Forest Research
Open Access

Divakara, Forest Res 2017, 6:2
DOI: 10.4172/2168-9776.1000201

Research Article OMICS International

Assessing Variability and Divergence of *Jatropha curcas* Linn. Germplasm Under *Ex-situ* Conditions

Divakara BN*

Institute of Wood Science and Technology, Bangalore, Karnataka, India

Abstract

An evaluation of 100 genotypes of *Jatropha curcas* L. was carried out to assess variability and character association and to identify diverse genotypes with superior growth traits. Variability studies revealed that, 39 accessions performed better in terms of above average values for volume index (479.41 cm^3), indicating better vigor of the plants. Genotypes IC 555380, IC 555381, IC 555379, IC 569133 were found to be superior on the basis of plant height (100.34 cm), collar diameter (3.59 cm), number of branches (3.34) and volume index (1054.91 cm^3) respectively. A wide range of variation was observed for plant height (41.11-100.34 cm), collar diameter (1.95-3.59 cm), branch number (1.36-3.34) and volume index (172.10-1045.91 cm^3). Estimates of broad sense heritability ranged from 5.28 to 29.78%, genetic advance in percent of the mean ranged between 4.24 and 32.82 with number of branches giving the lowest value and volume index giving the highest value. All the growth traits showed positive significant correlation at both genetic and phenotypic levels with volume index. Path analysis of growth traits revealed that the height (0.719) is the most pronounced trait contributing directly to volume index followed by collar diameter (0.206) and number of branches (0.110). Diversity analysis using Mahalanobis D^2 resulted in 7 clusters. Genotypes in cluster 2,3,4,5, and 6 have combination of desirable traits and can be directly selected for further improvement.

Keywords: *Jatropha curcas*; Co-efficient of variation; Heritability; Correlation; Diversity analysis; Genetic advance

Introduction

Biodiesel is a fast-developing alternative fuel in many developed and developing countries of the world because of demand, necessary policy support and technological availability. Biodiesel production from vegetable oils during 2004-05 was estimated to be 2.36 million tonnes globally. Of this, EU countries (1.93 million tonnes) and the USA (0.14 million tonnes) together accounted for 88% and rest of the world (0.29 million tonnes) for the remaining 12% [1]. Global biodiesel production is set to grow at slightly higher rates than for bioethanol-which maintains the largest share to reach 24 billion liters by 2017 [2] India consumes approximately 40 million tonnes of diesel and ranked fifth in the world after the US, China, Russia and Japan in terms of fossil fuel consumption. Many developed countries are using edible oil-seed crops such as soybean, rapeseed, groundnut, sunflower for production of bio-diesel. However, developing countries like India, having dearth of huge quantity of edible oil (6.31 million tonnes) for consumption, cannot afford to use edible oils for biodiesel production and hence non-edible oil seeds Jatropha *(Jatropha curcas)* is explored for this purpose.

Jatropha curcas commonly known as purging nut, physic nut is synonyms to *Curcas purgans* Medik, *Ricinus americanus* Miller, *Castiglionia lobata* Ruiz & Pavon, *Jatropha edulis* Cerv, 1. *acerifolia* Salisb, *Ricinus jarak* Thunb, *Curcas adansoni* Endl, *Curcas indica* A. Rich, *Jatropha yucatanensis* Briq, *Curcas curcas* (L.) Britton & Millsp. and belongs to family Euphorbiaceae. *J. curcas* is native of tropical America, but is now found abundantly in many tropical and sub-tropical regions throughout Africa and Asia because of likely distribution by Portuguese ships via the Cape Verde islands and Guinea Bissau to other countries in Asia and Africa [3]. *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, adoption to wide agro-climatic condition, bushy/shrubby nature and multiple uses of different plant parts [4] In view of these advantages, many investors, policy makers and clean development mechanism (CDM) project developers are interested to tackle the twin challenges of energy supply and GHG emission reduction. But unfortunately for several reasons, both technical and economical, the full potential of *J. curcas* is far from being realized. Apart from agronomic, socioeconomic and institutional constraints, planned crop improvement programs are lacking globally. Earlier research programs involving large-scale plantations launched in Brazil, Nicaragua and India indicated that the crop productivity is far too low to be commercialized. In extreme cases, the plantations failed to produce fruits. There is lack of bench mark descriptors and information on genetic variability, effects of environment and genotype x environment (G × E) interaction [5]. Improved varieties with desirable traits for specific growing conditions are not available, which makes growing jatropha a risky business.

