

Full Length Research Paper

## Genetic association, divergence and variability studies for seed yield and oil content and its contributing traits in *Jatropha* (*Jatropha curcas* L.)

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Accepted 12 February, 2013

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Genetic association, divergence and variability were studied in 24 accessions of *Jatropha curcas* L. for seed and oil yield and its contributing traits. Based on genetic divergence  $D^2$  statistics, 24 accessions were grouped into 14 clusters. Three accessions (BRS-12/05-UpA2, BRS-12/05-UpA3 and BRS-03/06-WbB) were included in cluster XI followed by clusters II, IV, VI, VII, VIII, X, XII and XIII (2 accessions in each case), whereas clusters I, III, V, IX, XIV included only 1 accession in each case. Intra and inter-cluster values ranged from 0.00 to 12.220 and 7.868 to 70.340, respectively and clusters XIV and VI were the most diverse, which could be used in hybridization programme. Phenotypic variances were higher than genotypic variances for all characters. Heritability coupled with genetic advance was higher for plant height (74.101%, 80.171), oil content (77.956%, 16.210) and fruit set (57.430%, 15.890). Substantial amount of genetic variability was noticed among the *Jatropha* accessions. Correlation and path coefficient analyses showed that seed yield/plant was significantly associated with fruit set whereas oil content was found to significantly correlate with plant height, stem diameter and number of branches/plant. Fruit set had the highest positive direct path followed by stem diameter towards seed yield/plant. Fruit set also indirectly contributed to seed yield/plant via plant height and stem diameter. Characters showing significant and positive correlation with seed yield and oil content can be used for genetic improvement of seed and oil yield which will ultimately enhance biodiesel productivity in *J. curcas*.

**Key words:** Divergence, interrelationship, *Jatropha curcas*, oil content, seed yield, variability.

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### INTRODUCTION

*Jatropha curcas* L., an important biodiesel plant, belongs to genus *Jatropha* (Family Euphorbiaceae), embraces about 175 species, which are distributed to Central and South Americas and Asia. About 9 species of *Jatropha* have been recorded in India. Out of these important ones are *J. curcas* L., *Jatropha gossypifolia* L., *Jatropha glandulifera* Roxb., *Jatropha multifida* L., and *Jatropha*

*podagrica* Hook. *J. curcas* is one of the most important biodiesel yielding crop, in India commonly known as Chandrajyot, Jangli arandi, Jamal gota, Kala aranda, Physic nut, Ratanjyot, etc., is a multipurpose plant with several attributes and considerable potential has evoked interest all over the tropics as a potential biofuel crop (Martin and Mayeux, 1985; Takeda, 1982). Global biofuel

production has tripled from 4.8 billion gallons in 2000 to about 16.0 billion in 2007, but still accounts for less than 3% of the global transportation fuel supply (Paul, 2007). Developed countries are using edible oil-seed crops such as soybean, rapeseed, groundnut, sunflower for production of biofuel. However, developing countries like India, having dearth of edible oil (6.31 million tonnes) for consumption, cannot afford to use edible oils for biofuel production and hence non-edible oil seeds such as *Jatropha* (*Jatropha curcas*), a renewable resource, a safe source of energy and a viable alternative to diesel, kerosene, LPG (Liquefied Petroleum Gas), furnace oil, coal and fuel wood (Martin and Mayeux, 1985), explored along with meeting additional criteria of greening the wastelands without compromising the food, fodder security and improve livelihoods (Wani et al., 2006; Reddy et al., 2008). The *J. curcas* oil has been identified as an efficient substitute to be used as fuel for diesel, its utilization as a new source of oil has tremendous scope in contributing to growing needs of country for energy resources. Many workers as Ginwal et al. (2004) reported 10 accessions from India having 33 to 39% seed oil content; Patolia et al. (2007) reported 26 to 35% seed oil content from Indian 23 accessions; Kaushik et al. (2007) reported 28 to 39% seed oil content from 24 Indian accessions in the same way for a different set of accessions seed yield/plant varying from 0.2 to more than 2 kg (Francis et al., 2005). However, high oil content of the seeds is an important crop characteristic, but if seed size, the number of seeds or number of fruits/plant is not accurately accounted for, oil yield/unit area are easily overestimated. In same way, *Jatropha* accessions that produce large seeds and high number of seeds or fruit/plant may be low in oil production per unit area, if oil content is low. In the ideal situation with a high number of seeds/plant in combination with high oil content per seed, it is justified to relate high oil yields with *J. curcas*. To gain maximum benefit from breeding efforts, identification of breeding lines with target traits seed yield and oil content is very important. Very limited information is available on quantitative genetic variation, such as heritability, genetic components of variation and correlation and path coefficients. Such 58 genetic interactions are prerequisite for conducting breeding programs (Eriksson et al., 2007). The importance of diversity for choosing parents for hybridization has been emphasised by several workers. The more diverse the parents, the greater the chances of achieving larger amount of heterotic expression and broad spectrum of variability in segregating generation (Arunachalam, 1981; Falconer, 1989). To create new variability for deriving improved parental lines, among existing diverse accessions appears essential oil (Arunachalam, 1981). The objective of this study was to evaluate genetic diversity, inter-relationship and path coefficients, variability, heritability (broad sense) and genetic gain among 24 accessions of *J. curcas* using cluster analysis on morphological traits.

