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Genetic diversity study in Niger (*Guizotia abyssinica* L.)

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Abstract
An experiment was undertaken by utilizing forty Niger genotypes for thirteen yield and yield contributing characters to assess genetic divergence. The analysis of variance has shown that there was significant variation among the genotypes in all the traits except capitulum diameter and 1000 seed weight. The magnitude of D^2 values of pooled data, location wise forty genotypes were grouped in 5, 4, 4, 8 and 4 clusters for E1, E2, E3, E4 and E5, respectively. Solitary clusters were found in all the environments it indicating their independent identity and importance due to the unique characters constituted by that genotypes. Environment wise the highest inter cluster distance for pooled data was observed between cluster II and VI (D=13.26), II and III (D=7.28), III and IV (D=7.89), IV and VIII (D=8.45), and I and IV (D=7.54) for E1, E2, E3, E4 and E5, respectively. The high intra and inter-cluster distance was observed in many clusters it indicated the extent of variability existed in the genotypes comprised in a particular cluster and will give high heterotic response and better segregants. On the basis of intra and inter cluster distances, cluster mean and per se performance, the genotypes *viz*., G1, G2, G4, G8, G9, G10, G24, G25, G26, G28, G32, G35, G36, G39 and G40 were found to be superior. These genotypes may serve as potential parents for breeding programme. Selection must be done on considering plant height, number of primary and secondary branches plant^{-1}, total number of capitulum plant^{-1}, capitulum diameter, number of seeds capitulum^{-1} and 1000 seed weight as their contribution towards total divergence is high.

Keywords: Niger, diversity, inter-cluster, heterotic, segregants and cluster mean

Introduction
The Niger (*Guizotia abyssinica* L.) is migrated to East Africa and India through the Persian Gulf traders along with other crops, which is popularly known as the 'Savannah complex' (Dagne, 2001) [1]. Niger although considered a minor oilseed crop, is important in terms of its 32 to 40% content of quality oil with 18 to 24% protein in the seed (Nagraj and Patil, 2004; Ramteke *et al*., 2001; Dagne and Jonsson, 1997) [9, 17, 2]. It is used as a substitute for olive oil, can be adulterated with rapeseed, sesame and linseed oil. Niger oil has good keeping quality and has < 70% unsaturated fatty acids free from toxins. The oil is considered good for health. It is premium oil because of high linoleic acid content (45-60 per cent) and oleic acid (13-39 per cent) (Dutta *et al*., 1994) [3]. Niger oil contains Omega 3 and Omega 6 fatty acids which are thought to help reduce the risk of heart disease and also to promote healthy skin. They are also used along with diet and exercise to help lower levels of a certain blood fat (triglyceride) and to raise levels of good cholesterol (HDL) (Ramdan and Morsel, 2003 and Staughton, 2017) [16, 23]. The crop is capable of giving better seed yield even under low soil fertility, moisture stress and poor crop management. Niger has an advantage of yielding oil and has good degree of tolerance to diseases, insect pests and attack of wild animals. Niger has great potential for soil conservation. These attributes favour its cultivation on hilly areas, marginal and sub marginal lands in and around the forests. Niger is primarily grown on the denuded soils in the tribal pockets under input starved conditions in India. Further it is the life line of tribal agriculture and economy (Ranganatha, 2013) [18].

Worlds occupies 5.60 lakh ha area under Niger cultivation with 1.52 MMT production and its productivity was 271kg/ha (USDA, 2018-19) [26]. It is grown in mainly India, Ethiopia, Nepal, Germany, Switzerland, France, USSR, Sudan, Uganda, Tanzania, Malawi, Zimbabwe, Central and South Africa. India is the most important country accounting for more than 50% of world niger area and production. India tops in area, production and total export for niger in the world. In India, niger is grown on an area of 2.52 lakh ha.

with the production of 0.85 MMT and its productivity was 337 kg/ha (FAO, 2018-19) [4]. India could earn the foreign exchange of Rs. 100 crores by export of niger seed and the oil meal. India is the largest exporter in the world and USA, Netherlands, Italy, Germany, Belgium and Spain are the regular buyers (Ranganatha *et al*., 2015) [19].

