



Variability in Seed Characteristics of *Jatropha curcas* Linn. From Hill Region of Uttarakhand

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ABSTRACT

Variability studies are the prerequisite and of paramount importance for developing tree improvement strategy. *Jatropha curcas* has recently come into prominence as source of bio-diesel. This species has naturalized stands spread all over India and due to varied climatic conditions across the country is likely to have a high degree of variability. In view of this, variability through seed characteristics was analyzed in its seeds. Significant differences were found among the seed sources for all the parameters studied. The mean fruit weight ranged from 2.21 to 3.41g, seed weight from 0.58 to 0.81g, seed length from 1.49 to 1.81cm, seed circumference from 2.97 to 3.51cm, seed moisture content from 6.20 to 10.44% and seed germination from 53.33 to 79.83%. The partition of total variance was influenced at phenotypic level through genotypic variance for seed length, seed circumference; seed moisture content and seed germination, while fruit weight and seed weight were influenced by environmental variance. In case of genetic component analysis, heritability value was found high for seed germination percentage (85.34%) coupled with moderate genetic gain which signifies that seed germination is under genetic control can be used for improvement of this species.

Key words: Seed source variation, Phenotypic, Genotypic, Environmental Variance, Heritability, Genetic Gain.

INTRODUCTION

Fast depleting fossil fuel resources, increasing oil prices apart from environment pollution have created an imperative need to search for other options such as bio-diesel [1-4]. Special interest has been shown in the cultivation of the tropical physic nut (*Jatropha curcas* Linn., Euphorbiaceae) for oil extraction, especially since it is drought resistant and can be cultivated on marginal land, without competing with food production [2,3,5]. It is a deciduous oil seed bearing tree species widely distributed in tropical and subtropical areas, especially in Central and South America, Africa, India and Southeast Asia [6]. In India it is commonly known as Ratanjot, Jamalghota, Jangliarand and Kalarand occurring almost and throughout India. *J. curcas* has spread beyond its original distribution because of its hardiness, easy propagation, drought endurance, high oil content, low seed cost, short gestation period, rapid growth, adaptation to wide agro-climatic conditions, bushy/shrubby nature and multiple uses of different plant parts [7-9]. Such a wide distribution of this species is likely to display a high degree of variation in its various characteristics and thus there is scope to determine the variability in the species in relation to different seed sources.

Many workers have been studied on the seed source variability of *J. curcas* in wide range of distribution for various parameters such as morphological, physiological and biochemical [10-14] and indicated the seed source variation occurred in *J. curcas* due to high degree of wide distribution. However, in our routine study we find significant differences in morphological and physiological parameters in narrow distribution range (i.e. in hill region of Uttarakhand). In view of this, genetic variability studies are required for the improvement programmes of *J. curcas* in this area.

Selection of the best source of a species for given region is necessary for achieving maximum productivity both in plantation botany as well as in agro forestry system. Seed source variability is an essential segment of tree improvement program that involves genetically superior reproductive material and better silviculture practices [15]. In variability experiments seeds are collected from number of widely scattered stands (usually natural) and studies are conducted in similar condition. The objective of conducting the seed source trial is to eventually arrive at conclusion as to which source is best for planting and breeding program in a particular region.

Seeds, which are principal means of propagation, contain a lot of variation depending upon the source of origin with regard to morphological and physiological characters [16]. The potential of a crop to respond favorably to breeding program depends upon the nature and magnitude of variability in its

characters. The genotypic and phenotypic correlation coefficients are measures of the degree of closeness of the linear relationship between pairs of variables. Heritability (H^2) is an approximate measure of the expression of a character. The present investigation reports the estimation of variability, heritability and genetic advance and gain in *J. curcas* among different seed sources.

MATERIAL AND METHODS

The experimental material was collected from 11 geographic locations (Table 1) having altitudes ranging from 336m to 1055m amsl of Uttarakhand Himalaya, India in 2007-2008. Discrepancies among seed sources occur on account of topographical barriers (aspect and distance) which forbid gene flow. Minimum of 10 parent trees were randomly selected for the study at each seed source. Mature fruits from these trees were collected and seeds were extracted manually from the fruit. Observations on fruit weight, seed weight, length, circumference and moisture content were recorded on 10 fruits of each seed source. Triplicate of 50 seeds were used for seed germination analysis.

