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Estimation of genetic variability for quantitative traits in Niger (*Guizotia abyssinica* L. f. Cass) genotypes

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Abstract

The field experiment conducted at the Zonal Agricultural Research Station, AICRP on Niger, Chhindwara (M.P), during the *kharif* season 2022-23. The experiments comprised of 12 Niger genotypes including one Check JNS 28. The mean sum of square due to genotypes had highly significant differences at 1% level for almost all characters except plant population which was significant difference at 5% level indicating a wide range of variability among of 12 genotypes for all the characters studied. The GCV and PCV were moderate too low for almost all the characters under studied. The highest PCV and GCV values were found particularly for seed yield due to very high variability available in this traits. Low PCV and GCV found for days to fifty percent flowering, plant height, number of branches per plant, number of capitula per plant, 1000 grain weight, days to maturity and plant population. All the traits under study showed low genetic advance ranging from 0.30 to 11.81 except high genetic advance in seed yield was 191.70. High heritability with high genetic advance over mean were recorded for seed yield. Days to fifty percent flowering, plant height, 1000 grain weight and days to maturity have high heritability coupled with low genetic advance.

Keywords: Estimation, genetic variability, *Guizotia abyssinica* L. f. Cass

Introduction

Niger (*Guizotia abyssinica* L.f. Cass) is an important minor oilseed crop grown in tropical and sub-tropical countries like India, Ethiopia, East Africa, West Indies and Zimbabwe. India ranks 1st in area, production and export of Niger in the world. India and Ethiopia are two major producers in the world. It is used as an oilseed crop in India where it provides about three percent of the edible oil requirement of the country (Getinet & Sharma, 1996). The wild form has oil content 20 to 35 percent while cultivated Niger has 36 to 42 percent (Patil *et al*, 2019) [7]. Niger crop is cultivated in sloppy and hilly areas which is unproductive, marginal or waste lands without any production management by the tribal farmers of Madhya Pradesh.

Knowledge of key genetic parameters is necessary for any crop improvement programmed which provides precise information for selection of particulars traits. Genetic parameters like genotypic (GCV) and phenotypic (PCV) Coefficient of variation, heritability, genetic advance and path coefficient analysis are very useful biometrical tool for measuring variability present in genotypes. In this concern under the present study, genetic background and breeding values of some important Niger genotypes were determined to find the suitability in inclusion for crop improvement traits. Niger is a completely out crossing species with self-incompatibility mechanism. Development of improved plant cultivars is restricted mainly due to limited genetic variability.

Method and Materials

The field experiment conducted at the Zonal Agricultural Research Station, AICRP on Niger, Chhindwara (M.P), during the *kharif* season 2022-23. The experiments comprised of 12 Niger genotypes including one Check JNS 28. These Niger genotypes were evaluated in RBD with three replication & 30 X 10cm spacing. The recommended agronomic practices were followed to raise a healthy crop. Observation were recorded on five randomly selected plants in each replication for genetic study with respect to different morphological characters *viz.*, days to fifty percentage flowering, days to maturity, plant height (cm), number of branches per plant, number of capitula per plant, 1000 seed weight (g), seed yield per plant (g) and plant population. Genotypic and phenotypic coefficient of variation were computed according to Burton and De vane (1953) [3] and heritability was worked out by using formula suggested by Hanson *et al* (1956).

Genetic advance was computed using the formula given by Robinson *et al* (1949) whereas genetic advance as percentage over mean was worked out as suggested by Johnson *et al* (1955) [5].

Result and Discussion

The analysis of variance for different quantitative characters as shown in table 1 revealed that the mean sum of square due to genotypes had highly significant differences at 1% level for almost all characters except plant population which was significant difference at 5% level indicating a wide range of variability among of 12 genotypes for all the characters studied. Similar result have been also reported by Patil, *et al.* (2019) [7], Baghel, *et al.* (2018) [11] and Suryanarayana, *et al.* (2018) [9].

In the present studies (table 2) the days to fifty percent flowering ranged from 64 to 69 with mean value 66, variation for plant height ranged from 105-135cm with mean an average value of 128cm. the observation data of number of branches per plant ranged between 9 to 13 with a general mean 10. The data of number of capitula per plant ranged from 20 to 41 with an average 33. The 1000 seed weight ranged between 3.8 to 4.4g with mean value 4.0g. The seed yield (kg/ha) 242 to 718 with a mean value 544 Kg/ha. The days to maturity variation ranged from 99 to 104 days with mean value 101 days and plant population ranged from 270 to 333 with mean value of 303.

