

Genetic Variability Studies for Yield and Yield Contributing Traits in Niger (*Guizotia abyssinica* L. f. Cass)

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ABSTRACT: Niger (*Guizotia abyssinica* L. f. Cass) seed oil is considered to be one of the best edible oils due to its high content of poly unsaturated fatty acid. In India, niger crop is mainly grown by tribals on marginal, unproductive, waste lands under rainfed conditions with minimal inputs. Till now, limited research has been done on understanding the existing genetic diversity in niger germplasm. Thus, the present study was conducted to assess the genetic variability and phylogenetic relationship among 208 niger genotypes based on six major agronomic traits. Results indicated that there is a significant variation ($p < 0.05$) observed among 208 accessions. Coefficient of variation was highest for seed yield per plant, followed by number of capitula per plant. The difference between phenotypic coefficient of variation and genotypic coefficient of variation is highest for seed yield per plant which implies that this trait is highly influenced by the environment. The maximum variations present among the studied accessions were captured in three principle components and they were grouped in to two clusters.

Keywords: Variability, Genetic diversity, Cluster analysis, Principal components, Niger.

INTRODUCTION

Niger ($2n=2x=30$) is an unexploited minor oilseed crop that is mainly grown in the tropical and subtropical countries like India, Ethiopia, West Indies and Zimbabwe. The crop is originated in the highlands of Ethiopia and India is considered as the secondary centre of diversity (Baagoe, 1974). Niger being self-incompatible in nature, is highly allogamous (Getinet and Sharma 1996). It is valued for its high polyunsaturated fatty acids content (50% linoleic acid and 38% oleic acid). India and Ethiopia are two major producers of niger in the world. Though India accounts for only 3% of niger oilseed production (Bulcha, 2007), it ranks first in area, production, and export in the world. Cultivation of niger is declining in India, from 4.14 lakh ha in 2005-06 to 2.18 lakh ha in 2017 due to low productivity and profitability. The major production constraints are low productivity of the available cultivars due to skewed source-sink relation, seed shattering and self-incompatibility. Assessing the genetic diversity and relation among the niger

accessions for seed yield and related components is thus prerequisite that may help in identifying the desired genotypes which could be used as donor for improving the seed yield in niger. Therefore, this study was executed with the objective of assessing the extent and pattern of genetic variability among the niger accessions.

MATERIALS AND METHODS

The present study was carried out using 208 niger accessions, and five checks (JNS9, JNS28, JNS30, IGPN 2004-1 and DNS4) in augmented randomized complete block design during *kharif* 2018-19. Five plants (excluding border plants) were randomly selected and tagged to record observations *viz.*, days to 50% flowering, plant height (cm), number of capitula per plant, number of branches per plant, seed yield per plant (g/pl). The oil content (%) was measured using Nuclear Magnetic Resonance spectroscopy (NMR MQC-5, UK).

The phenotypic and genotypic coefficients of variability (PCV and GCV), broad sense heritability (h^2_{bs}), genetic advance, multivariate analysis, including clusters and principal components of the accessions was computed as per the methods suggested by Burton (1952); Johnson *et al.* (1955); Rao (1952) respectively. Genetic distance between clusters was calculated using the generalized Mahalanobis D^2 statistics and the data was subjected to appropriate statistical analysis in R software v.4.2.1.0 using “augmented RCBD” package (Aravind *et al.*, 2021). Principle component analysis was done using “factoextra” and “princomp” packages in R.

RESULTS AND DISCUSSION

Descriptive Statistics and Analysis of Augmented Design.

The results on the mean, range and coefficient

of variation are presented in Table 1. The mean values were calculated for days to 50% flowering (42.53), plant height (92.82), number of capitula per plant (101.39), number of branches per plant (9.75), seed yield per plant (5.47) and oil content (35.88). The highest value of co-efficient of variation (C.V) was found in case of seed yield per plant (24.33 %), followed by number of capitula per plant (16.43 %), number of branches per plant (11.27 %), plant height (9.57 %); while days to 50 % flowering (4.94 %) and oil content (2.35 %) had lower C.V values. The graphical representation of phenotypic variability and frequency distribution for yield parameters and oil content with relation to checks are depicted in Fig. 1 and 2, respectively.