The key to success of any genetic improvement programme lies in the availability of genetic variability for desired traits. Genetic resource through exploration, introduction, characterization and evaluation will provide strong base for development of improved varieties by following different methods. Comprehensive work on collection, characterization and evaluation of germplasm for growth, morphology, seed characteristics and yield traits is still in its infancy in jatropha. The fact that jatropha has adapted itself to a wide range of edaphic and ecological conditions suggests that there exists considerable amount of genetic variability to be exploited for potential realization [6]. Species and provenance trials contribute fundamental information for further breeding and genetic improvement [7]. Keeping this in view and

***Corresponding author:** Divakara BN, Scientist, Institute of Wood Science and Technology, Bangalore-560 003, Karnataka, India, Tel: +919483253839; E-mail: bndsira@gmail.com

Received Mach 24, 2017; **Accepted** March 28, 2017; **Published** June 01, 2017

Citation: Divakara BN (2017) Assessing Variability and Divergence of *Jatropha curcas* Linn. Germplasm Under *Ex-situ* Conditions. Forest Res 6: 201. doi: 10.4172/2168-9776.1000201

Copyright: © 2017 Divakara BN. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

paucity of information in areas of genetic improvement, the present study was designed to exploit the resource base potentiality of one hundred accessions of *J. curcas* selected from various locations from India.

Materials and Methods

One hundred accessions of *J. curcas* were collected from Department of Biotechnology, Govt. of India under network project for multi-locational trial. *J. curcas* germplasm were collected systematically via exploration survey in different ecogeographical zones of India. Cuttings were collected from marked candidate plus trees (CPTs) and were planted in polybags filled with potting mixture of soil, sand and farm yard manure. (1:1:1). Regular weeding, watering operations were attended during nursery stage. Six month old rooted cuttings were planted as per randomized block design (RBD) with 4 replications along with boundary planting. In each replication, nine plants of each accession were planted at Nagari campus (23˚ 19' N latitude, 85˚ 12' E longitude) of the institute during December, 2010. Spacing of 3×3 m between plants and row were maintained. After one year of planting data on growth traits viz. plant height, collar diameter, number of branches and volume index were recorded. Plant height and collar diameter was measured using tape and digital caliper respectively and expressed in cm. All live primary and secondary branches were counted and recorded as total number of branches. Volume index was estimated by multiplying basal diameter with plant height and expressed as cm^3.

{Volume index=[Diameter (cm)]^2 × Height (cm)} [8]

Data analysis

Growth data recorded on 100 genotypes of *J. curcas* were used for Analysis of Variance (ANOVA) to understand the significance among the genotypes for growth traits [9]. The phenotypic variation for each trait was partitioned into components due to genetic (hereditary) and non-genetic (environmental) factors and estimated using the following formula [10]:

V_p=MSG/r; V_g=(MSG-MSE)/r; V_e=MSE

where, MSG, MSE and r are the mean squares of CPT's, mean squares of error and number of replications, respectively.

The phenotypic variance (V_p) is the total variance among phenotypes when grown over the range of environments, the genotypic variance (Vg) is the part of the phenotypic variance that can be attributed to genotypic differences among the phenotypes, and the error variance (V_e) is part of the phenotypic variance due to environmental effects. To be able to compare the variation among traits, phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were computed according to the method suggested by Burton:

PCV=(√Vp/X) × 100; GCV=(√Vg/X) × 100

Vp, Vg and X are the phenotypic variance, genotypic variance and grand mean for each studied trait respectively.

Broad sense heritability (h^2b) was calculated according to Allard as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p). Genetic advance (GA) expected was estimated following [11] as below:

GA=K·h^2b·√Vp;

where K is the selection differential (the value of K is 2.06 assuming selection of 5% of the genotypes).

GA was expressed in percent and mean using Genetic gain [(GA/X) × 100].

Phenotypic (r_p) and genotypic (r_g) correlations were further computed to examine inter-character relationships among growth traits following [9] as:

rp=Covp (x1, x2)/[Vp(x1) · Vp(x2)] ½

rg=Covg (x1, x2)/[Vg(x1) ·Vg(x2)] ½

Covp and Covg are phenotypic and genotypic covariances for any two traits x1 and x2, respectively, and Vp and Vg

are the respective phenotypic and genotypic variances for those traits. Path coefficient analysis was done using genotypic correlation coefficients following [12].

The genetic diversity of 100 accessions of *J. curcas* was estimated using Mahalanobis D^2 statistics [13]. The concept of Mahalanobis genetic distances, among the multivariate distance methods, has been shown to be robust [14] because of having vital utility in differentiating well defined plus trees, which is basic and fundamental for estimating the extent of diversity among the selected genotypes. The more diverse the parents within the overall limit of fitness, the greater the chances of obtaining a higher amount of heterotic expression and a broad spectrum of variability in segregating generations [15]. Owing to large amount of genetic variations encountered in open pollinated trees, it becomes an essential requirement to assess and analyze the extent of genetic divergence in the germplasm of a species. The clusters, derived from distance matrices, were formed according to criterion used by Tocher as described by [16]. This procedure starts with two closely associated genotypes (represented here by plus trees) and finds a third genotype which has the smallest average D^2 from the first two. Next, the fourth is chosen to have smallest average D^2 from the first three, and so on. There is an increase in the average D^2 within a cluster whenever an additional genotype is included. The limit for inclusion of a new genotype corresponds to the minimum generalized distance, above which the newly added genotype has to be considered outside the former cluster. Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal lntl, Software as suggested by Singh and Chaudhary [17].

