Full Length Research Paper

Variability and genetic diversity assessment in physic nut (*Jatropha curcas* L.)

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A trial was conducted to assess genetic parameters and diversity in physic nut (*Jatropha curcas* L.). Data were collected on ten biometric traits during year 2007 to 2008 and 2008 to 2009. Genotype Indira Gandhi Agricultural University (IGAU)-Raipur ranked first for seed yield (0.269, 0.492 kg/plant) in year 2007 to 2008 and 2008 to 2009, respectively. In 2007 to 2008, dry fruit yield/plant accounted highest phenotypic coefficient of variation (PCV) (40.27%) while seed yield/plant recorded highest genotypic coefficient of variation (GCV) (26.36%) in comparison to other traits. In contrast, in 2008 to 2009, seed yield/plant had highest PCV (45.88%) as well as GCV (34.27%). High estimates of heritabilities (h^2) coupled with high genetic gains (GA) were registered for number of fruit clusters/plant, seed yield/plant and dry fruit yield/plant for both years which implies that direct selection would be effective for improvement of these traits. The maximum Euclidean distance of 11.21% was registered between IGAU Raipur and Lower Sowan. Non-hierarchical Euclidean analysis grouped forty six genotypes of *J. curcas* into five non-overlapping clusters. The maximum (7.723) inter-cluster distance was noticed between cluster NC-I and NC-IV whereas, minimum (2.747) inter-cluster distances was in between NC-I and NC-V. Based on three methods of clustering namely; hierarchical clustering, non-hierarchical clustering and metroglyph clustering, pooled clusters were formed which were found to be effective in selection of genotypes for hybridization.

Key words: *Jatropha curcas*, variability, heritability, genetic advance, genetic diversity, euclidean distance, clustering.

INTRODUCTION

Jatropha curcas L., a recently domesticated crop is in highlights nowadays since its seed oil is used as fuel in the form of biodiesel and is safe from environmental point of view. This tropical physic nut (*J. curcas* L., Euphorbiaceae) have become the crop of interest for researchers and development organizations because of

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Table 1. List of *J. curcas* genotypes used for variability and diversity analysis.

S/no	Genotype name	Location	S/no	Genotype name	Location
National networking trial			**Progeny trial**		
1	IGAU Raipur	Chhattisgarh	21	Sitapur 30	Uttarakhand
2	IGAU Bilaspur		22	Rajasthan 31	Rajasthan
3	IGAU – Surzuja		23	Danibunger 28	Uttarakhand
4	TNMC-2	Tamil Nadu	24	Danibunger 29	
5	TNMC-3		25	Danibunger 27	
6	TNMC-4		26	Daultpur 25	
7	TNMC-5		27	Kamaluaganja 24	
8	TNMC-7		28	Kamaluaganja 22	
9	TNMC-22		29	Kaladungi road 15	
10	Sagar (S.F.R.I. Jabalpur)	Madhya Pradesh	30	Kaladungi road 16	
11	Indore (S.F.R.I. Jabalpur)		31	Golapar 12	
12	TFRI-1		32	Golapar 13	
13	TFRI-2		33	Golapar 11	
14	Pant Jat. Sel-1	Uttarakhand	34	Golapar 8	
15	Pant Jat. Sel-2		35	Golapar 9	
16	RJ-117	Maharashtra	36	Lamachaur 6	
17	PKVJ-MKV-1		37	Lamachaur 2	
18	PKVJ- DHW-1		38	Lamachaur 3	
19	PJ- 03004	Uttarakhand	39	Lamachaur 4	
20	PJ- 03031		40	Lamachaur 5	
Zonal Trial					
41	Jajhar Kotali	Jammu and Kashmir	44	Pant J Sel- 4	Uttarakhand
42	Lower Sowan		45	Pant J Sel-31	
43	Lower Dhearti		46	Pant J Sel-97	

its varied properties: drought resistance, rapid growth, easy propagation, low seed cost, high oil content, short gestation period, ability to grow on marginal and degraded lands, erosion controlling ability and not preferred by browsing animals (Heller, 1996; Sujatha et al., 2005; Sujatha et al., 2008).

Jatropha seed oil content ranged from 32 to 39% (Holla et al., 1993). Its oil is rich in unsaturated fatty acids: oleic acid (42 to 45%), linoleic acid (32 to 35%) (Holla et al., 1993; Chatakanonda, 2005; Getwichit, 2008). The present plant types of *Jatropha* are primitive types and low yielding which cannot be economically fitted well into present agricultural system. Hence, in order to harness the full potential of this crop, there is a need for evolving high yielding varieties with synchronous maturity and high seed and oil yield per hectare of land. The information regarding the introduction and genetic diversity of indigenous *J. curcas* population is lacking (Basha and Sujatha, 2007). However, breeding objectives should be aimed first for systematic collection of germplasm and evaluation of variability and diversity.

Therefore, germplasm evaluation and diversity analysis works have been reported, mostly by using candidate plus trees (CPTs). Ginwal et al. (2005) and Sunil et al. (2008) evaluated the variability for seed traits: size, oil content and yield components of *J. curcas*. Hence, the present study has been designed to assess variability, genetic parameters and the extent of genetic divergence for different growth and yield characters among different *J. curcas* genotypes obtained from different geographical regions of India.

