

Genetic divergence in 3 and 4 year old genotypes of physic nut [*Jatropha curcas* (L.)]

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(Received: December 2011; Revised: November 2012; Accepted: December 2012)

Abstract

Fifty six germplasm lines of physic nut collected from Aravali hills of Southern Rajasthan were assessed for 26 characters recorded for two consecutive years during 2007 and 2008 on 3 and 4 year old plants. The values of V statistics were 12040 and 10950 in first and second year, respectively which showed significant difference between the genotypes over the characters. The two year values indicated that sufficient diversity was present among the 56 genotypes of physic nut. The 56 genotypes were grouped into 8 clusters using Euclidean² values of 500 and 285 in the third and fourth year, respectively. The composition of clusters was slightly different in different years. With changing the age, genotypes also changed their cluster but most of the genotypes moved together and found place in one cluster. There was no relationship between genetic diversity and geographic distance. The contribution of vegetative characters towards genetic divergence was negligible. The characters like seed content, 100-seed weight, number of female flowers per inflorescence, oil content, kernel: shell ratio and weight per fruit were main contributors to total divergence. Cluster III and VIII in 3rd year and cluster VI and VIII in 4th year had maximum inter cluster distances. Cluster IV in 3rd year and cluster VIII in 4th year had highest mean values for maximum number of characters. Based on above results ARV-036 X ARV-020 and ARV-036 X ARV-023 are recommended for hybridization, as these genotypes showed good *per se* performance for seed yield and oil content and belong to the highly diverse clusters.

Key words: Genetic divergence, jatropha, Euclidean² distance, germplasm lines

Introduction

Jatropha curcas L. is considered as good renewable source of energy. Its oil can be directly used as fuel because of unique fatty acid composition. It is the hardiest plant having high degree of adaptability ranging

from tropical to subtropical climate [1]. It is highly cross-pollinated plant due to monoecious flowers. The genome of *Jatropha curcas* is relatively of small size. The karyotype of *J. curcas* is made up of 22 relatively small metacentric and submetacentric chromosomes whose size range from 1.21 to 1.24 μm [2]. It is commonly grown as a live fence around agricultural fields as it can be easily propagated, quick growing, less input demanding, not browsed by animals, does not harbour the crop damaging insects, tolerant to dry weather conditions and have wider adaptability. It is an environmentally safe and cost effective source of energy. Promotion of it as non-conventional source of energy will be boon for the society in the global context of increasing energy needs, spiralling prices of petroleum products and depleting petroleum reserves. It will also save the foreign exchange of the country and would be good source of income for the farmers [3]. There are no prominent varieties and the yield potential of present cultivars is very low. Therefore, intensive research is required for improving the seed yield and oil content. As it is a cross-pollinated and vegetatively propagated crop the hybrids can be developed using suitable parents for exploitation of heterosis. For identification of suitable parents genetic divergence is one of the important tool. In view of this, the present investigation was conducted to assess genetic divergence in jatropha genotypes of Southern Rajasthan at the age of 3 and 4 years.

Materials and methods

The stem cuttings of 56 selected plants collected from different locations of the Aravali hills of southern Rajasthan were planted at the Instructional Farm of

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Horticulture, Rajasthan College of Agriculture, Udaipur. The selection of plants was done based on area, location and density of plants in the area. More samples were taken from area having high density of plants. The experimental design was Completely Randomized Design (CRD) with 5 replications. Observations were recorded on five normal appearing plants of 3 and 4 year age stages for 26 vegetative, reproductive and quality characters during 2007 and 2008. Genetic divergence was measured by squared Euclidean distance [4].

