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Genetic variability for seed yield and its component traits in germplasm lines of Niger [(*Guizotia abyssinica* (L. f.) Cass.]

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Abstract
Niger (*Guizotia abyssinica* (L. f.) Cass) is a minor seed oil crop in India. Niger seeds contain 35-40 per cent oil and seed oil is good for human consumption. To assess the variability for yield and its yield attributing traits and also to derive the population for high yield and oil content by using mass selection, the study was carried out using 54 niger germplasm lines along with three standard varieties such as KBN-1, NO.71 and LOCAL for check using augmented design. Analysis of variance showed significant differences among the germplasm lines and also germplasm lines v/s checks. A wide range of variability was recorded for all yield attributing components. The high phenotypic and genotypic coefficient of variation was recorded for traits primary branches, secondary branches, number of capsules per plant. The PCV and GCV was observed moderate for capsule diameter, number of seeds per capsule, test weight and seed yield per plant and low for plant height, days to 50 per cent flowering and oil percentage. High heritability combined with high genetic advance was observed for primary branches, secondary branches, number of capsule per plant, capsule diameter and seed yield per plant. High heritability with moderate genetic advance was observed for plant height, days to 50% flowering, number of seeds per capsule. While high heritability with low genetic advance was observed for test weight and oil content.

Keywords: Niger, variability, PCV and GCV

Introduction
Niger (*Guizotia abyssinica* (L.f.) Cass) is an important minor oil seed crop in India. In India it occupied an area of about 2.61 lakh hectare with a production of 0.84 MT and productivity of 3.21 q/ha. In Indian it is grown in 10 states with larger area in Chhattisgarh with an area of 0.63 lakh hectare and with , production of 0.11 MT followed by MP, Maharashtra and Odisa. Niger crop is a highly cross pollinated, diploid species (2n=2x=30) belonging to the family Asteracea, tribe Heliantheae, subtribe Coriopsidinae. It has high oil percentage with Fatty acid composition of niger oil includes Linoleic acid (75-80%), palmitic acid (7-8%), stearic acids (7-8%) and 5 to 8 *per cent* oleic acid (5-8%) and henceniger oil is considered as one of the best oil for human consumption (Getinet and Teklewold, 1995) [6]. Niger is tolerant to drought condition and is semi-tolerant to the problematic soils like salinity and performs well under water logged soil conditions (Abebe, 1975) [1] and also resistant to insect pests. Though Niger crop has good economic values its improvement is neglected due to higher cross pollination and high level of self-incompatibility hence identification of good germ plasm line with a high seed yield and oil content is most important developing improved varieties over existing varieties. Thus the present experiment was conducted to evaluate germ plasm lines to assess variability present for yield and yield attributing traits.

Material and Methods
Genetic variability studies on yield and its components in Niger were conducted at University of Agricultural Sciences, GKVK during *Kharif* 2017. The experimental site is located at a latitude of 13° 4′ 55.92″North, longitude of 77° 34′34.57″ East and altitude of 899 meters above mean sea level and average annual rainfall is 779.7mm. The experimental material consisted of 54 Niger germplasm lines and 3 check varieties *viz.,* KBN-1, NO.71 and LOCAL. The experimental material was sown during 2017 using augmented statistical design with of nine blocks with three standard check varieties. Ten plants were randomly selected from every

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genotypic line and label each plant and fallow with the good agronomical practice and plant protection measures.

Phenotypic data analysis
The mean value was computed for yield and its related parameters for each of the 54 lines and subjected to biometrical analysis. The analysis of variance (Federer, 1961) [5] was carried out to separate variability components from total variability as per augmented design.

Estimation of genetic parameters
To know the genetic variability among the genotypes for yield and yield related traits will be estimated as mentioned below.

Co-efficient of variability
Both phenotypic and genotypic co-efficient of variability for all the characters will be estimated using formulae given by Burton and De Vane (1953) [4]. Heritability estimates were categorized according to Robinson et al., (1949) [11] and predicted genetic advance was estimated according to the formula given by Johnson et al., (1955) [8].

Parameters of variation
Range: The distribution of range was expressed by the limit of largest and the smallest value of each observation.

Mean: This was calculated by summing up of all the observations and dividing by the number of observations.

Heritability: Heritability in broad sense defined as the proportion of the genotypic variance to the total variance (phenotypic variance) was estimated by Hanson et al., (1956) [7].