Since, the beginning of agriculture, cultivated crops has been subjected to intensive natural, human selections and the trend continues. This has resulted in huge collection of different crop species, land races and varieties distributed throughout the world, which comprises valuable germplasm collection. The goal of every plant breeder is to develop superior varietal population; massive efforts are needed to obtain diverse types, generating variability and ultimately selection of desirable ideal genotypes. Genetic diversity which is pre-requisite for any successful breeding programme is of paramount importance. 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 the 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 among the genotypes of Niger.

Materials and Methods

The present experiment was conducted at five locations *viz*., ARS, Phondaghat (E1), ARS, Shirgaon (E2), Dept. of Agril. Botany, Dapoli (E3), RARS, Karjat (E4) and ARS, Plghar (E5) during *Kharif*, 2018 and *Kharif*, 2019. The experimental trial was included 40 niger genotypes (Table 1) laid out in Randomized Block design replicated thrice. Row to row and plant to plant spacing were maintained at 30 and 10 cm, respectively. All the agronomic package of practices was followed to grow a healthy crop in each replication. Randomly five plants were selected and tagged for observation in each entry. Observations were recorded on thirteen characters *viz*., days to 50 per cent flowering, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capitula plant^{-1}, capitulum diameter (cm), number of seeds capitulum^{-1}, 1000 seed weight (g), seed yield plant^{-1} (g), seed yield plot^{-1} (g), days to maturity, oil content (%) and protein content (%). The recorded data were analyzed as suggested by Panse and Sukhatme (1985) [11] for analysis of variance. Effective method suggested by Mahalanobis (1936) [6] known as Mahalanobis D^2 statistics 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 by Tocher's method (Rao, 1952) [20].

Results and Discussion

The mean sum of square (Table 2) was highly significant for all traits except capitulum diameter and 1000 seed weight, indicating the presence of wide variability in the genotypes. The tantamount findings were also reported by Sreedhar *et al.* (2006) [22], Patil (2007) [14], Parameshwarappa *et al*. (2009) [13], Parameshwarappa *et al*. (2011) [12], Sangita *et al*. (2012) [21], Yadav *et al*. (2012) [27], Goyal and Bisen (2017) [5], Misganaw (2017) [8], Naik *et al.* (2018) [10], Ram *et al.* (2018) [15], Suryanarayana *et al.* (2018b) [24] and Suryanarayana *et al.* (2019) [25].

The high level of D^2 value indicated wide range of divergence among the population of niger. Environment wise forty genotypes were grouped into 5, 4, 4, 8 and 4 clusters for E1, E2, E3, E4 and E5, respectively on the basis of magnitude of D^2 values (Table 3).

The pooled results of E1, the forty genotypes were grouped in 5 clusters on the basis of magnitude of D^2 values. Cluster I with 24 genotypes emerged as the largest cluster followed by cluster IV with 10 genotypes, cluster II with 4 genotypes whereas the cluster III and V contained only single genotype, thus these clusters remained solitary. On the basis pooled magnitude of D^2 values, the forty genotypes were grouped into 4 clusters during the experiment at E2. Cluster I with 30 genotypes emerged as the largest cluster followed by cluster III with 5 genotypes, cluster II with 4 genotypes while the cluster IV was solitary. In the investigation of E3, the forty genotypes were grouped in 4 clusters on the basis of magnitude of D^2 values. Cluster I with 32 genotypes emerged as the largest cluster followed by cluster II with 5 genotypes, cluster III with 2 genotypes whereas the cluster IV was solitary. On the basis of magnitude of D^2 values, the forty genotypes were grouped in 8 clusters during conducted the experiment at E4. Cluster I with 20 genotypes emerged as the largest cluster followed by cluster III with 7 genotypes, cluster II with 5 genotypes cluster VII with 3 genotypes and cluster VIII with 2 genotypes whereas the cluster IV, V and VI were solitary in regard to the multi-varietal composition. The results of E5, the forty genotypes were grouped in 4 clusters on the basis of magnitude of D^2 values. Cluster I with 27 genotypes emerged as the largest cluster followed by cluster III with 7 genotypes, cluster II with 5 genotypes while the cluster IV was solitary. The solitary clusters indicating their independent identity and importance due to the unique characters constituted by that genotypes. These genotypes may serve as potential parents for breeding programme. These results are in harmony with the findings of Sreedhar *et al.* (2006) [22], Patil (2007) [14], Parameshwarappa *et al*. (2009) [13], Parameshwarappa *et al*. (2011) [12], Sangita *et al*. (2012) [21], Goyal and Bisen (2017) [5], Misganaw (2017) [8], Naik *et al.* (2018) [10], Ram *et al.* (2018) [15], Suryanarayana *et al.* (2018b) [24] and Suryanarayana *et al*. (2019) [25].