## MATERIALS AND METHODS

### Description of the experimental plants

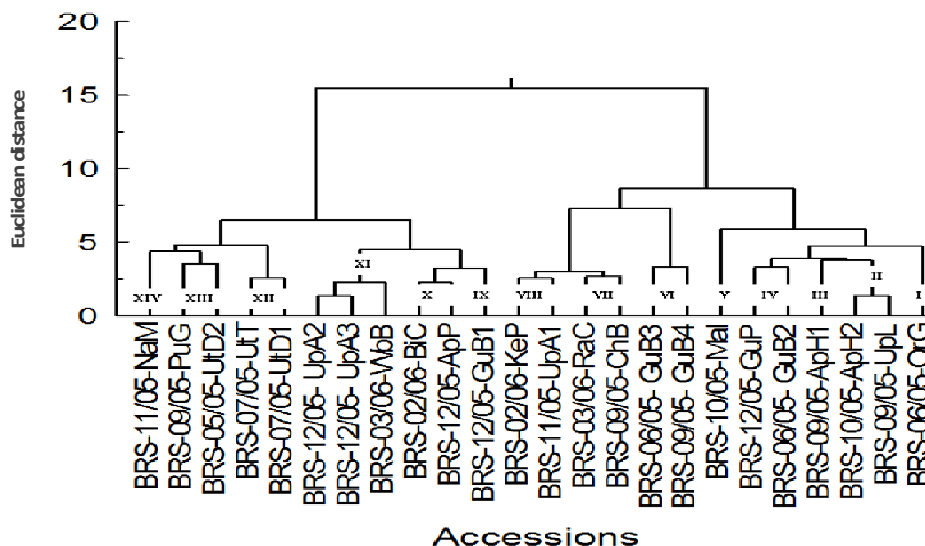
Twenty four accessions of *J. curcas* L., namely BRS-11/05-NaM, BRS-02/06-KeP, BRS-10/05-MaI, BRS-11/05-UpA1, BRS-09/05-PuG, BRS-12/05-UpA2, BRS-12/05-UpA3, BRS-03/06-WbB, BRS-02/06-BiC, BRS-03/06-RaC, BRS-09/05-ChB, BRS-12/05-APp, BRS-12/05-GuB1, BRS-12/05-GuP, BRS-06/05-OrG, BRS-06/05-GuB2, BRS-06/05-GuB3, BRS-09/05-GuB4, BRS-09/05-APh1, BRS-10/05-APh2, BRS-07/05-UtI, BRS-07/05-UtD1, BRS-05/05-UtD2, and BRS-09/05-UpL were collected from different locations of India (Table 1). The *Jatropha* accession cuttings were planted at Banthra Research Station (National Botanical Research Institute), Lucknow, UP, India during year 2005. All the recommended agronomic practices were adopted during the entire period (2005 to 2008) and the observations on plant height (cm), stem diameter (cm), number of branches/plant, inflorescence/plant, total male:female flowers ratio, pollen fertility (%), fruit set, fruit length (cm), fruit width (cm), fruit weight (g), number of seeds/fruit, seed weight/fruit (g), total seed yield/plant (g) and oil content percent (by NMR (Nuclear Magnetic Resonance) analyzer) were recorded (2007 to 2008) based on five randomly selected competitive plants for each accession and the mean values were utilized for statistical analysis.

### TD-NMR (Time domain Nuclear Magnetic Resonance) analysis for seed oil content

All NMR measurements were performed on a Maran bench-top pulsed NMR analyzer (Resonance Instruments, Witney, UK), equipped with a permanent magnet and 18 mm probe head, operating at 23.4 MHz. Prior to NMR analysis, pre-dried samples (<10 weight% moisture content) were equilibrated at 40°C for 30 min. The standard TD-NMR oil analysis method (ISO 10565, 1998) was used. The spin echo pulse sequence used 90 and 180° pulse widths of 6 and 12  $\mu$ s, respectively, and pulse spacing ( $\tau$ ) of 3.5 ms. Each run consisted of 16 scans with a recycle delay of 1 s, and acquisition of a single data point at  $t = 7$  ms. The TD-NMR instrument was calibrated for the *Jatropha* oil sample. TD-NMR sampling of *Jatropha* oil comprise different levels of oil contents, sampled in equal quantities for each testing. Each set consisted of 20 samples; 10 were used for constructing the calibration curves (training set), and the remaining 10 samples were used for validating the model (testing set). For each measurement, the NMR acquired signal was weight standardized and cross-correlated to the reference oil content obtained by the Soxhlet method to construct a linear calibration curve. This calibration was stored in the NMR computer program enabling the evaluation of unknown waste sample oil content using NMR analysis alone. Goodness of the fit ( $R^2$ ) was tested by comparing the calculated versus measured oil content in a linear regression fit. After training and testing of each level of oil content, TD-NMR analysis was used to characterize the oil contents of individual genotype. All TD-NMR screenings were conducted in three replicates. NMR sampling values represent average values of the screenings.

