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Studies on multienvironmental genetic variability in Niger (*Guizotia abyssinica* L.)

BS Thorat, SG Bhave and BD Waghmode

Abstract
The present experiment was conducted with forty niger genotypes at five locations in *Kharif*, 2018 and *Kharif*, 2019 in Randomized Block Design (RBD) with three replications for examine the genetic variability and its other parameters. The significant variation was present among the genotypes for all the traits except capitulum diameter and 1000 seed weight. The environment wise phenotypic coefficient of variation for various characters were ranged from 4.56 to 30.20 (E1), 3.98 to 20.88 (E2), 5.10 to 20.51 (E3), 3.50 to 27.91 (E4) and 5.30 to 23.66 (E5), respectively. The location wise range of genotypic coefficient of variation for various characters was 3.62 to 28.75 (E1), 3.07 to 17.14 (E2), 2.72 to 17.69 (E3), 2.63 to 25.70 (E4) and 3.32 to 20.67 (E5), respectively. The PCV greater than GCV was reported for all the traits under study indicating role of environment in the expression of these traits. The high magnitude of genotypic coefficient of variation for number of primary and secondary branches plant^{-1}, number of capitulum plant^{-1}, number of seeds plant^{-1}, seed yield plant^{-1} and seed yield plot^{-1} revealed the presence of high genetic variability. The environment wise heritability varied 26.93 to 90.58 per cent (E1), 28.78 to 77.92 per cent (E2), 28.55 to 85.97 per cent (E3), 35.88 to 84.80 per cent (E4) and 35.02 to 83.78 per cent (E5), respectively. The highest heritability was found in number of capitula^{-1}, days to 50 per cent flowering, number of seeds capitulum^{-1} and number of primary branches plant^{-1} while lowest in oil content and protein content. Most of the characters *i.e.*, days to 50 per cent flowering, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capitula plant^{-1}, number of seeds capitulum^{-1}, 1000 seed weight, seed yield plant^{-1}, seed yield plot^{-1} and days to maturity were exhibited high heritability coupled with high genetic advance indicating additive gene action in the expression of these characters while capitulum diameter, oil content and protein content under the control of non-additive gene action.

Keywords: Niger, variability, heritability, genetic advance and GAM

Introduction
The Niger (*Guizotia abyssinica* L.) belongs to the Compositae family with diploid chromosome number (2n=2x=30). The genus *Guizotia* is small with only six species, which are all native of tropical Africa (Chavan, 1961 and Arora *et al.*, 2003) [8, 4]. From the place of origin, it was 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) [9]. 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) [19, 25, 10]. It is used as a substitute for olive oil, can be adulterated with rapeseed, sesame and linseed oil. The oil from the seed is used to treat burns and in the treatment of scabies. The seed is eaten fried as a baby food (Chibto and litlit) and used as a condiment (Vles and Gottenbos, 1989) [32]. Niger oil has good keeping quality and has < 70% unsaturated fatty acids free from toxins. 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) [12]. 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) [24, 29]. 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) [26].

Worlds occupies 5.60 lakh ha area under Niger cultivation with 1.52 MMT production and its productivity was 271kg/ha (USDA, 2018-19) [31]. 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) [13]. 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) [27]. In Maharashtra, it is grown on an area of 28000 ha, with the production of 80000 MT and productivity is 286 kg/ha (Anonymous, 2018-19a) [2] which is very low compared to the national average. In Konkan region, 1530 ha area under niger cultivation with 452 MT production and its productivity is 295 kg/ha (Anonymous, 2018-19b) [3].

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.

An important step in cultivar development is studying the genetic variability found in genetic resources. The use of genetic resources to create new varieties is important for obtaining higher yields and for the technological transformations required for modernization of agribusiness. It is a dynamic process, but requires continuous enrichment and characterization of the materials maintained in germplasm collections. The genotypic and phenotypic coefficients of variation (GCV & PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the traits and the extent to which improvement is possible after selection. So, the present investigation was carried out for estimation of magnitude and extent of genetic variability, heritability and gene action in niger.

Materials and Methods

The present investigation was carried out at five locations *viz*., ARS, Phondaghat (E1), ARS, Shirgaon (E2), Dept. of Agril. Botany, Dapoli (E3), RARS, Karjat (E4) and ARS, Palghar (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 analysed as suggested by Panse and Sukhatme (1985) [21] for analysis of variance. The genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton and De Vane (1952) [7] and Johnson *et al.* (1955) [16] for heritability and genetic advance.

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 Rani *et al*. (2010) [28], Panda and Sial (2012) [20], Yadav *et al*. (2012) [33], Ahmad *et al.* (2016) [1], Benalli *et al*. (2017), Jay Laxami (2017) [15] and Kusumlata *et al*. (2018) [17].

