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Genetic variability and diversity in Niger [(*Guizotia abyssinica* (L.f.) Cass.]

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Abstract
An experiment was carried out on local collected Niger germplasm lines at the Zonal Agriculture Research Station, Igatpuri during *Kharif* 2022. Analysis of variance indicate that the mean sum of square due to genotypes were highly significant for all the characters. High genotypic coefficient of variation and phenotypic coefficient variation were observed for all the characters under study. High heritability accompanied with high genetic advance a percent were observed for seed yield per plot, number of capitula per plant and number seeds per capitula indicated that these characters are governed by additive gene effects. Twenty five germplasms were grouped into five clusters. Cluster I was biggest and consisted of 12 genotypes followed by cluster II and cluster III with 7 and 4 genotypes, respectively. The cluster IV and V were solitary. Intra cluster distance was ranged from zero (cluster IV and V) to 6.04 (cluster III). The highest intra cluster distance was observed in cluster III followed by cluster II and cluster I. From the inter cluster D^2 values of the five clusters, it can be seen that the highest divergence occurred between cluster I and III followed by cluster III and IV, cluster I and V suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination.

Keywords: Cluster, diversity, genetic variability, heritability, niger

Introduction
Niger [*Guizotia abyssinica* (L.f.) Cass.] is an important minor oilseed crop grown in Tropical and Subtropical countries like India, Ethiopia, East Africa, West Indies and Zimbabwe. India ranks first in area, production and export of Niger in the world. India and Ethiopia are two major producers in the world. Niger belongs to the Compositae family with diploid chromosome number (2n=2x=30). The genus Guizotia is small with only six species, which are all native of tropical Africa (Arora *et al*., 2003) [2]. Niger though a native of Tropical Africa, is wide spread and cultivated extensively in India since long. It is used as an oilseed crop in India where it provides about 3 percent of the edible oil requirement of the country (Getinet and Sharma, 1996) [7]. In Maharashtra, this oilseed crop is an important component of tribal agriculture and considered as lifeline for nutritional security but cultivated in poor and neglected soil under rainfed conditions.
The oil is considered good for health which is pale yellow with nutty taste and a pleasant odour and can be used as a substitute for olive oil provided it has good keeping quality and self-life. The seed itself is edible with no anti-nutritional factor but contains more crude fiber than most of the oilseed meal which is of high quality and is mainly used for culinary purpose, manufacture of cosmetics, soaps, paints, lubricating and lighting. Oilseed meal is used as cattle and poultry feed. The oil from the seed is used to treat burns and in the treatment of scabies. The press cake from oil extraction is used for livestock feed. Variability exists for morphological characters (Pradhan *et al.,* 1995) [17]; however these characters are not discrete and hence complicate the niger improvement programs. The study of amount of such genetic variability including the important economic traits in Niger can be achieved through mass selection (Panda and Sial, 2012) [12]. The information on genetic variability and diversity are of utmost importance to initiate the breeding programme to evolve high yielding varieties. Further direct selection for complex traits like seed yield is not effective. Knowledge of association of the simply inherited traits, which are less influenced by environment, is required to have sound selection criteria. Thus the present study was aimed at gathering information on existing genetic variability and diversity among seven attributes in twenty five gerplasm.

Material and Methods
The present investigation was carried out at the Zonal Agriculture Research Station, Igatpuri

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during *Kharif*, 2022. The experimental material comprised of 23local collected Niger germplasm lines and 2 check varieties. The experiment was sown in randomized block design with two replication in June, 2022. The experimental plot size of 3.00 x 0.60 m The objectives of present study to estimate the genetic variability, heritability, genetic advance and diversity. The crop was raised under recommended package of practices and prophylactic plant protection measures need based. Observations were taken on plot basis for days to 50% flowering, days to maturity and grain yield (q/ha). Ten randomly selected plants in each entry were taken up for recording data on plant height, number of branches per plant, number of capitula per plant and number of seeds per capitulum. Analysis of variance was performed following the standard procedures described by Panse and Sukhatme, 1985. Heritability (broad sense) and genetic advance were estimated as per Johnson *et al*. (1955) [9]. The analysis for divergence was done by following Mahalanobis (1936) [11] D^2 statistics.