The intra-cluster distance is another parameter, besides cluster mean for particular character, as it indicated the extent of variability existed in the genotypes comprised in a particular cluster. Location wise the highest intra cluster distance was observed for cluster IV (D=4.69), I (D=3.04), II (D=4.12), VIII (D=3.10) and III (D=3.61) for E1, E2, E3, E4 and E5, respectively (Table 4). The high intra cluster distance within a cluster indicated high degree of variability within the cluster offers scope for improvement by various selection methods. The similar results were also reported by Patil (2007) [14], Parameshwarappa *et al*. (2009) [13], Parameshwarappa *et al*. (2011) [12], Sangita *et al*. (2012) [21], Goyal and Bisen (2017) [5], Misganaw (2017) [8], Naik *et al.* (2018) [10], Ram *et al.* (2018) [15], Suryanarayana *et al.* (2018b) [24] and Suryanarayana *et al*. (2019) [25].

The inter-cluster studies indicated magnitude of genetic

divergence between the clusters. It showed that, how much this clusters were genetically diverse from each other. Environment wise the highest inter cluster distance for pooled data was observed between cluster II and VI (D=13.26), II and III (D=7.28), III and IV (D=7.89), IV and VIII (D=8.45), and I and IV (D=7.54) for E1, E2, E3, E4 and E5, respectively (Table 4). These clusters were found genetically diverse. Those genotypes reported maximum inter cluster distance indicated that these genotypes were included in these clusters will give high heterotic response and better segregants. The genotypes which included in that genetically diverse clusters could be used in hybridization programme for future crop improvement in niger. The lowest inter cluster distance was observed between cluster III and IV (D=4.52), I and II (D=4.88), I and IV (D=4.75), I and IV (D=3.20), and I and II (D=4.59) for E1, E2, E3, E4 and E5, respectively (Table 4). It indicating that genotypes present in these cluster might have genetical similarities with one another and appeared to have evolved from common gene pool. These results are in harmony with the findings of Sreedhar *et al.* (2006) [22], Patil (2007) [14], Parameshwarappa *et al.* (2009) [13], Parameshwarappa *et al.* (2011) [12], Goyal and Bisen (2017) [5], Naik *et al.* (2018) [10], Ram *et al.* (2018) [15], Suryanarayana *et al.* (2018b) [24] and Suryanarayana *et al.* (2019) [25].

Genotypes form cluster III, III, VII showed earliness for flowering and maturity with dwarf pant stature in E1, E3 and E4, respectively. In E2, early flowering and maturity of genotypes from cluster IV and dwarf plant height observed in cluster III. Also, in E5, genotypes found early flowering and dwarf statured plants in cluster IV and early matured genotypes reported in cluster II. The highest number of primary and secondary branches plant^{-1}, number of capitula plant^{-1}, capitulum diameter, number of seeds capitulum^{-1}, 1000 seed weight, seed yield plant^{-1}, seed yield plot^{-1}, oil content and protein content were found in genotypes consisted the cluster V (E1), clusters II and IV (E2 and E3), clusters VI and VIII (E4), and clusters III and IV (E5) (Table 5). D^2 analysis revealed that geographical distribution had no relation to genetic diversity as similar findings were in conformity with previous workers viz., Patil (2007) [14], Parameshwarappa *et al.* (2009) [13], Parameshwarappa *et al.* (2011) [12], Goyal and Bisen (2017) [5], Naik *et al.* (2018) [10], Ram *et al.* (2018) [15], Suryanarayana *et al.* (2018b) [24] and Suryanarayana *et al.* (2019) [25].

By studying the contribution of different characters towards the total divergence, breeder can get an idea about the characters, which are mainly responsible for the total divergence. This is important while selecting the parents in breeding programme. Location wise the contribution of various traits towards divergence was ranged from 0.00% (oil content) to 32.44 (number of capitula plant^{-1}), 1.28% (number of secondary branches plant^{-1}) to 26.28% (capitulum diameter), 0.26% (1000 seed weight) to 30.13% (days to 50 per cent flowering), 0.13% (protein content) to 33.59% (days to 50 per cent flowering) and 0.77% (1000 seed weight) to 32.56% (days to 50 per cent flowering) for ARS, E1, E2, E3, E4 and E5, respectively (Table 6).

