



VARIABILITY, HERITABILITY AND GENETIC ADVANCE OF SEED ATTRIBUTES IN *Pongamia pinnata*

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ABSTRACT

Studies were carried out in *Pongamia pinnata* progenies to elicit information about the seed attributes. Twenty progenies of *Pongamia pinnata* have been selected from the predominant growing areas in South India based on the plus trees characters. From these plus trees, seeds were collected and deployed for seed attributes viz., pod traits, seed traits and seed germination traits. The variability and heritability estimates indicated the presence of wider variation among the seed attributes investigated. Pod aspect ratio (20.09), seed width (24.00) and Germination value (30.44) exhibited higher PCV values and pod aspect ratio (18.26), Seed width (23.17) and germination value (29.98) exhibited higher GCV values in pod traits, seed traits and seed germination traits. Pod width (0.90), Seed width (0.93) and Germination value (0.97) exhibited high heritability and pod aspect ratio (34.19), seed width (46.09) and germination value (60.84) in genetic advance for pod traits, seed traits and seed germination traits and suggest that these traits are under strong genetic control and could be highly reliable for improvement of Pungam.

KEYWORDS: Pungam; Variability; Pod and Seed Traits; Biofuel; TBOs.

INTRODUCTION

The economic development of India and other countries is based on Self-reliance in energy. The recent oil crises and depleting fossil fuel reserves have rekindled interest in promotion of tree-borne oil seed species (Scott *et al.*, 2008). There are several trees to produce oil for biofuel production. Among the several TBOs, *Pongamia pinnata* (L.) Pierre is a perennial, fast-growing, leguminous tree, widely distributed on the Indian subcontinent (Murphy *et al.*, 2012) that has a high potential for high oil seed production and ability to grow on marginal lands-supports its cultivation as a potential biofuel crop for biodiesel industry. As the plant is an efficient and potential biodiesel crop, it is necessary to establish extensive plantations comprising elite varieties of these trees, with higher potential to produce oil seeds (Siddiqui *et al.*, 1993). In the recent past, research has been directed to explore plant based biofuel sources as a supplement or substitute of fossil fuel. Biofuels are renewable and environmentally safe. The most common type of biofuels that are being developed and used at present is bio-ethanol and bio-diesel. At present, bio-diesel is reported to substitute about 10% of the world diesel consumption (Choo and Ma, 2000). In view of economic, environmental and health benefits associated with the use of bio-diesel, planners have decided to develop bio-fuel programme in the country and targets are fixed to replace 5% and 10%, of petro diesel by bio-diesel by the year 2010 and 2015 respectively. To meet these targets, India should produce about 19 lakhs tonnes and 38 lakh tonnes of bio-diesel respectively. Under Indian conditions, only such plant sources can be considered for bio-diesel, which produce non-edible oil in appreciable quantity and can be grown in

large scale on non-crop marginal and wastelands. Seeds of more than 100 species of forest plants-Oil seeds (TBOs) have been identified as source of fatty oils with an estimated potential of 11.3 lakh tones (Gulati *et al.*, 1984). However the realized potential of such oils is 6.6 lakh tones (Anon, 1994). It has been recorded that fatty oils derived from *Jatropha curcas* and *Pongamia pinnata* (Karanj) are excellent feed stock for bio-diesel production (Srinivas *et al.*, 2001). Seed is one of the most important inputs for forest nursery production and plantation establishment (Laurisen and Olesen, 1990). The seed used for large scale plantation programme must be genetically superior to produce goods and services. A good quality seed should possess uniform size, weight, colour and freedom from pest and disease to produce vigorous seedlings. But several studies indicated the presence of variations in seed size and other seed physical attributes (Patil *et al.*, 2011 and Raut *et al.*, 2011). The knowledge of genetic variability and association between pod, seed and germination traits is considered to provide considerable help in genetic improvement of Pungam improvement programme. Heritability is of key importance in estimating gains that can be obtained from selection programmes. Of the two types of heritabilities, broad sense heritability has a limited application in tree improvement and is of primary use when both additive and non additive variation can be transferred from parent to offspring. It is important to know about the heritability of traits to be selected. However, variation studies using seed attributes in *Pongamia pinnata* is not attempted and hence the current study is conceived to assess the existing variability for incorporation and promotion through agroforestry.

MATERIALS AND METHODS

Selection of superior genetic resources of pungam

The predominant *Pongamia pinnata* L. growing areas of Southern India viz., Tamil Nadu, Karnataka and Kerala were identified. Initially the trees were morphologically selected based on 'comparison check tree selection' method in plantation and 'subjective grading' method in natural population. The selected trees are referred as Plus Trees (Zobel and Talbert, 1984).

