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Studies on genetic components and character association among *Jatropha* (*Jatropha curcas* L.) genotypes

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Abstract

The present investigation was carried out at Medicinal Plant Research and Development Centre of the G.B. Pant University of Agriculture and Technology, Pantnagar during the year 2011-14. The forty six open pollinated genotypes of *Jatropha curcas* collected from various parts of the country and planted in Randomized Block Design. All the genotypes showed sufficient genetic variability. The PCV and GCV indicated that the values of PCV were higher than of GCV, but the difference was very closer between these two estimates for all parameters. The highest heritability observed for seed yield per plant and seed yield per ha and total number of branches per plant, days to flower initiation, collar diameter and plant height parameter. High estimates of genetic advance recorded for seed yield per ha, plant height and total number of branches per plant. Seed yield per ha showed highly significant positive correlation with total no. of branches, collar diameter and seed index. The diverse genotypes having high heritability, genetic advance and positive correlation of phenotypic and genotypic correlation would be helpful in selection and improvement of genetic population in breeding program.

Keywords: *Jatropha curcas*, heritability, genetic advance, PCV and GCV etc

Introduction

Jatropha (*Jatropha curcas* L.) belongs to the family Euphorbiaceae having 175 species and has originated from tropical America and has spread all over the tropics and subtropics of Asia and Africa (Mabberley, 2008) [19]. Native place of the *J. Curcas* is to South America (Ramawat, 2010) [27] and it was introduced to the tropical and sub-tropical regions of Asia and Africa by the Portuguese (Mabberley, 2008) [19]. From the oil-bearing crops the renewable energy source produced that is biodiesel, which is gaining attention due to low emission profiles and environmental benefits (Ma and Hanna, 1999) [18]. It has been promoted that the biodiesel production from non-edible oil crops such as *Pongamia pinnata*, *Azadirachtra indica*, and *Jatropha curcas* L. (Bankovi'c, et al., 2012; Borugadda and Goud, 2012) [4, 7]. Among all the crops, the oil is rapidly growing from *J. curcas* for biodiesel production, due to the high oil yield and long productive period of the crop (Ong, et al., 2011; Achten, et al., 2008) [23, 1]. As a drought-resistant crop with the adaptability to grow on marginal soils, the cultivation is becoming favorable in developing countries due to its contribution to rural development (Ong, et al., 2011; Achten et al., 2010; Conran, et al., 2013) [23, 2, 10].

Besides its use for biodiesel production, it has been used for the preparation of soaps and cosmetics, cloth dye, and medicine (Moniruzzaman, et al., 2017) [21], and its waste biomass is utilized as fertilizer, adsorbent, briquettes, resin and bioactive compost (Primandari, et al., 2018) [26]. *Jatropha curcas* is reported to be a polymorphic species, and it displays great variation in plant architecture, fruiting capacity, seed yield and seed oil content (Xu et al., 2012; Guan et al., 2013) [35, 14]. The seed oil content ranges from 30% to 65% (Basha, et al., 2009; Nzikou, et al., 2009) [9, 22]. More than 1,000,000 ha of *Jatropha* has been propagated throughout the world, the majority (about 85%) concentrated in Asian countries such as India (the largest cultivator), China, and Myanmar; 12% is found in Africa and 2% in Latin America (Edrisi, et al., 2015) [12].

Material and Methods

The present investigation was carried out at Medicinal Plant Research and Development Centre (MRDC) of the G.B. Pant University of Agriculture and Technology, Pantnagar. The trial was initiated in July 2005 under the project National Network on Integrated Development

of Tree-Born Oilseed. The present study was carried out during the year 2011-14. The experimental material for present study comprised of forty six open pollinated genotypes of *Jatropha curcas* collected from various parts of the country (Table 1). All forty six genotypes were planted during July, 2005 in Randomized Block Design (RBD) with three replications at, Medicinal Plant Research and Development Center (MRDC), G.B. Pant University of Agriculture and Technology, Pantnagar. Utilizing pre grown nursery plants. Each plot has one row with sixteen plants and the plant to plant and row to row spacing was kept 3x3 m. Standard agronomic practices were carried out during crop growth period and harvesting of ripe fruits was done during Dec-Jan every year.

