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Evaluation of Genetic Variability for Quantitative and Qualitative Characters in Niger [*Guizotia abyssinica* (L.f) Cass] Local Germplasm

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A B S T R A C T

A study was undertaken to determine the extent of genetic variability for seed yield and ten other quantitative characters and two qualitative characters in 45 genotypes of Niger. The analysis of variance revealed significant differences among genotypes for all the characters. High genotypic coefficient and phenotypic coefficient of variation was recorded for number of secondary branches per plant followed by number of capitula per plant, 1000 seed weight, seed yield per plant, number of seed per capitula and number of primary branches per plant, days to 50% flowering. The lower magnitude of GCV and PCV was observed in protein content, plant height, oil content, days to maturity and diameter of capitula. The high estimates of heritability in broad sense was observed for number of secondary branches per plant followed by number of capitula per plant, 1000 seed weight and number of seeds per capitula. Highest estimate of GA was noticed for number of secondary branches per plant. While, medium to low estimates of GA observed for number of capitula per plant, 1000 seed weight, seed yield per plant, number of seeds per capitula, number of primary branches per plant, days to 50% flowering, diameter of capitula, days to maturity, oil content, protein content, plant height. High heritability coupled with high genetic advance was recorded in number of capitula per plant, number of secondary branches per plant, 1000 seed weight, and number of seeds per capitula, which indicated the predominance of additive gene effects. Improvement in these characters could be exercised by simple selection due to fixable additive gene effects.

Introduction

Niger (*Guizotia abyssinica* (L.f) Cass) is named after the French historian Guizot. It belongs to the family Compositae/Asteraceae, tribe Helianthoides and subtribe Verbeninae. It is an oilseed crop cultivated in Indian subcontinents and East African Countries. It is self-incompatible crop having diploid chromosome 2n=30. It is minor crop grown mostly in India and Ethiopia where it is known as Ram til, Kala til, Karala, Gurellu, Tilangi and Neuk, Noog and Nug.

Niger is the native of highlands of Ethiopia and originated from *G. scabre* subsp. *Schimperi,* where it is a common weed in fields with grown Niger. The wild form has oil content of 24 to 35%, while the cultivated Niger has 36 to 42% oil with fatty acid composition of 75 to 80% linoleic acid, 7 to 8 % palmitic and stearic acid and 5 to 8 % oleic

acid. Indian Niger oil reported higher in oleic acid (25%) and lower in linoleic acid (55%). Niger has a 10-30% protein content. Niger is a dicotyledonous herb, moderately to well branched, grows up to two meter tall. Niger plant like other compositae is highly cross pollinated oilseed crop mostly grown on marginal and sub marginal land.

In India the Niger is grown on an area of 2.61 lakh ha mainly during *Kharif*, and average productivity in India is 321 kg/ha with production 0.84 lakh tonnes. India is the largest exporter of Niger in the world to USA, Netherland, Italy, Germany, Belgium, and Spain are the regular buyer. Whereas, USA is the largest buyer in the world. The export of the Niger seed continuously increased. In Maharashtra, it is grown on an area of 0.141 lakh ha with the production of 0.023 lakh MT and productivity is 165 kg/ha (2016-17). India tops in area, production and total export for Niger in the world.

Information regarding genetic variability present in population and estimates of heritability are pre requisites for designing an effective breeding programme for improvement of any crop. Therefore, it is necessary to collect, conserve and study the genetic diversity among various crops in the form of germplasm for establishing the wide genetic base for the posterity.

Selection of parents is of paramount importance in any breeding programme, so as to get maximum heterosis and a wide spectrum of variability in the segregating generations.

Materials and Methods

The experimental material comprising forty five genotypes of Niger were grown in Randomized Block Design with two replications at the research farm of Department of Genetics and plant breeding, College of Agriculture, Dhule, during *Kharif* season of 2018. Each entry was represented by single row of 4.5 m length with spacing of 30 cm between rows. Data were recorded on five randomly and competitive plants of each genotype from each replication for twelve quantitative characters viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capitula per plant, number of seeds per capitula, diameter of capitula (cm), 1000 seed weight (g), seed yield per plant (g), protein content (g), oil content (g). The mean of five plants was subjected to statistical analysis. The data for different characters were statistically analyzed for significance by using analysis of variance technique described by Panse and Sukhatme (1985). The adapted design was Randomized Block Design (RBD) with two replications. The significance of mean sum of square for each character was tested against the corresponding error degrees of freedom using "F" Test (Fisher and Yates, 1967). The components of variances were used to estimate genetic parameters like phenotypic and genotypic coefficient of variation (PCV and GCV) as per the formula given by Burton and De Vane (1953). Heritability in broad sense was calculated according to the formula given by Allard (1960) and expressed in percentage. Genetic advance was estimated by using Burton (1953).