The environment wise phenotypic variances (Table 3) for different characters were ranged from 0.01 to 529.51 (E1), 0.01 to 580.68 (E2), 0.01 to 975.19 (E3), 0.01 to 342.40 (E4) and 0.01 to 667.32 (E5), respectively. The location wise range of genotypic variances for various characters from 0.01 to 212.37, 0.01 to 254.48, 0.01 to 284.22, 0.00 to 103.93 and 0.01 to 193.51 for E1, E2, E3, E4 and E5, respectively. The location wise environmental variances were ranged from 0.00 to 317.14 (E1), 0.00 to 326.21 (E2), 0.00 to 690.97 (E3), 0.00 to 238.48 (E4) and 0.00 to 473.81 (E5), respectively for various characters. The highest genotypic, phenotypic and environmental variance (Table 3) was found in number of primary and secondary branches plant^{-1}, number of capitula plant^{-1}, number of seeds capitulum^{-1}, seed yield plant^{-1}, seed yield plot^{-1} while lowest in capitulum diameter. In general, the magnitudes of phenotypic variances were greater than genotypic variances for all the traits. This is because of the addition of environmental variance into the phenotypic variance. These findings were in conformity to those of Rani *et al*. (2010) [28], Yadav *et al.* (2012) [33], Ahmad *et al.* (2016) [1], Benalli *et al.* (2017), Kusumlata *et al.* (2018) [17] and Fekadu (2020) [14].

The environment wise phenotypic coefficient of variation (Table 4) for different traits were ranged from 4.56 to 30.20 (E1), 3.98 to 20.88 (E2), 5.10 to 20.51 (E3), 3.50 to 27.91 (E4) and 5.30 to 23.66 (E5), respectively. The location wise range of genotypic coefficient of variation for various characters was 3.62 to 28.75 (E1), 3.07 to 17.14 (E2), 2.72 to 17.69 (E3), 2.63 to 25.70 (E4) and 3.32 to 20.67 (E5), respectively. The high magnitude of genotypic coefficient of variation (Table 4) for number of primary and secondary branches plant^{-1}, number of capitulum plant^{-1}, number of seeds plant^{-1}, seed yield plant^{-1} and seed yield plot^{-1} revealed the presence of high genetic variability. In the present study, the highest GCV and PCV was found in number of primary and secondary branches plant^{-1} while lowest in days to maturity. In general, phenotypic coefficients of variation (PCV) were found to be maximum than corresponding genotypic coefficients of variation (GCV) for all the characters. This is because of the insertion of environmental coefficient of variation into the phenotypic coefficient of variation. The similative results were also reported by Panda and Sial (2012) [20], Ahmad *et al*. (2016) [1], Dudhe *et al.* (2017) [11], Kusumlata *et al.* (2018) [17], Suryanarayana *et al.* (2018a) [30] and Fekadu (2020) [14].

The environment wise heritability (Table 4) was ranged from 26.93 to 90.58 per cent (E1), 28.78 to 77.92 per cent (E2), 28.55 to 85.97 per cent (E3), 35.88 to 84.80 per cent (E4) and

35.02 to 83.78 per cent (E5), respectively. The highest heritability (Table 4) was found in number of capitula^{-1}, days to 50 per cent flowering and number of primary branches plant^{-1} while lowest in 1000 seed weight, plant height, number of seeds capitulum^{-1} and oil content. These traits were governed by additive genes and selection for improvement of these traits may useful. The tantamount findings were also reported by Rani *et al.* (2010) [28], Ahmad *et al.* (2016) [1], Dudhe *et al.* (2017) [11], Kusumlata *et al.* (2018) [17], Suryanarayana *et al.* (2018a) [30] and Fekadu (2020) [14].

The environment wise genetic advance (Table 4) was ranged from 0.12 to 22.38 per cent (E1), 0.14 to 21.75 per cent (E2), 0.15 to 18.75 per cent (E3), 0.08 to 11.57 per cent (E4) and 0.11 to 10.38 per cent (E5), respectively whereas genetic advance per cent mean was ranged from 3.87 to 56.36 per cent (E1), 3.39 to 28.99 per cent (E2), 3.00 to 32.59 per cent (E3), 4.07 to 48.75 per cent (E4) and 4.07 to 37.20 per cent (E5), respectively. The maximum genetic advance and genetic advance per cent mean (Table 4) was found in number of primary and secondary branches plant^{-1}, number of capitula^{-1}, number of seeds capitulum^{-1}, seed yield plant^{-1} and seed yield plot^{-1}. These genotypes were controlled by additive genes and selection is beneficial for such traits. These findings were in conformity to those of Rani *et al.* (2010) [28], Panda and Sial (2012) [20], Ahmad *et al.* (2016) [1], Dudhe *et al.* (2017) [11], Kusumlata *et al.* (2018) [17], Suryanarayana *et al.* (2018a) [30] and Fekadu (2020) [14].