The data were recorded on five randomly selected competitive plants in each replication and each genotype for seven character seed yield/plant (kg), seed yield (kg/ha), plant height (cm), collar diameter (cm), days to flower initiation, total number of branches/plant and seed index (g). The analysis of variance was analyzed by the formula given by Cochran and Cox (1992) [9], heritability (Allard, 1960) [3], genetic advance (Allard, 1960; Burton and Devane, 1953) [3, 8], correlation analysis (Searle, 1961) [31] and coefficient of variation (Burton and Devane, 1953) [8].

Result and Discussion

Analysis of Variance

The results of analysis of variance for Randomized Block Design for seven characters of Forty six genotypes have been presented in Table 2. The pooled data over the two years (2011-12 and 2012-13) for different characters has been presented below. Analysis of variance exhibited highly significant differences among the genotypes for the traits viz. seed yield/plant, seed yield ha/kg, plant height, collar diameter; total no. of branches/plant, and seed index and significant differences was observed for the entire trait. It means there is the sufficient genetic variability present among the genotypes. Das *et al.*, (2010) [11] observed high variability for Seed yield/plant (g), Plant height (cm), Collar diameter (cm), Total no. of branches/plant, Seed index (g) etc. similar observation also reported by Kumar *et al.*, (2008) [17] for seed yield/plant (g), plant height (cm), collar diameter (cm), total no. of branches/plant, seed index (g) etc.

Heritability and Genetic Advance

The genetic variability among different genotypes for different parameters has been showed in Table 3. The estimates of phenotypic (PCV) and genotypic coefficient (GCV) of variation indicated that the values of PCV were higher than of GCV, but the difference was very closer between these two estimates for all the cases. This indicates that greater role of genetic components and expression of characters under study was less influenced due to environmental factors. The results in accordance with the findings of Rao *et al.*, (2009a) [29] in *Jatropha*, Sridhar *et al.*, (2009) [33] and Patel *et al.*, (2010a) [25] in castor.

According to Mac Whirter (1979) [20] heritability estimates can be divided into three categories which are low heritability ($h^2 < 0.2$), medium heritability ($0.2 > h^2 < 0.5$), and high heritability ($h^2 > 0.5$). In the pooled analysis all the characters showed highest heritability viz. seed yield per plant and seed yield per ha and total no. of branches per plant, days to flower initiation, collar diameter, plant height and moderate heritability was observed for seed index. The estimates of

heritability were observed to be high for yield and contributing characters. This indicated that phenotypic based selection would be effective for the improvement of the traits. According to Baraskar *et al.*, (2014) [5] genetic advance estimates can be divided into three classes which are high (>20%), moderate (10-19%) and low (<10%). High estimates of genetic advance recorded for seed yield per ha, plant height and total number of branches per plant and collar diameter and days to flower initiation showed moderate and low genetic advance was recorded for seed yield per plant and seed index. The magnitude of high genetic advance is useful in identification and selection for appropriate characters.

Finally it was concluded that seed yield per plant and seed yield per ha has high heritability coupled with high genetic advance which is in accordance with the findings of Gohil and Pandaya (2009) [13] in *Jatropha*. The determination of the extent of variation is not possible which is heritable through genotypic coefficient of variation alone. For the prediction of genetic advance for any quantitative characters and exercising selection procedure the knowledge of heritability helps to plant breeder (Baraskar *et al.*, 2014, Guleria *et al.*, 2019) [5, 15]. The genotypic coefficient of variation together with heritability estimate would give the best picture expected for selection than the heritability value alone (Burton, 1952).