### Statistical analysis

Genetic divergence between accessions was worked out using Mahalanobis  $D^2$  statistics (Mahalanobis, 1936) and the clustering of accessions were done following Tocher's method as described by Rao (1952). Ward's hierarchical clustering (Indostat Cluster Package, 1994) was used for grouping of the accessions in clusters. For analysis of variance (ANOVA), Panse and Sukhatme



**Figure 1.** Euclidean dendrogram for twenty four accessions of *Jatropha* (*Jatropha curcas* L.).

(1978) method was followed. Genotypic, phenotypic and environmental variances ( $\delta^2g$ ,  $\delta^2p$  and  $\delta^2e$ ), genotypic and phenotypic coefficients of variations (GCV and PCV%), heritability broad sense ( $h^2B$ ) and genetic advance (GA%) and genetic gain (%) were estimated according to Singh and Chaudhary (1985).

$$GCV = \frac{\sqrt{\delta^2g}}{\bar{x}} \times 100$$

$$PCV = \frac{\sqrt{\delta^2p}}{\bar{x}} \times 100$$

Broad sense heritability ( $h^2B$ ) was calculated as:

$$h^2B = \frac{\delta^2g}{\delta^2p} \times 100$$

where  $\delta^2g$  = genetic variance,  $\delta^2p$  = phenotypic variance and  $\bar{x}$  = general mean of character.

Expected genetic advance (GA) =  $i \delta p h^2$

$$GA (\%) = \frac{GA}{\bar{x}} \times 100$$

For genotypic and phenotypic correlation coefficients and path coefficient analysis, the method of Dewey and Lu (1959) was followed.

## RESULTS AND DISCUSSION

Source and grouping of clusters for 24 accessions of *J. curcas* are presented in Table 1. Clusters II, IV, VII, VIII, X, XI, XII and XIII having accessions from different geographical sources shows that genetic divergence has no relationship with geographical divergence. The absence of relationship between genetic diversity and geographical diversity indicated that forces other than

geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection, are perhaps responsible for genetic diversity (Nagarajan and Prasad, 1980). On the basis of non-hierarchical Euclidean cluster analysis, 24 accessions were grouped into 14 clusters (Figure 1 and Table 2). The maximum number of 3 accessions were included in cluster XI followed by clusters II, IV, VI, VII, VIII, X, XII and XIII (2 accessions in each case), whereas clusters I, III, V, IX, and XIV included only 1 accession in each case. The cluster pattern proved that geographical diversity need not necessarily be related to genetic diversity. Clusters VI and XIV were most diverse with maximum (70.340) followed by clusters VI and XI (67.312), clusters VI and XIII (66.750) inter-cluster distance (Table 2). Highly divergent accessions would produce a broad spectrum of variable attributes enabling further selection and improvement. Inter-cluster distance between the cluster VII and VIII was the lowest (7.868) indicating that involved accessions are closely related. Intra cluster distance ranged from 0.00 to 12.220. Intra-cluster distance was the highest for cluster XIII (12.220) while the clusters I, III, V, IX and XIV were the lowest (0.00). Cluster mean for various plant characteristics of different clusters for *J. curcas* accessions are presented in Table 3. Cluster I had the highest values for Inflorescence/plant (10.00), fruit set (52.44%) and oil content (30.75%). Cluster II had the highest value for pollen grain fertility (91.82%), while cluster III showed the highest values for number of branches/plant (16.67) and cluster V had maximum seeds/fruit (2.78) and seed yield/plant (41.97 g). Cluster VI showed the highest values for plant height (233.84 cm), stem diameter (4.60 cm), fruit length (2.50 cm), fruit width (2.22 cm), fruit weight (2.65 g) and seed weight/fruit (1.49 g). Cluster X showed maximum male: female flower ratio (32.83).