It is obvious the yield is the dependent character governed by several other yield contributing characters, which are affected by different environments in different locations. Therefore, changes in variability in character among genotypes for breeding cannot be made only on the basis of yield potential. Hence to improve it, selection must be done considering plant height, number of primary and secondary branches plant^{-1}, number of capitulum plant^{-1}, capitulum diameter, number of seeds capitulum^{-1}, 1000 seed weight as their contribution towards total divergence is more. The similar results were also reported by Parmeshwarappa *et al.* (2009) [13], Parmeshwarappa *et al.* (2011) [12], Goyal and Bisen (2017) [5], Naik *et al.* (2018) [10], Ram *et al.* (2018) [15], Suryanarayana *et al.* (2018b) [24] and Suryanarayana *et al.* (2019) [25].

Table 1: List of genotypes/varieties and their sources

Sr. No.	Genotype code	Name of Genotypes	Source	Sr. No.	Genotype code	Name of Genotypes	Source
1.	G1	GP-54	ZARS, Igatpuri	21.	G21	NMLT-12	ZARS, Igatpuri
2.	G2	GP-57	ZARS, Igatpuri	22.	G22	NMLT-13	ZARS, Igatpuri
3.	G3	IGPN 14-2	ZARS, Igatpuri	23.	G23	NMLT-14	ZARS, Igatpuri
4.	G4	IGPN 14-6	ZARS, Igatpuri	24.	G24	NMLT-15	ZARS, Igatpuri
5.	G5	IGPN 14-9	ZARS, Igatpuri	25.	G25	NGR -1	ARS, Shirgaon
6.	G6	IGPN 15-1	ZARS, Igatpuri	26.	G26	NGR -3	ARS, Shirgaon
7.	G7	IGPN 15-3	ZARS, Igatpuri	27.	G27	NGR -4	ARS, Shirgaon
8.	G8	IGPN 15-4	ZARS, Igatpuri	28.	G28	NGR -5	ARS, Shirgaon
9.	G9	IGPN 15-5	ZARS, Igatpuri	29.	G29	NGR -6	ARS, Shirgaon
10.	G10	NMLT-1	ZARS, Igatpuri	30.	G30	NGR -18	ARS, Shirgaon
11.	G11	NMLT-2	ZARS, Igatpuri	31.	G31	NGR -22	ARS, Shirgaon
12.	G12	NMLT-3	ZARS, Igatpuri	32.	G32	NGR -24	ARS, Shirgaon
13.	G13	NMLT-4	ZARS, Igatpuri	33.	G33	Devadi Local 2	Devadi, Solapur
14.	G14	NMLT-5	ZARS, Igatpuri	34.	G34	Devadi Local 3	Devadi, Solapur
15.	G15	NMLT-6	ZARS, Igatpuri	35.	G35	Devadi Local 4	Devadi, Solapur
16.	G16	NMLT-7	ZARS, Igatpuri	36.	G36	Devadi Local 5	Devadi, Solapur
17.	G17	NMLT-8	ZARS, Igatpuri	37.	G37	Modnimb Local 2	Modnimb, Solapur
18.	G18	NMLT-9	ZARS, Igatpuri	38.	G38	Sahyadri	ZARS, Igatpuri
19.	G19	NMLT-10	ZARS, Igatpuri	39.	G39	Phule Karala	ZARS, Igatpuri
20.	G20	NMLT-11	ZARS, Igatpuri	40.	G40	Phule Vaitrna	ZARS, Igatpuri

Table 2: Environment wise analysis of variance for quantitative and qualitative traits in 40 genotypes of Niger

Sr. No.	Characters	ARS, Phondaghat (E1)			ARS, Shirgaon (E2)			Dept. of Agril. Botany, Dapoli (E3)		
		Replication	Treatment	Error	Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78	2	39	78
1.	DFPF	11.56	20.67**	1.82	2.79	25.64**	2.21	2.10	37.84**	1.95