MATERIALS AND METHODS

Experimental material

The experimental material for present study comprised of 46 open pollinated genotypes of *J. curcas* obtained from various parts of the country. The genotypes studied (Table 1) were part of the National Networking Trial on *J. curcas* coordinated under National Oilseed

and Vegetable Oil Development (NOVOD) board, Gurgaon, India, Progeny Trial and Zonal Trial. An extensive survey was conducted to select the CPTs of *J. curcas* from different locations of Uttarakhand, India. The selection of CPTs was done on the basis of phenotypic examination of traits of economic value that is, dry fruit and seed yield potential, number of fruit clusters/plant, number of branches, collar diameter, disease resistance etc.

Layout plan

The *J. curcas* genotypes were planted on 27 to 29 July, 2005 by using around 120 days old plantlets in completely randomized block design, with three replications, at Medicinal Plant Research and Development Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India. Single row of one genotype was planted with plant to plant and row to row spacing of 3 m. The standard agronomic practices were carried out during crop growth period. Trial was under rainfed condition and after harvesting of fruits, plants were pruned every year. The year 2006 to 2007 was counted as zero year. Five representative plants from each plot were randomly selected and tagged. The data were recorded on ten quantitative characters on selected plant for two years (2007 to 2008 and 2008 to 2009).

Statistical analysis

The mean values of observations recorded on five random plants were used for computation of various genetic parameters. The analysis of variance (ANOVA) was done as per Panse and Sukhatme (1954). PCV and GCV were estimated and expressed in percentage following Burton and Devane (1953). Heritability in broad sense and genetic advance (GA) were calculated for each character by following the method of Allard (1960). GA as percent of mean for each character was estimated as suggested by Johnson et al. (1955). Pooled data of both years were used for diversity analysis and clustering of genotypes. The Euclidean distance coefficients and principal component analysis based on morphological data were computed using NT SYS PC 2.11v (Rohlf, 2000) software and non-hierarchical Euclidean cluster analysis was carried out as per the Beale (1969) and Spark (1973). The metroglyph and index score analysis was carried out for the eight characters of high variability as per the procedure given by Anderson (1957).

RESULTS AND DISCUSSION

Mean performance and variability

Amongst all the genotypes studied TNMC-2 was earliest (17.33, 20.0 days) in flowering while genotype PKVJ-MKV-1 had late duration (53.42, 54.14 days) of flowering for 2007 to 2008 and 2008 2009, respectively. Seed yield/plant ranged from 0.060 to 0.269 kg with a general mean of 0.138 kg in year 2007 to 2008. Whereas, it ranged from 0.105 to 0.492 kg with a general mean of 0.194 kg during year 2008 to 2009 (Table 2). Amongst all the genotypes studied, IGAU-Raipur ranked first for seed yield (0.269, 0.492 kg) in both years, respectively. Genotype Lower Sowan was lowest yielder (0.060 kg) in

year 2007 to 2008 while Pant J Sel-97 recorded lowest yield (0.105 kg) in year 2008 to 2009.

The ANOVA for ten quantitative characters of *J. curcas* revealed highly significant differences (P < 0.01) among the genotypes for all the characters studied except collar diameter during year 2007 to 2008 and plant height during year 2008 to 2009. Pooled analysis of variance over two years exhibited significant differences for days to flower initiation (after July), fruit clusters/plant, seed yield/plant and dry fruit yield/plant due to genotypes and genotype × year interaction as well. Significant genotype × environment interaction unveiled that environment had significant influence on expression of these traits. In the present study, all the traits showed enhanced mean performance except days to flower initiation (decreased), number of primary branches/plant and number of fruits/cluster (both traits shown nearly consistent performance) in the second year 2008 to 2009 (Figure 1).

A peruse of the Table 2 indicated that PCVs were generally higher than corresponding GCVs of all the characters studied. During year 2007 to 2008 dry fruit yield/plant showed highest PCV (40.27%) while, seed yield/plant recorded highest GCV (26.36%). In year 2008 to 2009 seed yield/plant had the highest PCV and GCV (45.88 and 34.27%). There was decrease in magnitude of PCV as well as GCV in year 2008 to 2009 as compared to 2007 to 2008 for all the traits except seed yield and dry fruit yield. An assessment of PCV and GCV indicated high amount of variability for the traits: seed yield/plant, dry fruit yield/plant, and fruit clusters/plant whereas, primary branches/plant, secondary branches/plant, days to flower initiation and fruits/cluster accounted fairly good amount of variability. The probable reason of high magnitude of variability in yield and its component traits may be that the material under study includes genotypes which are progenies of CPTs and selection from CPTs. These CPTs were obtained from wild unadapted germplasm which do not have any breeding history and growing naturally in their habitats in different geographical regions of India. Various workers conducted studies on germplasm evaluation in *J. curcas*. Kaushik et al. (2001) studied the biochemical changes in seed and pods during the development of *J. curcas*. Kaushik (2003) and Srivastava et al. (2007) tested maturity indices of fruit development in physic nut.

Heritability and genetic advance

Heritability denotes the effectiveness by which selection of genotypes can be made on the basis of their phenotypic performance. The utility of heritability estimates is increased when they are used in association with the selection differential and expected genetic gain (Johnson et al., 1955). As suggested by Robinson (1965),

Table 2. Mean performance, variability and estimates of genetic parameters for yield and yield contributing characters of *J. curcas*.