Table 1: Descriptive statistics of yield parameters and oil content in 208 genotypes of niger

Trait	Mean	Range	Coefficient Of variation %		
Days to 50% flowering (DFF)	42.53	38.55-71.55	4.94		
Plant height (PH)	92.82	66.63-136.63	9.57		
No. of capitula/plant (Capitula)	101.39	62.06-162.26	16.43		
No. of branches/plant (Branches)	9.75	4.52-17.52	11.27		
Seed yield/plant (SYP)	5.47	0.65-11.44	24.33		
Oil content %	35.88	27.34-39.91	2.35		

ns: $p>0.05$; *: $p<0.05$; **: $p<0.01$

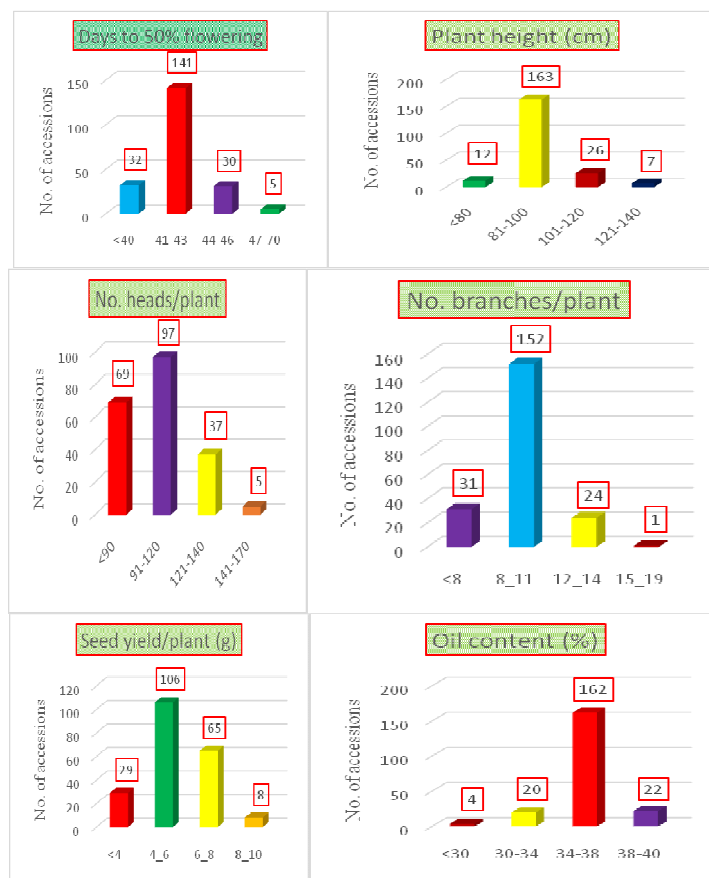


Fig. 1. Phenotypic variability in niger genotypes.