The genetic architecture of the population can be measured by the idea of estimates of heritability and genetic advance (Baraskar *et al.*, 2014) [5]. High heritability along with high genetic advance indicates the presence of additive gene action for improvement of that trait by various selection methods. The moderate genetic advance accompanied with high heritability which indicates the presence of both additive and non-additive gene action for that traits. High heritability coupled with low genetic advance which clearly indicates the presence of non-additive gene action and selection is not rewarding for such traits. For such types of traits the recombination breeding and recurrent selection may be used for population improvement (Guleria *et al.*, 2019) [15].

Correlation Analysis

The correlation analysis for different characters of *Jatropha* are presenting in Table 4. The results indicated that seed yield per plant showed positive and highly significant genotypic as well as phenotypic correlations with seed yield per ha, collar diameter, total no. of branches per plant, seed index, the reason behind this association may be the plants with thick collar diameter are suppose to possess well developed root system which supports more production of branches in accordance with the findings of Sharma (2009) [32]. Whereas negative and significant correlation with plant height. Seed yield per ha shows highly significant positive correlation with total no. of branches, collar diameter and seed index which was also reported by Parthiban, *et al.*, (2011) [24] in *Jatropha* whereas, negative and highly significant correlation with plant height. Plant height represented highly significant and positive correlations at both genotypic and phenotypic levels with total no of branches per plant, days to flower initiation and negative correlation for collar diameter. Collar diameter showed significant positive correlation with seed index and days to flower initiation. Days to flower initiation showed positive and highly significant positive correlations with seed index, and negative correlation with seed yield per plant and seed yield per ha, this was in accordance with the findings of Rao, *et al.*, (2008) [28] in *Jatropha*. In the present investigation, it was observed that the magnitude of genotypic correlation

coefficients was higher than their corresponding phenotypic correlation coefficients (Yadav, *et al.*, 2004, in castor) ^[36] and significant correlations were found between most of the economic characters studied. These findings are in accordance with Umamaheswari, *et al.*, (2009) ^[34] and Das *et al.*, (2010)

^[11] in *Jatropha*. Correlation studies provide better understanding of yield components which helps plant breeder during selection (Robinson *et al.*, 1951; Johanson *et al.*, 1955) ^[30, 16].

Table 1: Information of genotypes collected from different zones in research program

S. No.	Name of genotype	Place of collection
1.	IGAU Raipur	Chhattisgarh
2.	IGAU Bilaspur	
3.	IGAU- Surzuja	
4.	Jajhar kotali	Jammu & kashmir
5.	Lower Sowan Cheack	
6.	Low Dhearti	
7.	Sagar (SFRI. Jabalpur)	Madhya Pradesh
8.	Indor (SFRI. Jabalpur)	
9.	TFRI-1	
10.	TFRI-2	
11.	RJ-117	Maharashtra
12.	PKVJ-MKV-1	
13.	PKVJ- DHW-1	Rajasthan
14.	Rajasthan 31	
15.	TNMC-2	Tamilnadu
16.	TNMC-3	
17.	TNMC-4	
18.	TNMC-5	
19.	TNMC-7	
20.	TNMC-22	Uttarakhand
21.	PJ-03004	
22.	PJ03103	
23.	Pant J. Sel-1	
24.	Pant J. Sel-2	
25.	Sitapur 30	
26.	Danibunger28	
27.	Danibunger29	
28.	Danibunger27	
29.	Daultpur 25	
30.	Kamaluaganja 24	
31.	Kamaluaganja 22	
32.	Kaladungi rd 15	
33.	Kaladungi rd 16	
34.	Golapar 12	
35.	Golapar 13	
36.	Golapar 11	
37.	Golapar 8	
38.	Golapar 9	
39.	Lamachaur -6	
40.	Lamachaur -2	
41.	Lamachaur -3	
42.	Lamachaur -4	
43.	Lamachaur -5	
44.	Pant J Sel- 4	
45.	Pant J Sel-31	
46.	Pant J Sel-97	

