association between the traits. Strong association between pod characters and 100 seed weight, 100 seed weight and growth parameters [7] and seed germination and seedling traits [11] was established.

### 3.4 Path Analysis

Correlation measurement does not consider the dependence of one variable on the other. The direct contribution of each component to the main component and the indirect effect on its association with other components cannot be differentiated from mere correlation studies. A statistical method called path coefficient analysis developed by Wright, 1921 [43] fulfills this lacuna. Path coefficient analysis is further helpful in knowing the relative contribution of different traits to the trait of major interest.

Path analysis (Table 5) revealed that initial seed germination (genotypic=0.695; phenotypic=0.667) is the most pronounced character contributing directly to seed storability followed by 100 seed weight ( $g=0.440$ ;  $p=0.266$ ) and seed length ( $g=0.048$ ;  $p=0.044$ ). Whereas, seed thickness showed directly negative effect ( $g=-0.304$ ;  $p=-0.143$ ) on seed storability. The direct effects were about less than half of the correlation value. A usual trend in majority of the tree species is that, more vigorous the seeds, the better will be the germination. Vigour is a measure of weight (100 seed weight) and size (length and width). The correlation coefficient and path analysis only analyses the relationship and dependence of variables but cannot measure the effect of genotypes/provenances on dependent variable.

**Table 1. Mean performance of selected genotypes for seed physical traits in relation to seed storability in *Pongamia pinnata***

<i>Pongamia</i> genotype	Seed length (mm)	Seed width (mm)	Seed thickness (mm)	100 seed weight (g)	Seed germination %-BA	Seed germination %-AA	Seed size (mm <sup>3</sup> )	Seed length: % Reduction in width (Ratio) SG	
TOIL 1	22.83	12.69	8.09	132.94	90 (72)	32 (35)	2344	1.80	58
TOIL 2	23.39	14.54	8.99	168.68	65 (54)	0 (4)	3057	1.61	65
TOIL 3	21.59	13.98	6.94	111.11	90 (72)	33 (35)	2095	1.54	57
TOIL 4	19.72	14.92	6.28	123.77	75 (60)	53 (47)	1848	1.32	22
TOIL 5	21.16	12.32	7.62	121.03	100 (86)	77 (62)	1986	1.72	23
TOIL 6	21.16	15.73	5.77	115.82	85 (67)	75 (60)	1921	1.35	10
TOIL 7	23.28	12.17	6.97	108.78	90 (72)	62 (52)	1975	1.91	28
TOIL 8	20.48	13.75	6.34	104.79	60 (51)	48 (44)	1785	1.49	12
TOIL 9	19.61	12.69	5.97	103.27	70 (57)	0 (4)	1486	1.55	70
TOIL 10	21.90	17.03	5.96	139.61	65 (54)	45 (42)	2223	1.29	20
TOIL 11	22.27	11.15	7.97	105.90	75 (60)	47 (43)	1979	2.00	28
TOIL 12	19.86	14.15	8.08	151.37	85 (67)	85 (67)	2271	1.40	0
TOIL 13	20.22	14.57	6.18	123.05	85 (67)	65 (53)	1821	1.39	20
TOIL 14	21.91	13.41	6.94	121.24	87 (69)	85 (67)	2039	1.63	2
TOIL 15	20.82	12.25	7.32	121.16	30 (33)	0 (4)	1867	1.70	30
TOIL 16	21.57	16.93	7.99	125.07	75 (60)	36 (37)	2918	1.27	39
TOIL 17	24.78	15.61	6.34	140.35	45 (42)	35 (36)	2452	1.59	10
TOIL 18	18.49	12.40	5.59	85.00	80 (63)	10 (18)	1282	1.49	70
TOIL 19	20.27	12.66	7.69	113.46	55 (48)	0 (4)	1973	1.60	55
TOIL 20	21.19	13.33	6.99	133.52	95 (78)	62 (52)	1974	1.59	33
TOIL 21	20.51	14.65	7.65	124.03	95 (78)	80 (63)	2299	1.40	15
TOIL 22	21.85	15.11	8.97	184.45	70 (57)	59 (50)	2961	1.45	11
TOIL 23	20.79	14.21	5.66	108.13	95 (78)	50 (44)	1672	1.46	45
TOIL 24	20.73	14.32	7.51	128.04	75 (60)	37 (37)	2229	1.45	38
<b>Mean</b>	<b>21.27</b>	<b>13.90</b>	<b>7.07</b>	<b>124.77</b>	<b>77 (63)</b>	<b>45 (40)</b>	<b>2090</b>	<b>1.53</b>	<b>32</b>
<b>S.E</b>	0.64	0.12	0.26	0.42	2.28 (2.01)	0.70 (0.62)			
<b>C.D at 5%</b>	1.82	0.36	0.73	1.18	6.48 (5.73)	2.00 (1.76)			
<b>C.V%</b>	5.21	1.59	6.28	0.58	5.16 (5.57)	2.72 (2.68)			