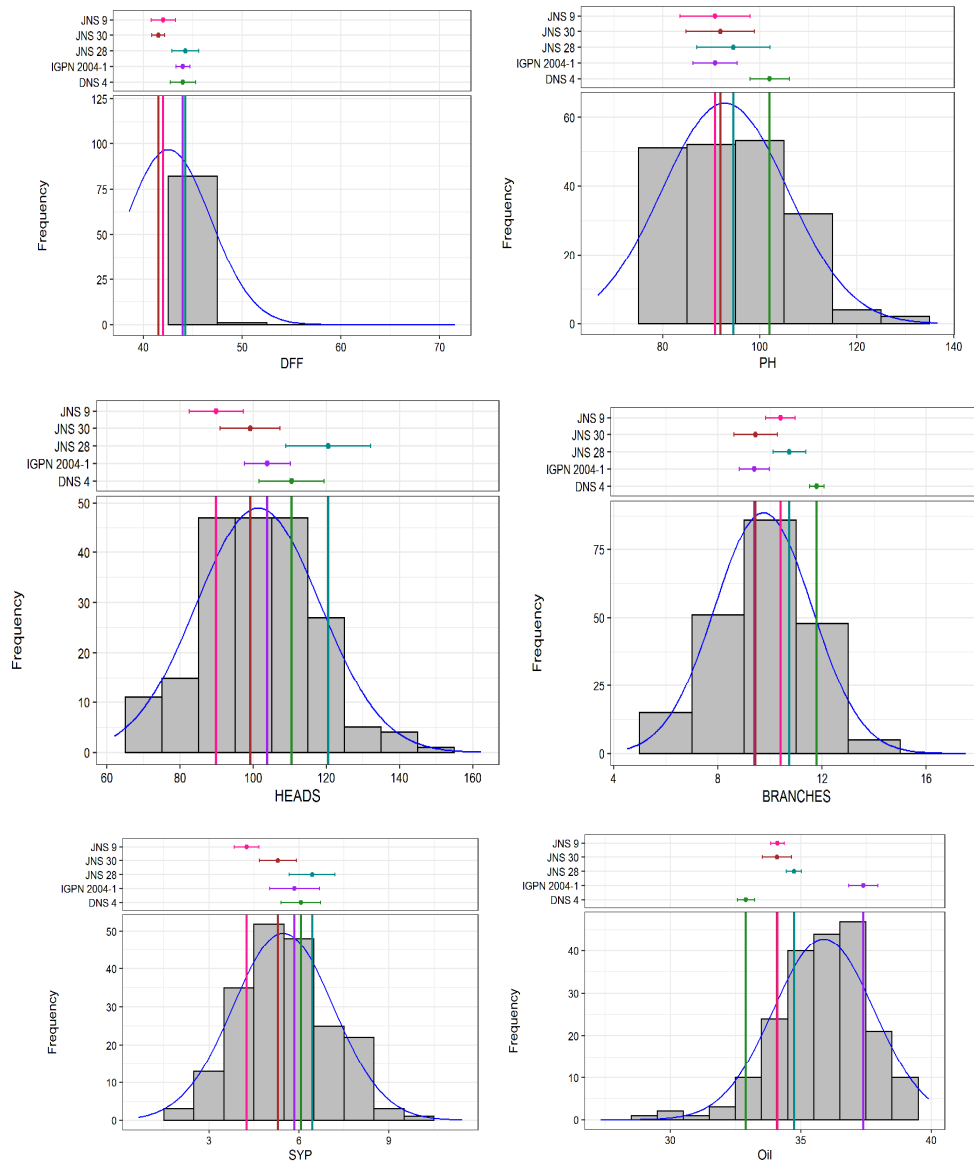


Fig. 2. Frequency distribution for yield parameters and oil content in relation to checks.

The ANOVA revealed significant mean sum of squares for all traits for different sources of variation (Table 2). The source of variation for block (excluding treatments) and entries (excluding blocks) were found to be significant for all the traits analyzed. The traits *viz.*, branches per plant (BPP), seed yield per plant (SYP) and oil content (OC) were significant in the checks.

However, the adjusted block effects were non-significant for all traits, indicating homogeneity of evaluation blocks. Similarly, the mean square due to checks *v/s* genotypes was significant for all the traits except days to 50% flowering (DFF) and plant height (PH), indicating that the treatments were significantly different from checks.

Table 2: Analysis of variance of augmented block design.

Source of Variation	Degrees of freedom	DF	PH	Capitula	BPP	SYP	OC
Block (ignoring treatments)	3	34.93**	2289.07**	7679.34**	78**	9.07**	6.37**
Treatment (ignoring block)	207	17.06**	71.66**	303.61*	2.57 ^{ns}	2.24**	3.68**
Check	4	6.7 ^{ns}	9.73 ^{ns}	41.11 ^{ns}	3.98*	2.65**	11.26**
Blocks (eliminating treatments)	3	6.18 ^{ns}	1.73 ^{ns}	313.98 ^{ns}	2.43 ^{ns}	0.2 ^{ns}	0.7 ^{ns}
Entries (ignoring block)	207	17.48**	104.65**	409.84**	3.67*	2.37**	3.76**
Genotypes	202	17.75**	106.5**	396.64**	3.64*	2.4**	3.49**
Test vs check	1	7.06 ^{ns}	12 ^{ns}	4208.41**	7.27*	3.35*	28.8**
Error	12	4.43	5.97	97.74	1.22	0.5	0.71

ns: p>0.05; *: p<0.05; **: p<0.01

Genetic Variability, Heritability and Genetic Advance. The genetic variability exhibited medium GCV for number of branches per plant (15.97) followed by seed yield per plant (12.55) and capitula per plant (10.83) (Table 3). The GCV was low for days to 50% flowering followed by plant height and oil content. High PCV was recorded for seed yield per plant (27.4) and medium PCV for plant height, number of capitula per plant and number of branches per plant. These results are in accordance with Saraswat and Bisen (2022); Suryanarayana *et al.* (2018); Baghel *et al.* (2018).