2.	PH (cm)	15.04	271.81**	34.21	6.50	113.62**	39.57	32.10	235.52**	44.21
3.	NPBPP	0.23	13.33**	0.99	0.63	9.62**	1.34	0.17	7.63**	0.92
4.	NSBPP	4.52	53.63**	3.49	2.18	30.00**	5.10	2.26	23.50**	3.29
5.	NCPP	0.23	404.45**	13.55	6.47	90.96**	19.30	7.94	170.62**	13.15
6.	CD (cm)	0.001	0.03	0.001	0.01	0.02	0.001	0.001	0.03	0.001
7.	NSPC	17.11	43.37**	10.27	1.79	32.33**	7.60	3.66	42.27**	9.16
8.	1000 SW (g)	0.04	0.05	0.02	0.03	0.06	0.02	0.02	0.10	0.03
9.	SYPp (g)	0.26	0.23**	0.08	0.03	0.23**	0.06	0.23	0.26**	0.09
10.	SYPP (g)	638.71	954.25**	317.14	612.87	1089.64**	326.21	2619.18	1543.62**	690.97
11.	DM	1.71	38.56**	2.99	0.01	24.60**	3.93	15.27	42.39**	10.13
12.	OC (%)	2.43	10.11**	4.80	4.31	7.44**	3.36	1.07	6.32**	2.88
13.	PC (%)	1.06	3.36*	0.66	2.76	3.71*	1.31	1.51	2.58*	0.66

*Significant at 5% level of significance **Significant at 1% level of significance

DFPF: Days to 50 per cent flowering PH: Plant height NPBPP: No. of primary branches plant^{-1} NSBPP: No. of secondary branches plant^{-1}

NCPP: No. of capitula plant^{-1} CD: Capitulum diameter NSPC: No. of seeds capitulum^{-1} SW: Seed weight

SYPp: Seed yield plant^{-1} SYPP: Seed yield plot^{-1} DM: Days to maturity OC: Oil content

PC: Protein content

Table contd…

Table 2: Environment wise analysis of variance for quantitative and qualitative traits in 40 genotypes of Niger

Sr. No.	Characters	RARS, Karjat (E4)			ARS, Palghar (E5)		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFPF	0.09	37.30**	2.13	3.39	33.47**	2.03
2.	PH (cm)	45.61	90.93**	30.45	11.82	144.00**	39.91
3.	NPBPP	0.64	12.48**	0.70	1.41	11.60**	1.09
4.	NSBPP	4.08	29.19**	2.50	13.58	30.90**	4.02
5.	NCPP	36.88	112.91**	10.22	3.70	109.77**	10.18
6.	CD (cm)	0.01	0.01	0.001	0.001	0.02	0.001
7.	NSPC	1.93	11.80**	4.41	5.26	30.96**	9.27
8.	1000 SW (g)	0.02	0.12*	0.06	0.07	0.09	0.05
9.	SYPp (g)	0.01	0.11*	0.04	0.06	0.16**	0.07
10.	SYPP (g)	128.34	550.26**	238.48	297.46	1054.34**	473.81
11.	DM	3.26	19.80**	4.05	7.39	45.24**	6.44
12.	OC (%)	2.13	8.29**	2.13	3.28	7.36**	2.78
	PC (%)	0.23	3.59*	1.31	6.00	3.08*	1.18

*Significant at 5% level of significance **Significant at 1% level of significance

DFPF: Days to 50 per cent flowering PH: Plant height NPBPP: No. of primary branches plant^{-1} NSBPP: No. of secondary branches plant^{-1}

NCPP: No. of capitula plant^{-1} CD: Capitulum diameter NSPC: No. of seeds capitulum^{-1} SW: Seed weight

SYPp: Seed yield plant^{-1} SYPP: Seed yield plot^{-1} DM: Days to maturity OC: Oil content

PC: Protein content

Table 3: Environment wise grouping of 40 niger genotypes of pooled data into different clusters by Tochers' method

Cluster No.	ARS, Phondaghat (E1)		ARS, Shirgaon (E2)			Dept. of Agril. Botany, Dapoli (E3)		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	24	G3, G4, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G17, G19, G21, G22, G23, G29, G30, G31, G33, G34, G35, G37	I	30	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G30, G31, G33, G34, G35, G37, G39	I	32	G1, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G27, G28, G29, G30, G31, G33, G34, G35, G37, G39
II	4	G25, G26, G27, G28	II	4	G32, G36, G38, G40	II	5	G24, G32, G36, G38, G40
III	1	G39	III	5	G25, G26, G27, G28, G29	III	2	G25, G26
IV	10	G1, G2, G10, G16, G18, G20, G24, G32, G38, G40	IV	1	G24	IV	1	G2
V	1	G36						