**Table 1.** Source and grouping of clusters of 24 accessions of *Jatropha curcas* L.).

Cluster	Accessions with their sources
I	BRS-06/05-OrG (Ganjam, Orissa)
II	BRS-09/05-UpL (Lucknow, Uttar Pradesh), BRS-10/05-ApH2 (Hyderabad, Andhra Pradesh)
III	BRS-09/05-ApH1 (Hyderabad, Andhra Pradesh)
IV	BRS-06/05- GuB2 (Banaskantha, Gujrat), BRS-12/05-GuP (Panchmahal, Gujrat)
V	BRS-10/05-Mal (Imphal, Manipur)
VI	BRS-09/05- GuB4 (Banaskantha, Gujrat), BRS-06/05-GuB3 (Banaskantha, Gujrat)
VII	BRS-09/05-ChB (Bilaspur, Chhatisgarh), BRS-03/06-RaC (Chittorgarh, Rajsthan)
VIII	BRS-11/05-UpA1 (Allahabad, Uttar Pradesh), BRS-02/06-KeP (Palakkad, Kerala)
IX	BRS-12/05-GuB1 (Banaskantha, Gujrat)
X	BRS-12/05-ApP (Papumpare, Arunachal Pradesh), BRS-02/06-BiC (West Champaran, Bihar)
XI	BRS-03/06-WbB (Bankura, West Bengal), BRS-12/05-UpA3 (Allahabad, Uttar Pradesh), BRS-12/05-UpA2 (Allahabad, Uttar Pradesh)
XII	BRS-07/05-UtD1 (Dehradun, Uttarakhand), BRS-07/05-UtT (Tehri, Uttarakhand)
XIII	BRS-05/05-UtD2 (Dehradun, Uttarakhand), BRS-09/05-PuG (Gurdaspur, Punjab)
XIV	BRS-11/05-NaM (Mon, Nagaland)

**Table 2.** Estimates of inter- and intra-cluster distances for seed and oil and other characters in *Jatropha curcas* accession.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	0.000	19.770	16.850	15.370	24.240	28.410	30.645	43.785	43.420	61.745	55.190	57.655	59.810	59.000
II		1.760	10.920	10.273	25.585	37.617	20.205	20.860	20.655	26.420	26.310	18.378	18.225	19.420
III			0.000	13.805	35.220	21.540	20.325	26.110	27.380	35.985	40.147	31.020	35.505	30.620
IV				10.510	21.020	21.872	16.920	23.763	28.255	41.135	41.385	36.778	34.835	35.645
V					0.000	33.890	25.790	29.285	38.910	47.830	40.700	56.075	48.210	60.500
VI						10.760	20.625	30.095	46.035	57.330	67.312	64.193	66.750	70.340
VII							7.130	7.868	13.730	19.353	28.565	30.358	29.865	34.675
VIII								6.400	12.115	11.673	20.193	22.585	20.140	25.715
IX									0.00	9.090	10.877	21.485	15.300	22.720
X										5.020	10.237	12.555	17.470	24.845
XI											5.100	17.968	13.485	26.973
XII												6.510	15.403	18.090
XIII													12.220	17.315
XIV														0.000

Variability parameters of metrical traits comprising range and mean values of accessions, GCV and PCV, heritability (broad sense) and genetic

advance are presented in Table 4. Coefficients of variation ranged from 4.329 (fruit length) to 75.355 (seed yield/plant). High values of genotypic

(2043.977) and phenotypic (2758.367) variances were noted for plant weight followed by fruit set (103.607, 180.407), oil content percent (79.427,

**Table 3.** Cluster mean values for various plant characteristics of different cluster for *J. curcas* accessions.

Character/ Cluster	Plant height (cm)	Stem diameter (cm)	No. of branches /plant	Inflorescence/ plant	Male:female flower ratio	Pollen grain fertility (%)	Fruit set (%)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seeds /fruit	Seed weight /fruit (g)	Seed yield/plant (g)	Oil content (%)
Cluster I	224.67	4.33	11.33	10.00	16.14	77.53	52.44	2.41	2.01	1.79	2.07	0.99	24.01	30.75
Cluster II	173.17	3.39	8.67	6.00	15.16	91.82	23.92	2.32	1.89	1.36	1.78	0.80	13.01	28.36
Cluster III	219.00	4.57	16.67	6.67	21.84	79.93	18.33	2.39	2.00	1.42	1.80	0.84	9.37	28.43
Cluster IV	192.67	4.17	8.77	6.17	9.00	89.84	27.72	2.39	2.11	1.91	2.09	1.07	14.53	29.61
Cluster V	144.67	3.63	8.33	5.00	14.41	86.90	29.00	2.41	1.94	2.27	2.78	1.29	41.97	18.41
Cluster VI	233.84	4.60	15.17	6.84	22.75	78.16	18.00	2.50	2.22	2.65	2.70	1.49	9.15	29.81
Cluster VII	131.17	3.89	5.67	5.33	27.76	81.60	16.86	2.39	2.17	1.98	2.22	1.37	8.31	17.44
Cluster VIII	121.84	3.12	4.00	2.67	28.73	81.34	7.415	2.45	2.05	2.05	2.28	1.14	6.58	18.70
Cluster IX	88.67	2.97	4.00	3.33	19.84	70.82	12.83	2.30	2.01	1.48	1.46	1.36	7.08	15.67
Cluster X	89.00	2.57	3.67	1.50	32.83	77.00	5.00	2.17	1.94	1.39	1.95	1.05	2.955	12.91
Cluster XI	94.67	2.41	2.11	2.00	19.78	69.67	11.67	2.13	1.85	1.62	1.77	0.69	14.66	7.74
Cluster XII	149.17	3.00	3.17	2.00	29.32	86.44	7.00	2.01	1.87	1.34	1.67	0.56	1.68	26.81
Cluster XIII	121.92	2.71	2.64	2.00	24.55	78.05	9.33	2.07	1.86	1.48	1.72	0.62	8.17	17.27
Cluster XIV	145.00	3.30	2.00	1.00	21.81	87.65	4.33	2.50	2.00	0.95	1.00	0.33	8.16	25.96

