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Assessment of genetic divergence in niger (*Guizotia abyssinica* L.)

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Abstract

A field experiment was conducted with 30 genotypes to study the genetic divergence using Mahalanobis D^2 statistics. The genotypes were grouped into seven clusters based on D^2 values for 7 characteristics indicating the presence of large amount of diversity among the genotypes. Maximum number of genotypes were grouped in cluster I (12) followed by cluster III (9), cluster IV (3), cluster V & cluster II with 2 genotypes in each cluster, whereas cluster VI and VII are solitary with single genotype in each cluster.

The intra cluster distance ranged from 0.00 to 52.45. The highest intra cluster distance was observed for cluster III (52.45) followed by cluster IV (37.70), cluster I (27.20), cluster V (24.68), cluster II (3.22), cluster VI and cluster VII (0.0). The inter cluster D^2 values ranged from 17.11 to 200.17. The maximum inter cluster distance (200.17) was noticed between cluster VI and VII followed by cluster V and VI (167.08). Since the clusters VI and VII had a single genotype with maximum inter cluster distance indicated that the genotypes included in these clusters will give high heterotic response and better segregants

Keywords: Genetic diversity, D^2 -analysis in niger

Introduction

Niger (*Guizotia abyssinica* L.) is an important minor oilseed crop of tropical and subtropical areas of the world. It is grown in the marginal and sub marginal lands in India. In India it is mainly grown in tribal areas of Andhra Pradesh, Madhya Pradesh, Gujarat, Maharashtra, Orissa, Chhattisgarh and Karnataka states. The extent of cultivable area in India is 2.53 lakh hectares with a production of 0.83 lakh tonnes and productivity of 326 kg/ha. It is important in terms of its quality oil and protein in the seed. Its oil is used in food, paints and soaps as an illuminant. Niger seeds contain about 40% edible oil with fatty acid composition of 75-80% linoleic acid, 7-8% palmitic and stearic acids and 5-8% oleic acid. The seeds are eaten fried, used as a condiment or dried powder and mixed with flour to make sweet cakes.

Genetic variability and divergence are of greater interest to the plant breeder as they play a vital role in framing a successful breeding programme. Genetic diversity analysis is essential for selection of diverse parents in hybridization programme to produce wide range of gene recombination for quantitatively inherited traits than those between closely related ones. Mahalanobis' generalized distance estimated by D^2 statistics (Rao, 1952)^[4]. is a unique tool to study the magnitude of genetic divergence and mean performance of characters in different clusters.

Material and Methods

The present experiment was conducted at Regional Agricultural Research Station, Chintapalle during *rabi*, 2010. The experimental material comprised of 30 niger genotypes were laid out in Randomized Block Design (RBD) with three replications. Each genotype was sown in 10 rows of 4 m length with a spacing of 30 cm between rows and 10 cm within a row. All the recommended package of practices were followed to raise a healthy crop. The observations were recorded on five randomly selected competitive plants in each replication for plant height (cm), number of branches per plant, number of capitula per plant, number of seeds per capitula and observations for days to 50% flowering, days to maturity and grain yield q/ ha were recorded on per plot basis. Genetic distance between clusters was calculated using the generalised Mahalanobis' D^2 statistics (1936)^[3]. Intra and inter cluster distance, cluster means

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and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985) [6].

Results and Discussion

Analysis of variance revealed significant differences among the genotypes for all the characters studied, indicating the existence of wide range of genetic divergence among them. The statistical distance (Mahalanobis D^2) between a pair of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two genotypes considered at a time. The genotypes were grouped into seven clusters based on D^2 values indicating the presence of large amount of diversity among the genotypes (Table 1). Maximum number of genotypes were grouped in cluster I (12) followed by cluster III (9), cluster IV (3), cluster V & cluster II with 2 genotypes in each cluster, whereas cluster VI and VII are solitary with single genotype in each cluster.

The intra and inter cluster distances revealed that inter cluster distance was greater than intra cluster distance (Table 2). The maximum intra cluster distance was recorded in cluster III (52.45) followed by cluster IV (37.70), cluster I (27.20), cluster V (24.68), cluster II (3.22), cluster VI and cluster VII (0.0). The intra cluster distance in cluster III was highest (52.45) indicating the presence of wide genetic diversity among the genotypes present within this cluster.