Results and Discussion

Analysis of variance revealed significant differences among genotypes for all the characters. Studies of genetic variability exhibited high phenotypic and genotypic coefficients of variation, heritability and genetic advance as percent of mean for the traits viz., Genetic advance as a per cent of mean was observed highest for number of

secondary branches per plant followed by number of capitula per plant. Whereas, it was found medium for 1000 seed weight, seed yield per plant and number of seeds per capitula, number of primary branches per plant and days to 50% flowering. While low estimates of GA observed for plant height, Protein content, oil content, days to maturity and diameter of capitula indicating simple selection can be practiced for improvement of these characters (Table 1). It shows that the presence of variability and choice of material is appropriate.

Improvement of economic characters like yield through selection is conditioned by the nature and magnitude of variability existing in such populations. However, the phenotypic expression of complex character like yield is a combination of genotype, environment and their interaction. This indicates the need for partition of overall variability into heritable and non-heritable components with the help of appropriate statistical techniques. Possibility of achieving improvement in any crop plants depends largely on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and environmental components. The genotypic component being the heritable part of the total variability, its magnitude for yield and its component characters influence the selection strategies to be adopted by the breeders.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters, indicating that the characters were less influenced by the environment. Therefore, selection for the improvement of these traits.

The differences between GCV and PCV values was more for plant height, diameter of capitula, 1000 seed weight and seed yield per plant indicating that selection based on phenotypic observation may not be very effective for these traits (Table 2 and 3).

Table.1 Analysis of variance for twelve characters in Niger

Sr. No	Characters	Mean sum of square		
		Replication	Genotype	Error
1	Days to 50 per cent flowering	0.100	95.622**	7.622
2	Days to maturity	5.877	65.018**	26.673
3	Plant height (cm)	740.173	11275.376**	8486.941
4	No. of primary branches / plant	2.116	20.370**	5.074
5	No. of secondary branches / plant	10.410	260.910**	12.331
6	No. of capitula / plant	105.408	1582.885**	94.286
7	No. of seeds / plant	1.534	49.349**	8.527
8	Diameter of capitula (cm)	0.009	0.011**	0.005
9	1000 seed weight (g)	0.047	0.462**	0.072
10	Seed yield/ plant (g)	0.065	1.108**	0.258
11	Protein content (%)	0.531	2.131**	0.707
12	Oil content (%)	4.513	4.954**	2.021

*, ** Indicates significance at 5% and 1% level, respectively.

Table.2 List of Niger genotypes with origin

Sr. No.	Genotype	Source
1	DHLN – 1	Igatpuri (Nasik)
2	DHLN – 2	Igatpuri (Nasik)
3	DHLN – 3	Igatpuri (Nasik)
4	DHLN – 4	Igatpuri (Nasik)
5	DHLN – 5	Igatpuri (Nasik
6	DHLN – 6	Akole (Ahamednagar)
7	DHLN – 7	Sakri (Dhule)
8	DHLN – 8	Trimbakeshwar (Nasik)
9	DHLN – 9	Akole (Ahamednagar)
10	DHLN – 10	Dhadgoan (Nandurbar)
11	DHLN – 11	Dhadgaon (Nandurbar)
12	DHLN – 12	Sakri (Dhule)
13	DHLN – 13	Trimbakeshwar (Nasik)
14	DHLN – 14	Trimbakeshwar (Nasik)
15	DHLN – 15	Akole (Ahamednagar)
16	DHLN -16	Tarahabad (Nasik)
17	DHLN – 17	Surgana (Nasik)
18	DHLN – 18	Surgana (Nasik)
19	DHLN – 19	Tarahabad (Nasik)
20	DHLN – 20	Saler-Muler (Nasik)
21	DHLN – 21	Saler-Muler (Nasik)
22	DHLN – 22	Saler-Muler (Nasik)
23	DHLN – 23	Saler-Muler (Nasik)
24	DHLN – 24	Surgana (Nasik)
25	DHLN – 25	Surgana (Nasik)
26	DHLN – 26	Mahabaleshwar (Satara)
27	DHLN – 27	Mahabaleshwar (Satara)
28	DHLN – 28	Mahabaleshwar (Satara)
29	DHLN – 29	Kosbad (Thane)
30	DHLN – 30	Kosbad (Thane)
31	DHLN – 31	Tarahabad (Nasik)
32	DHLN – 32	Tarahabad (Nasik)
33	DHLN – 33	Igatpuri (Nasik)
34	DHLN – 34	Igatpuri (Nasik)
35	DHLN – 35	Akole (Ahamednagar)
36	DHLN – 36	Akole (Ahamednagar)
37	DHLN – 37	Surgana (Nasik)
38	DHLN – 38	Surgana (Nasik)
39	DHLN – 39	Kosbad (Ahamednagar)
40	DHLN – 40	Tarahabad (Nasik)
41	DHLN – 41	Sakri (Dhule)
42	DHLN – 42	Sakri (Dhule)
43	DHLN - 43(Phule Karala)	Peth (Nasik)
44	DHLN - 44(Phule Vaitarna)	Trimbakeshwar (Nasik)
45	DHLN - 45(IGP - 76)	Niphad (Nasik)

