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Vinod Kumar
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Rajani Bisen
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Correspondence
Vinod Kumar
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Assessment of genetic divergence in Niger germplasm

Vinod Kumar Goyal and Rajani Bisen

Abstract
Seventy one niger germplasm were evaluated to explore the nature and magnitude of genetic divergence for yield and its contributing traits during *kharif* 2015-16 using Mahalanobis's D^2 Statistics. The data were recorded on eleven important yield attributing traits from the germplasms raised in randomized complete block design (RCBD) under three replications. Highly significant differences existed among the genotypes tested for all the traits. Cluster analysis revealed wide range of diversity in the genotypes grouped in eleven clusters. Out of eleven, Cluster II was the largest among all clusters followed by cluster I, cluster IX, cluster X, cluster VII, cluster XI and cluster IV. Cluster III, V, VI and VIII were monotypic. The highest intra cluster distance was recorded by cluster X followed by cluster IX, cluster XI, cluster IV, cluster VII, cluster II and Cluster I. The highest inter cluster distance was observed between the clusters VII and XI followed by clusters IV and XI and clusters VI and VII. The characters like seed yield per plant, 1000 seed weight and number of capitula per plant exhibited major contribution towards the genetic divergence. These traits should be considered as more important and due consideration to any breeding program. On the basis of inter and intra-cluster distance coupled with cluster means of different traits, the genotypes classified in clusters IX, IV, XI, VII, II, VI and V were found to be superior and may be utilized in breeding programmes.

Keywords: Genetic diversity; germplasm and Niger

1. Introduction
Niger (*Guizotia abyssinica* (L.f.) Cass.) being an oilseed crop is mainly cultivated in Indian subcontinent and East African Countries (Getinet and Sharma, 1996) [4]. Niger though a native to Tropical Africa, is wide spread and extensively cultivated in India since long and constitutes about 50% of Ethiopian and 3% Indian oilseed production. In India, it is primarily grown on the degraded soils in hilly and tribal pockets under input starved conditions over an area of about 3 lakh ha with larger area in Chhattisgarh, MP, Maharashtra and Odisha. It can be grown successfully without chemicals. In MP, it is grown in 0.43 lakh ha area with production of 0.16 lakh tonnes and productivity of 372 kg /ha (Anonymous, 2014-15) [1].

Niger seeds contain about 40% edible oil with fatty acid composition of 75-80% linoleic acid, 7-8% palmitic and steric acids, and 5-8% oleic acid (Dutta *et al*. 1994). However, keeping quality of niger is poor due to high content of unsaturated fatty acids. The oil is used for culinary purposes, manufacturing paints, soft soaps and for lighting and lubrication. Moreover, consuming niger seed oil is beneficial from public health point of view because it contains minor quantities of substances such as tocopherols, phospholipids and sterols that provide protection against cardiovascular disorders and cancer (Ramadan and Morsel, 2002) [9]. Niger seed cake is a valuable cattle feed, particularly for milch cattle. Niger meal with 30% protein and 17% crude fibre in India could replace linseed cake in calf ration.

Niger is a completely out crossing species with self-incompatibility mechanism. Variability exists for morphological characters (Pradhan *et al*. 1995) [8]; however these characters are not discrete and hence, complicate the niger improvement programs. Consequently, varieties identification or genetic purity assessment are difficult. Development of improved plant cultivars is restricted mainly due to limited genetic variability. Due to narrow genetic pool it is not possible to restructure the niger crop. Wide genetic diversity is very important in selecting the parents for hybridization programmes to identify herterotic crosses and obtain desirable recombination in the segregating generations (Banerjee and Kole, 2009) [2]. The systemic management of plant genetic resources is very important to augment productivity of niger. The present study is thus aimed to analyze genetic diversity among niger germplasm

for selection of parents for hybridization programme and important yield components for high yield based on 71 germplasm accessions through Mahalanobis D^2 statistics.

Materials and Methods

The present investigation was conducted at Project Coordinating Unit (Sesame and Niger) Research Farm, JNKVV, Jabalpur (M.P.) during *kharif* 2015-16. Jabalpur is situated in 'Kymore plateau and Satpura hills agro-climatic region of Madhya Pradesh. The soil of the experiment is medium black with uniform topography and free from water logged conditions. Jabalpur has sub-tropical, semi-arid climate. The average rainfall is about 1200 mm. The minimum and maximum temperatures range between 22^0C to 35^0C, respectively during the *kharif* season. The experiment consisted of 71 niger germplasm laid out in a Randomized Block Design replicated thrice. The distance between rows was maintained at 0.40 m and plant to plant was 0.15 m. All recommended cultural practices for growing niger were applied equally. The observations were recorded on days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, number of capitula/plant, 1000 seed weight, seed length and seed yield/plant (g). The oil content (%) was analyzed using Nuclear magnetic Resonance Spectrophotometer. The genetic divergence was estimated using Mahalanobis D^2 statistics (1928).