Results

ANOVA obtained for all the growth traits *viz*. plant height, collar diameter, number of branches and volume index showed significant variation among the selected 100 genotypes of *J. curcas* indicating the presence of adequate variability. The variability analysis revealed that 39 accessions performed better in terms of above average values for volume index (479.41 cm^3), among the accessions evaluated in the field, indicating the vigor of the plants. Similarly, 41, 51 and 41 accessions recorded value that are more than the average for plant height (58.38 cm), collar diameter (2.68 cm), and number of branches (2.10), respectively (Table 1). Genotype IC 555380, IC 569133 recorded highest plant height and volume index with 100.34 cm and 1045.91 cm^3 respectively, whereas, IC 555381 recorded highest collar diameter (3.59 cm). Though range is a crude measure of variability present in genotypes, it does give an idea of spread of variation for a particular character. A wide spread of variation was observed for plant height (41.11-100.34 cm), collar diameter (1.95-3.49 cm), number of branches (1.36-3.34) and volume index (172.10-1045.91 cm^3) (Table 3). In general, the study revealed that more than 40% of the evaluated genotypes recorded values greater than average for different growth traits showing the superiority of the collection which can be used in improvement program.

S. No.	Genotypes	Plant height (cm)	Collar diameter (cm)	Number of branches	Volume index (cm^3)
1	IC 555379	76.01	3.46	3.34	923.52
2	IC 555383	65.28	3.4	3.09	753.9
3	IC 555381	79.86	3.57	2.52	1041.69
4	IC 560688	58.31	2.56	1.93	419.2
5	IC 560687	56.38	2.77	1.92	495.58
6	IC 555380	100.34	3.05	2.34	952.77
7	IC555382	67.54	2.91	1.93	585.48
8	IC 564010	71.87	2.95	1.83	636.94
9	IC 564011	76.42	3.05	1.94	732.35
10	IC 569122	60.1	2.41	1.58	352.08
11	IC 558217	57.52	2.65	1.9	415.01
12	IC 569134	49.68	2.61	1.65	354.44
13	IC 564020	61.12	2.88	2.4	511.76
14	IC 565667	85.03	3.3	2.79	938.18
15	IC 558214	80	3.49	2.69	1024.06
16	IC 558221	81.58	3.19	2.33	881.51
17	IC 566614	66.22	2.78	2.03	566.88
18	IC 558209	59.99	2.69	1.86	438.72
19	IC 566533	45.92	2.52	2.05	294.1
20	IC 569135	47.94	2.15	1.48	251.27
21	IC 569130	62.7	3.25	2.83	712.66
22	IC 558222	69.88	2.81	1.68	566.62
23	IC 558213	74.79	2.94	2.04	737.61
24	IC 566535	83.94	3.16	2.33	845.82
25	IC 569133	87.9	3.43	2.78	1045.92
26	IC 566603	53.3	2.61	2.31	404.99
27	IC 565669	51.9	2.72	2.97	403.08
28	IC 566612	63.59	3.03	2.32	683.71
29	IC 569142	44.62	2.3	1.36	280.72
30	IC 566532	48.56	2.39	1.41	284.75
31	IC 566538	56.61	2.5	2	377.18
32	IC 558215	41.12	2.33	1.8	241.67
33	IC 566536	67.3	3.33	1.96	852.42
34	IC 564023	70.63	2.88	1.88	706.81
35	IC 566602	51.69	2.55	1.79	382.89
36	IC 566607	52.94	2.62	1.63	397.87
37	IC 566604	72.25	3.48	2.14	967.09
38	IC 564013	55.6	2.81	2.32	498.83
39	IC 565668	73.86	2.65	1.93	515.08
40	IC 569131	67.09	3.04	2.86	679.46
41	IC 558212	56.79	2.48	1.48	435.78
42	IC 566601	48.88	2.3	1.74	329.91
43	IC 558210	61.04	2.78	2.04	512.65
44	IC 569129	60.15	2.92	2	533.88
45	IC 550790	61.08	2.63	1.9	512.75
46	IC 528114	65.21	2.82	2.36	572.53
47	IC 471359	61.54	2.71	2.29	452.41
48	IC 471360	48.34	2.23	1.74	300.18
49	IC 471356	68.47	2.59	2.38	613.72
50	IC 468910	63.5	2.72	1.81	540.04
51	IC 471358	51.51	2.3	2	283.73
52	IC 471344	52.86	2.83	2.44	482.26
53	IC 471352	64.25	2.96	1.84	640.17
54	IC 468909	43.03	2.28	1.85	240.98
55	IC 471353	43.67	2.34	1.44	239.82
56	IC 471349	41.11	2.14	1.58	239.38
57	IC 471126	43.15	2.15	2.65	243.6
58	IC 468908	50.54	2.33	1.79	323.51
59	IC 471346	45.76	2.22	2.38	271.85
60	IC 468919	47.88	2.72	2.88	374.51