Table Contd…

Table 3: Environment wise grouping of 40 Niger genotypes of pooled data into different clusters by Tochers' method

Cluster No.	RARS, Karjat (E4)		Cluster No.	ARS, Palghar (E5)	
	Number of Genotypes	Name of the Genotypes		Number of Genotypes	Name of the Genotypes
I	20	G3, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G29, G30, G31	I	27	G1, G2, G3, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G30, G31, G33, G34, G35, G37
II	5	G1, G2, G4, G6, G10	II	5	G25, G26, G27, G28, G29
III	7	G33, G34, G35, G37, G38, G39, G40	III	7	G4, G10, G32, G36, G38, G39, G40
IV	1	G28	IV	1	G24
V	1	G5			
VI	1	G36			
VII	3	G25, G26, G27			
VIII	2	G24, G32			

Table 4: Environment wise average intra and inter cluster divergence (D & D^2) of pooled data in 40 genotypes of Niger

ARS, Phondaghat						ARS, Shirgaon					Dept. of Agril. Botany, Dapoli				
Cluster	I	II	III	IV	V	Cluster	I	II	III	IV	Cluster	I	II	III	IV
I	3.90 (15.21)	5.87 (34.46)	5.36 (28.73)	5.98 (35.76)	9.78 (95.65)	I	3.04 (9.24)	4.88 (23.81)	5.05 (25.50)	6.29 (39.56)	I	3.70 (13.69)	5.93 (35.16)	5.66 (32.40)	4.75 (22.56)
II		2.62 (6.86)	8.41 (70.73)	9.17 (84.09)	13.26 (175.83)	II		2.98 (8.88)	7.28 (53.00)	5.14 (26.42)	II		4.12 (16.97)	7.59 (57.61)	5.67 (32.15)
III			0.00 (0.00)	4.52 (20.43)	5.64 (31.81)	III			3.01 (9.06)	5.99 (35.88)	III			1.73 (2.99)	7.89 (62.25)
IV				4.69 (22.00)	6.68 (44.62)	IV				0.00 (0.00)	IV				0.00 (0.00)
V					0.00 (0.00)										

RARS, Karjat									ARS, Palghar				
Cluster	I	II	III	IV	V	VI	VII	VIII	Cluster	I	II	III	IV
I	2.46 (6.05)	4.76 (22.66)	4.52 (20.43)	3.20 (10.24)	3.26 (10.63)	6.70 (44.89)	4.49 (20.16)	8.24 (67.90)	I	2.65 (7.02)	4.59 (21.07)	5.30 (28.09)	7.54 (56.85)
II		2.69 (7.24)	4.46 (19.89)	5.06 (25.60)	3.72 (13.84)	4.86 (23.62)	4.57 (20.88)	4.74 (22.47)	II		2.64 (6.97)	6.17 (38.07)	6.45 (41.60)
III			3.09 (9.55)	5.50 (30.25)	5.16 (26.63)	4.24 (17.98)	6.00 (36.00)	6.36 (40.45)	III			3.61 (13.03)	4.94 (24.40)
IV				0.00 (0.00)	3.41 (11.63)	7.79 (60.68)	3.57 (12.74)	8.45 (71.40)	IV				0.00 (0.00)
V					0.00 (0.00)	6.79 (46.10)	3.31 (10.96)	7.31 (53.44)					
VI						0.00 (0.00)	7.78 (60.53)	4.69 (22.00)					
VII							2.53 (6.40)	7.40 (54.77)					
VIII								3.10 (9.61)					

Table 5: Environment wise cluster mean performance of pooled data for 13 characters in 40 genotypes of Niger