Results and Discussion

To estimate D^2 values, correlated means of characters were transformed to standard uncorrelated means using Tocher's method. The statistical distance (Mahalanobis D^2) between pair of germplasms were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two germplasms considered at a time.

All 71 genotypes used for the study were grouped into eleven clusters based on divergence analysis. Out of eleven clusters, Cluster II was the largest among all clusters comprising 19 germplasm followed by cluster I (18 germplasm), cluster IX (9 germplasm), cluster X (6 germplasm), cluster VII (6 germplasm), cluster XI (5 germplasm) and cluster IV (4 germplasm). Clusters III, V, VI and VIII were monotypic (Table 1 and Fig1 and 2). The discordance among diversity patterns and geographical distribution of genotypes found in this investigation implies that the parental lines for hybridization should be selected based on genetic diversity rather than the geographical distribution.

The inter and intra cluster D^2 mean values are presented in Table 2. The highest intra cluster distance was recorded in Cluster X (257.23) followed by Cluster IX (204.45), Cluster XI (193.54), Cluster IV (183.33), Cluster VII (180), Cluster II (139.6) and Cluster I (116.76). The inter cluster distance was highest between the clusters VII and XI (1464.36) followed by cluster IV and XI (1061.66), VI and VII (866.37), II and XI (775.52), VII and IX (766.94), V and VII (673.6), IV and VI (645.53), IV and V (635.24) and clusters IX and XI (600.95). The lowest inter cluster distance was observed between clusters V and VIII (86.4).

Table 1: Distribution of niger germplasm in different clusters

Cluster No.	No. of germplasm	Germplasm included in the cluster
1	18	M-3, GA-10,IGP-11, BPB-1, NC-63592, CH-7, IGP-50, EC-158673, EC-158672, MUTUNAY, 41-50, IGP-234, N-35, NO.5, NC-63586, GA-23, NC-62587 and PHULE-4
2	19	5-64, 5-70, NC-63591, NC-63595, COMP-II, CH-53, 89-25, BHC-120, 71-41, 87-14, 41-52, NC-63597, GA-5, NC-63588, IGP-37, NO.1, GA-2, GHETA NO.1 and 18-64
3	1	89-20
4	4	5-5, NO.36, 5-1, 87-32
5	1	EC-158670
6	1	NO.14
7	6	5-20, 23-4, GA-8, NA-48, DB-500, 52-26
8	1	5-9
9	9	KOMKEMP, RCR-64, RCR-5-4, IGP-76, CWA-1, 5-4, EC-158671, EC-158669, 34-14
10	6	N-20, NR-73-13, IGP-38, NR-76-14, IGPN-2004-1, PHULE-2
11	5	COMB-2, CH-32, CH-4, GOUDAGUDA, EC-158660

Table 2: Inter and intra cluster D^2 values for different clusters in niger germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	116.76	213.68	308.87	390.37	166.73	226.26	605.5	172.57	257.28	316.87	458.88
Cluster II		139.6	199.1	299.13	248.46	393.02	304.16	190.7	320.83	338.17	775.52
Cluster III			0	475.57	244.65	250.94	341.82	284.38	346.83	275.5	676.78
Cluster IV				183.33	635.24	645.53	348.15	457.43	736.6	446.95	1061.66
Cluster V					0	228.96	673.6	86.4	152.38	389.01	448.68
Cluster VI						0	866.37	295.62	360.37	242.64	174.25
Cluster VII							180	520.76	766.94	572.21	1464.36
Cluster VIII								0	246.85	301.88	509.59
Cluster IX									204.45	557	600.95
Cluster X										257.23	535.51
Cluster XI											193.54