In the present studies (table 2) the phenotypic coefficient of variance was higher than genotypic coefficient of variances for all the characters, but the differences were narrow indicating low environmental influence in the expression for days to fifty percent flowering, plant height, 1000 grain weight and days to maturity, thus the selection based on phenotypic performance would be reliable. Those traits which showed less variation between PCV and GCV can be directly selected for further breeding programmes. Number of branches per plant, number of capitula per plant, seed yield and plant population were reported high differences between PCV and GCV which indicated greater environmental influence while these characters need more improvement for direct selection.

The GCV and PCV were moderate too low for almost all the characters under studied. These finding also reported by Sarawat, *et al.* (2022) [8] for the traits days to fifty percent flowering, days to maturity, plant height, number of branches per plant and 1000 seed weight.

The highest PCV and GCV values were found particularly for seed yield due to very high variability available in this traits. Low PCV and GCV for days to fifty percent flowering, plant

height, number of branches per plant, number of capitula per plant, 1000 grain weight, days to maturity and plant population were indicating less variability existed in these characters. Similar results have also been reported by Gururaja, *et al.* (2021) [4] for days to fifty percent flowering, Bhoite, *et al.* (2021) [2] for days to maturity and Tiwari, *et al.* (2016) [10] for the traits days to fifty percent flowering, days to maturity, plant height and 1000 seed weight. Moderate estimate of PCV and GCV was obtained for seed yield per plant.

Heritability is conjunction with genetic advance would give a more reliable index of selection value (Johanson, *et al.* 1955). Present study revealed that all the traits under study showed low genetic advance ranging from 0.30 to 11.81 except high genetic advance in seed yield was 191.70.

High heritability with high genetic advance over mean were recorded for seed yield. The results are in live with the finding of Sarawat, *et al.* (2022) [8]. It shows genotypic variance for these character due to high additive gene effect (Panse, 1957). Hence, there is an ample scope for selection for these traits. The selection based on phenotypic performance of these character would be useful for achieving desired results.

The number of capitula per plant had high heritability value coupled with moderate genetic gain suggesting that the predominance role of both additive and non additive gene action in the expression of these traits. Hence, these traits can be improved by mass selection.

High heritability coupled with low genetic advance indicates non additive gene action. Days to fifty percent flowering, plant height, 1000 grain weight and days to maturity have high heritability coupled with low genetic advance. The results are in live with the finding of Suryanarayana, *et al.* (2018) [9] for the trait days to fifty percent flowering.

Table 1: Analysis of variance (ANOVA) for 8 characters in Niger genotypes

S. No	Source	Mean sun of square		
		Replication	Genotypes	Error
	DF	2	11	22
1	Days to fifty percent flowering	1.027	4.505**	0.330
2	Plant height (cm)	4.341	75.98**	11.59
3	Number of branches per plant	0.444	2.444**	0.626
4	Number of capitula per plant	5.444	43.60**	4.838
5	1000 seed weight (g)	0.010	0.082**	0.003
6	Seed yield (Kg/ha)	1506	3721**	3397
7	Days to maturity	1.256	5.64**	0.605
8	Plant population	25.86	358.21*	116.5

Significant level: 1% (**) highly significant and 5% (*) significant

Table 2: Estimation of genetic and phenotypic coefficient of variability, Heritability, genetic advance and genetic advance over mean for 8 characters in Niger

S. No	Traits	Range		Mean	Coefficient of variance (%)		Heritability (%)	Genetic advance	Genetic advance as percentage of mean
		Min.	Max.		GCV	PCV			
1	Days to fifty percent flowering	64	69	66	1.77	1.97	0.80	2.18	3.28
2	Plant height (cm)	105	135	128	3.60	4.47	0.64	7.68	5.98
3	Number of branches per plant	9	13	10	7.14	10.19	0.49	1.12	10.32
4	Number of capitula per plant	20	41	33	10.73	12.59	0.72	6.31	18.87
5	1000 seed weight (g)	3.8	4.4	4.0	3.98	4.27	0.86	0.30	7.65
6	Seed yield (Kg/ha)	242	718	544	19.50	22.25	0.76	191.70	35.22
7	Days to maturity	99	104	101	1.27	1.49	0.73	2.28	2.25
8	Plant population	270	333	303.5	2.95	4.62	0.40	11.81	3.89

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