*Arc sine transformation values are in parenthesis; BA=Before Aging; AA=After Aging*

**Table 2. ANOVA for seed physical characters affecting seed storage of *Pongamia pinnata***

Mean sum of squares	Character					
	Seed length (mm)	Seed width (mm)	Seed thickness (mm)	100 Seed weight (g)	Seed germination (%) -BA	Seed germination (%) -AA
Treatments (d.f = 23)	5.811**	6.124**	3.014**	1380.696**	874.577**	2276.309**
Error (d.f = 46)	1.229	0.049	0.198	0.519	15.565	1.487

*d.f* = Degrees of freedom; BA=Before Aging; AA=After Aging  
 \*\* Significant at 1% level

**Table 3. Genetic estimates of seed physical traits in relation to seed storability in *Pongamia pinnata***

Seed physical and physiological trait	Range	GV	PV	GCV	PCV	$h^2$ (bs) (%)	GA as (%) of mean
Seed length (mm)	18.49 - 24.78	1.527	2.752	5.811	7.807	55.4	8.910
Seed width (mm)	11.15 – 17.03	2.025	2.074	10.238	10.363	97.6	20.838
Seed thickness (mm)	5.59 – 8.99	0.939	1.137	13.698	15.073	82.6	25.644
100 seed weight (g)	85 – 184.45	460.059	460.578	17.190	17.200	99.9	35.392
Seed Germination (%) -BA	30 – 100	286.338	301.902	22.112	22.705	94.8	44.360
Seed Germination (%) -AA	0 - 85	757.868	760.574	61.480	61.590	99.6	126.423

GV=Genotypic Variance; PV=Phenotypic Variance; GCV=Genotypic Coefficient of Variation; PCV=Phenotypic Coefficient of Variation;  $h^2$  (bs) = Heritability at broad sense; GA= Genetic Advance; BA=Before Aging; AA=After Aging

**Table 4. Correlation matrix of seed physical traits in relation to seed storability in *Pongamia pinnata***

Seed physical and physiological trait		SW	ST	100 SWt	SG -BA	SG-AA
SL	G	0.084	0.389	0.487	-0.167	0.024
	P	0.031	0.281*	0.357**	-0.110	0.028
SW	G	1.000	-0.175	0.500	-0.064	0.197*
	P	1.000	-0.161	0.494***	-0.066	0.194
ST	G		1.000	0.663	-0.042	-0.017
	P		1.000	0.601***	-0.038	-0.009
100 SWt	G			1.000	-0.146	0.141
	P			1.000	-0.143	0.142
SG-BA	G				1.000	0.638*
	P				1.000	0.623*

\* Significant at 5% level, \*\* Significant at 1% level, \*\*\* Significant at both 5% and 1% level  
 SL= Seed length; SW= Seed width; ST= Seed thickness; 100 S Wt=100 Seed weight; BA=Before Aging; AA=After Aging; SG=Seed Germination; G=Genotypic; P=Phenotypic