61	IC 471345	51.74	2.26	1.38	281.62
62	IC 471357	42.54	2.52	2.19	301.81
63	IC 471343	54.24	2.71	2.04	449.23
64	IC 468907	53.91	2.23	1.42	282.36
65	IC 540920	59.28	2.5	2.07	413.15
66	IC 468917	52.9	2.45	2.54	319.79
67	IC 471354	43.44	2.31	2.12	267.47
68	IC 471355	43.1	2.38	1.61	261.82
69	IC 471124	51.54	2.38	1.79	307.31
70	IC 540922	58.56	2.46	1.79	359.96
71	IC 553592	74.96	3.17	3.01	754.89
72	IC 553591	60.7	2.5	1.72	385.95
73	IC 561232	53.37	2.03	2.13	227.11
74	IC 561231	62.33	3.26	1.99	999.95
75	IC 561235	55.11	2.45	1.82	352.58
76	IC 569353	50.74	2.77	3.24	408.17
77	IC 561230	45.12	2.68	1.93	321.28
78	IC 569361	58.26	2.81	2.1	477.47
79	IC 569355	49.72	3.08	2.23	713.71
80	IC 561229	55.28	2.62	1.95	382.32
81	IC 569362	49.47	2.55	1.41	331.8
82	IC 569356	52.84	2.56	2.1	346.3
83	IC 550431	50.97	2.51	2.53	338.35
84	IC 550449	54.53	2.74	2	411.77
85	IC 561292	55.91	2.57	1.94	381.65
86	IC 569349	47.89	2.52	1.54	315.59
87	IC 568554	55.84	2.54	1.96	363.6
88	IC 561290	57	2.81	2.35	522.66
89	IC 569346	62.01	2.61	2.21	439.05
90	IC 561291	52.44	2.49	2	323.5
91	IC 568552	53.3	2.61	2.94	362.17
92	IC 561287	46.81	2.06	2.5	194.88
93	IC 569342	51.54	2.41	2.17	301.89
94	IC 569344	46.69	1.95	2.17	183.28
95	IC 569343	51.71	2.26	1.78	262.08
96	IC 560620	73.44	3.08	2.76	700.84
97	IC 560627	57.32	2.51	1.71	374.25
98	IC 560653	39.82	2.11	1.66	172.09
99	IC 560626	69.86	2.81	2.37	565.93
100	IC 566889	55.47	2.73	2.53	429.88
	Mean	**58.38**	**2.68**	**2.1**	**479.42**
	SEM	**1.7**	**0.2**	**0.08**	**22.07**
	CD	**5.25**	**0.62**	**0.25**	**68.2**

Table 1: Mean performance of *J. curcas* genotypes for morphometric traits.

Genetic estimates and association of traits

The amount of genetic variations and association was evident from the study of PCV, GCV and correlation analysis presented in Tables 2 and 3. The magnitude of PCV was higher than the corresponding GCV for all the growth traits. Highest values of GCV and PCV were recorded for volume index (33.75%, 71.47%) followed by plant height (15.89%, 29.12%). The highest heritability of 29.78% was recorded for plant height. In general, all the growth traits viz. plant height, collar diameter, number of branches, volume index recorded low to moderate heritability with genetic advance in that order. The genetic advance (per cent of mean) ranged from 4.25% for number of branches to 32.82% for volume index.

All the 12 (6 genotypic and 6 phenotypic) correlations of growth traits *viz.* plant height, collar diameter, number of branches and volume index (Table 3) were found to be significant and positive correlated at both genotypic and phenotypic level. Measure of correlation does not consider the dependence of one variable on the other. Therefore, the direct contribution of each component to the dependent character (volume index) and the indirect effect through other components cannot be differentiated from mere correlation studies. A statistical method called path coefficient analysis developed by [18] 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 of growth traits revealed that, the plant height (0.719) is the most pronounced character contributing directly to volume index followed by collar diameter (0.206) and number of branches (0.110) (Table 4). This suggests that, plant height in *J. curcas* should invariably be given attention in the selection of plants at nursery stage for high volume index.