Sr. No.	Characters	ARS, Phondaghat (E1)						ARS, Shirgaon (E2)					Dept. of Agril. Botany, Dapoli (E3)				
		Clusters						Clusters					Clusters				
		I	II	III	IV	V	PM	I	II	III	IV	PM	I	II	III	IV	PM
1.	DFPF	50.05	46.75	48.67	50.62	49.17	49.05	50.36	49.42	43.97	41.50	46.31	49.41	46.30	40.58	50.67	46.74
2.	PH (cm)	131.73	123.04	119.00	138.52	119.33	126.32	125.33	130.13	118.50	121.83	123.95	141.83	143.50	124.50	134.00	135.96
3.	NPBPP	8.22	5.83	9.17	11.22	13.00	9.49	9.41	12.29	8.60	13.33	10.91	8.40	10.40	6.92	11.83	9.39
4.	NSBPP	14.24	10.38	19.50	21.05	24.67	17.97	19.60	25.54	17.40	25.83	22.09	15.68	19.73	13.17	19.17	16.94
5.	NCPP	35.28	26.96	50.50	51.58	67.33	46.33	37.57	44.58	29.83	43.83	38.95	39.81	49.33	29.33	59.00	44.37
6.	CD (cm)	1.08	0.92	1.18	1.09	1.27	1.11	1.05	1.15	0.94	1.07	1.05	1.07	1.22	0.96	1.12	1.09
7.	NSPC	32.28	31.13	39.67	35.40	42.17	36.13	30.16	35.92	26.90	30.67	30.91	31.47	39.37	30.00	29.67	32.63
8.	1000 SW (g)	2.63	2.37	2.75	2.70	2.88	2.67	2.57	2.72	2.33	2.73	2.59	2.57	2.78	2.20	2.72	2.57
9.	SYPp (g)	2.61	2.58	2.55	2.89	3.57	2.84	2.73	3.43	2.74	3.39	3.07	3.38	4.10	3.42	3.59	3.62
10.	SYPP (g)	221.75	226.50	226.17	238.43	269.50	236.47	223.80	253.67	229.53	271.67	244.67	226.52	261.20	247.17	264.00	249.72
11.	DM	85.41	77.21	83.17	85.20	84.83	83.16	83.52	83.42	78.70	74.17	79.95	81.07	79.80	73.08	82.67	79.16
12.	OC (%)	36.22	35.33	39.00	37.87	40.67	37.82	37.86	40.17	36.53	40.17	38.68	38.99	41.73	39.25	40.00	39.99
13.	PC (%)	18.29	17.58	19.33	19.08	21.17	19.09	18.91	21.67	19.07	20.83	20.12	19.80	21.97	19.42	19.17	20.09

DFPF: Days to 50 per cent flowering, PH: Plant height, NPBPP: No. of primary branches $plant^{-1}$, NSBPP: No. of secondary branches $plant^{-1}$, NCPP: No. of capitula $plant^{-1}$, CD: Capitulum diameter NSPC: No. of seeds $capitulum^{-1}$, SW: Seed weight, SYPp: Seed yield $plant^{-1}$, SYPP: Seed yield $plot^{-1}$, DM: Days to maturity, OC: Oil content, PC: Protein content, PM: Population Mean

Table Contd…

Table 5: Environment wise cluster mean performance of pooled data for 13 characters in 40 genotypes of Niger

Sr. No.	Characters	RARS, Karjat (E4)									ARS, Palghar (E5)				
		Clusters									Clusters				
		I	II	III	IV	V	VI	VII	VIII	PM	I	II	III	IV	PM
1.	DFPF	52.83	48.47	55.05	48.33	48.00	55.50	45.17	47.42	50.10	49.54	41.73	49.24	41.17	45.42
2.	PH (cm)	136.23	138.23	144.60	136.83	135.50	141.83	128.11	136.00	137.17	136.99	135.33	143.10	131.83	136.81
3.	NPBPP	6.26	8.83	9.79	6.50	6.00	11.17	7.33	12.42	8.54	8.33	8.27	11.74	13.83	10.54
4.	NSBPP	12.39	16.27	16.45	12.00	11.33	20.83	13.50	22.33	15.64	15.61	15.00	21.19	25.33	19.28
5.	NCPP	33.24	44.33	38.00	30.17	37.83	43.17	32.72	51.67	38.89	33.29	33.37	45.83	49.33	40.46
6.	CD (cm)	0.98	1.01	1.05	0.87	0.97	1.18	0.92	0.98	1.00	0.99	0.97	1.12	1.05	1.03
7.	NSPC	20.35	22.43	21.38	18.00	22.83	25.67	19.17	22.33	21.52	23.83	22.90	29.79	28.83	26.34
8.	1000 SW (g)	2.39	2.57	2.53	1.68	2.51	2.68	2.22	2.59	2.40	2.52	2.15	2.64	2.67	2.50
9.	SYPp (g)	2.29	2.49	2.52	2.34	2.62	2.85	2.28	2.76	2.52	2.50	2.59	2.78	3.08	2.74
10.	SYPP (g)	191.72	211.63	188.14	191.33	191.83	231.17	195.22	222.92	203.00	214.14	202.27	241.19	260.50	229.53
11.	DM	88.71	86.67	86.83	86.33	85.83	86.83	81.39	82.83	85.68	84.59	74.83	83.52	78.17	80.28
12.	OC (%)	36.32	37.80	37.36	36.33	37.67	40.83	35.28	40.08	37.71	36.75	36.17	39.62	40.33	38.22
13.	PC (%)	18.70	19.50	19.79	18.50	18.83	22.17	18.17	21.58	19.66	18.62	18.83	20.33	20.17	19.49