### 3.5 Divergence Studies

On the basis of cluster analysis (Table 6), 24 accessions were grouped in to five clusters (Table 6). The maximum number of 15 accessions were included in cluster I followed by cluster II (5 accessions) and cluster V (2

accessions). In contrast, clusters III and IV included only one accession each. The cluster pattern exhibited that geographical diversity need not to necessarily be correlated with genetic diversity. The inter- and intra-cluster distances are presented in Table 7. The intra cluster distances ranged from 0 to 23.79 with maximum

value in cluster V followed by II and cluster I. Minimum intra cluster distance was found in cluster III and IV. The highest inter cluster distance was found between clusters IV and V (78.29) followed by clusters III and IV (56.29) indicating wider genetic diversity between the trees in these groups and selection of parents from such clusters for hybridization programs would help to achieve novel hybrids. The minimum inter cluster distance was observed between clusters I and II (24.56).The minimum inter-cluster distance indicated that trees in these clusters were of close relationship. Hence, selection of parents from these two clusters is to be avoided. Cluster mean indicated significant

variation among clusters particularly for 100 seed weight and initial seed germination (Table 8). The cluster V recorded maximum cluster mean values for all seed physical parameters viz., seed length, seed width, seed thickness and 100 seed weight, while cluster III recorded maximum initial seed germination and germination after seed storage. The clusters, having high inter-cluster distance and high mean value, would produce divergent trees and therefore should be selected. Thus it may be suggested that crosses involving genotypes under cluster V and III may result in substantial segregates and further selection for overall improvement of species [7,40].

**Table 5. Phenotypic (P) and Genotypic (G) path coefficient analysis of seed physical traits on storability of *Pongamia pinnata***

Seed physical and physiological trait		Seed length (mm)	Seed width (mm)	Seed thickness (mm)	100 Seed weight (g)	Seed germination- before aging	Seed germination- after aging
Seed length (mm)	G	<b>0.048</b>	0.004	0.019	0.023	-0.008	0.024
	P	<b>0.044</b>	0.001	0.013	0.016	-0.005	0.028
Seed width (mm)	G	-0.003	<b>-0.035</b>	0.006	-0.018	0.002	0.198
	P	0.003	<b>0.083</b>	-0.013	0.041	-0.006	0.194
Seed thickness (mm)	G	-0.118	0.053	<b>-0.304</b>	-0.202	0.013	-0.017
	P	-0.040	0.023	<b>-0.143</b>	-0.086	0.006	-0.010
100 seed weight (g)	G	0.214	0.220	0.292	<b>0.440</b>	-0.065	0.142
	P	0.095	0.132	0.160	<b>0.266</b>	-0.038	0.142
Seed germination – before aging	G	-0.116	-0.045	-0.030	-0.102	<b>0.695</b>	0.638
	P	-0.074	-0.044	-0.026	-0.096	<b>0.667</b>	0.624

Genotypic Residual Effect = 0.7034; Phenotypic Residual Effect = 0.7266; SL= Seed length; SW= Seed width; ST= Seed thickness; 100SWt=100 Seed weight; BA=Before Aging; AA=After Aging; SG=Seed germination; G=Genotypic; P=Phenotypic

**Table 6. Clustering pattern among 24 genotypes of *Pongamia pinnata* by Tocher’s method**

Cluster	Number of genotypes	Genotypes
Cluster I	15	TOIL 16, TOIL 24, TOIL 4, TOIL 20, TOIL 13, TOIL 21, TOIL 5, TOIL 14, TOIL 6, TOIL 23, TOIL 7, TOIL 3, TOIL 8, TOIL 11 and TOIL 1
Cluster II	5	TOIL 15, TOIL 19, TOIL 9, TOIL 17 and TOIL 10
Cluster III	1	TOIL 12
Cluster IV	1	TOIL 18
Cluster V	2	TOIL 2 and TOIL 22