Character / Genetic parameter	Days to flower initiation (DFI)	Primary branches/ plant (PBP)	Secondary branches/plant (SBP)	Collar diameter (cm) (CD)	Plant height (cm) (PH)	Fruit clusters/plant (FCP)	Fruits/ cluster (FC)	100-seed weight (g) (100-SW)	Seed yield/ Plant (kg) (SYP)	Dry fruit yield/ plant (kg) (DFY)
2007 to 2008										
Mean	44.26	10.04	39.67	13.26	261.22	26.43	5.40	51.30	0.138	0.216
Range	17.33-53.42	7.00-13.60	27.47-56.73	12.24- 14.74	230.73-286.33	11.58- 51.17	3.23- 7.02	41.42- 62.63	0.060-0.269	0.095- 0.396
SEM±	2.88	1.12	4.05	0.56	9.61	3.43	0.47	4.05	0.023	0.039
PCV (%)	17.78	23.14	21.57	7.42	7.26	31.36	18.97	13.48	39.91	40.27
GCV (%)	13.72	12.59	13.4	1.18	3.48	21.83	11.29	7.32	26.36	25.17
h^2(b) (%)	59.55	29.59	40.35	2.52	23.05	48.46	35.41	29.54	43.61	39.06
GA as % of the mean	21.8	14.14	17.95	0.38	3.45	31.33	13.89	8.19	35.51	32.4
2008 to 2009										
Mean	42.87	9.83	51.47	13.89	298.98	30.86	5.16	57.63	0.194	0.299
Range	20.0-54.17	6.93-11.87	43.53- 60.40	12.59-14.95	265.13-322.47	15.60-54.73	4.17- 6.16	49.01-62.32	0.105-0.492	0.159-0.759
SEM±	2.87	0.86	3.16	0.44	10.26	3.74	0.42	1.46	0.034	0.046
PCV (%)	15.22	18.03	12.51	6.28	6.34	29.45	15.42	5.58	45.88	43.21
GCV (%)	9.84	9.61	6.59	2.93	2.22	20.63	6.07	3.4	34.27	33.7
h^2(b) (%)	41.82	28.39	27.74	21.81	12.22	49.08	15.49	37.16	55.79	60.81
GA as % of the mean	13.11	10.58	7.15	2.81	1.6	29.78	4.84	4.27	51.55	54.13
Pooled over two years										
Mean	43.56	9.94	45.59	13.57	280.10	28.64	5.28	54.39	0.166	0.257
Range	18.67- 53.78	7.37-12.73	35.5- 56.73	12.62-14.92	259.1-302.73	13.59-52.95	3.7- 6.53	47.57-61.14	0.083-0.359	0.127- 0.571
SEM±	2.04	0.71	2.48	0.36	7.03	2.54	0.318	1.83	0.0208	0.0305

heritability values can be categorized as, low (5 to 10%), moderate (10 to 30%) and high (30 to 60%). During year 2007 to 2008, high estimates of heritability and GA as percent of mean were observed for fruit clusters/plant (48.46 and 38.33%), seed yield/plant (43.61 and 35.51%), dry fruit yield/plant (39.06 and 32.40%), whereas primary branches/plant (29.59, 14.14%), and registered moderate estimates of heritability as well as GA (Table 2). Like 2007 to 2008, dry fruit

yield/plant (60.81 and 54.13%), seed yield/plant (55.79 and 51.55%), fruit clusters/plant (49.08 and 29.78%) recorded high estimates of GA in comparison to other yield parameters investigated in year 2008 to 2009. Hence, selection will be effective for improvement of traits namely, dry fruit yield/plant, seed yield/plant and fruit clusters/plant.

Kaushik et al. (2007) evaluated the variability for seed traits: size, oil content, yield components of

J. curcas and recorded highest heritability for oil content (99%) followed by seed weight (96%). Rao et al. (2008) while evaluating seed characters: seed morphology and oil content as well as growth characters: plant height, female to male flower ratio and seed yield reported highest heritability for female to male flower ratio (99.95%) followed by oil content (99.61%). Rafii et al. (2012) assessed six accessions of *J. curcas* for seed and vegetative traits. They found significant
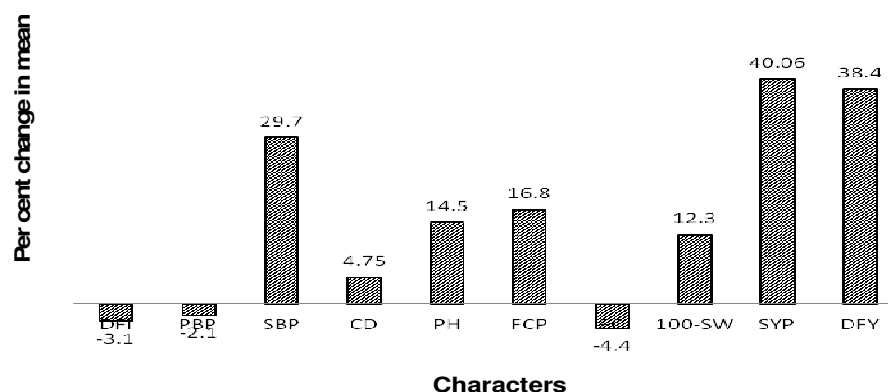
Figure 1. Change in mean performance of *J. curcas* for different traits in second year (2008-09).

