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Analysis of genetic divergence in Niger {*Guizotia abyssinica* (L.f) Cass.}

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Abstract
The present investigation was carried out at Zonal Agriculture Research Station, Igatpuri at ZARS, Igatpuri during *rabi*-2020. This experiment comprises 30 genotypes including two checks. The analysis of variance has manifested significant variation among the studied genotypes for all the traits. The multivariate analysis carried out using Mahalanobis D^2-statistics, indicated wider genetic diversity in the genotypes of niger. Total six clusters have formed of which, cluster IV was largest with eight genotypes. Seven genotypes formed in cluster I and II each, while cluster V and VI were monogenotypic. The maximum inter cluster distance was observed between cluster V and VI (D=13.64) followed by cluster III and VI (D=11.91), cluster I and VI (D= 11.03), cluster II and V (D=11.03). Maximum intra cluster distance observed within cluster III (D=6.03) while lowest intra cluster distance was observed within cluster I (D=4.33. The variance for cluster means were high for number of seeds per capitulla (31.49 per cent) followed by diameter of capitulla (19.31 per cent), seed yield per plant (19.08 per cent), days to maturity (10.34 per cent) and days to 50% flowering (9.20 per cent) while, number of capitula per plant (4.37 per cent), number of branches per plant (3.68 per cent) and plant height (2.53 per cent) contributed least to the divergence. Based on inter-cluster distances, cluster mean and *per se* performance the genotypes *viz;* GP-20.14, GP-20-17, GP-20-23, GP-20-24 and GP-20-27 were identified as potential parent for future endeavors for improvement of Niger.

Keywords: Cluster, genetic diversity, mean, Niger, seed yield per plant

Introduction
Niger (*Guizotia abyssinica* (L.f.) Cass) is one of the minor oil seed crops of India. Its cultivation mainly for its oil and seed. The Ethiopia Niger seed contains about 35 to 40 percent oil with fatty acid composition of 75-80% linoleic acid, 7-8% palmitic and stearic acids and 5-8% oleic acid. (Getinet and Teklewold, 1995) [2]. However, Indian Niger types contain 25% oleic and 55% linoleic acids (Nasirullah *et al*., 1982) [7].

Genetic diversity has paramount importance in breeding and It is pre-requisite for any successful breeding programme. Genetic divergence among the parents play a vital role in cultivar improvement because a cross involving genetically diverse parents is likely to generate more variability in segregating generations, and also which can be used for the desired improvement.

Generally, plant breeders select the parents on the basis of phenotypic diversity. Hence the knowledge of genetic diversity among the parents with respect to characters which are to be improved is essential. 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. Keeping these things in view, an effort has been made in the present study to evaluate a set of Niger genotypes with the objective to study the nature and magnitude of divergence.

Materials and Methods
The experimental material comprising thirty genotypes of Niger were grown in Randomized Block Design with two replications at the research farm of Zonal Agriculture Research Station, Igatpuri Dist. Nashik during *rabi* season of 2020. Each entry was represented by single row of 3.0 m length with spacing of 30 cm between rows and 10 cm between plant to plant.. Data were recorded on five randomly and competitive plants of each genotype from each replication for eight quantitative characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, diameter of capitulum (cm), number of capitulum per

plant, number of seeds per capitulum and seed yield per plant (g.) Effective method suggested by Mahalanobis (1936) [6] known as "Mahalanobis D^2 statistics" or "D^2 technique" is widely used to know genetic diversity in the germplasm. It was conducted to estimate the intra and inter cluster distances and to group the genotypes into different clusters and a logical grouping of genotypes following Tocher's method (Rao, 1952).

Result and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied. On the basis of D^2 statastics, the thirty genotypes evaluated for eight characters were grouped into six clusters by using the Tocher's method as described by Rao (1952) [12]. Cluster IV was largest with 8 genotypes followed by cluster I and III (7 genotypes), cluster II (6 genotypes), while cluster V and VI were monogenotypic. In the present investigation grouping of genotypes into six 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 Pulate *et al.,* (2013) [11], Khuntey and Kumar (2015) [4], Bisen *et al.,* (2016) [1] and Goyal and Bisen (2017) [3], Surayanarayana *et al*., (2018) [14] and Patil *et al*., (2019) [10].

The maximum intra cluster distance was observed for cluster III (D=6.03) followed by cluster IV (D=5.99) suggesting that genotypes present in these clusters might have different genetical architecture (Table 2). However, lowest intra cluster distance was observed in cluster I (D=4.33) indicating that genotypes present in these cluster might have genetical similarities with one another and appeared to have evolved from common gene pool. Cluster V and VI showed no intra cluster distance due to its monogenotypic nature.