Germination percentage was calculated according to ISTA, [17]99 using the formula (Germination% = Number of germinated seeds \times 100/ Total number of seeds). For analysis of variance; genotypic, phenotypic and environmental variances were calculated using the following equations according to [18].

$$\text{Genotypic variance (GV)} = (\text{Mt} - \text{Me}) / r$$

$$\text{Phenotypic variance (PV)} = \text{GV} + \text{Me}$$

$$\text{Environmental variance (EV)} = \text{Me}$$

Where: Mt= Mean Square for treatments, Me= Mean Error variance and r= Number of replicates.

Phenotypic, genotypic and environmental coefficients of variation were calculated by using the formula as suggested by BURTON and DEVANE [19]:

$$\text{Phenotypic coefficient of variation \% (PCV)} = \sqrt{\text{PV}/x} \times 100$$

$$\text{Genotypic coefficient of variation \% (GCV)} = \sqrt{\text{GV}/x} \times 100$$

$$\text{Environmental coefficient of variation \% (ECV)} = \sqrt{\text{EV}/x} \times 100$$

x = population mean for each trait

For estimation of genetic components, heritability in broad sense (H^2), the ratio of genetic variance to the total phenotypic variance, was estimated as suggested by [19,20]. Genetic advance (GA) is the expected increase in the magnitude of a particular character when a selection pressure of chosen intensity (i) is applied. This was calculated as per [20].

$$\text{GA} = \text{GV} / \text{PV} \times i \times \sqrt{\text{PV}}$$

Where, i = selection intensity (2.06)

Genetic gain (GG) expressed in percentage of mean was computed by using the formula given by Johanson *et al.* [20].

Statistical analysis

The data were statistically analyzed using mean and standard deviation. Analysis of Variance (ANOVA) was applied to test the variations between different seed sources through seed characteristics. Least significant difference (Lsd at 5% level) was also subjected on significant findings.

RESULTS AND DISCUSSION

Variations between studied parameters among seed sources are given in Table 2. Fruit weight was found maximum ($3.41 \pm 1.32\text{g}$) in Shergarh and minimum ($2.21 \pm 0.03\text{g}$) in Bachelikhal seed source. Seed weight, seed length and seed circumference were found maximum in Metakund ($0.81 \pm 0.11\text{g}$, $1.81 \pm 0.05\text{cm}$ and $3.51 \pm 0.16\text{cm}$ respectively) and minimum in Bachelikhal ($0.58 \pm 0.05\text{g}$, $1.49 \pm 0.07\text{cm}$ and $2.97 \pm 0.12\text{cm}$ respectively). Seed moisture content was found maximum in Laltappar ($10.44 \pm 0.92\%$) and minimum in Kamera ($6.20 \pm 0.46\%$). Seeds from Gandhari had highest germination percentage ($79.83 \pm 0.29\%$) while Metakund seed source had minimum (53.33 ± 2.88). All these differences between the seed sources were statistically significant at $P < 0.001$ level of significance with their respective Lsd value.

Table 1. Geographical coordinates of selected seed sources of *J. curcas*.

S.No.	Seed source	Aspect	Elevation (m)	Latitude (N°)	Longitude (E°)
1	Shergarh	South-East	336	30°03'678"	78°12'729"
2	Lalthapar	South-East	366	30°12'330"	78°33'021"

3	Naithana	South- West	550	30°13'633"	78°46'333"
4	Metakund	South-West	704	30°10'330"	78°63'011"
5	Bamot	South-West	787	30°16'267"	79°10'250"
6	Saknidhar	South- East	828	30°05'420"	78°32'240"
7	Kamera	South-East	838	30°19'048"	79°01'782"
8	Bachelikhal	South-West	925	30°05'198"	78°35'022"
9	Gandhari	South- West	970	30°18'902"	79°02'422"
10	Chopra	South- West	1046	30°19'224"	79°03'412"
11	Devlakha	South-West	1055	30°19'518"	79°03'252"

Table 2. Variation between different seed sources of *J. curcas* on the basis of seed characteristics