Table 3. Eigen vectors, eigen roots and associated variation for first three principal components in *J. curcas.*

Character	Eigen vectors		
	1	2	3
Days to flower initiation	-0.087	0.325	0.370
Primary branches/ plant	0.218	-0.310	-0.282
Secondary branches/ plant	0.916	0.125	0.279
Collar diameter (cm)	0.257	-0.385	-0.222
Plant height (cm)	0.034	0.204	0.129
Fruit clusters/ plant	-0.161	-0.120	0.168
Fruits/ cluster	-0.059	-0.688	0.465
100- seed weight (g)	0.062	0.118	0.568
Seed yield /plant (kg)	0.071	0.300	-0.272
Dry fruit yield/ plant (kg)	0.013	0.003	0.006
Eigen roots	169.26	140.81	40.72
Variation (%)	37.62	31.31	9.05
Cumulative proportion of variation (%)	37.62	68.93	77.98

variation for plant height, seed thickness, seed breath, seed numbers and highest heritability for plant height (23.04%).

Genetic diversity

Three methods of clustering: hierarchical clustering, non-hierarchical clustering, and metroglyph analysis were employed to assess the effect of geographical origin on diversity of genotypes with reference to selecting parents for hybridization. Selection of parents based on the extent of genetic divergence has been successfully utilized in different crop species by different workers (Moll et al., 1962; Murty and Arunachalam, 1966; Mahto, 1994; Sihag et al., 2004).

Hierarchical cluster analysis

Pooled quantitative data of *J. curcas* were subjected to principal component analysis. Based on the correlation matrix, eigen roots (eigen values) and eigen vectors were computed (Table 3). The first three components accounted for 77.98% of the total variation. The minimum Euclidean distance of 0.96% was between genotypes Danibunger 27 and Danibunger 29, while the maximum of 11.21% was registered between genotypes namely, IGAU Raipur and Lower Sowan. The UPGMA phenogram (Figure 2) grouped forty six accessions of *J. curcas* at 2.86 Euclidean coefficient distance into six hierarchical clusters: HC-I, HC-II, HC-III, HC-IV, HC-V and HC-VI. Cluster HC-II is the largest cluster amongst all the clusters with 18 genotypes grouped in it and this

Table 4. Grouping of *J. curcas* genotypes based on different methods of clustering.

Cluster No.	Hierarchical clusters (HC)			Cluster No.	Non–hierarchical clusters (NC)			Cluster No.	Metroglyph clusters (MC)		
	Genotypes No.	Total no. of genotypes	Locations of genotypes		Genotypes No.	Total no. of genotypes	Locations of genotypes		Genotypes No.	Total no. of genotypes	Locations of genotypes
HC-I	1, 10	2	M. P., Chhattisgarh	NC-I	4, 7, 22, 41, 42, 43, 44, 45, 46	9	T. N., Rajasthan, J. & K., Uttarakhand	MC-I	36, 39, 41, 42, 43, 44, 46	7	Uttarakhand, J&K
HC-II	2, 3, 5, 6, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22	18	Chhattisgarh, T.N., MP, Uttarakhand , Maharashtra, Rajasthan	NC-II	28, 30, 31, 34, 37, 38, 40	7	Uttarakhand	MC-II	2, 4, 7, 8, 9, 12, 14, 17, 21, 22, 23, 24, 25, 27, 32, 33, 35, 37, 40, 45	20	Chhattisgarh, T.N., MP, Uttarakhand , Maharashtra, Rajasthan
HC-III	41, 42, 43, 44, 45, 46	6	Uttarakhand, J&K, Rajasthan	NC-III	2, 3, 5, 6, 11, 13, 15, 16, 17, 18, 19, 20	12	Chhattisgarh, T. N., M.P., Uttarakhand, Rajasthan, Maharashtra	MC-III	3, 5, 6, 11, 13, 16, 18, 19, 26, 28, 29, 30, 31, 34, 38	15	Chhattisgarh, T.N., MP, Maharashtra, Uttarakhand
HC-IV	23, 24, 25, 26, 27, 29, 32, 33, 35, 36, 37, 39, 40	13	Uttarakhand	NC-IV	1, 10	2	M. P., Chhattisgarh	MC-IV	15, 20	2	Uttarakhand
HC-V	28, 30,31 ,34, 38	5	Uttarakhand	NC-V	8 , 9, 12, 14, 21, 23, 24, 25, 26, 27, 29, 32, 33, 35, 36, 39	16	T. N., M. P., Uttarakhand	MC-V	1, 10	2	M. P., Chhattisgarh
HC-VI	4	1	T.N.								

cluster is most diverse since entries of this cluster had their origin from six different geographical regions: Chhattisgarh, TN, MP Uttarakhand, Rajasthan and Maharashtra. Cluster HC-IV and HC-V showed that geographical diversity can be used as a criterion of genetic diversity because all entries in these two clusters hail from Uttarakhand state only.

Non-hierarchical Euclidean cluster analysis

A non-hierarchical Euclidean cluster analysis grouped forty six genotypes of *J. curcas* in five non-overlapping clusters (Table 4). The clustering pattern of genotypes does not correspond to the area of collection in general. Cluster NC-V had highest number of genotypes (16) while cluster NC-IV consisted of only two genotypes. However, clustering of genotypes from different regions in a single cluster like cluster NC-I (TN, Rajasthan, Jammu and Kashmir, Uttarakhand), NC-III (Chhattisgarh, Tamil Nadu, MP, Uttarakhand, Rajasthan, Maharashtra) and NC-V (TN, MP, Uttarakhand) indicated that there was no association between ecogeographical distribution of genotypes and genetic divergence as genotypes selected under diverse locations clustered together. On the other hand, genotypes from the same geographic region were distributed in different clusters. This shows that geographic diversity is not always a marker of genetic diversity and therefore, it is not sufficient as an index of genetic diversity and this kind of genetic diversity might be due to differential selection pressure, adaptation and acclimatization, selection parameters, and environmental settings (Das and Gupta, 1984). Murty and Arunachalam (1966) stated that genetic drift and selection in different environment could cause greater diversity than geographic diversity. However, in some cases influence of geographic origin affected the clustering pattern of genotypes. The cluster NC-II had all the genotypes from Uttarakhand. Likewise, majority of genotypes in cluster NC-V hail from Uttarakhand. These results are in the direction of earlier workers (Singh and Shukla, 1994; Mishra et al., 1995; Ghafoor et al.,

Table 5. Index scores and signs used for 8 characters of *J. curcas* in metroglyph analysis.