Twenty five Candidate Plus Trees (CPTs) were identified based on the morphometric and qualitative traits from different locations of Southern India viz., Tamil Nadu, Karnataka and Kerala and furnished in table 1. The characteristics pod, seed and germination attributes of the each of the progenies were evaluated as below with 250 pods of three replications in each of the sources.

TABLE 1. Location details of superior progenies of *Pongamia pinnata*

Sl.No.	State	Location	Latitude	Longitude	Altitude (m)	Name of the CPTs
1	Tamil Nadu	Anjetti	12°19'N	77°45'E	554	CPT PP 01
2	Tamil Nadu	Denkanikottai	12°31'N	77°46'E	890	CPT PP 02
3	Tamil Nadu	Hosur	12°43'N	77°49'E	883	CPT PP 03
4	Tamil Nadu	Palacodu	12°17'N	78°04'E	521	CPT PP 05
5	Tamil Nadu	Mettupalayam	11°17'N	76°57'E	256	CPT PP 06
6	Tamil Nadu	Sirumugai	11°19'N	77°01'E	302	CPT PP 07
7	Tamil Nadu	Coimbatore	10°59'N	76°54'E	398	CPT PP 08
8	Tamil Nadu	Tanjore	10°50'N	79°07'E	47	CPT PP 09
9	Tamil Nadu	Viluppuram	11°55'N	79°30'E	41	CPT PP 10
10	Tamil Nadu	Krishnagiri	12°30'N	78°12'E	497	CPT PP 04
11	Tamil Nadu	Tindivanam	12°13'N	79°37'E	46	CPT PP 11
12	Puducherry	Puducherry	11°54'N	79°47'E	554	CPT PP 12
13	Karnataka	Honnavaara	14°15'N	74°26'E	14	CPT PP 13
14	Karnataka	Hubli	15°22'N	75°04'E	648	CPT PP 14
15	Karnataka	Sirsi	14°39'N	74°52'E	624	CPT PP 15
16	Karnataka	Udupi	13°20'N	74°43'E	15	CPT PP 16
17	Karnataka	Mangalore	12°54'N	74°51'E	25	CPT PP 17
18	Karnataka	Shimoga	13°53'N	75°33'E	585	CPT PP 18
19	Karnataka	Sagar	14°09'N	75°00'E	604	CPT PP 19
20	Karnataka	Tumkur	13°20'N	76°09'E	815	CPT PP 20
21	Karnataka	Hiregutti	14°34'N	74°23'E	54	CPT PP 21
22	Kerala	Trivandrum	08°29'N	76°59'E	25	CPT PP 22
23	Kerala	Thrissur	10°29'N	76°17'E	50	CPT PP 23
24	Kerala	Kottayam	09°33'N	76°32'E	14	CPT PP 24
25	Kerala	Upala	12°41'N	79°54'E	10	CPT PP 25

Statistical analysis

The data gathered from the evaluation were analyzed using GENRES software and tabulated. The significance test was carried out by referring to the standard 'F' table of Snedecor (1961). The observations recorded from the seed attributes were subjected to following genetic estimations.

Variability studies

These parameters were estimated as per the method described by Johnson *et al.*, (1955).

Genotypic variance

$$(G.V) (\sigma^2_g) = (\sigma^2_g - \sigma^2_e)/r$$

Where,

σ^2_g = Genotypic mean square

σ^2_e = Error variance

r = Number of replications

Phenotypic variance

$$(P.V) (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance

σ^2_e = Error variance

Phenotypic (PCV) and genotypic (GCV) coefficients of variances were computed following Burton (1952).

Phenotypic co-efficient of variability

Phenotypic co-efficient of variability was arrived by using the formula as given below

$$\text{(Phenotypic variance)}^{1/2}$$

$$\text{PCV (\%)} = \frac{\text{General mean}}{\text{General mean}} \times 100$$

General mean

Genotypic co-efficient of variability

Genotypic co-efficient of variability was arrived by using the formula as given below

$$\text{(Genotypic Variance)}^{1/2}$$

$$\text{GCV (\%)} = \frac{\text{General mean}}{\text{General mean}} \times 100$$

General mean

Heritability (h^2)

Broad sense heritability (h^2) was calculated according to Lush (1940)

$$h^2 = \sigma^2_g / \sigma^2_p$$

$$\text{Heritability percentage} = h^2 \times 100$$

Genetic advance

Genetic advance was worked out after Johnson *et al.*, (1955).

$$\text{Genetic advance (GA)} = [(\text{Genotypic variance} / (\text{Phenotypic variance})^{1/2})] \times K$$

Where,

K = 2.06, a selection differential at 5 % selection intensity

Genetic advance as percentage of mean

$$\text{GA as percentage of mean} = \text{GA} / \text{Grand mean} \times 100$$

The biometrical traits for describing the genetic parameters, the values recorded in the study were classified as presented.