Results and Discussion
Analysis of variance
Augmented design makes use to evaluate large number of genotypes to know their performance with standard checks in random replication in all the blocks. In the present study, 54 germ plasm lines were evaluated for yield and yield related traits along with 3 standard checks. The Analysis of variance revealed significant mean sum of squares for almost all the yield related traits for different sources of variation (Table 1).These findings are similar with the result of Ammara et al., (2015) [3]. The mean value and the range for plant height was (97.76, 85.09-120.68 cm), primary branches (6.35, 3.90-10.86), secondary branches (11.94, 6.98-19.16),days to flowering (43.37, 36.0-48.0 days), number of capsule per plant (42.89, 25.12-64.20), capsule diameter (1.10, 0.72-1.38 cm), number of seeds per capsule (32.00, 24.60-40.70), test weight (2.90, 2.20-3.68 g), seed yield per plant (3.17, 2.04-4.10 g) and oil content (34.68, 30.28-38.21%) (Table2).

Genotypic and phenotypic coefficient of variation
PCV and GCV components are used to measure the genetic variability present in the population. The PCV and GCV values give an idea about the magnitude of variability present in a genetic population. The graphical representation of PCV and PCV shown in figure.1. Based on the percentage value PCV and GCV are categorized as low (less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Sivasubramanian and Madhavamenon (1973) [12]. The PCV were marginally higher than the corresponding GCV

indicating some amount of environment influence on the expression of traits. In our experiment high genotyphic coefficient of variation and phenotypic coefficient of variation were noticed for primary branches per plant, secondary branches per plant and number of capsules per plant, results are represented in table 2, similar results were reported by Kusumlata B. et al., 2018 [9] in niger crop. Whereas moderate PCV and GCV were reported for capsule diameter, number of seeds per plant, test weight and seed yield for plant. Traits like plant height, days to 50% flowering, and oil percentage were show low PCV and GCV were computed.

Heritability (Broad sense)
Heritability shows the degree of variation due changes in genetic constitution that result in changes in the phenotypic level of trait under study. Heritability is helpful in the selection of elite genotypes from different genetic constitution material. Heritability is generally expressed as low (< 50%), moderate (50-70%), and high (> 70%) as based on the percentage of heritability as suggested by Robinson (1966). High heritability for the traits indicated that characters are less influenced by the environment and it is mainly due to genetic constitution hence that the selection for such traits become useful for further improvement. Low heritability for traits it indicates these traits are highly affected by environmental effects and selection of such characters for genetic improvement will not be useful. The present experimented study most of the characters exhibit a high broad sense heritability. High heritability was recorded for the trait plant height (cm), primary branches, secondary branches, days to 50% flowering, number of capsule per plant, number of seeds per capsule, capsule diameter, seed yield per plant (g) and oil content (%). Whereas test weight (g) exhibited a low heritability, Similar results were revealed by (Tiwari et al., 2016) and (Ahmad et al., 2016) [13, 2].

Genetic advance as per cent mean
Genetic advance as per cent mean indicated the mean genotypic value over the parental population. Genetic advance along with the heritability is more important and accurate to knowing the genetic gain under selection process. Genetic advance as per cent of mean was categorized as high (>20%), moderate (10% -20%), and low (<10%) as suggested by Johnson et al.,(1973). If particular trait showed higher the genetic advance as per cent mean value it indicated that the trait is governed by a additive genes action these traits are considering for further crop improvement programme by using appropriate breeding method. While if the genetic advance value is low, it indicates that the character is governed by non-additive genes may be useful. Our experimental results the traits like primary branches per plant, secondary branches per plant, number of capsule per plant and capsule diameter and seed yield per plant (g) were show higher value of genetic advance, similar results were obtained by Ahmad et al., (2016) and Rani et al., (2010) [2, 10]. It indicated that these traits are governed by additive gene action selection of these traits for further crop improvement is most valuable than the traits which are involving in non-additive gene action. Whereas trait like plant height, days to 50 per cent flowering and number of seeds for per capsule exhibited a medium genetic advance

Table 1: Analysis of variance for yield and yield attributing traits in Niger germ plasm lines

| Sourse of Variation	DF	Characters									
		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
Blocks	8	9.23	0.36	0.57	1.28	5.40	37.90	0.01	0.09	0.14	0.04
Genotypes+Checks	56	82.83**	3.15**	12.92**	10.26**	108.47**	14.44**	0.02**	0.17**	0.43**	3.04**
Checks	2	31.60**	0.96*	3.72*	1.81	57.94	45.93**	0.01	0.56**	1.30*	4.28**
Genotypes	53	83.51**	3.28**	12.54**	10.65**	111.08**	12.35**	0.01*	0.15*	0.24*	2.64**
Checks Vs Genotypes	1	149.47**	0.23	51.79**	6.32**	71.50**	62.32**	0.27**	0.03	8.91**	21.50**
Error	16	3.00	0.15	0.73	1.81	3.41	2.16	0.03	0.01	0.12	0.42