Traits	Mean	Range	Genotypic co-efficient of variance (GCV)	Phenotypic coefficient of variance (PCV)	Heritability (%)	Genetic Advance (%) of mean
Plant height (cm)	58.38	41.11-100.34	15.89	29.12	30.0	17.87
Collar diameter (cm)	2.68	1.95 -3.49	8.25	23.02	13.0	6.09
Number of branches	2.10	1.36 -3.34	8.98	39.06	5.28	4.25
Volume index (cm^3)	479.42	172.09 - 1045.92	33.75	71.47	22.29	32.82

Table 2: Mean, range, genotypic and phenotypic coefficient of variation, heritability and genetic advance for morphometric traits in *J. curcas*.

Traits		Collar diameter	Number of branches	Volume index
Plant height	G	0.97**	0.46**	0.97**
	P	0.69**	0.38**	0.82**
Collar diameter	G		0.86**	0.99**
	P		0.45**	0.93**
Number of branches	G			0.62**
	P			0.43**
**Significant at *P*=0.01				

Table 3: Genotypic (G) and Phenotypic (P) correlation coefficient for morphometric traits in *J. curcas*.

Traits	Plant height	Collar diameter	Number of branches
Plant height	0.719	0.200	0.050
Collar diameter	0.700	0.206	0.094
Number of branches	0.330	0.176	0.110
Residual effect=0.1724			

Table 4: Path analysis of morphometric traits with volume index.

Divergence studies

All 100 genotypes of *J. curcas* were subjected to divergence studies using Mahalanobis D^2 statistics and genotypes under investigation grouped into 7 clusters, indicating wide diversity (Table 5). The maximum number of genotypes (83) was included in cluster-VII followed by cluster-I with 7 genotypes. The cluster II, Ill, IV, V, and VI contained two genotypes each. Intra and inter-cluster divergence suggests the distance (divergence) between the genotypes of different clusters (Table 6). Cluster VII contained 83 genotypes and showed maximum intra cluster distance (1.77) closely followed by cluster I (1.67) because the genotypes were from different locations. Thus, the genotypes in cluster VII and I were most heterogeneous and can be best used for within group hybridization. The highest inter-cluster distance (Table 6) was found between cluster I and II (1.83) followed by I and VII (1.79) suggesting wide diversity between these groups. Cluster means indicated a wide range of variation for all the growth traits (Table 7). Cluster I recorded maximum values for plant height (63.94 cm), collar diameter (2.98 cm), number of branches (2.38) and volume index (625.59 cm^3) followed by cluster III except for trait plant height. Cluster I had genotype (IC 555381) containing high collar diameter (3.57 cm) and volume index (1041.69 cm^3) and cluster I had genotype (CPT-15) containing high seed length and 2D surface area. The contribution of individual characters to the diversity has been worked out, the trait volume index contributed maximum to genetic diversity in respect of per cent contribution and rank total, 44.75 and 2215 respectively.

Discussion

The study of growth traits of *J. curcas* wild accessions collected from the natural populations following planting in a common place is useful step in ascertaining genetic variability of the populations. Significant variation among genotypes was observed for all the growth traits. Growth traits are important characters that can be improved upon by selection and breeding programme. Though the selection of superior trees was carried out intensively and clonal superiority over seed raised plants was established [19], genetic superiority *per se* needs to be determined. The genetic estimates can be very useful tools in predicting the amount of gain expected in short period. The variation among genotypes is commonly used as an estimate of total genetic variation and to calculate the degree of genetic control for a particular trait [20]. Higher difference between PCV and GCV for all growth traits and moderate estimates of heritability (broad sense) for all growth traits under study revealed the influence of environment on variability present. However, it should be noted that estimation of heritability is of little significance in coherent selection breeding programs unless accompanied by sufficient genetic gain [21]. Due to large differences in the phenotypic variation between different traits, genetic advance is not directly related to heritability values. In the present study, low to moderate genetic advance values for growth traits indicate that improvement could be made in these characters. Results are in similar lines with [22] in *J. curcas*. This could be due to extreme variation in the material investigated, and smaller values for genetic advance are expected in further selection cycles in a more improved material. Within the growth traits volume index showed maximum advance indicating that the progress in shifting the genotypic mean and gene frequencies of plant growth in the population could be achieved in the desired direction by selection to fit into agroforestry systems, which inturn controls bearing habit and seed and oil yield. High heritability for growth parameters have been reported in *Tectona grandis* [23] and accompanied by high genetic advance in *Prosopis cineraria* [24].