Table 2: Pooled Analysis of variance (ANOVA)

Source of variation	d.f.	Seed yield / plant (kg)	Seed yield / ha (kg)	Plant height (cm)	Collar diameter (cm)	Days to flower initiation	Total no. of branches/plant	Seed index (g)
Replication	2	0.000004	23.34	15.43	5.54	0.08	3.12	0.71
Treatment	45	0.015**	18457.41**	574.622**	151.081**	71.388**	641.990**	3.134**
Error	90	0.000013	13.85	53.01	1.82	0.12	4.85	0.99
SEm.		0.002	2.15	4.20	0.78	0.20	1.27	0.58
CD. at 5%		0.006	6.04	11.81	2.19	0.57	3.57	1.62

SEm: Standard error of mean, CD = Critical difference

Table 3: Pooled estimation of genetic parameters for yield and different yield contributing characters of *Jatropha curcas* L. over two years

Genetic parameters	Seed yield/plant (kg)	Seed yield/ha (kg)	Plant height (cm)	Collar diameter (cm)	Days to flower initiation	Total no. of branches/plant	Seed index (g)
PCV (%)	40.45	40.95	3.57	9.56	28.62	12.85	2.15
GCV (%)	40.39	40.90	3.13	9.39	28.55	12.71	1.12
ECV (%)	2.11	1.94	1.72	1.79	2.07	1.92	1.64
h ² (b) (%)	99.70	99.70	76.60	96.40	99.40	97.70	41.50
SEm	0.002	2.14	4.20	0.78	0.20	1.27	0.577
GM	0.17	191.67	421.08	75.04	17.07	114.65	60.65
GA	0.14	161.33	23.77	14.27	10.01	29.68	1.12

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, ECV= Environmental coefficient of variation, h² (b) = Heritability in broad sense, GM= General mean, GA= Genetic advance

Table 4: Pooled estimates of genotypic and phenotypic correlation coefficients between different characters over two years

Character		Seed yield/plant (Kg)	Seed yield/ha (kg)	Plant height (cm)	Collar diameter (cm)	Days to flower initiation	Total no. of branches/plant
Seed yield/plant (Kg)	rg						
	rp						
Seed yield/ha (kg)	rg	0.998**					
	rp	0.996**					
Plant height (cm)	rg	-0.248**	-0.242**				
	rp	-0.217*	-0.212*				
Collar diameter (cm)	rg	0.228**	0.244**	-0.065 ^{NS}			
	rp	0.224**	0.239**	-0.040 ^{NS}			
Days to flower initiation	rg	-0.107 ^{NS}	-0.101 ^{NS}	0.213*	0.188*		
	rp	-0.107 ^{NS}	-0.100 ^{NS}	0.182*	0.182*		
Total no. of branches/plant	rg	0.515**	0.508**	0.589**	0.041 ^{NS}	0.163 ^{NS}	
	rp	0.500**	0.493**	0.500**	0.043 ^{NS}	0.163 ^{NS}	
Seed index (g)	rg	0.206*	0.220**	0.213*	0.376**	0.325**	0.128 ^{NS}
	rp	0.132 ^{NS}	0.136 ^{NS}	0.153 ^{NS}	0.243**	0.182*	0.081 ^{NS}

rg= genotypic correlation, rp= phenotypic correlation

Conclusion

In the present study the forty six diverse genotypes of *Jatropha curcas* showed high genetic diversity where the phenotypic coefficient of variation very closer to genotypic coefficient of variation which showed the expression of characters were less influenced due to environmental factors. Almost all the characters showed high heritability and highest genetic advance along with heritability for seed yield per ha, plant height and total number of branches per plant means the selection would be effective in phenotypic based improvement of these traits. The well performed genotypes for the genetic estimates of the characters could be used in breeding program for selection and hybridization program for improvement the characters.

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