*significance at 5% level of significance
**significance at 1% level of significance
X1- Plant height (cm), X2- Primary branches, X3 - Secondary branches, X4 - Days to 50% flowering, X5 - Number of capsule per plant, X6 - Number of seeds per capsule, X7 - Capsule diameter, X8 - Test weight (g), X9 - Seed yield per plant (g), X10 - Oil content (%)

Table 2: Estimation of genetic variability parameters for yield and yield related traits in Niger germplasm lines

Sl. No	Character	Mean	Range		Coefficient of variation (%)		h²bs (%)	GAM (%)
			Min.	Max.	PCV	GCV		
1	Plant height	97.76	85.09	120.68	9.33	9.16	96.40	18.56
2	Primary branches⁻¹	6.35	3.90	10.86	28.51	27.82	95.19	55.99
3	Secondary branches⁻¹	11.94	6.98	19.16	27.22	26.27	93.08	52.28
4	Days to 50% flowering	43.37	36.00	48.00	7.52	6.85	82.96	12.87
5	Number of capsule per plant	42.89	25.12	64.20	21.69	21.26	96.07	42.99
6	Capsule diameter (cm)	1.10	0.72	1.38	12.22	11.23	84.40	21.28
7	Number of seeds per capsule	32.00	24.60	40.70	11.20	10.22	83.24	19.24
8	Test weight (g)	2.90	2.20	3.68	13.11	12.32	22.09	5.98
9	Seed yield per plant (g)	3.17	2.04	4.10	16.50	16.34	98.09	33.38
10	Oil content (%)	34.68	30.28	38.21	4.25	4.20	98.06	8.50
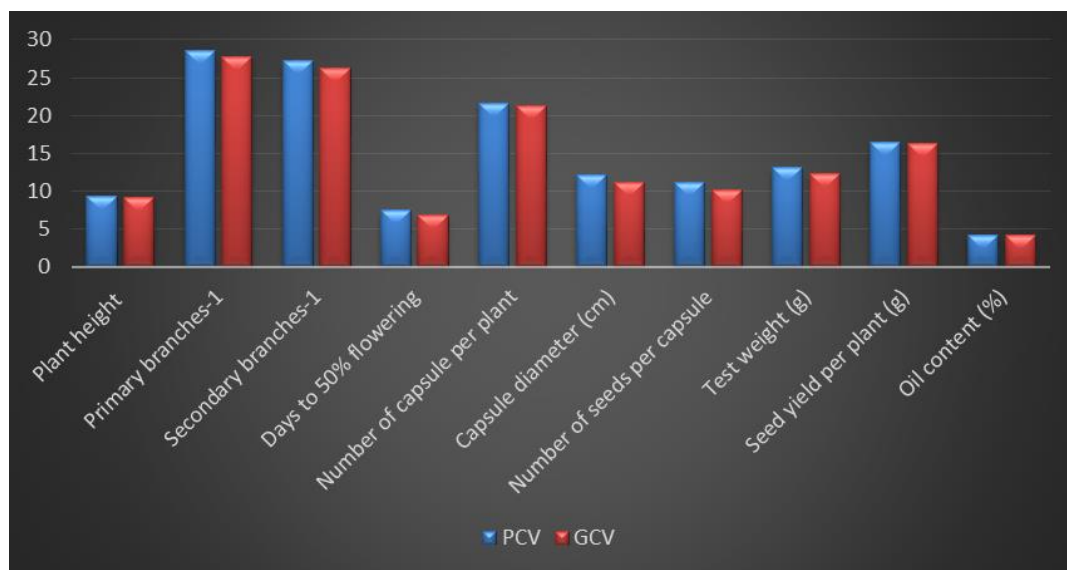
Fig 1: Graphical representation of Genotypic and phenotypic coefficient of variation parameters for yield and yield related traits in niger germplasm lines

Conclusion
Genetic variability of 54 Niger germ plasm lines exhibited sufficient variability for yield and yield related traits this variability can be utilised to develop superior population having higher seed yield and oil percentage through mass selection breeding programme.

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