**Table 4.** Estimation of genetic variables for seed and oil and other biometric characters in *Jatropha* (*Jatropha curcas* L.).

S/N	Character	Range	Mean	F cal	CV	$\delta^2g$	$\delta^2p$	$\delta^2e$	GCV%	PCV%	$h^2B$	GA
1	Plant height (cm)	82.67-234.67	146.308±51.044	9.58	18.613	2043.977	2758.367	714.390	30.901	35.897	74.101	80.171
2	Stem diameter (cm)	2.13-4.67	3.344±0.792	7.18	15.317	0.54	0.80	0.26	21.976	26.749	67.5	1.244
3	No. of Branches/plant	1.67-16.67	6.425±4.499	12.57	34.217	18.59	23.41	4.82	67.103	75.301	79.411	7.915
4	Inflorescence/plant	1.00-10.00	4.028±2.501	7.77	38.562	5.447	7.857	2.41	57.941	69.589	69.325	4.003
5	Male:female flower ratio	0.17-38.95	21.109±8.442	1.85	33.111	14.06	63.51	49.45	17.7636	37.754	22.138	3.634
7	Pollen grain fertility %	3.67-58.67	81.455±7.911	4.78	7.691	49.487	88.727	39.24	8.637	11.564	55.774	10.823
8	Fruit set %	0.17-38.97	15.670±11.366	5.05	55.923	103.607	180.407	76.800	64.957	85.715	57.430	15.890
9	Fruit length (cm)	66.94-94.84	2.308±0.156	7.3	4.329	0.02	0.03	3.00	6.128	7.505	66.667	0.239
10	Fruit width (cm)	2.33-52.44	1.988±0.134	6.09	4.743	0.013	0.023	0.01	5.810	7.686	57.143	0.180
11	Fruit weight (g)	1.98-2.58	1.6838±0.468	20.61	10.606	0.21	0.24	0.01	27.216	29.095	87.500	0.883
12	Seeds/fruit	1.80-2.30	1.973±0.415	8.27	12.661	0.153	0.213	0.06	19.852	23.416	71.875	0.684
13	Seed weight/fruit (g)	0.95-3.03	0.969±0.330	9.97	18.726	0.1	0.13	0.03	32.641	37.217	76.923	0.571
14	Seed yield/plant (g)	1.00-2.78	10.470±8.953	3.86	75.355	59.423	121.673	62.249	73.626	105.354	48.838	11.098
15	Oil content %	0.331-65	20.683±9.315	11.61	22.93	79.427	101.887	22.460	43.090	48.803	77.956	16.210

CV = Coefficient of variance,  $\delta^2g$  = genotypic variance,  $\delta^2p$  = phenotypic variance,  $\delta^2e$  = environmental variance, GCV = genotypic coefficient of variance, PCV = phenotypic coefficient of variance,  $h^2B$ =heritability (broad sense), GA=genetic advance.

**Table 5.** Interrelationship for biometric characters calculated from twenty four accessions of *Jatropha* (*Jatropha curcas* L.).