The ultimate goal of the tree improvement is to improve tree species for growth and yield. Growth and yield traits are complex and the end product depends on the interplay of many physiological and morphological attributes, hence improvement based on per se performance alone might prove to be less effective. This can be overcome through the selection of superior genotypes for which often an indirect selection is performed. In genetic improvement of growth and seed traits of *J. curcas* clear understanding of the relationships among different growth and seed traits is very essential. As variation among genotypes used for estimation of genetic variation and genetic

Cluster	Number of accessions	Accessions
I	7	IC 555379, IC 555383, IC 555381, IC 560688, IC 560687, IC 561292, IC 568554
II	2	IC 566601, IC 471360
III	2	IC 564013, IC 561290
IV	2	IC 569356, IC 561291
V	2	IC 569134, IC 569349
VI	2	IC 558217, IC 561229
VII	83	IC 555380, IC 555382, IC 564010, IC 564011, IC 569122, IC 564020, IC 565667, IC 558214, IC 558221, IC 566614, IC 558209, IC 566533, IC 569135, IC 569130, IC 558222, IC 558213, IC 566535, IC 569133, IC 566603, IC 565669, IC 566612, IC 569142, IC 566532, IC 566538, IC 558215, IC 566536, IC 564023, IC 566602, IC 566607, IC 566604, IC 565668, IC 569131, IC 558212, IC 558210, IC 569129, IC 550790, IC 528114, IC 471359, IC 471356, IC 468910, IC 471358, IC 471344, IC 471352, IC 468909, IC 471353, IC 471349, IC 471126, IC 468908, IC 471346, IC 468919, IC 471345, IC 471357, IC 471343, IC 468907, IC 540920, IC 468917, IC 471354, IC 471355, IC 471124, IC 540922, IC 553592, IC 553591, IC 561232, IC 561231, IC 561235, IC 569353, IC 561230, IC 569361, IC 569355, IC 569362, IC 550431, IC 550449, IC 569346, IC 568552, IC 561287, IC 569342, IC 569344, IC 569343, IC 560620, IC 560627, IC 560653, IC 560626, IC 566889

Table 5: Clustering of *J. curcas* genotypes.

Clusters	I	II	III	IV	V	VI	VII
I	**1.67 (2.80)**	1.83 (3.34)	1.23 (1.52)	1.48 (2.18)	1.69 (2.86)	1.40 (1.95)	1.79 (3.19)
II		**0.15 (0.02)**	1.22 (1.48)	1.19 (1.43)	1.24 (1.54)	1.30 (1.70)	1.60 (2.57)
III			**0.17 (0.03)**	0.71 (0.51)	1.02 (1.03)	0.80 (0.64)	1.42 (2.00)
IV				**0.18 (0.03)**	0.75 (0.56)	0.42 (0.18)	1.46 (2.14)
V					**0.19 (0.04)**	0.71 (0.50)	1.64 (2.70)
VI						**0.22 (0.05)**	1.43 (2.05)
VII							**1.77 (3.12)**

Table 6: Average inter and intra cluster distance and D^2 values of *J. curcas* genotypes.

Traits/ Cluster	I	II	III	IV	V	VI	VII
Plant height (cm)	63.94	48.61	56.30	52.64	48.79	56.40	58.61
Collar diameter (cm)	2.98	2.27	2.81	2.52	2.56	2.63	2.66
Number of branches	2.38	1.74	2.34	2.05	1.59	1.92	2.10
Volume index (cm^3)	625.59	315.04	510.74	334.90	335.01	398.67	479.20

Table 7: Cluster wise mean values of different traits in *J. curcas*.

gain, co-variance estimates between traits can be used to estimate genetic correlations between the traits [25]. Correlation establishes the extent of association between seed traits and its attributes so that these components may form additional criteria for selection in breeding program. Correlated quantitative traits are of a major interest in an improvement program, as the improvement of one character may cause simultaneous correlated changes in the other characters. Genotypic and phenotypic correlation coefficients between various characters under study revealed that magnitude of correlation coefficient at genotypic level was higher than their corresponding phenotypic coefficient of correlations. The present study indicates the correlation of volume index to all growth traits in *J. curcas* therefore, volume index can be considered as important trait for early selection. The correlations seen can be explained by the fact that during the phonological succession of appearance of physiological and morphological determinants of yield; the number of branches contributed to higher number of flowers which in turn contributed to higher number of female flowers which finally culminated in higher yield. Significant association among crown area, branches/plant and volume index indicate that plants with good growth habit tend to develop more 100-seed weight and in turn more seed oil.

Genetic diversity in plant species is a gift to mankind as it forms the basis for selection and further improvement. The information on the genetic structure and diversity relationship of CPT provide a basis for planning and conducting future collections and efficient utilization of genetic resources to realize the potentiality for maximizing growth and yield. The clustering pattern in this study revealed that geographical diversity need not necessarily be related to genetic diversity. This kind of genetic diversity might be due to differential adoption, selection criteria, selection pressure and environment [26]. This indicated that genetic drift produce greater diversity than the geographic diversity [27]. Absence of any relationship between genetic diversity and geographical distribution is in accordance with the findings of Kaushik [28], Gohil [29] and Pandya [30] in *J. curcas*. The trees that originated in one region had been distributed into different clusters indicated that trees with same geographic origin could have undergone change for different characters under selection.