Results and discussion

The values of V statistics were 12040 and 10950 at 3 and 4 year age of the plants, respectively. It showed significant difference between the genotypes over the characters and indicate significant diversity among the 56 genotypes of physic nut. The genetic divergence in *Jatropha curcas* has also been reported by Kaushik *et al.* [5], Rao *et al.* [6], Das *et al.* [7] and Sunil *et al.* [8]. The studies on genetic diversity at morphological and molecular level in *Jatropha curcas* populations has also revealed moderate to high magnitude of divergence with a wide genetic base in India [9] and abroad [10, 11]. The 56 genotypes were grouped into 8 clusters in both the years using 500 and 285 Euclidean² distance as cut of point, respectively. However, composition of clusters was slightly different in different years. At 3 year age, cluster I contained maximum number of genotypes i.e., 19 followed by 8 in cluster IV and VII, 6 in cluster II, 5 in cluster III and VIII, 4 in cluster V and 1 in cluster VI. At 4 year age, cluster V contained maximum number of genotypes i.e., 16 followed by 11 in cluster VI, 6 in cluster IV, 5 in cluster VIII, 4 in cluster I, 3 in cluster II and 1 in cluster III. The comparison of clusters and relative position of genotypes can be more clearly depicted through Ward's minimum variance dendrograms (Figs. 1&2). At age 3 and 4 year genotypes formed different clusters but, most of the genotypes moved together and found place together in one cluster (Table 1). The distribution of