Result and Discussion
Analysis of variance indicate that the mean sum of square due to genotypes were highly significant for all the characters indicating the presence of wide variability in the genotypes. The tantamount findings were also reported by Panda and Sial (2012) [12], Patil *et al.,* (2013) [16], Bisen *et al.,* (2015) [5] and Thorat *et al*., (2022) [23].

The seed yield per plant ranged from 3.50 g (IGPN-2007) to 8.75 g (IGPN-2006) with a mean value 5.23 g. Days to 50% flowering was ranged from 92 (IGPN-2205) to 101 (IGPN-2004-1) with an average value 95.56. Variation for days to maturity ranged between 122 (IGPN-2205) to 132 (IGPN-2006) with a general mean 126.14. Variation for plant height ranged between 121.5 (IGPN-2212) to 145.0 cm (IGPN-2001) with an average value of 130.90. The observation data of number of capitula per plant ranged between 20.50 (IGPN-2009) to 45.0 (IGPN-2001) with a general mean 30.20. The trait seeds per capitula ranges between 17.50 (IGPN-2010) to 37.50 (IGPN-2008) with average value of 26.46. Similar results were reported by Saraswat *et al*., (2023) [21] Bhoite *et al*., (2021) [4], Baghel *et al.,* (2018) [3] for seed yield per plant, Ahmad *et al.,* (2016) for test weight, Tiwari *et al.,* (2016) [24] for seed per capitulla.

Coefficient of variation provides a relative measure of variance among the different traits. Results revealed that the values of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the traits. High genotypic coefficient of variation and phenotypic coefficient variation were noticed for seed yield per plot, number of capitula per plant and number seeds per capitula. Similar observation were reported by earlier by Bhoite *et al*., (2021) [4] and Baghel (2018) [3] for seed yield, Suryanarayana *et al.,* (2018) [22] for number of capitulla per plant and Pradhan *et al.,* (1995) [17] for number of seeds per capitula. The moderate GCV and PCV were recorded in number of branches per plot, however, lowest GCV and PCV observed in days to 50% flowering days to maturity and plant height. Similar results have been reported by Panda and Sial (2012) [12].

In the present investigation each traits showed high estimates of broad sense heritability. The high heritability was recorded for the trait seed yield per plant (g) and number of branches per plant (96.20%), number of capitula per plant (81.00%), number of seeds per capitula (80.20%), days to 50% flowering (72.50%), days to maturity (68.90%) followed by

plant height (cm) (62.90%). These results are in accordance with Bhoite *et al*., (2021) [4] and Vinod and Rajani (2016) [25]. Genetic advance is the improvement in the mean genotypic value of selected plants over the parental population. Heritability estimates along with genetic advance are normally more helpful in predicting gain under selection than heritability estimates alone. However it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.,* 1955) [9].

The magnitude of genetic advance as percent of mean was categorized as high (> 20%), moderate (10% - 20%), and low (< 10%). If the value of genetic advance is high, it shows that the character is governed by additive genes and selection will be rewarding for improvement of such trait. If the value of genetic advance is low, it indicates that the character is governed by non-additive genes may be useful.

Genetic advance a percent mean recorded high for seed yield per plant (66.48%) followed by number of capitula per plant (43.35%), number of seeds per capitula (36.91%) and number of branches per plant (35.60). These results are conformity with Bhoite *et al*., (2021) [4] and Rani *et al*., (2010) [20]. In the present study, seed yield per plant, number of capitula per plant and number seeds per capitula expressed high heritability accompanied with high genetic advance a percent reveals that these characters are governed by additive gene effects. Selection may be effective in such cases.

On the basis of D^2 statistics, the thirty genotypes evaluated for seven characters were grouped into five clusters by using the Tocher's method as described by Rao (1952) [19]. Cluster I was largest with 12 genotypes followed by cluster II with 7 and cluster III with 4 genotypes, while cluster IV and V were monogenotypic. In the present investigation grouping of genotypes into five clusters (Table 3) suggested the presence of substantial amount of genetic diversity in the material under investigation. The similar results depicted by earlier while evaluating niger genotypes Parmeshwarappa *et al.,* (2011) [14], Pulate *et al.,* (2013) [18], Khuntey and Kumar (2015) [10], Bisen *et al.,* (2016) [6] and Goyal and Bisen (2017) [8], Surayanarayanan *et al*., (2018) [22] and Patil *et al*., (2019) [15].