Characters	Score 1		Score 2		Score 3	
	Below average values	Sign	Average values	Sign	Above average values	Sign
Days to flower initiation	<41	○	41-45	⟲	>45	⟍○
Primary branches/ plant	<9	○	9-11	♂	>11	♂
Secondary branches/ plant	<42	○	42-48	⟋○	>45	⟋○
Plant height (cm)	<275	○	275-285	○⟍	>285	○⟍
Fruit clusters/ plant	<28	-	28-35	-	>35	-
Fruits/ cluster	<5	○	5-5.5	○⟍	>5.5	○⟍
100- seed weight (g)	<52	○	52-55	○	>55	○
Seed yield/ plant (kg)	<0.150	-	0.150-0.200	-	>0.200	-

2001; Kaushik et al., 2007).

The average inter and intra cluster distances is depicted in Figure 3. The average intra-cluster distances ranged from 1.595 (NC-II) to 2.238 (NC-I). Maximum intra-cluster distance (2.238) exhibited is by NC-I which is an indicator of selection of parents for hybridization within cluster. The maximum inter-cluster distance (7.723) was recorded between NC-I and NC-IV which indicated wider genetic diversity between the genotypes in these groups and selection of parents from such clusters for hybridization programmes would help to achieve new combination of genotypes. Kaushik et al. (2007) using non-hierarchical Euclidean cluster analysis divided 24 accessions of *J. curcas* in six non-overlapping clusters based on seed traits and oil content. They found highest inter cluster distance (5.129) between cluster VI and V. Genetic diversity in *J. curcas* based on biochemical markers like, peroxidase enzyme activity (Kumar et al., 2005) and molecular markers: random amplified polymorphic DNA (RAPD), inter simple sequence repeats (ISSR), sequenced characterized amplified region (SCAR) and amplified fragment length polymorphism (AFLP) (Basha and Sujatha, 2007; Xiang et al., 2007; Pamidiamarri et al., 2009; Subramanyam et al., 2009) have also been assessed by many workers.

The cluster mean for some of the important traits is depicted by bar diagram (Figure 4a and b). Genotypes possessed more number of fruit clusters/plant, 100-seed weight, seed yield/plant and dry fruit yield/plant belonging to cluster NC-IV while, cluster NC-I had genotypes with lowest value for these variables.

**Metroglyph and index score analysis**

The Index scores and signs were used for clustering of

genotypes in metroglyph analysis (Table 5), based on which a scatter diagram (Figure 5) was prepared. Each genotype is represented by the glyph; the X-coordinate for each glyph being the fruit clusters/plant and Y-coordinate the seed yield/plant (kg). Remaining six characters have been represented by rays at different positions on the glyph and the index score by the length of rays. An examination of the scatter diagram revealed that five clusters could be distinguished on the basis of morphological variation. The cluster MC-I was represented by the seven genotypes belonging to Uttarakhand. The second cluster consisted of 20 genotypes originated in different states. The third cluster contained 15 genotypes, and cluster fourth and fifth have two genotypes each. The frequency diagram (Figure 5) shows the index score of 46 genotypes of *J. curcas*. The range of index score was from 11 to 22. Haritha and Sekhar (2003) compared D^2 statistics and metroglyph analysis and found that metroglyph analysis may be more desirable for preliminary clustering of large numbers of genotypes. Abbas et al. (2010) grouped 40 mungbean germplasm accessions into eight clusters based on 100-seed weight and seed yield using metroglyph analysis.

Comparison of three methods of clustering

A comparison of three methods of clustering (Table 5) namely; hierarchical clustering, non-hierarchical clustering and metroglyph clustering, and it was noted that genotype no. 1 (IGAU Raipur) and no. 10 (Sagar, SFRI) were always grouped together separately in a single group that is, HC-I (hierarchical clustering), NC-IV (non-hierarchical clustering) and MC-V (metroglyph analysis).