S. No.	Seed Sources	Fruit weight (g)	Seed weight (g)	Seed length (cm)	Circumference (cm)	Moisture content (%)	Germination (%)
1	Shergarh	3.41±1.32	0.71±0.21	1.68±0.14	3.42±0.13	10.26±0.72	54.15±1.44
2	Lalthapar	2.93±0.77	0.62±0.17	1.69±0.10	3.24±0.20	10.44±0.92	61.67±3.82
3	Naithana	2.67±0.20	0.71±0.03	1.65±0.03	3.30±0.03	9.71±1.58	62.28±0.67
4	Metakund	3.08±0.77	0.81±0.11	1.81±0.05	3.51±0.16	9.19±0.48	53.33±2.88
5	Bamot	2.39±0.56	0.62±0.15	1.72±0.09	3.24±0.11	7.67±0.59	67.50±2.50
6	Saknidhar	2.62±0.15	0.71±0.02	1.60±0.02	3.17±0.03	9.28±0.19	77.35±0.54
7	Kamera	2.30±0.35	0.69±0.05	1.72±0.05	3.31±0.05	6.20±0.46	70.83±1.57
8	Bachelikhal	2.21±0.03	0.58±0.05	1.49±0.07	2.97±0.12	8.90±0.49	65.33±1.13
9	Gandhari	2.87±0.17	0.73±0.04	1.71±0.05	3.29±0.07	7.34±0.46	79.83±0.29
10	Chopra	2.59±0.40	0.69±0.08	1.69±0.08	3.23±0.13	9.03±0.75	57.29±1.91
11	Devlakha	2.50±0.20	0.68±0.03	1.68±0.03	3.20±0.07	7.56±0.26	71.13±0.22
Mean (seed sources)		2.69±0.36	0.69±0.62	1.68±0.08	3.26±0.14	8.69±1.33	65.52±8.83
P value (Lsd at 5%)		<0.001 (0.48)	<0.001 (0.09)	<0.001 (0.06)	<0.001 (0.09)	<0.001 (0.10)	<0.001 (1.66)
Magnitude of variation (%)		35.19	28.40	17.68	15.38	40.61	33.20

Table 3. Variances and coefficient of variability for seed characteristics of *J. curcas*

S.No.	Parameters	GV	PV	EV	GCV	PCV	ECV
1	Fruit weight	0.085	0.424	0.339	10.86	24.22	21.65
2	Seed weight	0.003	0.014	0.011	7.260	17.01	15.38
3	Seed length	0.006	0.011	0.005	4.449	6.195	4.310
4	Seed circumference	0.016	0.029	0.013	3.914	5.248	3.496
5	Seed moisture content	1.560	2.085	0.525	14.36	16.62	8.334
6	Seed germination	20.92	24.51	3.594	6.980	7.556	2.893

Table 4. Estimate of genetic components for seed characteristics in *J. curcas*

S.No.	Parameters	H ² %	GA	GG
1	Fruit weight	20.11	0.27	10.03
2	Seed weight	18.20	0.04	6.38
3	Seed length	51.58	0.11	6.58
4	Seed circumference	55.63	0.20	6.014
5	Seed moisture content	74.84	2.23	25.62
6	Seed germination	85.34	8.70	13.28

In present investigation the partition of total variance revealed that maximum variance was recorded at phenotypic level through genotypic variance for seed length, seed circumference, seed moisture content and seed germination, while fruit weight and seed weight were influenced by environmental variance (Table 3). However, phenotypic, genotypic and environmental coefficients of variation showed same pattern as variance.

Table 4 depicts the genetic components variation in *J. curcas*. Heritability values varied between 85.34% (seed germination percentage) to 18.19% (seed weight). Similarly maximum value of genetic advance was calculated for seed germination (8.7) and minimum for seed weight (0.04). On the other hand the values of genetic gain were found maximum for moisture content (25.62%) and minimum for seed circumference (6.014%).

The region being lower part of Himalayas represents a wide range of habitat diversity in respect of slope, aspect, altitude and edaphic factor on account of its topography. *J. curcas* occurs as isolated patches in the region distantly placed from each other. Due to the wide geographical distribution there is considerable scope of genetic variation in *J. curcas* seeds, which are the principal means of propagation. Seed contain a lot of variation from one origin to another origin with regard to morphological variation and physiological differences which could be genetic in nature as a result of adaptation to diverse environmental condition prevailing throughout their distributional range (Mathur *et al.*, 1984). Variation refers to the observable differences in individuals for a particular trait. In present investigation average fruit weight was found 2.69 ± 0.36 g, seed weight (0.69 ± 0.62 g), seed length (1.68 ± 0.08 cm), seed circumference (3.26 ± 0.14 cm), seed moisture content (8.69 ± 1.33 %) and seed germination (65.52 ± 8.83 %) in all seed sources with significant differences (Table 2). Seed morphological parameters were taken to examine the seed source variation in *Grewia oppositifolia* by Uniyal *et al.*, [21]. Ginwal *et al.*, [10], determined the variation in *J. curcas* seeds collected from Central India having wide distribution range. Their observations revealed that the magnitude of variation was 29% in seed germination, 24% in seed weight and 6% in seed length. While in present investigation, which represents comparatively narrow distribution range the magnitude of variation was observed 33% in seed germination, 28% in seed weight and 18% in seed length. This indicates that variations in characteristics of *J. curcas* seeds also occur in a narrow distribution range and specifies the good scope in improvement of this species. The seed sources significantly different from each other and represent isolated populations. Morpho-physiological parameters were studied by Saikia *et al.*, [14] for estimation of source variation and genetic differences in *J. curcas* from 17 states of India. Significant trait differences were observed in all the seed characters viz., seed morphology and oil content as were observed in growth characters viz., plant height, and female to male flower ratio and seed yield in the progeny trial of *J. curcas* for evaluating genetic association, and variability in seed and growth characters e.g. Rao *et al.*, [12]. Variability in seed traits and oil content of 24 accessions of *J. curcas* collected from different agroclimatic zones of Haryana state, India were assessed and significant differences was obtained ($P < 0.05$) in seed size, 100-seed weight and oil content between accessions by Kaushik *et al.*, [11].