The differences between GCV and PCV were very low for days to 50% flowering and oil content which indicates that the traits are not influenced by the environment. The difference is high for number of branches per plant, and plant height, very high for number of capitula per plant and seed yield per plant, indicating high environmental influence and complexity of these traits (Fig. 3). The presence of high genetic variability is an indication of good scope for their improvement through hybridization followed by selection. High heritability was recorded for days to

50% flowering, number of branches per plant and oil content. Amsalu (2020) also reported high heritability for plant height. But the present results for seed yield per plant and capitula per plant are in contrast with the results of Baghel (2018); Suryanarayana *et al.* (2018). High heritability coupled with high genetic advance as percent of mean was recorded for number of branches per plant (Patil *et al.*, 2013) revealing the influence of additive gene action for this trait. Hence, the improvement of this trait can be made through direct phenotypic selection. High heritability coupled with low genetic advance as percent mean was recorded for oil content, indicating the effect of non-additive gene action. Similar results were reported by Gururaja *et al.* (2021). Low heritability coupled with low genetic advance as percent of mean was recorded for plant height, indicating that this trait is highly influenced by environmental effects and selection would be ineffective. In contrast, Baghel *et al.* (2018); Suryanarayana *et al.* (2018) reported high heritability and high genetic advance as a percent of mean for plant height.

Table 3: Estimates of genetic variability parameters of niger genotypes.

Trait	Mean	GCV	GCV category	PCV	PCV category	Heritability broadsense	hBS category	Genetic Advance	Genetic Advance of Mean	GAM category
DFF	42.53	8.58	Low	9.9	Low	75.02	High	6.52	15.33	Medium
PH	92.82	5.75	Low	11.17	Medium	20.54	Low	5.67	6.11	Low
Capitula	101.39	10.83	Medium	19.71	Medium	30.2	Medium	12.45	12.28	Medium
Branches	9.75	15.97	Medium	19.58	Medium	66.58	High	2.62	26.87	High
SYP	5.47	12.55	Medium	27.4	High	20.98	Low	0.65	11.86	Medium
OIL	35.88	4.65	Low	5.21	Low	79.73	High	3.07	8.57	Low

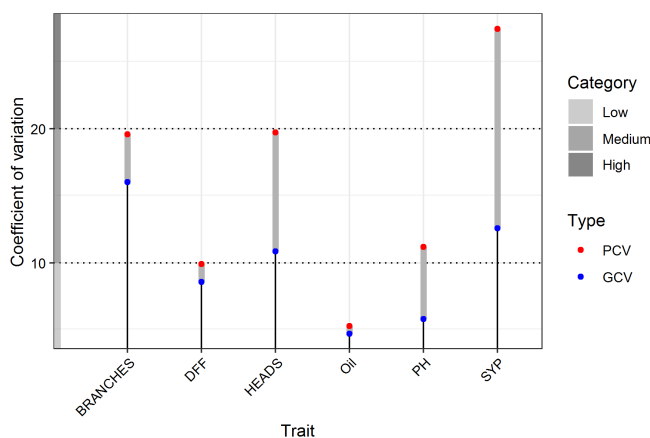


Fig. 3. Phenotypic and genotypic coefficient of variability plot.

Principal Component Analysis. Eigen vector values, percentage of variance and the cumulative percentage are presented in Table 4. In this case, three components had Eigen values greater than 1.0. PCA 1, 2 and 3 had Eigen values of 1.646, 1.041 and 1.031 respectively. Together they accounted for 61.998 percent of the variability of the genotypes used for the diversity analysis. Days to 50% flowering (0.072) and oil content (0.201) showed positive loadings in PC 1 and the

remaining parameters showed negative loadings (Table 5). In PC2, seed yield per plant (0.58) showed positive loadings and the remaining factors showed negative loadings. The biplot diagram (Fig. 4) between PC 1 and PC2 explained the distribution and the nature of diversity for both variables and the genotypes. The loading plot depicted that almost all the genotypes and variables showed high degree of variation.

Plant height, capitula per plant, branches per plant and seed yield per plant have the largest participation in the divergence and carry the largest portion of its variability (Fig. 5). The results of PCA are in accordance with the results obtained by Gebeyehu *et al.* (2021).