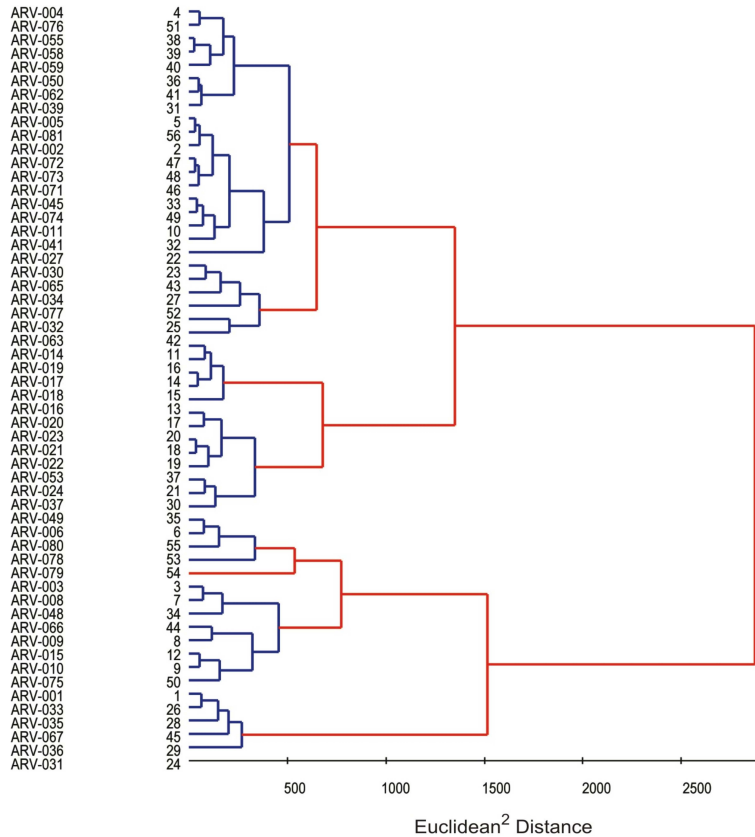


Fig. 1. Ward's minimum variance dendrogram at 3 year age

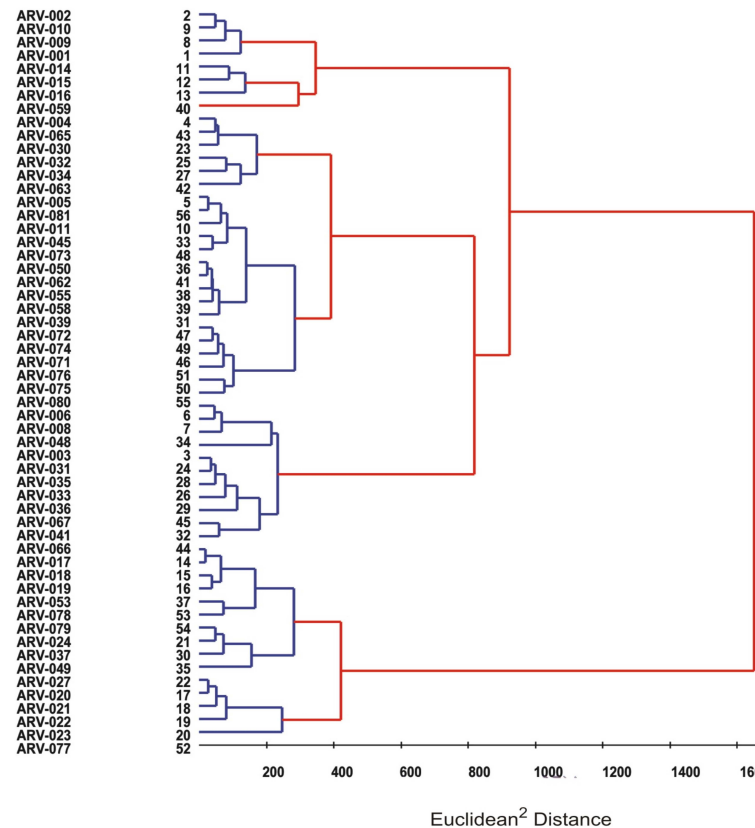


Fig. 2. Ward's minimum variance dendrogram at 4 year age

cluster values were maximum between clusters VI and VIII (664.01) and minimum between clusters IV and V (239.46). The intra-cluster Euclidean² value was maximum in cluster II (224.27) followed by cluster VI (212.84), VII (202.94), VIII (201.14), IV (189.92), I (165.69) and V (151.49) (Table 3).

The characters contributed more towards divergence at 3 year age also contributed high at 4 year age. These were seed content, 100-seed weight, number of female flowers per inflorescence, oil content, kernel: shell ratio, weight per fruit, number of male flowers per secondary branch, acid value and iodine

Table 4. Contribution (%) of characters to total divergence

S.No. Characters	Contribution (%)	
	at 3 year age	at 4 year age
1 Plant height	0.00	0.00
2 Stem girth	0.00	0.00
3 Number of primary branches/plant	0.00	0.00
4 Number of fruiting branches/plant	0.00	0.00
5 Number of flushes per fruiting branch	0.00	0.00
6 Number of fruits per fruiting branch	0.00	0.00
7 Petiole length	0.06	0.00
8 Area of fully matured leaf	0.58	0.00
9 Diameter of fruiting branch	0.00	0.00
10 No. of primary branches/inflorescence	1.23	3.00
11 No. of secondary br./inflorescence	0.00	2.00
12 No. of male flowers/secondary branch	4.74	5.00
13 No. of female flowers/secondary br.	0.00	2.00
14 No. of female flowers/inflorescence	9.16	10.00
15 Ratio of male to female flowers	0.06	2.00
16 Fruit diameter	0.00	1.00
17 Weight per fruit	6.75	2.00
18 Seeds per fruit	0.00	0.00
19 100 Seed weight	27.01	15.00
20 Fruit yield per plant	0.00	0.00
21 Seed yield per plant	5.97	0.00
22 Seed content	11.17	32.00
23 Kernel : shell ratio	15.45	4.00
24 Oil content	10.45	9.00
25 Acid value	2.86	6.00
26 Iodine value	4.48	5.00

value. The contributions of these characters were 92.07 and 88.00 percent at 3 and 4 years of age, respectively (Table 4). The genotypes having high mean values for these characters found places in five clusters in both the years. At 3 year age cluster IV had maximum mean values for weight per fruit, 100-seed weight, seed yield per plant, seed content, kernel: shell ratio and oil content and cluster VI for acid value and iodine value. Similarly cluster II, III and VII for number of primary branches per inflorescence, number of female flowers per inflorescence and number of male flowers per secondary branch, respectively (Table 5). At 4 year age cluster VIII had highest mean values for number of primary branches per inflorescence, 100-seed weight, seed yield per plant and kernel: shell ratio, cluster II for number of female flowers per inflorescence and iodine value and cluster III for number of male flowers per secondary branch and acid value. Similarly, cluster VII had highest mean value for seed content and oil content and cluster IV for weight per fruit (Table 6). The genotypes with high mean values for 100-seed weight, seed yield per plant and kernel: shell ratio moved together and found place in cluster IV and VIII at 3 and 4 year age, respectively. The characters having maximum mean values in cluster IV and VIII was 76.8 and 22.0 per cent at 3 and 4 year of age, respectively. The low contribution of these characters in second year was on account of shifting of genotypes with higher seed content in cluster VII and increase of contribution of this character from 11.17 in first year to 32 per cent in second year. The mean value of these characters may also be considered while selecting the diverse genotypes. The genetic divergence was less dependent on vegetative characters like plant height, stem girth, number of primary branches per plant, number of fruiting branches per plant, petiole length, area of fully matured leaf and diameter of fruiting branch as contribution of these characters was very low.