Since improvement is targeted for desired growth traits, cluster I is ideal for getting higher improvements because of higher mean value for all growth traits. Hence genotypes from cluster I having most heterogeneous individuals may be directly selected and utilized for breeding program for within group hybridization. Earlier studies, in crop plant had indicated that inter-mating of divergent groups would lead to greater opportunity for crossing over which would release

latent variation by breaking up predominantly repulsion linkage [31] and utilization of diverse parents in breeding was also stressed by [32]. This kind of study can help to identify the better genotypes of *J. curcas* having better yield and oil content. Therefore, the best genotypes selected will improve the poor sites for agroforestry systems and energy plantations in the wastelands [33-35].

Thus, it may be suggested that crosses involving under cluster I and VII may result in substantial segregates and further selection for overall improvement of species. Cluster 11 showed the minimum intra genetic distance (0.15) between them revealing that these genotypes were somewhat similar in genetic constitution and hybridization amongst these groups not showing sufficient variability [36].

The character contributing maximum diversity can be given more emphasis for the purpose of fixing priority of parents in hybridization program. It is suggested to effect crosses between genotypes selected from most distant clusters with high mean performance to get desirable transgressive segregates [37]. In general, the cluster I and II exhibited high and low mean values, respectively for most of the characters. It is also suggested that for creating variability and developing the best selection a large number of divergent lines, instead of few should be used in the hybridization [38].

Conclusions

From the above study, identification of good genotype may be graded based on crown area, volume index and seed weight is advantageous. Since traits *viz.,* height and volume index are having high heritability and genetic advance, consideration may be given for further improvement by selection and breeding. Genotypes IC 569133, IC 555381, IC 558214 were found to be superior on the basis of volume index, hence these genotypes may be given importance for massive afforestation programme. The present study can however serve as a pointer to be compared with the results to be obtained at later stages especially seed and oil yield and also to establish the correlations. This study would perspectively determine whether genetic analysis at early stage is reliable. If reliable, genetic assessment for other population can also be carried out with suitable correlation factors of the extent of relationship can be determined.

Acknowledgements

The authors are grateful to Department of Biotechnology, New Delhi for financial assistance and sharing the germplasm under network.