Scree plot explained the percentage of variation by a graph between Eigen Values and Principal Components (Fig. 6). It is clearly depicted in the graph that the maximum variation was observed in PC1, PC2 and PC3.

Table 4: Eigen values, percentage of variance and cumulative percentage of variance of niger genotypes.

Principal Component	Eigen values (Latent roots)	Percentage of variance	Cumulative percentage of variance
PC 1	1.646	27.438	27.438
PC 2	1.041	17.366	44.804
PC 3	1.031	17.193	61.998
PC 4	0.908	15.134	77.132
PC 5	0.820	13.68	90.812
PC 6	0.551	9.187	100.00

Table 5: Contribution of first three principal components to variation in niger genotypes.

Trait	PC 1	PC 2	PC 3
DFF	0.072	-0.776	-0.297
PH	-0.453	-0.108	-0.047
Capitula	-0.62	-0.101	-0.019
Branches	-0.588	-0.037	-0.093
SYP	-0.131	0.58	-0.602
OIL	0.201	-0.43	-0.732

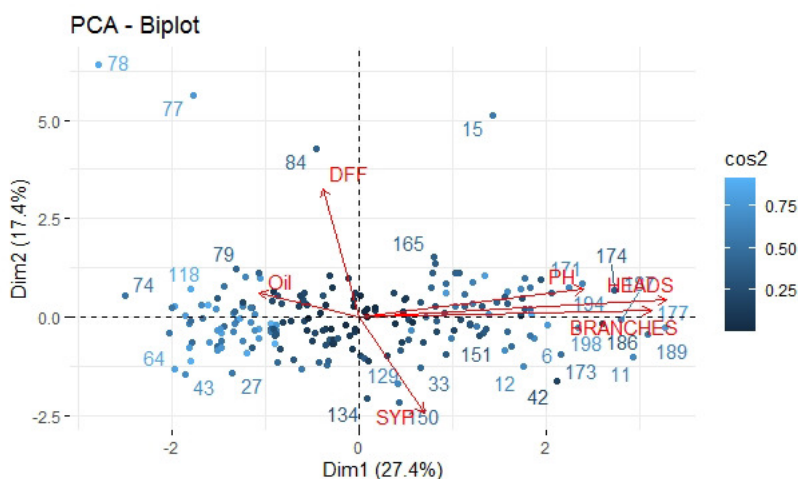


Fig. 4. PCA Biplots.

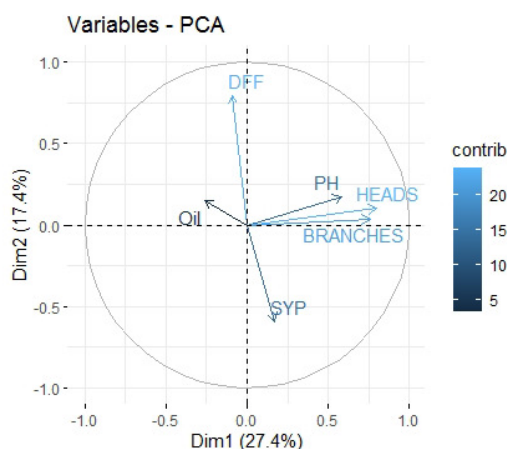


Fig. 5. PCA variables.

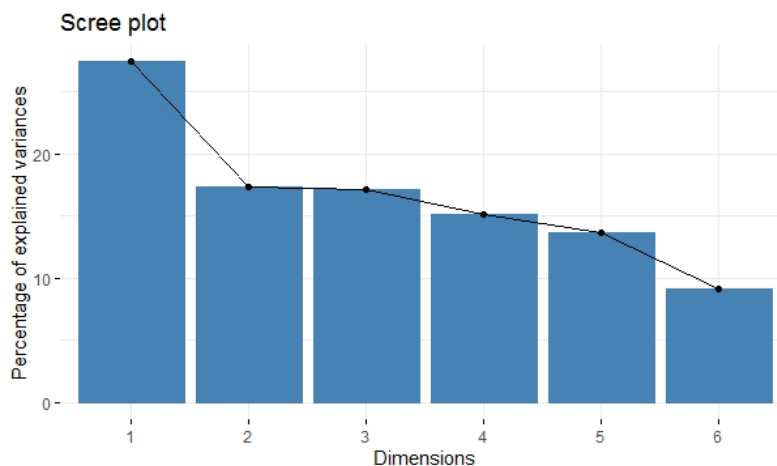


Fig. 6. Scree plot constructed using six principal components.