Character	Plant height (cm)	Stem diameter (cm)	No. of Branches/plant	Inflorescence /plant	Male:female flower ratio	Pollen grain fertility (%)	Fruit set (%)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seeds /fruit	Seed weight /fruit (g)	Seed yield/plant (g)	Oil content (%)
Plant height (cm)	1.000	0.831**	0.860**	0.781**	-0.337	0.347	0.587**	0.485*	0.458*	0.418*	0.389	0.247	0.201	0.667**
Stem diameter (cm)		1.000	0.865**	0.848**	-0.130	0.272	0.637**	0.659**	0.736**	0.558**	0.502*	0.504*	0.316	0.674**
No. of Branches/plant			1.000	0.846**	-0.221	0.190	0.599**	0.551**	0.499*	0.480*	0.527**	0.451*	0.283	0.556**
Inflorescence/plant				1.000	-0.327	0.199	0.874**	0.557**	0.503*	0.450*	0.480*	0.460*	0.439*	0.497*
Male:female flower ratio					1.000	-0.164	-0.398*	-0.196	0.127	0.075	-0.036	0.046	-0.389	-0.137
Pollen grain fertility %						1.000	0.220	0.145	0.035	-0.139	0.051	-0.217	0.066	0.400*
Fruit set %							1.000	0.365	0.250	0.319	0.346	0.250	0.691**	0.404*
Fruit length (cm)								1.000	0.695**	0.498*	0.405*	0.548**	0.246	0.321
Fruit width (cm)									1.000	0.722**	0.535**	0.730**	0.017	0.327
Fruit weight (g)										1.000	0.822**	0.778**	0.334	0.194
Seeds/fruit											1.000	0.742**	0.393	0.107
Seed weight/fruit (g)												1.000	0.174	0.103
Seed yield/plant (g)													1.000	0.125
Oil content %														1.000

\*Significant at P=5%; \*\*Significant at P=1% levels.

101.887) and seed yield/plant (59.423, 121.673). The values of phenotypic variances are higher than genotypic variances for all the traits. Genotypic coefficients of variation ranged from 5.810 (fruit width) to 73.626% (seed yield/plant). Heritability ranged from 22.138 (male:female flower ratio) to 87.50% (fruit weight). Heritability coupled with genetic advance was higher for plant height (74.101%, 80.171), oil content (77.956%, 16.210) and fruit set (57.430%, 15.890). Yield is ultimate expression of various yield contributing characters; direct selection for yield could be misleading (Islam and Rasul, 1998; Nath and Alam, 2002). This is difficult to judge what proportion of observed variability is heritable and what proportion is non-heritable, that is, environmental. If variability in population is largely due to genetic cause with least environmental effect, probability of isolating superior genotype is a prerequisite for obtaining higher yield. The pro-

cess of breeding such population is primarily conditioned by magnitude and nature of interactions of genotypic and environmental variations in plant characters. So it becomes necessary to partition the observed variability into its different components and to have an understanding of parameters such as genetic coefficient of variation, heritability and genetic advance. There are a few reports on genetic characterisation and systematic assessment of phenotypic characteristics of different accessions of *J. curcas*. A large variation in seed size and oil content in seeds from various parts of the world were noticed by some workers, while they exhibited high genetic similarity. Kaushik et al. (2007) reported the predominant role of the environment in the higher phenotypic coefficient of variation in some characters in 24 Indian accessions *J. curcas* originating from different agroclimatic zones. Large differences in morphological and bioche-

mical phenotype for seed size and seed oil content were observed in our results.

Recently, Sunil et al. (2008) recorded the phenotypic traits of *J. curcas* plants *in situ* at 4 different ecogeographical regions of India. They noticed pronounced differences in the 9 characters they assessed for a total of 162 accessions in the 4 zones. Similar differences were noticed in the number of fruits and seed oil content and composition. Environment related developmental differences have been noticed in *J. curcas* by Sunil et al. (2008) are reminiscent, since he did not undertake genetic characterisation of the accessions, the reason for the variability is not clear.

Interrelationship for biometric characters calculated from twenty four accessions of *Jatropha* (*J. curcas* L.) are presented in Table 5. Plant height had significant and positive correlation coefficients with stem diameter (0.831), number of branches/