**Table 7. Cluster means for 6 quantitative traits of *Pongamia pinnata* (Tocher’s method)**

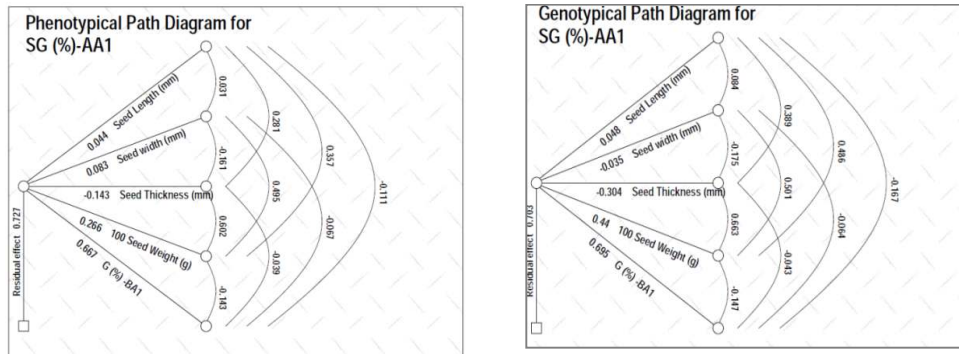
Cluster	SL (mm)	SW (mm)	ST (mm)	100 SWt (g)	SG (%)- BA	SG (%)- AA
Cluster I	21.29	13.72	6.99	119.15	84.78	56.18
Cluster II	21.48	14.10	6.65	123.57	53.00	15.67
Cluster III	19.86	14.15	8.08	151.37	85.00	84.67
Cluster IV	18.49	12.73	5.59	85.00	80.00	10.00
Cluster V	22.62	15.16	8.98	176.57	67.50	29.50

SL= Seed length; SW= Seed width; ST= Seed thickness; 100SWt=100 Seed weight; BA=Before Aging; AA=After Aging; SG=Seed germination; G=Genotypic; P=Phenotypic

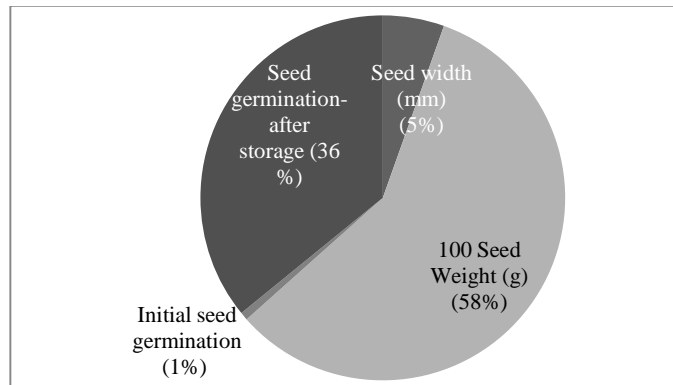


**Table 8. Intra cluster (Diagonal) and inter cluster average distance (D<sup>2</sup>) in *Pongamia pinnata* genotypes (Tocher Method)**

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	16.17	24.56	28.81	31.95	55.79
Cluster II		22.05	33.67	35.65	48.48
Cluster III			0.00	56.29	37.34
Cluster IV				0.00	78.29
Cluster V					23.79



**Fig. 1. Genotypic and phenotypic path analysis of five traits and their effects on seed storability in *Pongamia pinnata* genotypes**



**Fig. 2. Relative contribution of different characters towards genetic diversity in *Pongamia pinnata* genotypes**

**4. CONCLUSION**

Among the 24 *Pongamia* genotypes, TOIL 12 recorded highest seed seed storability and lowest values were recorded with TOIL 18. Seed germination after storage exhibited high positive significant correlation with initial seed germination and seed width. Initial seed germination is the most pronounced character contributing directly to seed storability followed by 100 seed weight and seed length. Whereas, seed thickness showed direct negative effect on seed storability.

Cluster V recorded maximum cluster mean values for all seed physical parameters while

cluster III recorded maximum for initial seed germination and germination after seed storage. It may be suggested that crosses involving genotypes under cluster V and III may result in substantial segregates and further selection for overall improvement of species with good seed storability.

This kind of study revealed the existence of substantial variation and diversity which can be utilized to identify *Pongamia pinnata* genotypes for genetic resource conservation and further tree improvement programmes of the species with better seed storability.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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