Cluster Analysis. The 208 Niger genotypes exhibited significant differences for 6 characters. The presence of significant differences among genotypes for all the characters justified further calculation of D^2 (Sharma, 1998). The dendrogram obtained from the cluster analysis grouped the 208 niger accessions into two clusters based on the averages clustering method (Fig. 7). The D^2 values were based on the mean of genotypes; Cluster I was the largest cluster which consisted of 144 accessions followed by Cluster II which comprised of 64 accessions. The check IGPN 2004-1 was grouped in Cluster I. The checks, JNS9,

JNS28, JNS30 and DNS4 were in Cluster II. The mean value of genotypes in each cluster was computed and cluster means are presented in Table 6. There was a considerable difference among the clusters for plant height, no. of capitula per plant and no. of branches per plant. Similar results were found by Goyal and Bisen (2017); Suryanarayana *et al.* (2018) in 28 genotypes. Parameshwarappa *et al.* (2009); Ahirwar *et al.* (2017) reported the presence of seven clusters in 52 accessions and eight clusters in 114 niger seed genotypes respectively.

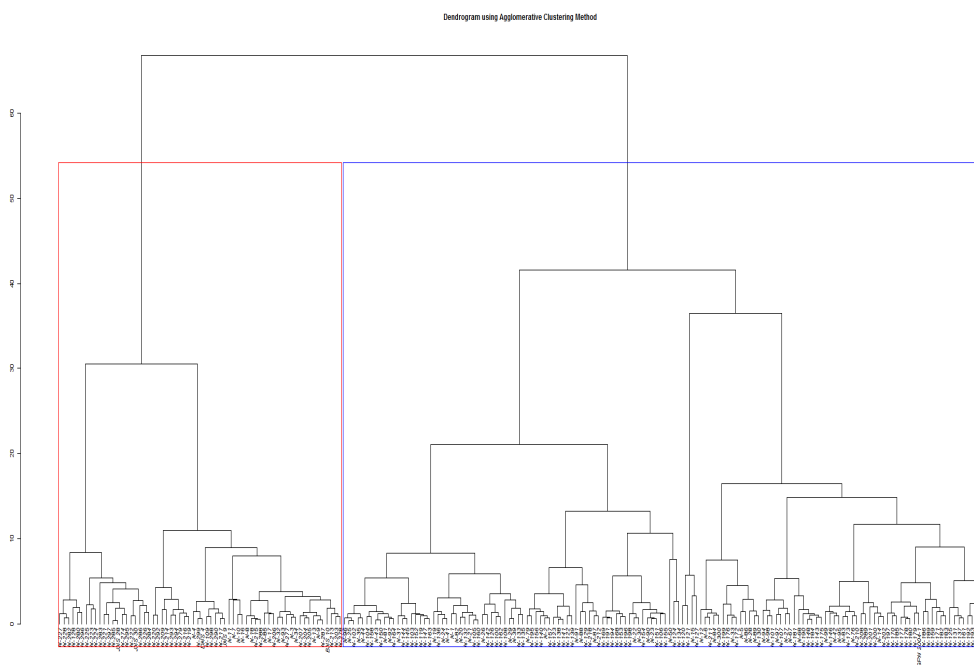


Fig. 7. Dendrogram using agglomerative clustering method.

Table 6: Cluster means.

Cluster	DFP	PH	Capitula	Branches	SYP	Oil
1	42.61	89.1	93.12	9.19	5.57	36.06
2	42.27	101.93	120.36	11.06	5.25	35.5

CONCLUSIONS

The present study on variability analysis concluded that seed yield and number of capitula have high coefficient of variation. Thus, selecting these traits would be effective for transferring characters to next generation. A high difference was observed between PCV and GCV for seed yield, indicating that the direct selection for this trait is not viable. The high heritability for the oil content indicated that direct selection is highly effective for this trait. From the multivariate analysis, it is concluded that 208 niger accessions with five checks are included in two clusters with a cumulative variation of 61.99% indicating to have large variation, revealing that these accessions could be used as trait-specific donors for niger improvement programme.

FUTURE SCOPE

The traits with high GCV and high heritability can be used in the direct selection of desirable genotypes and their further utilization in crop improvement programmes.

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Conflict of Interest. None.

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