Moreover, it may be concluded that these two genotypes
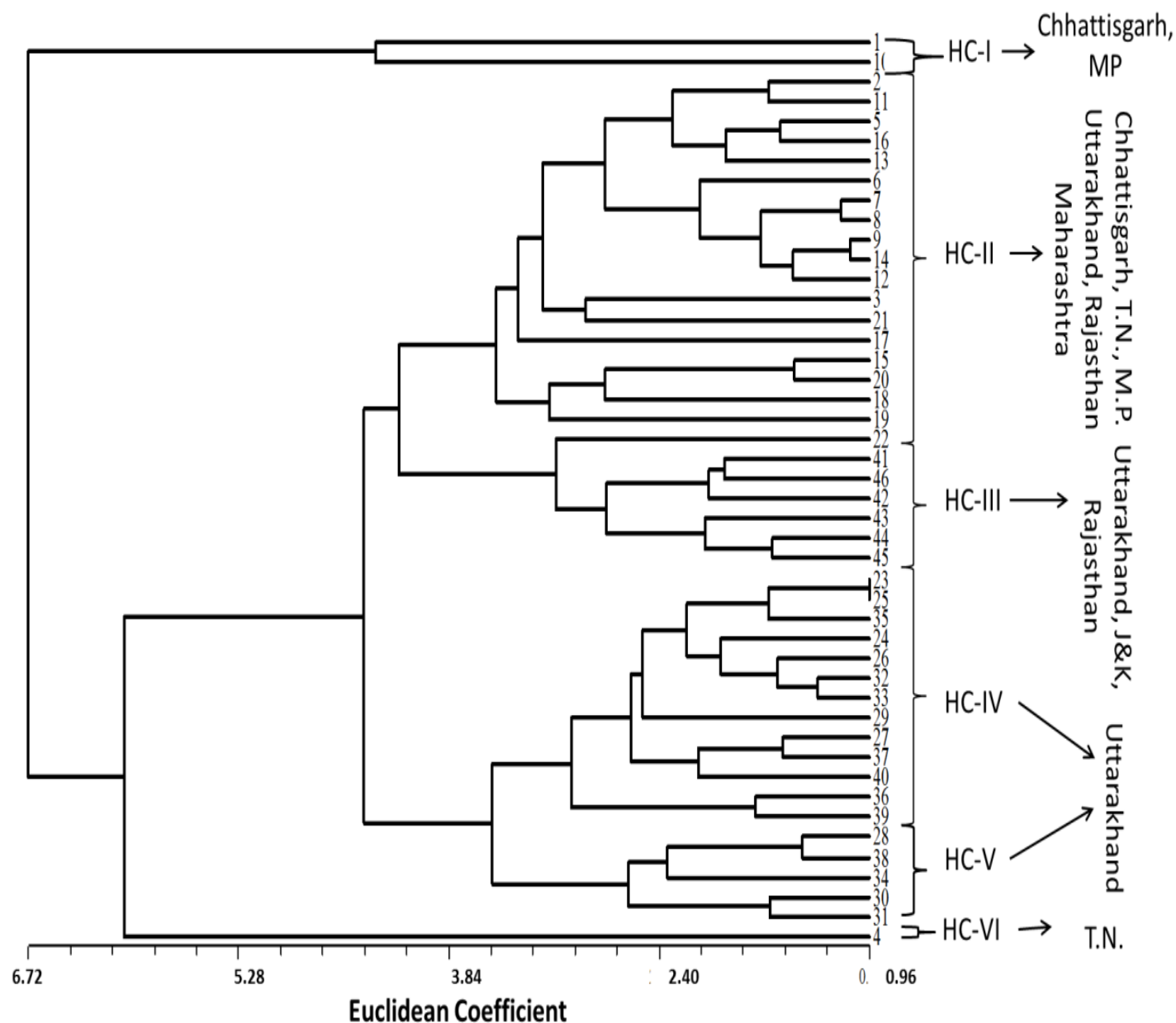
Figure 2. Morphological variability phenogram of *J. curcas* genotypes based on Euclidean distance and UPGMA clustering.

are more diverse from the rest of the genotypes studied. Based on three methods of clustering, pooled clusters were formed which depicted that common genotypes were always grouped together in different methods of clustering (Table 6). Genotypes which were repeatedly coming together in different clusters were more closely related to each other.

So, crossing in between members of pooled clusters may generate more variability for yield and its attributing traits as compared to crossing based on single method of clustering.

Conclusion

The present study is clearly indicating considerable genetic differences and substantial amount of variability among all the genotypes for seed yield and its

Table 6. Pooled clusters formed for grouping of *J. curcas* genotypes based on three different methods of clustering.