The maximum inter cluster distance was between cluster III and VIII at 3 year age and between cluster VI and VIII at 4 year age. In first year ARV-017 and ARV-019 in cluster III and ARV-035 and ARV-036 in cluster VIII and in second year ARV-036, ARV-041 and ARV-035 in cluster VI and ARV-020, ARV-021 and ARV-023 in cluster VIII showed high *per se* performance for seed yield. The best performing genotypes ARV-021 and ARV-023 clustered in cluster IV at 3 year age and in VIII at 4 year age. The cluster IV showed second highest inter-cluster distance from the cluster VIII at 3 year age. Further ARV-036 showed

Table 5. Cluster means for the characters at 3 year age

Cluster	Plant height	Stem girth	No. of primary branches/plant	No. of fruiting branches/plant	No. of flushes/fruiting branch	No. of fruits/fruiting branch	Petiole length	Area of full matured leaf	Diameter of fruiting branch
I	1.533	18.75	3.326	8.800	1.097	2.763	10.912	130.572	1.499
II	1.518	17.82	3.400	5.700	1.189	2.542	11.892	132.963	1.567
III	2.087	22.75	3.400	14.760	1.288	3.802	11.490	123.742	1.564
IV	2.404	24.36	3.400	13.000	1.242	4.234	13.529	128.135	1.413
V	1.130	15.43	3.500	6.200	1.350	2.720	11.214	126.940	1.549
VI	1.150	15.08	2.400	2.800	1.240	3.366	9.408	125.590	1.610
VII	1.561	18.95	3.400	10.625	1.140	2.733	9.196	116.869	1.508
VIII	2.129	23.29	3.960	12.640	1.337	3.644	14.455	144.320	1.443
Probability	0.000	0.002	0.372	0.124	0.018	0.010	0.000	0.022	0.187
Cluster	No. of primary branches/inflorescence	No. of secondary branches/inflorescence	No. of male flowers/secondary branch	No. of female flowers/secondary branch	No. of flowers/inflorescence	Ratio of male to female flowers	Fruit diameter	Weight per fruit	
I	2.046	7.469	21.454	1.349	11.269	16.806	2.036	2.256	
II	2.187	7.597	19.242	1.497	11.015	13.436	2.074	2.511	
III	2.016	7.364	19.596	1.716	20.156	11.450	2.080	2.410	
IV	2.010	7.793	22.705	1.320	12.349	18.187	2.035	2.528	
V	2.040	7.515	16.763	1.523	13.875	11.346	2.074	2.192	
VI	2.000	7.400	18.500	1.520	13.100	12.174	1.852	1.648	
VII	2.053	7.461	23.461	1.544	13.967	15.338	2.002	1.953	
VIII	2.020	7.730	21.700	2.164	13.098	10.360	2.042	2.410	
Probability	0.335	0.571	0.080	0.002	0.000	0.000	0.032	0.000	
Cluster	Seeds/fruit	100 seed weight	Fruit yield per plant	Seed yield/plant	Seed content	Kernel : shell ratio	Oil content	Acid value	Iodine value
I	2.882	57.284	74.584	50.091	66.901	1.382	33.185	6.419	109.897
II	2.807	67.913	53.851	33.887	63.720	1.428	33.815	6.389	101.893
III	2.944	64.765	92.509	65.978	71.237	1.409	34.982	7.434	113.174
IV	2.930	67.941	112.091	81.112	72.709	1.683	39.732	8.509	103.368
V	2.820	53.078	39.105	27.134	69.109	1.198	36.006	8.105	95.973
VI	2.480	55.726	36.020	20.268	56.222	0.988	38.200	13.240	133.264
VII	2.820	43.235	70.416	44.974	62.327	1.099	31.109	8.302	99.394
VIII	2.848	49.369	105.649	57.472	54.932	1.150	29.738	5.884	116.435
Probability	0.011	0.000	0.007	0.003	0.000	0.000	0.000	0.135	0.004

high mean seed yield than ARV-035 in both the years, ARV-020 was identified as the best genotype based on consistent high per se performance and ARV-023 had highest seed yield at 4 year age and at par to