**Table 6.** Path coefficient analyses for seed yield/plant and oil content in *Jatropha curcas* germplasm.

Character	Direct effect	Indirect effects via													Correlation with Seed yield/plant (g) [with oil content]
		Plant height (cm)	Stem diameter (cm)	No. of Branches /plant	Inflorescence /plant	Male :female flower ratio	Pollen grain fertility (%)	Fruit set (%)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seeds /fruit	Seed weight /fruit (g)	Oil content [Seed yield/plant (g)]	
Plant height (cm)	-0.550 [0.152]	- [-]	0.972 [1.369]	0.099 [-0.123]	-0.994 [-0.823]	0.083 [0.029]	-0.020 [0.584]	0.715 [0.358]	0.104 [0.005]	-0.317 [-0.353]	0.161 [0.132]	0.077 [-0.132]	-0.023 [0.075]	-0.106 [-0.081]	0.201 [0.667**]
Stem diameter (cm)	1.170 [1.648]	-0.457 [0.126]	- [-]	0.099 [-0.124]	-1.080 [-0.895]	0.032 [0.011]	-0.016 [0.046]	0.776 [0.388]	0.142 [0.007]	-0.509 [-0.567]	0.215 [0.177]	0.099 [-0.170]	-0.047 [0.154]	-0.108 [-0.127]	0.316 [0.674**]
No. of Branches/plant	0.116 [-0.143]	-0.473 [0.130]	1.012 [1.425]	- [-]	-1.077 [-0.892]	0.055 [0.189]	-0.011 [0.032]	0.730 [0.365]	0.118 [0.006]	-0.345 [-0.385]	0.185 [0.152]	0.104 [-0.179]	-0.042 [0.138]	-0.089 [-0.114]	0.283 [0.556**]
Inflorescence/plant	-1.273 [-1.054]	-0.429 [0.118]	0.992 [1.398]	0.098 [-0.121]	- [-]	0.081 [0.027]	-0.012 [0.034]	1.065 [0.533]	0.120 [0.006]	-0.348 [-0.388]	0.173 [0.143]	0.095 [-0.163]	-0.043 [0.141]	-0.079 [-0.177]	0.439* [0.497*]
Male:female flower ratio	-0.247 [-0.085]	-0.185 [-0.051]	-0.152 [-0.214]	-0.026 [0.032]	0.416 [0.345]	- [-]	0.009 [-0.028]	-0.485 [-0.243]	-0.042 [-0.002]	-0.088 [-0.098]	0.029 [0.024]	-0.007 [0.012]	-0.004 [0.014]	0.022 [0.157]	-0.389 [-0.137]
Pollen grain fertility (%)	-0.058 [0.168]	-0.190 [0.053]	0.318 [0.449]	0.022 [-0.027]	-0.254 [-0.210]	0.041 [0.014]	- [-]	0.268 [0.134]	0.031 [0.002]	-0.024 [-0.027]	-0.053 [-0.044]	0.010 [-0.017]	0.020 [-0.066]	-0.064 [-0.027]	0.066 [0.400*]

plant (0.860), inflorescence/plant (0.781), fruit set percent (0.587) and oil content percent (0.667), respectively. Stem diameter had significant and positive correlation coefficients with number of branches/plant (0.865), inflorescence/plant (0.848), fruit set percent (0.637), fruit length (0.659), fruit width (0.736), fruit weight (0.558) and oil content percent (0.674), respectively. Branches/plant showed significant and positive correlation coefficients with inflorescence/plant (0.846), fruit set percent (0.599) and fruit length (0.551). Inflorescence/plant had positive and significant correlation coefficients with fruit set

percent (0.874) and fruit length (0.557). Fruit set percent had positive and significant correlation coefficients with seed yield/plant (0.691). Fruit length had positive and significant correlation coefficients with fruit width (0.695) and fruit weight (0.548), respectively. Fruit width had positive and significant correlation coefficients with fruit weight (0.722), seeds/fruit (0.535) and seed weight/fruit (0.730), respectively. Fruit weight had positive and significant correlation coefficients with seeds/fruit (0.822) and seed weight/fruit (0.778), respectively. Seeds/fruit had positive and significant correlation coefficients with seed weight/fruit (0.742).

Path coefficient analyses for seed yield/plant and oil content for *J. curcas* germplasm are presented in Table 6. Stem diameter (1.170), fruit set (1.218), fruit length (0.215), fruit weight (0.385) and seed/fruit (0.197) showed significant and positive direct path effect on seed yield/plant, while plant height (-0.550), inflorescence/plant (-1.273), male:female flower ratio (-0.247), fruit width (-0.692) and oil content percent (-0.160) showed significant and negative direct path effect on seed yield/plant. Plant height (0.972), number of branches/plant (1.012), inflorescence/plant (0.992), pollen grain fertility percent (0.318), fruit

Table 6. Contd.