The inter cluster distances varied from 17.11 to 200.17. The maximum inter cluster distance (200.17) was noticed between cluster VI and VII followed by cluster V and VI with an inter cluster distance of 167.08. Since the clusters VI and VII had single genotype with maximum inter cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters are likely to produce wide variability with desirable segregants for yield and yield

components. The lowest inter cluster distance was noticed between cluster II and IV (17.11) followed by clusters II and VI (22.33) indicating the close relationship and similarities for most of the traits of the genotypes in these clusters

The per cent contribution towards genetic divergence by seven contributing characters was presented in Table 3. The maximum percentage of contribution towards genetic divergence was displayed by grain yield q/ha (47.35) followed by number of seeds per capitula (25.05), days to 50% flowering (17.24), number of capitula per plant (7.35), plant height (1.83) and number of branches per plant (1.14) respectively. Similarly, Suryanarayana *et al.*, (2018) [7], and Kumar and Bisen (2017) [2]. In a study of genetic diversity in niger reported seed yield and number of capitula per plant contributed maximum towards genetic divergence. Bisen *et al.*, (2016) [1]. Reported seed yield, days to maturity, number of capitula per plant and 1000 seed weight contributed maximum towards genetic divergence. Plant height, number of capitula per plant and seed yield per plant contributed maximum towards genetic diversity was reported by Swetha and Parameshwarappa (2016) [5].

The cluster mean values for seven characters are presented in Table 4. Highest and lowest cluster mean values for plant height, days to 50% flowering, days to maturity, number of branches per plant were recorded in cluster VII and cluster VI respectively. When considering the number of capsules per plant, cluster V recorded the highest and cluster II recorded the lowest cluster mean value. Whereas for number of seeds per capitula, cluster V recorded the highest and cluster VII recorded the lowest cluster mean values. Genotypes in the cluster V registered the highest and cluster VII registered the lowest mean value for seed yield. Hence utilization of outstanding genotypes from these clusters will be useful for developing high yielding varieties.

Table 1: Cluster composition of 30 niger genotypes

Cluster No	No of genotypes in each cluster	Cluster members
Cluster 1	12	JNS-30, DNS-2, DNS-4, BNC-15, JNS-10, JNS-28, IGPN-2005-10, PCN-8, BNM-1, JNS-204, JNS-206 and JNS-08-04.
Cluster 2	2	JNS-255 and JNS-501.
Cluster 3	9	ONC-162, DNC-08-5, IGPN-08-16, ONC-21, IGPN-76, IGPN-8004, BAU-09-01, JNS-107 and JNS-119.
Cluster 4	3	BAU-09-01, DNC-02-02 and JNS-502.
Cluster 5	2	DNC-08-02 and ONC-22.
Cluster 6	1	IGPN-8007
Cluster 7	1	KGN-2

Table 2: Average intra and inter cluster D^2 values among seven clusters in niger

	I	II	III	IV	V	VI	VII
I	27.20(5.21)	29.97(5.47)	44.43(6.6)	43.90(6.62)	80.58(8.97)	48.19(6.94)	120.95(10.99)
II		3.22(1.79)	54.57(7.38)	17.11(4.13)	126.58(11.25)	22.33(4.72)	119.04(10.91)
III			52.45(7.24)	60.50(7.77)	63.02(7.93)	79.34(8.90)	100.12(10.00)
IV				37.70(6.14)	126.83(11.26)	41.56(6.44)	123.97(11.13)
V					24.68(4.96)	167.08(12.92)	76.07(8.72)
VI						0.0(0.0)	200.17(14.14)
VII							0.0(0.0)

Table 3: Contribution of characters towards genetic divergence in niger

Character	No of times ranked first	% Contribution towards divergence
Plant height (cm)	8	1.83
Days to 50 % Flowering	75	17.24
Days to Maturity	0	0
Number of Branches per Plant	5	1.14
Number of Capsules per Plant	32	7.35
Number of Seeds per Capsule	109	25.05

Seed Yield (Q/ha)	206	47.35
Total	435	100

Table 4: Cluster means for seven characters in 30 genotypes of niger.

Cluster No	Plant Height (cm)	Days to 50% Flowering	Days to Maturity	Number of Branches per Plant	Number of Capsules per Plant	Number of Seeds per Capsule	Seed Yield (Q/ha)
Cluster I	107.96	45.50	101.55	7.53	48.46	33.37	6.8
Cluster II	114.30	44.00	100.00	7.53	44.60	30.12	5.1
Cluster III	106.12	46.07	101.81	8.05	53.86	30.69	7.3
Cluster IV	116.44	43.33	99.33	8.11	45.86	29.40	5.8
Cluster V	116.61	49.00	105.00	8.83	63.70	34.01	9.0
Cluster VI	87.93	42.00	99.00	7.13	49.33	30.60	4.7
Cluster VII	129.80	51.00	106.66	9.46	54.40	27.22	5.3

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