Table.3 Parameters of genetic variability for different characters in Niger

Sr. No	Characters	General Mean	$\sigma^2 g$	$\sigma^2 p$	$\sigma^2 e$	GCV (%)	PCV (%)	ECV (%)	h^2 (BS %)	GA	GA as per cent of mean
1	Days to 50 per cent flowering	75.366	44.000	51.622	7.622	8.801	9.533	3.663	85.230	12.615	16.738
2	Days to maturity	105.344	19.172	45.846	26.673	4.156	6.427	4.902	41.820	5.833	5.537
3	Plant height (cm)	189.885	31.686	224.571	192.885	2.964	7.892	7.314	14.110	4.355	2.293
4	No. of primary branches /plant	23.362	7.648	12.722	5.074	11.837	15.267	9.642	60.120	4.147	18.907
5	No. of secondary branches /plant	42.583	124.289	136.620	12.331	26.180	27.448	8.246	90.970	21.905	51.440
6	No. of capitula /plant	105.404	744.299	838.586	94.286	25.883	27.473	9.212	88.760	52.947	50.232
7	No. of seeds / capitula	28.480	20.410	28.938	8.527	15.862	18.888	10.253	70.530	7.816	27.443
8	Diameter of capitula (cm)	0.918	0.002	0.008	0.005	5.817	10.113	8.272	33.090	0.063	6.893
9	1000 seed weight (g)	2.326	0.194	0.267	0.072	18.968	22.236	11.603	72.770	0.775	33.332
10	Seed yield/plant (g)	3.831	0.425	0.683	0.258	17.020	21.578	13.264	62.210	1.059	27.654
11	Protein content (%)	34.380	0.712	1.419	0.707	2.454	3.465	2.446	50.160	1.231	3.580
12	Oil content (%)	39.396	1.466	3.487	2.021	3.073	4.740	3.609	42.030	1.617	4.104

High genotypic coefficient and phenotypic coefficient of variation was recorded for number of secondary branches per plant followed by number of capitula per plant, 1000 seed weight, seed yield per plant, number of seed per capitula, number of primary branches per plant, days to 50% flowering showing greater scope for selection for improvement of these characters. Similar results were reported by Borole and Patil (1997), Sreedhar (2003), Patil and Duhoon (2005), Thakur and Reddy (2012), Kumar and Bisen (2016), Kusumlata *et al.,* (2018).

High heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression. Lower values of genetic advance indicate the prevalence of narrow range of variability, high G X E interaction (non-additive gene action). In the present investigation, high heritability coupled with high genetic advance was observed for number of capitula per plant followed by number of secondary branches per plant, number of days to 50% flowering, indicating the predominant role of additive gene action in the inheritance of these characters. Thus, while selection emphasis on these traits in niger should be effective for increasing seed yield. These results are in conformity with results of Mathur and Gupta (1993), Borole and Patil (1997), Patil (2000), Kenjale *et al.,* (2003), Sreedhar (2003), Ahmad *et al.,* (2003) and Patil and Duhoon (2005), Patil *et al.,* (2013), Ekhlaque *et al.,* (2016), Kumar and Bisen (2016).

High heritability with low genetic advance or low heritability with low genetic advance is observed for any given character, presence of non-additive gene action may be suspected. High heritability coupled with low genetic advance was observed, for 1000 seed weight, seed yield per plant. This indicates non-additive gene action and selection in early genotypes for such traits may not be effective. Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1953). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.,* 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Table 3). In conclusion, the material chosen differed in their genotypic make up as evidenced by the significant differences among them in respect of all the quantitative characters studied. Phenotypic coefficients of variations estimate were slightly higher than the genotypic coefficients of variation for all the trait, indicating low environmental influence on the expression of all the traits.

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