Character	Direct effect	Indirect effects via													Correlation with Seed yield/plant (g) [with oil content]
		Plant height (cm)	Stem diameter (cm)	No. of Branches /plant	Inflorescence /plant	Male :female flower ratio	Pollen grain fertility (%)	Fruit set (%)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seeds /fruit	Seed weight /fruit (g)	Oil content [Seed yield/plant (g)]	
Fruit set (%)	1.218 [0.609]	0.323 [0.089]	0.745 [1.049]	0.069 [-0.086]	-1.113 [-0.922]	0.098 [0.034]	-0.013 [0.037]	-	0.078 [0.004]	-0.173 [-0.193]	0.123 [0.101]	0.068 [-0.117]	-0.023 [0.076]	-0.064 [-0.278]	0.691** [0.404*]
Fruit length (cm)	0.215 [0.011]	-0.267 [0.074]	0.771 [1.087]	0.064 [-0.079]	-0.709 [-0.587]	0.048 [0.017]	-0.008 [0.024]	0.444 [0.222]	-	-0.481 [-0.536]	0.192 [0.158]	0.080 [-0.138]	-0.051 [0.168]	-0.051 [-0.099]	0.246 [0.321]
Fruit width (cm)	-0.692 [-0.771]	-0.252 [0.069]	0.860 [1.212]	0.058 [-0.071]	-0.641 [-0.530]	-0.031 [-0.010]	-0.002 [0.005]	0.305 [0.152]	0.149 [0.008]	-	0.278 [0.229]	0.106 [-0.182]	-0.068 [0.223]	-0.052 [-0.007]	0.017 [0.327]
Fruit weight (g)	0.385 [0.317]	-0.230 [0.063]	0.652 [0.919]	0.055 [-0.069]	-0.573 [-0.474]	-0.018 [-0.006]	0.008 [-0.023]	0.389 [0.195]	0.107 [0.006]	-0.500 [-0.557]	-	0.162 [-0.279]	-0.073 [0.238]	-0.031 [-0.135]	0.334 [0.194]
Seeds/fruit	0.197 [-0.340]	-0.214 [0.059]	0.587 [0.827]	0.061 [-0.075]	-0.611 [-0.506]	0.009 [0.003]	-0.003 [0.008]	0.421 [0.211]	0.087 [0.004]	-0.371 [-0.413]	0.316 [0.260]	-	-0.069 [0.227]	-0.017 [-0.159]	0.393 [0.107]
Seed weight/fruit (g)	-0.093 [0.306]	-0.136 [0.037]	0.589 [0.830]	0.052 [-0.065]	-0.585 [-0.485]	-0.011 [-0.004]	0.013 [-0.037]	0.304 [0.152]	0.118 [0.006]	-0.505 [-0.562]	0.299 [0.246]	0.147 [-0.252]	-	-0.016 [-0.070]	0.174 [0.103]
Oil content [Seed yield/plant (g)]	-0.160 [-0.403]	-0.367 [0.030]	0.788 [0.521]	0.064 [-0.040]	-0.632 [-0.463]	0.034 [0.033]	-0.023 [0.011]	0.492 [0.421]	0.069 [0.003]	-0.226 [-0.013]	0.075 [0.106]	0.021 [-0.134]	-0.010 [0.053]	-	0.125 [0.125]

Residual = 0.12252 [Residual = 0.30930]. Values for path coefficients of oil content are given in [ ].

set (0.745), fruit length (0.771), fruit width (0.860), fruit weight (0.652), seeds/fruit (0.587), seed weight/fruit (0.589), and oil content percent (0.788) showed significant and positive indirect path effect via stem diameter on seed yield/plant. Plant height showed significant positive indirect effect via stem diameter (0.972) and fruit set (0.715), while it showed significant negative

indirect effect via inflorescence/plant (-0.994) and fruit width (-0.317) on seed yield/plant. Stem diameter (1.648), fruit set (0.609) and fruit weight (0.317) showed significant and positive direct path effect on oil content, while inflorescence/plant (-1.054), fruit width (-0.771), seeds/fruit (-0.340) and seed yield/plant (-0.403) showed significant and negative direct path effect on oil content

percent.

### Conclusion

The diverse accessions can be utilized for improvement of yield productivity. From the foregoing, it is evident that the accessions from



clusters VI, XI, XIII and XIV may be used for hybridization programme (as accessions from cluster VI with accessions of clusters XI, XIII and XIV) to generate wide range of variability and provide transgressive segregants for enhanced yield. In cluster XI, oil content is relatively lower (7.74%) as compared to cluster XIII and XIV but having higher seed yield/plant as compared to cluster XIII and XIV. For ideal situation with a high seed yield/plant in combination with high oil content, the parents may be selected from diverse clusters (cluster VI and XI) having contrast values for both traits. BRS-06/05- GuB3, BRS-09/05- GuB4, BRS-06/05-OrG and BRS-11/05-NaM being genetically diverse from the rest of the accessions could be used in hybridization with all the clusters.

Association and path coefficient analyses revealed that parents for hybridization should be selected of short height, thick stem with multiple branches, inflorescence having less male:female ratio and high fruit set percent, fruit of higher length and lower width with higher fruit weight, it will improve seed yield/plant and oil content percent of this crop.

The present study reveals that there exists considerable amount of genetic divergence and variability in this particular species in India with respect to oil content and seed yield and its contributing traits which offers scope for breeding. Based on correlation and path coefficient studies, it is evident that selection of short stature plant with more branches consisting least male:female flower ratio, fruit width, higher fruit set percent and fruit length will be appropriate for hybridization to increase seed and oil content in this crop.

## ACKNOWLEDGEMENTS

The authors are thankful to the Director, CSIR-National Botanical Research Institute, Lucknow for the encouragement and facilities offered for the conduction of experiment.

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