The maximum intra cluster distance was observed for cluster III (D=6.04) followed by cluster II (D=5.76) suggesting that genotypes present in these clusters might have different genetical architecture (Table 4). However, lowest intra cluster distance was observed in cluster I (D=4.39) indicating that genotypes present in these cluster might have genetically similarities with one another and appeared to have evolved from common gene pool. Cluster IV and V showed no intra cluster distance due to its mono-genotypic nature.

Maximum inter cluster distance was observed between cluster I and III (D=19.08) followed by cluster III and VI (D=17.96), cluster I and V (D= 13.60), cluster II and III (D=10.88) indicating wide divergence among these clusters. These also suggest that genotype present in one cluster differ entirely from those presenting other clusters. The minimum inter cluster distance was found between cluster I and IV (D=6.37). The less inter cluster distance between these clusters revealed that genetic constitution of genotypes had close proximity.

Based on mean performance of clusters for 7 characters (Table 5), it was observed that cluster VI exhibited the highest number of seeds per capitula and days to maturity. All these characters appeared to have played important role in determining seed yield per plant of these cluster. Yadav *et al*

(2020) also reported number of seeds per capitula was contributed highest percent to genetic diversity.

On the basis of intra and inter cluster distances, cluster mean and per se performance, the genotypes *viz.*, IGPN-2001, IGPN-2006, IGPN-2008, IGPN-2201, IGPN-2209 and IGPN-2210 were found to be superior. These genotypes may serve as potential parents for future breeding programme.

Table 1: Analysis of variance for seed yield and its component in Niger

Source of variation	d.f	Mean sum of squares						
		Days to 50% flowering	Days to Maturity	Plant height (cm)	Number of branches/plant	Number of capitula per plant	Number of seeds per capitula	Seed yield per plot (g)
Replications	1	0.02	0.98	16.82	0.09	0.80	7.22	0.26
Genotypes	24	12.95**	15.35**	84.25*	4.78**	123.0*	69.83*	6.17**
Error	24	3.56	4.77	31.24	0.18	13.33	13.80	0.24

*,**: Significant at 5% and 1% levels respectively.

Table 2: Genetic parameters of variation for seed yield and its component in Niger

S. N.	Characters	Mean	Range		GCV%	PCV%	Heritability (%)	Genetic advance as% mean
			Min.	Max.				
1	Seed yield/plant (g)	5.23	3.50	8.75	32.91	33.55	96.20	66.48
2	Days to 50% flowering	95.56	92.0	100.50	2.27	2.67	72.50	3.98
3	Days to Maturity	126.14	121.50	132.0	1.82	2.20	68.90	3.12
4	Plant height (cm)	130.90	121.50	145.0	3.93	4.96	62.90	6.42
5	Number of branches/plant	8.61	6.25	11.90	17.62	17.97	96.20	35.60
6	Number of capitula per plant	30.20	20.50	45.00	23.38	25.97	81.00	43.35
7	Number of seeds per capitula	26.46	17.50	37.50	20.00	22.33	80.20	36.91

Table 3: Distribution of niger genotypes into different clusters

Cluster	Genotypes	Number of genotypes included in cluster
I	IGPN-2002, IGPN-2003, IGPN-2004, IGPN-2007, IGPN-2009, IGPN-2010, IGPN-2204, IGPN-2208, IGPN-2211, IGPN-2212, IGPN-2213 and IGPN-2214	12
II	IGPN-2202, IGPN-2203, IGPN-2206, 2207, 2209, IGPN-2004-1 and IGPN-8004,	7
III	IGPN-2001, IGPN-2006, IGPN-2008 and 2201	4
IV	IGPN-2205	1
V	IGPN-2210	1

Table 4: Intra (diagonal) and inter-cluster distance among five clusters in niger

Cluster	I	II	III	IV	V
I	4.39	10.38	19.08	6.37	13.60
II		5.76	10.88	9.58	7.43
III			6.04	17.96	8.95
IV				0.00	11.89
V					0.00

Table 5: Cluster means performance for seven characters studied in Niger

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of capitula per plant	No. of seed per capitula	Seed yield per plant (g)
I	93.83	124.67	126.96	7.47	23.71	21.17	3.77
II	96.93	127.14	134.93	9.05	32.43	29.57	6.11
III	98.75	129.00	137.63	11.15	42.88	34.38	8.23
IV	92.00	121.50	124.00	7.20	31.00	28.00	3.67
V	98.00	130.00	130.00	10.30	41.00	35.00	6.19

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