DFPF: Days to 50 per cent flowering, PH: Plant height, NPBPP: No. of primary branches plant^{-1}, NSBPP: No. of secondary branches plant^{-1}, NCPP: No. of capitula plant^{-1}, CD: Capitulum diameter NSPC: No. of seeds capitulum^{-1}, SW: Seed weight, SYPp: Seed yield plant^{-1}, SYPP: Seed yield plot^{-1}, DM: Days to maturity, OC: Oil content, PC: Protein content, PM: Population Mean

Table 6: Environment wise contribution of various characters towards divergence of pooled data in 40 genotypes of Niger

Sr. No.	Environments	ARS, Phondaghat (E1)		ARS, Shirgaon (E2)		Dept. of Agril. Botany, Dapoli (E3)		RARS, Karjat (E4)		ARS, Palghar (E5)	
	Characters	Times ranked 1st	Per cent contribution	Times ranked 1st	Per cent contribution	Times ranked 1st	Per cent contribution	Times ranked 1st	Per cent contribution	Times ranked 1st	Per cent contribution
1.	DFPF	100	12.82%	141	18.08%	235	30.13%	262	33.59%	254	32.56%
2.	PH (cm)	50	6.41%	21	2.69%	39	5.00%	9	1.15%	46	5.90%
3.	NPBPP	62	7.95%	103	13.21%	82	10.51%	242	31.03%	127	16.28%
4.	NSBPP	24	3.08%	10	1.28%	51	6.54%	4	0.51%	15	1.92%
5.	NCPP	253	32.44%	24	3.08%	139	17.82%	143	18.33%	103	13.21%
6.	CD (cm)	159	20.38%	205	26.28%	80	10.26%	27	3.46%	116	14.87%
7.	NSPC	23	2.95%	60	7.69%	8	1.03%	22	2.82%	8	1.03%
8.	1000 SW (g)	4	0.51%	30	3.85%	2	0.26%	16	2.05%	6	0.77%
9.	SYPp (g)	36	4.62%	24	3.08%	16	2.05%	11	1.41%	18	2.31%
10.	SYPP (g)	3	0.38%	63	8.08%	13	1.67%	9	1.15%	24	3.08%
11.	DM	34	4.36%	27	3.46%	36	4.62%	16	2.05%	10	1.28%
12.	OC (%)	0	0.00%	23	2.95%	11	1.41%	18	2.31%	18	2.31%
13.	PC (%)	32	4.10%	49	6.28%	68	8.72%	1	0.13%	35	4.49%

E1: ARS, Phondahgat; E2: ARS, Shirgaon; E3: Department of Agril. Botany, Dapoli; E4 : RARS, Karjat; E5 : ARS, Palghar

DFPF: Days to 50 per cent flowering	PH: Plant height	NPBPP: No. of primary branches plant^{-1}	NSBPP: No. of secondary branches plant^{-1}
NCPP: No. of capitula plant^{-1}	CD: Capitulum diameter	NSPC: No. of seeds capitulum^{-1}	SW: Seed weight
SYPp: Seed yield plant^{-1}	SYPP: Seed yield plot^{-1}	DM: Days to maturity	OC: Oil content
PC: Protein content			

Conclusion

It is concluded that the high intra and inter-cluster distance was observed in many clusters it indicated the extent of variability existed in the genotypes comprised in a particular cluster and will give high heterotic response and better segregants. Selection must be done on considering plant height, number of primary and secondary branches plant^{-1}, total number of capitulum plant^{-1}, capitulum diameter, number of seeds capitulum^{-1} and 1000 seed weight as their contribution towards total divergence is high. On the basis of intra and inter cluster distances, cluster mean and per se performance, the genotypes *viz*., G1, G2, G4, G8, G9, G10, G24, G25, G26, G28, G32, G35, G36, G39 and G40 were found to be superior. These genotypes may serve as potential parents for breeding programme.

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