In present investigation the majority of characters (seed length, seed circumference, seed moisture content and seed germination) were influenced by genotypic variations and only two characters (seed weight and fruit weight) were under the influence of environmental variation. Similar trend was obtained in growth, physiological and biochemical parameters of *Dalbergia sissoo* Roxb. by Rawat and Nautiyal [22]. These differences may partly be due to the genetic factors and partly due to the environmental effect. The observed value of a trait is the phenotypic value of that individual. The related magnitude of these components determines the genetic properties of any particular species [23]. The extent of variability in *Eucalyptus grandis* W.Hill. was assessed by Subramanian *et al.* [24] through genotypic and phenotypic variance, and genotypic and phenotypic coefficient of variation. For proper utilization of observed variation in a species, it is a prerequisite to know the extent of variation and its cause, whether it is due to genetic (heritable) or the environmental and phenotypic (non-heritable) factors. Study of genetic variation in *Acacia catechu* on individual tree and its seed characteristics had been done by Gera and Gera [25]. A detailed review about biology and genetic improvement of *J. curcas* was given by Divakara [26].

The proportion of total variation, which is heritable, is termed as heritability in broad sense [27]. Knowledge of its magnitude gives an idea about scope of effecting genetic improvement through selection. Heritability in broad sense may give useful indication about the relative value of selection in the material at hand, to arrive at a more reliable conclusion. Heritability and associated genetic gain

should be considered jointly. Volker *et al.* [28] has shown that heritability estimates along with genetic gain is more useful than the heritability alone in predicting the resultant effect for selecting the best genotype for given trait. Higher heritability value accompanied by high genetic gain have earlier been reported for seed weight in *Graewia optiva* L. [29] and *Celtis australis* L. [23]. Moderately high heritability estimates associated with moderate genetic advance have earlier been reported for plant height in *Terminalia* species [31] and for seed weight in *Dalbergia sissoo* Roxb. [32] which supports to present finding. High heritability (85.34%) and moderate genetic advance (13.28) value of germination suggesting that high heritability may not necessarily lead to increased genetic gain unless sufficient genetic variability existed in the germplasm. The findings of the present investigation are similar with that of Sardana *et al.* [33,34] observations in *Pea*. Johanson *et al.* [35] observed that a high genetic gain is usually more useful than the heritability value alone in predicting the best individual or seed source and therefore, a heritability estimate alone does not necessarily mean an increased genetic advance. High heritability (broad sense) may be due to non-additive gene action so it shall be reliable only if accompanied by high genetic gain [22]. Although Ramachandra [35] and Devgiri *et al.* [36] in *Accacia catechu* and *Heracleum candicans* respectively reported higher amount of expected genetic gains indicating a wide scope of genetic improvement. Similar results were reported by Gera and Gera in 2006 for *Accacia catechu*. Gingwal *et al.* [10] determine source variation in *J. curcas* seeds collected from ten locations in Central India, a significant seed source variation was observed in seed morphology (colour, size and weight), seed germination (viability, germination percentage), seedling height, collar diameter, leaf/plant, and seedling biomass. The significance of this type of studies and seed source testing in forest tree improvement is well realized [37-39]. In spite of significant differences in studied parameters the limited scope of genetic improvement of the species was found through genetic component analysis.

Thus it is clear that considerable genetic differences exist in all the seed characteristics among the different seed sources of *J. curcas*. Matakund was found as a superior seed source on the basis of seed morphological characters such as fruit weight, seed weight, seed length and seed circumference. On the other hand in case of seed germination Gandhari emerged as superior seed source. The study revealed that, there was clear difference in seed characteristics among the seed sources. The variations in most studied parameters are under genotypic control among seed sources. It is suggested that the seed germination was found superior character for selection of elite seed source for tree improvement program on the basis of heritability value.

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