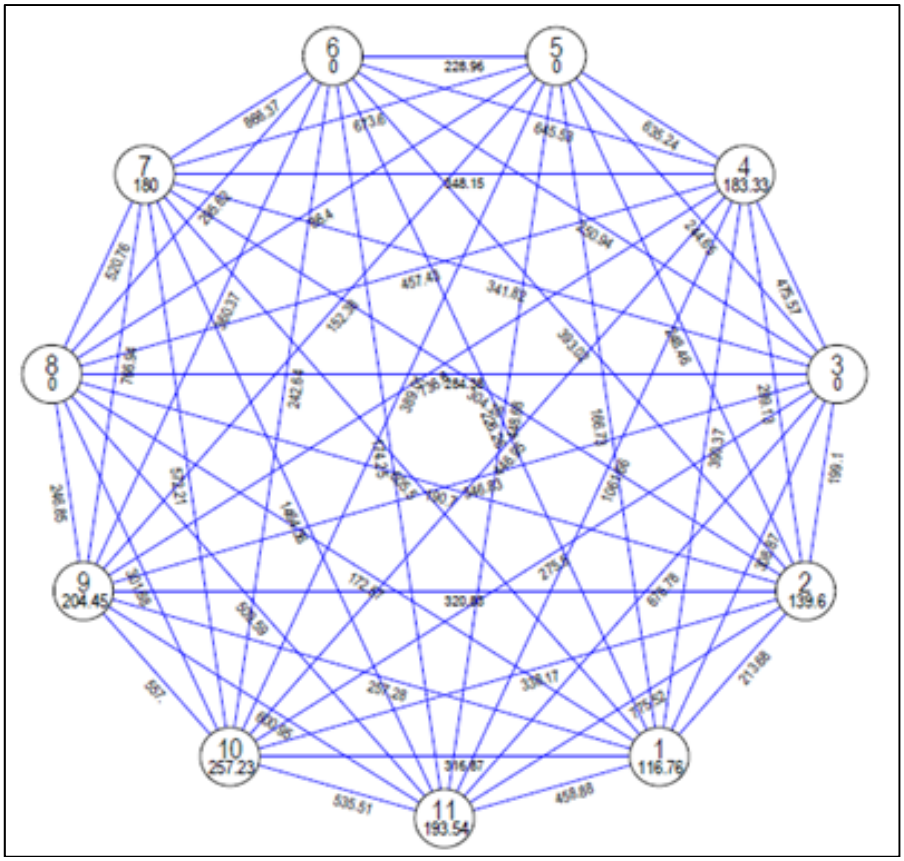

Fig 1: Diagram showing inter and intra cluster distances

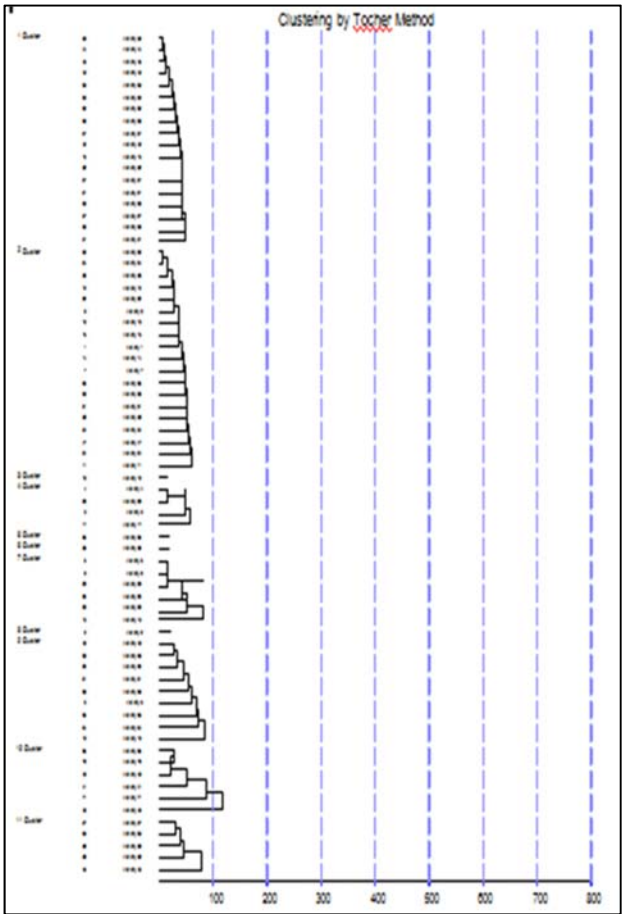

Fig 2: Clustering of 71 genotypes in 11 clusters by Tocher method

The trait seed yield per plant (40.6%) contributed maximum to genetic divergence followed by 1000 seed weight (23.3%), number of capitula per plant (17.67%), oil content (%) (7.04%), seed length (5.84%), number of primary branches per plant (4.19%) and number of secondary branches per plant (0.85%) (Table 3). Low contribution was shown by days to 50% flowering (0.06%) and plant height. Similar reports have been given by Parameshwarappa *et al*. (2011) [7] in niger, Kumhar and Solanki (2009) [5] and Rao (2006) [10] for seed yield per plant in sesame.