ARV-020 at 3 year age. Thus ARV-036 X ARV-020 and ARV-036 X ARV-023 cross combinations would be the best to obtain superior plants in F₁. The F₁ will be segregating generation because parents are

Table 6. Cluster means for the characters at 4 year age

Cluster	Plant height	Stem girth	No. of primary branches/plant	No. of fruiting branches/plant	No. of flushes/fruiting branch	No. of fruits/fruiting branch	Petiole length	Area of full matured leaf	Diameter of fruiting branch
I	1.750	27.78	2.950	8.450	1.095	2.963	8.264	101.400	1.544
II	1.996	29.62	3.600	17.800	1.307	4.333	11.435	128.267	1.541
III	1.600	29.85	3.600	13.400	1.040	3.300	10.378	133.290	1.402
IV	1.800	27.84	3.600	9.367	1.153	3.083	12.126	133.798	1.541
V	1.706	29.09	3.388	10.088	1.135	3.242	10.682	131.005	1.512
VI	2.057	32.28	3.782	15.236	1.253	3.891	11.749	136.963	1.497
VII	2.327	33.01	3.460	15.640	1.276	4.252	12.358	130.136	1.494
VIII	2.578	34.79	3.560	15.520	1.184	4.336	12.890	120.656	1.434
Probability	0.010	0.026	0.487	0.038	0.027	0.020	0.027	0.000	0.628

Cluster	No. of primary branches/inflorescence	No. of secondary branches/inflorescence	No. of male flowers/secondary branch	No. of female flowers/secondary branch	No. of flowers/inflorescence	Ratio of male to female flowers	Fruit diameter	Weight per fruit
I	2.000	5.780	24.410	1.260	12.330	19.437	1.970	1.864
II	2.000	7.617	28.380	1.567	17.330	18.225	2.067	2.273
III	2.040	7.350	28.750	1.520	10.700	18.922	2.052	2.344
IV	2.020	7.574	20.581	1.449	11.161	14.651	2.088	2.603
V	2.017	7.559	23.184	1.341	10.251	17.619	2.013	2.199
VI	2.004	7.581	24.110	1.579	12.000	15.770	1.989	2.183
VII	2.000	7.511	21.353	1.532	12.171	14.241	2.008	2.405
VIII	2.120	7.976	20.750	1.000	8.848	20.750	2.044	2.417
Probability	0.182	0.000	0.022	0.001	0.000	0.003	0.059	0.000

Cluster	Seeds/fruit	100 seed weight	Fruit yield per plant	Seed yield/plant	Seed content	Kernel : shell ratio	Oil content	Acid value	Iodine value
I	2.770	43.286	104.396	69.889	67.980	1.205	31.792	8.429	100.499
II	2.920	58.785	167.344	113.443	68.138	1.375	32.220	10.081	118.191
III	2.880	62.552	142.046	98.882	69.568	1.252	32.572	26.098	101.338
IV	2.820	67.524	107.448	68.034	63.384	1.366	32.738	7.342	103.655
V	2.855	55.853	94.342	63.286	66.807	1.297	32.065	6.255	111.658
VI	2.793	50.059	126.161	72.405	57.459	1.069	31.363	5.772	112.821
VII	2.908	61.998	150.837	109.535	72.788	1.553	39.795	6.098	107.746
VIII	2.920	67.985	235.848	170.469	72.523	1.618	36.735	9.882	104.257
Probability	0.179	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.439

heterozygous, so clones may be developed from superior plants and tested at different locations.

In conclusion, for development of high oil content

clone genotypes ARV-079 and ARV-049 could be used as parents and can be crossed with ARV-036 or ARV-035 (having high inter cluster distance and good seed yield) and with ARV-020 or ARV-023 (having high per

se performance for seed yield and for most of the positively correlated characters with seed yield). High seed yield and oil yield is expected from the above hybrids. If not in hybrid, individual plant may be tested for these characters and desired one may be multiplied through vegetative propagation to obtain the superior clones for high seed yield and oil content.

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