| Pooled cluster no.	Cluster no.	Common genotypes	Total genotypes
1	HC-I, NC-IV, MC-V	1,10	2
2	HC-II, NC-III, MC-III	3, 5, 6, 11, 13, 16, 18, 19	8
3	HC-III, NC-I, MC-I	41, 42, 43, 44, 46	7
4	HC-IV, NC-V, MC-II	23, 24, 25, 27, 32, 33, 35,	7
5	HC-V, NC-II, MC-III	28, 30,31 ,34, 38	5
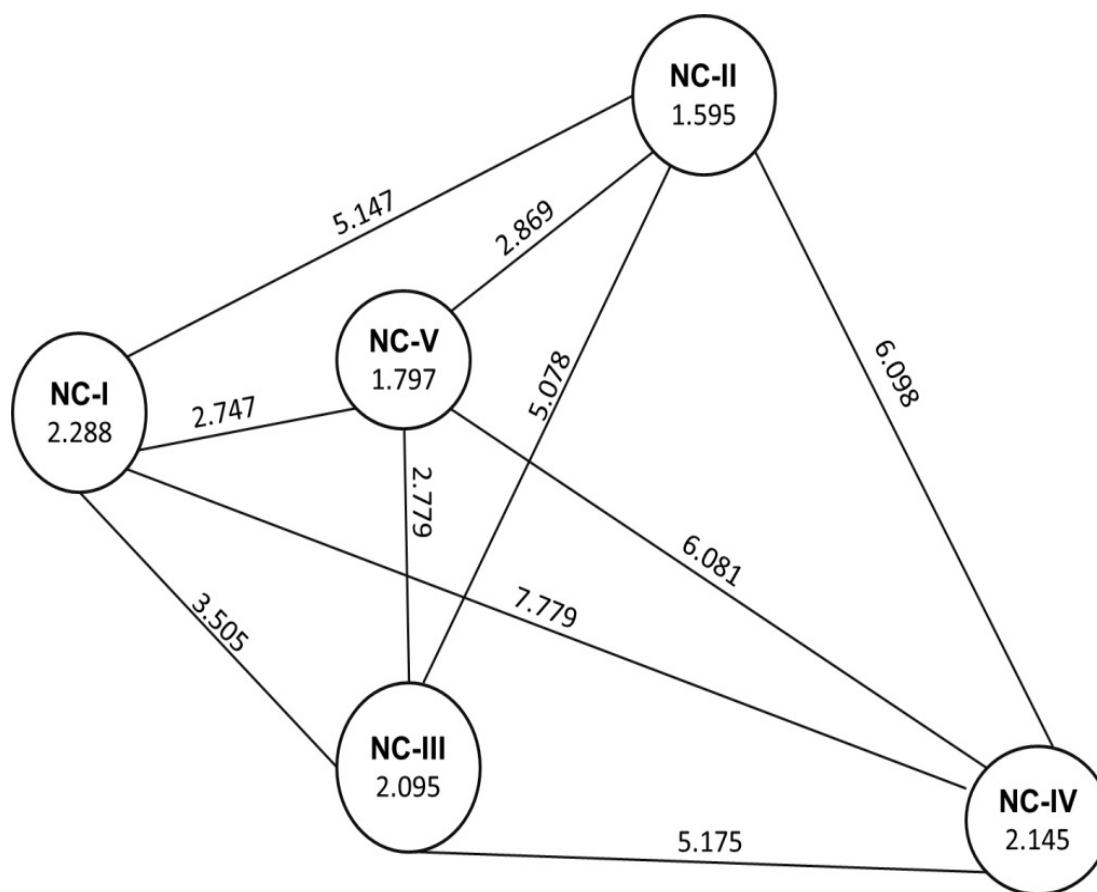
Figure 3. Cluster diagram showing inter and intra-cluster distance between five non-hierarchical clusters of *J. curcas.*

component traits in *J. curcas*. High heritabilities coupled with high genetic gains were found for traits like number of fruit clusters/plant, seed yield/plant and dry fruit yield/plant, reflecting that most likely the heritability is due to additive gene effects, and selection may be effective for further improvement in these traits. Selection of genotypes for hybridization based on two or three methods of clustering may be more effective to generate more variability and to produce heterotic progenies and transgressive segregants rather than based on single method of clustering.

Fruit clusters/ plant   **100 Seed weight (g)**

(a)

Cluster mean

(b)   **Seed yield /plant (kg)**   **Dry fruit yield/plant (kg)**
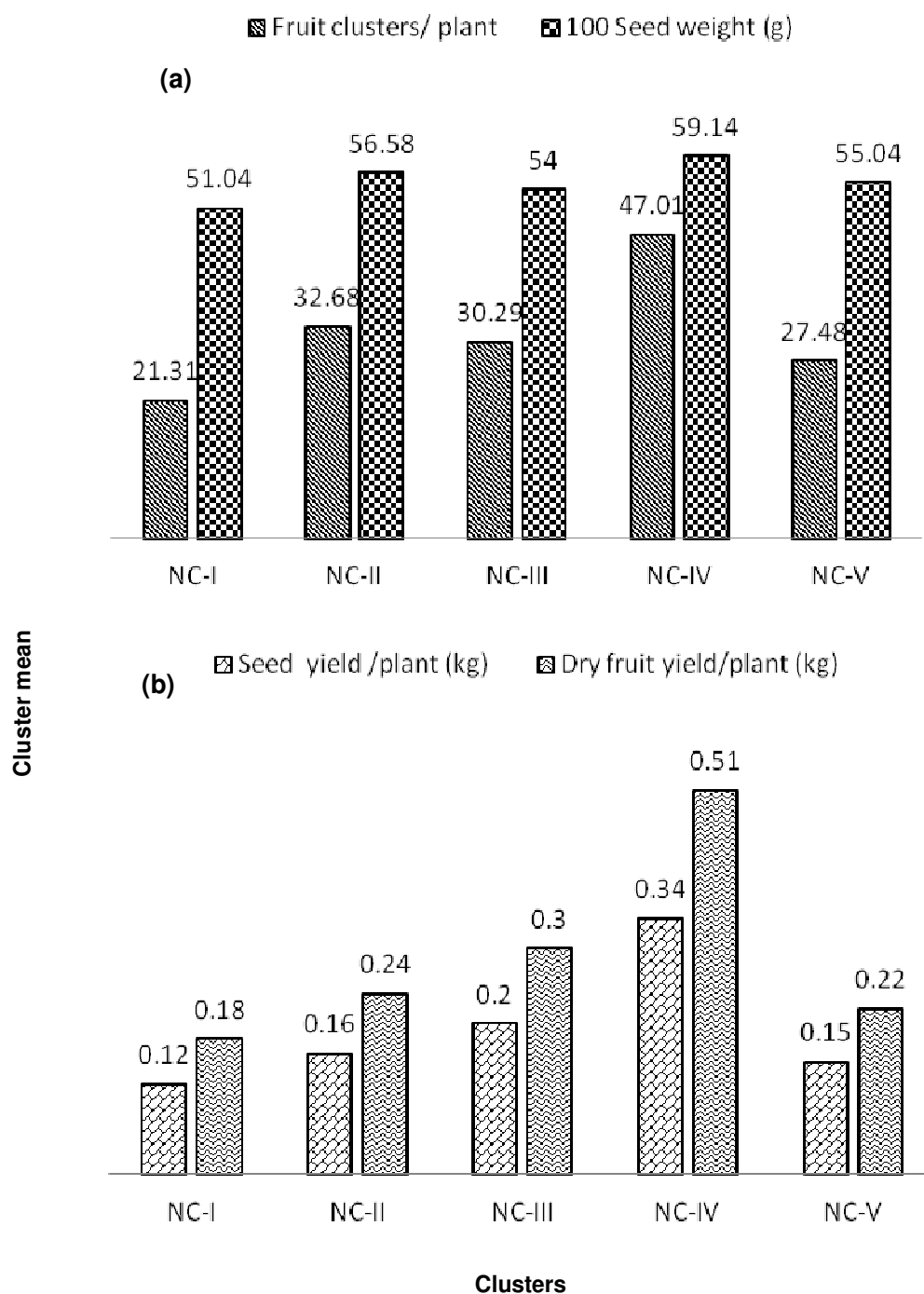
Clusters