Table 3: Contribution of different characters toward clustering in niger germplasm

S. No.	Source	Times ranked 1st	Contribution %
1	DFF	1	0.06
2	PH	2	0.08
3	PB	104	4.19
4	SB	21	0.85
5	CP	439	17.67
6	DM	11	0.44
7	TSW	579	23.3
8	SL	145	5.84
9	oil %	175	7.04
10	SY/P	1009	40.6

The cluster mean values of different characters are presented in Table 4. The highest cluster mean values were recorded for characters days to 50% flowering (45.67) and oil content (%) (41.9) in cluster V, number of primary branches (12.67), plant height (109.67) and days to maturity (105.33) in cluster VI, number of secondary branches (22.47), number of capitula per plant (96.73), seed length (0.5), 1000 seed weight (4.78) and seed yield per plant (13.49) in cluster XI. The lower cluster

mean values for days to 50% flowering (42.51) were found in cluster II, days to maturity (101.67) in cluster III, plant height (80.67), number of primary branches per plant (7.67), number of secondary branches per plant (13.33) and seed length (0.33) in cluster VIII, number of capitula per plant (65.67), 1000 seed weight (4.36), oil content (%) (35.21) and seed yield per plant (2.94) in cluster VII.

Table 4: Cluster mean for yield and yield contributing traits in niger germplasm

	DFF	PH	PB	SB	CP	DM	TSW	SL	oil %	SY/P
Cluster I	43.93	92.04	9.65	18.19	83.57	102.96	4.71	0.47	40.19	8.57
Cluster II	42.51	97.53	9.49	16.89	74.37	102.53	4.57	0.41	37.88	6.11
Cluster III	43.33	109.33	9	18.67	70	101.67	4.4	0.42	37.04	6.84
Cluster IV	44.5	96.33	10.58	18.25	91.92	103.67	4.52	0.4	38.71	5.57
Cluster V	45.67	97.67	8.33	15	70.33	103.67	4.73	0.42	41.9	8.7
Cluster VI	45.33	109.67	12.67	22.33	89.33	105.33	4.61	0.49	36.85	11.32
Cluster VII	42.78	101.83	10.17	15.61	65.67	102.72	4.36	0.34	35.21	2.94
Cluster VIII	43.33	80.67	7.67	13.33	68	102.33	4.63	0.33	39.42	7.44
Cluster IX	43.15	100.93	8.74	16.44	72.85	102.59	4.72	0.46	37.33	8.34
Cluster X	43.39	83.72	9.61	17	74.89	102.39	4.38	0.4	36.95	7.98
Cluster XI	44.2	99.73	10.93	22.47	96.73	103.6	4.78	0.5	37.15	13.49

Conclusions

Cluster analysis revealed the wide range of diversity in the germplasms were grouped in eleven clusters. On the basis of inter-cluster distance and cluster mean values, the genotypes of cluster IX, IV, XI, VII, II, VI and V were found superior and may be further utilized in breeding programmes. Thus, geographic origin cannot be considered as sole criteria for the selection of desirable donors for breeding programmes.

References

1. Anonymous. 4th Advance Estimates, Agriculture Statistics Division, Directorate of Economics and Statistics, New Delhi, 2014-15.
2. Banerjee PP, Kole PC. Analysis of Genotypic Diversity in Sesame (*Sesamum indicum* L.) Based on Some Physiological Characters. Czech Journal of Genetics and Plant Breeding. 2009; 45:72-78.
3. Dutta PC, Helmersson S, Kebedu E, Getinet A Appliqvist L. Variation in lipid composition of niger seed (*Guizotia abyssinica* Cass) samples collected from different regions in Ethiopia. Journal of the American Oil Chemists Society. 1994; 71:839-843.
4. Getinet A, Sharma SM. Niger [*Guizotia abyssinica* (L.f.) Cass.]: Promoting the conservation and use of underutilized and neglected crops, International Plant Genetic Resources Institute, Rome. 1996; 59.
5. Kumhar SR, Solanki ZS. Genetic diversity and variability in sesame (*Sesamum indicum* L.). Journal of Oilseeds Research. 2009; (26):162-164.
6. Mahalanobis PC. A statistical study at Chinese head measurement. Journal of Asiatic Society. 1928; 25:301-377.
7. Parameshwarappa SG, Palakshappa MG, Shindhe GG. Genetic diversity studies in germplasm collections of niger (*Guizotia abyssinica*). Plant Archives. 2011; 11(2):1071-1074.
8. Pradhan K, Mishra RC, Paikaray RK. Genetic variability and character association in niger. Indian Journal of Genetics and Plant Breeding. 1995; 55:457-459.
9. Ramadan MF, Morsel JT. Proximate neutral lipid composition of niger (*Guizotia abyssinica* Cass.) Seed. Czech journal of food sciences. 2002; 20:98-104.
10. Rao SVSG. D^2 statistics in sesame (*Sesamum indicum* L.). Crop Research. 2006; 31(2):261-263.