References

1. Parikh J (2005) Growing our own oils. Biofuels India 3: 7.
2. Heller J (1996) Physic nut Jatropha curcas L. Promoting the conservation and use of underutilized and neglected crops. Institute of Plant Genetic and Crop Plant Research, Gatersleben/International Plant Genetic Resource Institute, Rome, Italy.
3. Jones N, Miller JH (1992) Jatropha curcas: a multipurpose species for problematic sites. ASTAG Technical Paper - Land Resources. Volume I. Washington DC, USA. World Bank, pp: 1-12.
4. Jongschaap REE, Corre WJ, Bindraban PS, Brandenburg WA (2007) Claims and facts on Jatropha curcas L. Wageningen, The Netherlands: Plant Research International.
5. Rao GR, Korwar GR, Shanker AK, Ramakrishna YS (2008) Genetic associations, variability and diversity in seed characters, growth, reproductive phenology and yield in Jatropha curcas (L.) accessions. Trees, Structure and Function 22: 697-709.
6. Burley J, Wood PJ (1976) A manual on species and provenance research with particular reference to the Tropics. Tropical Forestry Papers No. 10. Department of Forestry, Commonwealth Forestry Institute, University of Oxford.
7. Achten WMJ, Mathijs E, Verchot L, Singh VP, Aerts R, et al. (2007) Jatropha biodiesel fueling sustainability? Biofuels Bioprod Biorefin 1: 283-291.
8. Johanson HW, Robinson HF, Comstock RE (1955) Estimate of Genetic and environmental variability in soyabeans. Agron J 47: 314-318.
9. Burton GW (1952) Quantitative inheritance of grass. Proceedings 6th International Grassland Congo Held at Pennsylvania State College, PA, USA 1: 74-83.
10. Allard RW (1999) Principles of plant breeding. 2nd edn. John Wiley & Sons, New York, USA.
11. Goulden CH (1952) Some distance properties of latent root and vector methods used in multivariate analysis. Biometrica 53: 325-338.
12. Allen GS (1960) Factors affecting the viability and germination behaviour of coniferous seed. IV. Stratification period and incubation temperature. Pseudostuga menziesii (Mirb) Franco. For Chron 36: 18-19.
13. Kumar A (1995) Genetic improvement of Casuarina equisetifolia. PhD Thesis, Forest Research Institute (Deemed University), Dehradun, India.
14. Bagchi SK, Sharma VP (1989) Biometrical studies on seed characters of *Santalurn alburn* L. Silvae Genet 38: 152-153.
15. Chaturvedi OP, Pandey N (2004) Correlation and path analysis studies between biomass and other characters in Bornbax ceiba L. Silvae Genet 53: 5-6.
16. Foster GS (1986) Provenance variation of eastern cottonwood in the lower Mississippi valley. Silvae Genet 35: 32-38.
17. Foster GS, Shaw DV (1988) Using clonal replicates to explore genetic variation in a perennial plant species. Theor Appl Genet 76: 788-794.
18. Gohil RH, Pandya B (2008) Genetic diversity assessment in physic nut (Jatropha curcas L.). International Journal of Plant Production 2: 321-326.
19. Francis G, Edinger R, Becker K (2005) A concept for simultaneous wasteland reclamation, fuel production, and socioeconomic development in degraded areas in India: need, potential and perspectives of jatropha plantations. Nat Resour Forum 29: 12-24.
20. Gera M, Gera N, Sharma S (2001) Estimation of variability in growth characters of forty clones of Tectona grandis. Indian Forester 127: 639-643.
21. Ginwal HS, Rawat PS, Srivastava RL (2004) Seed source variation in growth performance and oil yield of Jatropha curcas Linn. in Central India. Silvae Genet 53: 186-192.
22. Gomez AK, Gomez AA (1984) Statistical procedure for agricultural research. John Wiley and Sons Inc.
23. Johnsen O, Dietrichson J, Skaret G (1989) Phenotypic changes in progenies of northern clones of Picea abies L. grown in a southern seed orchard. III. Climate changes and growth in a progeny trial. Scand J For Res 4: 343-350.
24. Kaura SK, Gupta SK, Chowdhury JB (1998) Morphological and oil content variation in seeds of Azadirachta indica A. Juss. (Neem) from northern and western provenances of India. J Plant Foods Hum Nutr 52: 132-136.
25. Kaushik N, Kumar K, Kumar S, Kaushik N, Roy S (2007) Genetic variability and divergence studies in seed traits and oil content of Jatropha (J. curcas L.) accessions. Biomass Bioenergy 31: 497-502.
26. Keuls M (1952) The use of the Studentized range in connection with an analysis of variance. Euphytica, pp: 112-122.
27. Kumar A, Sharma S (2008) An evaluation of multipurpose oil seed crop for industrial uses (Jatropha curcas L.): a review. Ind Crops Prod 28: 1-10.
28. Levene H (1960) Robust tests for equality of variances. In: Olkin I (ed.), Contributions to probability and statistics: essays in honour of Harold Hotelling. Stanford University Press, Stanford, USA, pp: 278-292.
29. Newman D (1939) The distribution of range in samples from a normal population expressed in terms of an independent estimate of standard deviation. Biometrica 63: 395-400.
30. www.oecd.org/publishing/corrigenda
31. Singh YP, Kumar A, Chauhan BPS (1981) Genetic divergence in pearl millet. Indian Genetics 41: 186-190.
32. Singh AK, Singh SB, Singh SM (1996) Genetic divergence in scented and fine genotypes of rice. Ann Agric Res 17: 163-166.

33. Solanki KR, Muthana KO, Jindal SK, Arora GO (1984) Variability, heritability and correlation for growth parameters in Prosopis cineraria. J Tree Sci 3: 86-88.

34. Tefera H, Assefa K, Hundera F, Kefyalew T, Teferra T (2003) Heritability and genetic advance in recombinant inbred lines of tef (Eragrostis tef). Euphytica 131: 91-96.

35. Thoday JM (1960) Effect of disruptive selection. III. Coupling and repulsion. Heredity 14: 35-49.

36. Veerendra HCS, Ramalakshmi S, Mallesha BB (1999) Variation in seed characterstics in provenances of sandal (*Santalum album* L.). Ind For 125: 308-312.

37. Vivekananda P, Subramaninan S (1993) Genetic divergence in rainfed rice. Oryza 39: 60-62.

38. Ward JH (1963) Hierarchical grouping to optimize an objective function. J Am Stat Assoc 38: 236-244.

Citation: Divakara BN (2017) Assessing Variability and Divergence of *Jatropha curcas* Linn. Germplasm Under *Ex-situ* Conditions. Forest Res 6: 201. doi: 10.4172/2168-9776.1000201

OMICS International: Open Access Publication Benefits & Features

Unique features:

- Increased global visibility of articles through worldwide distribution and indexing
- Showcasing recent research output in a timely and updated manner
- Special issues on the current trends of scientific research

Special features:

- 700+ Open Access Journals
- 50,000+ editorial team
- Rapid review process
- Quality and quick editorial, review and publication processing
- Indexing at major indexing services
- Sharing Option: Social Networking Enabled
- Authors, Reviewers and Editors rewarded with online Scientific Credits
- Better discount for your subsequent articles

Submit your manuscript at: http://www.omicsonline.org/submission