Figure 4. (a) and (b) represents bar diagrams depicting cluster means of five non-hierarchical clusters for some important yield contributing traits of *J. curcas.*
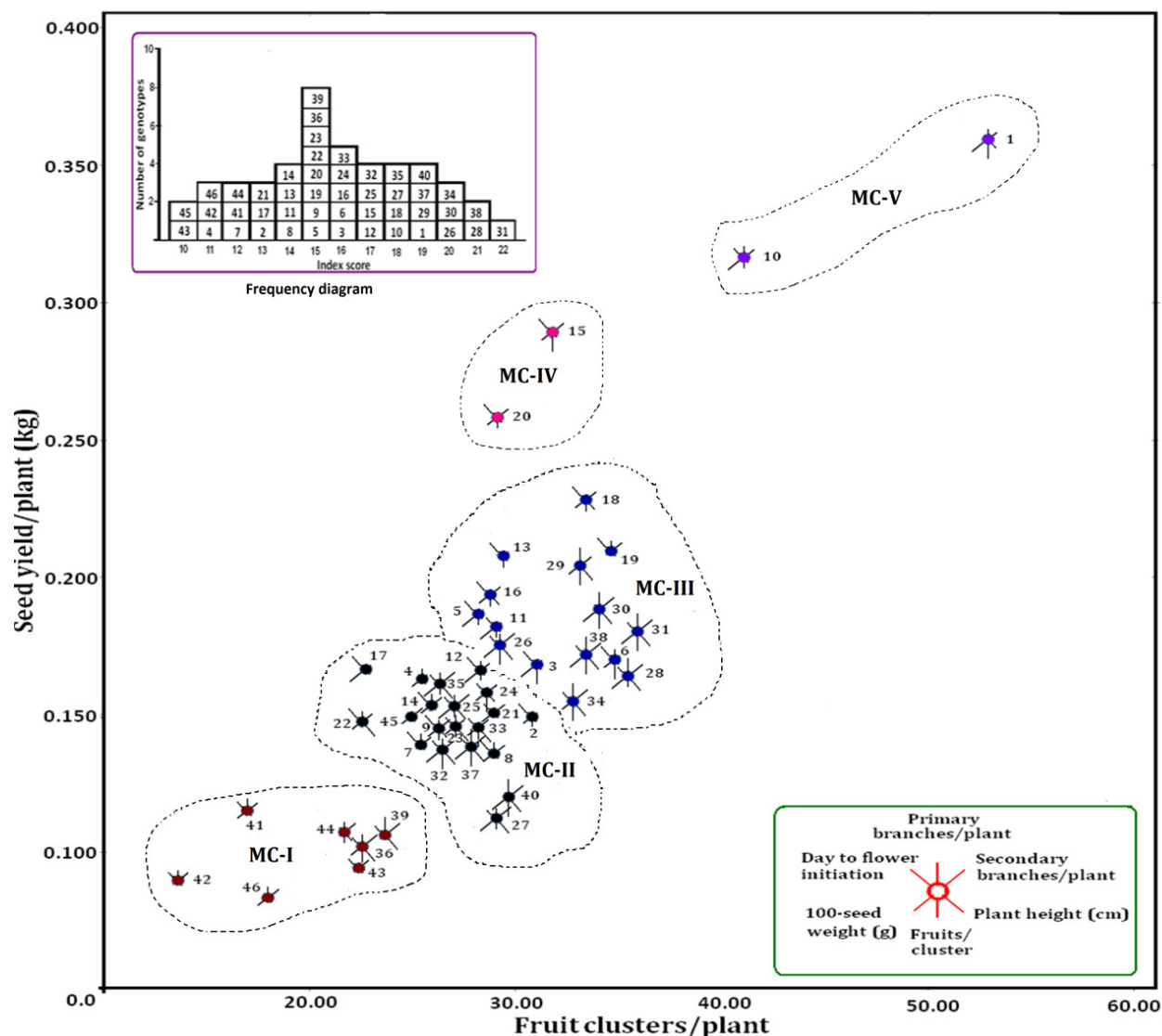
Figure 5. Scatter diagram showing clustering of *J. curcas* genotypes based on metroglyph analysis.

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