Maximum inter cluster distance was observed between cluster V and VI (D=13.64) followed by cluster III and VI (D=11.91), cluster I and VI (D= 11.03), cluster II and V (D=11.03) 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 III (D=6.88). The less inter cluster distance between these clusters revealed that genetic constitution of genotypes had close proximity.

Based on mean performance of clusters for 8 characters (Table 3), it was observed that cluster VI exhibited the highest number of capitulum per plant, number of seeds per capitulum, plant height and number of branches per plant. All these characters appeared to have played important role in determining seed yield per plant of these cluster.

Cluster II was characterized by less days to 50 per cent flowering whereas cluster I was observed for days to maturity. Cluster V was characterized by highest diameter of capitulla. On the basis of mean performance of different clusters, it was observed that cluster VI and I, II were performing well for most of the characteristics.

The variance of cluster mean provides information on relative importance of different characters towards seed yield per plant. The present study revealed that number of seeds per capitulla was (31.49 per cent) contributed more to genetic diversity followed by diameter of capitulla (19.31 per cent), seed yield per plant (19.08 per cent), days to maturity (10.34 per cent) and days to 50% flowering (9.20 per cent). However, number of capitula per plant (4.37 per cent), number of branches per plant (3.68 per cent) and plant height (2.53 per cent) contributed least to the divergence.

Yadav *et al.* (2020) [15] also reported number of seeds per capitulla was contributed highest per cent to genetic diversity. Patil *et al.,* (2007) [9] observed more divergence for number of capitulum per plant and seed yield per plant. Kumar, S. (1999) [5] reported that days to maturity has maximum contribution towards divergence. Sreedhar *et. al.* (2006) [13] were also of same opinion.

On the basis of inter cluster distances, cluster mean and performance observed in the present study, the genotypes *viz*., GP-20.14, GP-20-17, GP-20-23, GP-20-24 and GP-20-27 were found to be superior. These genotypes may be used further in hybridization programme for crop improvement.

Table 1: Distribution of Niger genotypes into different clusters

Cluster	Genotypes	Number of genotypes included in cluster
I	GP-20-11, GP-20-22, GP-20-24, GP-20-25, GP-20-26, GP-20-27, GP-20-24,	07
II	GP-20-06, GP-20-19, GP-20-09, GP-20-10, GP-20-18, GP-20-07	06
III	GP-20-20, GP-20-21, IGPN-2004-1, IGPN-8004, GP-20-12, GP-20-23, GP-20-13,	07
IV	GP-20-03, GP-20-16, GP-20-05, GP-20-08, GP-20-01, GP-20-15, GP-20-04, GP-20-02,	08
V	GP-20-14,	01
VI	GP-20-17,	01

Table 2: Intra (diagonal) and inter-cluster distance among six clusters in Niger

Cluster	I	II	III	IV	V	VI
I	4.33	8.35	6.88	7.63	7.25	11.03
II		4.95	8.94	8.26	11.03	6.99
III			6.03	9.75	7.43	11.91
IV				5.99	8.04	10.14
V					0.00	13.64
VI						0.00

Table 3: Cluster means performance for ten characters studied in Niger

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	Diameter Of capitulula (mm)	No. of capitulula per plant	No. of seed per capitulula	Seed yield per plant (g)
I	52.57	84.64	86.57	8.14	16.75	70.46	27.40	18.31
II	51.50	85.33	83.17	7.67	11.04	56.44	26.45	15.88

III	53.93	87.33	83.43	8.83	16.50	68.08	23.06	16.73
IV	54.44	86.81	80.50	6.86	8.65	50.70	20.07	14.71
V	59.00	92.00	79.00	7.05	14.35	52.35	17.80	16.60
VI	57.00	90.00	89.50	9.30	10.30	78.00	39.75	19.20
Population mean	53.33	86.43	83.38	7.87	13.09	61.48	24.34	16.47

Table 4: Per cent contribution of eight characters towards genetic divergence in Niger.

Sr. No.	Characters	No. of times appearing first in ranking	Contribution per cent
1	Days to 50% flowering	40	9.20
2	Days to maturity	45	10.34
3	Plant height (cm)	11	2.53
4	No. of branches per plant	16	3.68
5	Diameter of capitulula	84	19.31
6	No. of capitulula per plant	19	4.37
7	No. of seeds per capitulula	137	31.49
8	Seed yield per plant (g)	83	19.08
	Total		100.0

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