RESULTS

The variability estimates viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean of seed attributes of *Pongamia pinnata* are analyzed and presented in Table 2-4.

The variability and heritability estimates indicated the presence of wider variation among the pod traits investigated. In general, the PCV values were higher than their corresponding GCV values for all pod traits. Among pod traits, pod aspect ratio exhibited higher PCV value (20.09) followed by pod width (17.85), pod length (15.60).

Pod thickness (5.97) and hundred pod weight (9.62) registered lower PCV values. In case of GCV value, pod aspect ratio (18.26) exhibited higher values followed by pod width (16.90) and pod length (14.62). The heritability studies among the pod traits are very high except for the Pod thickness and hundred pod weight. Pod width (0.90) exhibited high heritability followed by pod length (0.88) and pod aspect ratio (0.83). The genetic advance is moderate in pod aspect ratio (34.19), pod width (32.94) and pod length (28.24) and low genetic advance in Pod thickness (4.31) and hundred pod weight (13.26) (Table 2).

TABLE 2. Genetic estimates of Pod attributes in *Pongamia pinnata*

S.No	Traits	GCV	PCV	Heritability	GA (%) of Mean
1.	Pod length (mm)	14.62	15.60	0.88	28.24
2.	Pod width (mm)	16.90	17.85	0.90	32.94
3.	Pod thickness (mm)	3.53	5.97	0.35	4.31
4.	Hundred pod weight (g)	7.87	9.62	0.67	13.26
5.	Pod Aspect ratio	18.26	20.09	0.83	34.19

The variability and heritability estimates indicated the presence of wider variation among the seed traits investigated. In general, the PCV values were higher than their corresponding GCV values for all seed traits. Among seed traits, seed width (24.00) exhibited higher PCV value followed by seed aspect ratio (23.03), seed length (17.43) and hundred seed weight (16.71). Seed thickness (6.86), seed oil content (9.95) and pod seed ratio (11.74) registered lower PCV values. In case of GCV value, seed width (23.17) exhibited higher values followed by seed aspect

ratio (21.22), seed length (16.46) and hundred seed weight (16.00). The heritability studies among the seed traits are high. Seed width (0.93) exhibited high heritability followed by hundred seed weight (0.92), seed length (0.89), seed aspect ratio (0.83) and seed oil content (0.74). The genetic advance is high in seed width (46.09), seed aspect ratio (40.27), seed length (32.00) and low genetic advance in seed thickness (6.85), pod seed ratio (13.25) and seed oil content (15.10) (Table 3).

TABLE 3. Genetic estimates of Seed attributes in *Pongamia pinnata*

S.No	Traits	GCV	PCV	Heritability	GA (%) of Mean
1.	Seed length (mm)	16.46	17.43	0.89	32.00
2.	Seed width (mm)	23.17	24.00	0.93	46.09
3.	Seed thickness (mm)	4.78	6.86	0.48	6.85
4.	Hundred seed weight (g)	16.00	16.71	0.92	31.58
5.	Seed Aspect ratio	21.22	23.03	0.85	40.27
6.	Pod seed ratio	8.69	11.74	0.55	13.25
7.	Seed oil content (%)	8.54	9.95	0.74	15.10

The variability and heritability estimates indicated the presence of wider variation among the seed germination traits investigated. In general, the PCV values were higher than their corresponding GCV values for all seed germination traits. Among seed germination traits, germination value (30.44) exhibited higher PCV value and germination percentage (13.56), Peak value (13.96) and mean daily germination (17.60) registered lower PCV values. In case of GCV value, germination value (29.98) exhibited higher values and germination percentage (12.76),

Peak value (13.10) and mean daily germination (16.51) registered lower values.. The heritability studies among the seed germination traits are high. Germination value (0.97) exhibited high heritability followed by germination percentage (0.89), Peak value (0.88) and mean daily germination (0.88). The genetic advance also high in germination value (60.84) followed by Peak value (25.30), germination percentage (24.74) and mean daily germination (31.91) (Table 4).

TABLE 4. Genetic estimates of Seed germination attributes in *Pongamia pinnata*

S.No	Traits	GCV	PCV	Heritability	GA (%) of Mean
1.	Germination Percentage	12.76	13.56	0.89	24.74
2.	Germination Value	29.98	30.44	0.97	60.84
3.	Peak Value	13.10	13.96	0.88	25.30
4.	Mean Daily germination	16.51	17.60	0.88	31.91

DISCUSSION

The knowledge of existing variability within population is essential for any selection procedure to be effective. The assessment of genetic variability is necessary to evaluate

the performance of individual genotypes. According to Allard (1960), genotypic coefficient of variation measures the extent of variability for a trait and aids to compare the variability among the different traits. The measures of

genotypic and phenotypic coefficient of variations are needed to understand the effect of environment on different traits. In the present study of seed attributes, the information obtained from 25 progenies in *Pongamia pinnata* showed that the estimates of genotypic coefficient of variation were lesser than the estimates of phenotypic coefficient of variation indicating that the characters studied were influenced by non-additive gene action. In the present investigation, Pod aspect ratio exhibited higher PCV value (20.09) followed by pod width (17.85), pod length (15.60) in pod traits; seed width (24.00) exhibited higher PCV value followed by seed aspect ratio (23.03), seed length (17.43) and hundred seed weight (16.71) in seed traits; Germination value (30.44) exhibited higher PCV value and germination percentage (13.56), Peak value (13.96) in seed germination traits. In case of GCV value, pod aspect ratio (18.26) exhibited higher values followed by pod width (16.90) and pod length (14.62) in pod traits; Seed width (23.17) exhibited higher values followed by seed aspect ratio (21.22), seed length (16.46) and hundred seed weight (16.00) in seed traits; Germination value (29.98) exhibited higher values and germination percentage (12.76), Peak value (13.10) and mean daily germination (16.51) registered lower values in seed germination traits. Similar results were earlier reported in pungam which indicated that the phenotypic variances were found to be greater than the corresponding genotypic variances for all the seed characters. The results indicated that the expressions of these characters were influenced by the environmental factors (Sahoo *et al.*, 2011) and the results are in consonance with the findings of current study. The estimates of heritability help the breeder in the selection programme. Johnson *et al.*, (1955) suggested that heritability estimates in conjunction with genetic advance are usually more helpful in predicting its resultant effect for selecting the best individuals. The environment influences the variability of quantitative traits. Though the genetic coefficient of variation revealed the extent of genetic variability in the genotypes for their various characters, it did not indicate the variation to be heritable. The heritability estimates helps to assess the heritable portion of variation and the selection would be more effective if the estimates of the heritability are high. Genetic improvement depends upon the nature and magnitude of existing variability and also on the degree of transmission of traits or heritability (Zobel and Talbert, 1984). Pod width (0.90) exhibited high heritability followed by pod length (0.88) and pod aspect ratio (0.83) and the genetic advance is moderate in pod aspect ratio (34.19), pod width (32.94) and pod length (28.24) and low genetic advance in Pod thickness (4.31) and hundred pod weight (13.26) in pod traits. Seed width (0.93) exhibited high heritability followed by hundred seed weight (0.92), seed length (0.89), seed aspect ratio (0.83) and seed oil content (0.74) and the genetic advance is high in seed width (46.09), seed aspect ratio (40.27), seed length (32.00) and low genetic advance in seed thickness (6.85), pod seed ratio (13.25) and seed oil content (15.10) in seed traits. Germination value (0.97) exhibited high heritability followed by germination percentage (0.89), Peak value (0.88) and mean daily germination (0.88) and the genetic advance also high in germination value (60.84) followed by Peak value (25.30), germination percentage (24.74) and mean daily germination (31.91) in seed germination traits.

The higher heritability estimated by some of the seed character revealed the inheritance nature of this characters and the associated selection effect. Though heritability estimates give useful indication of the relative values of selection based on phenotypic expression, it does not give more reliable conclusion unless genetic gain under selection is taken into consideration along with heritability. Similar results were earlier reports in pungam which indicated that the heritability was high (>80%) for hundred seed weight (96.10%), hundred pod weight (90.97%) and seed thickness (86.11%). Such high levels of heritability may be due to the control of additive gene action in expression of these characters. Pod length, pod thickness, and seed length had moderate heritability (60-80%). Pod breadth and seed breadth showed low heritability (<60%) indicating that these two characters were controlled by non-additive type of gene action. The genetic advance ranged from 13.11 per cent to 55.49 per cent. High values of genetic advance are indicative of additive gene action involved in the expression of various polygenic traits and low values are of non-additive gene action (Sahoo *et al.*, 2011). Hence these indicated seed attributes could act as a reliable indicator for selection in these species.

CONCLUSION

The seed attributes of twenty five *Pongamia pinnata* genotypes evaluated. The variability and heritability estimates indicated the presence of wider variation among the seed attributes investigated. The variability studies indicated that the characters are least influenced by environment. However most growth traits exhibited higher heritability coupled with maximum genetic advance and suggest that these traits are under strong genetic control and are reliable.

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