Most of the characters *i.e.*, days to 50 per cent flowering, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capitula plant^{-1}, number of seeds capitulum^{-1}, 1000 seed weight, seed yield plant^{-1}, seed yield plot^{-1} and days to maturity were under the control of additive gene action (Table 4) in the expression of these characters. Therefore, improvement of these traits having high heritability along with and high genetic advance would be more effective if the selection in the present material could be rigorously applied. These results are in harmony with the findings of Patil and Duhoon (2005) [22], Rani *et al.* (2010) [28], Yadav *et al.* (2012) [33], Dudhe *et al.* (2017) [11] and Suryanarayana *et al.* (2018a) [30]. On the other hand, characters *viz.*, capitulum diameter, oil content and protein content showed high heritability coupled with low genetic advance, indicating substantial contribution of non-additive gene action in the expression of these traits. Therefore, improvement of these traits having high heritability along with and low genetic advance would be less effective if the selection in the present material could be rigorously applied. The similative quests were also reported by Mathur and Gupta (1993) [18], Pradhan *et al.* (1995) [23] and Borole and Patil (1997) [6].

Table 1: List of genotypes/varieties and their sources

Sr. No.	Genotype code	Name of Genotypes	Source	Sr. No.	Genotype code	Name of Genotypes	Sourse
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 2: Table Contd…

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 components of variation of pooled data 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)			RARS, Karjat (E4)			ARS, Palghar (E5)		
		$б^2p$	$б^2g$	$б^2e$	$б^2p$	$б^2g$	$б^2e$	$б^2p$	$б^2g$	$б^2e$	$б^2p$	$б^2g$	$б^2e$	$б^2p$	$б^2g$	$б^2e$
1.	DFPF	8.10	6.28	1.82	10.02	7.81	2.21	13.91	11.96	1.95	12.51	10.48	2.03	13.86	11.72	2.13
2.	PH (cm)	113.41	79.20	34.21	64.26	24.68	39.57	107.98	63.77	44.21	74.61	34.70	39.91	50.61	20.16	30.45
3.	NPBPP	5.10	4.11	0.99	4.10	2.76	1.34	3.16	2.24	0.92	4.59	3.50	1.09	4.63	3.92	0.70
4.	NSBPP	20.21	16.71	3.49	13.40	8.30	5.10	10.03	6.74	3.29	12.98	8.96	4.02	11.40	8.90	2.50
5.	NCPP	143.85	130.30	13.55	43.18	23.89	19.30	65.64	52.49	13.15	43.38	33.20	10.18	44.45	34.23	10.22
6.	CD (cm)	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.00	0.00
7.	NSPC	21.30	11.03	10.27	15.84	8.24	7.60	20.20	11.04	9.16	16.50	7.23	9.27	6.87	2.47	4.41
8.	1000 SW (g)	0.03	0.01	0.02	0.03	0.01	0.02	0.05	0.02	0.03	0.06	0.01	0.05	0.08	0.02	0.06
9.	SYPp (g)	0.13	0.05	0.08	0.11	0.06	0.06	0.15	0.06	0.09	0.10	0.03	0.07	0.06	0.02	0.04
10.	SYPP (g)	529.51	212.37	317.14	580.68	254.48	326.21	975.19	284.22	690.97	667.32	193.51	473.81	342.40	103.93	238.48
11.	DM	14.85	11.86	2.99	10.82	6.89	3.93	20.88	10.75	10.13	19.37	12.93	6.44	9.30	5.25	4.05
12.	OC (%)	6.57	1.77	4.80	4.72	1.36	3.36	4.03	1.15	2.88	4.31	1.53	2.78	4.18	2.05	2.13
13.	PC (%)	1.56	0.90	0.66	2.11	0.80	1.31	1.30	0.64	0.66	1.81	0.63	1.18	2.07	0.76	1.31

$б^2p$: Phenotypic variance, $б^2g$: Genotypic variance and $б^2e$: Environmental variance
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 4: Environment wise estimates of genetic parameters of pooled data 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)					
		PCV	GCV	H^2b	GA	GAM	Ga	PCV	GCV	H^2b	GA	GAM	Ga	PCV	GCV	H^2b	GA	GAM	Ga
1.	DFPF	5.72	5.03	77.55	4.55	9.13	A	6.43	5.67	77.92	5.08	10.32	A	7.67	7.11	85.97	6.61	13.59	A
2.	PH (cm)	8.07	6.75	69.83	15.32	11.61	A	6.42	3.98	38.41	6.34	5.08	A	7.37	5.66	59.06	12.64	8.97	A
3.	NPBPP	25.46	22.85	80.61	8.75	42.27	A	20.88	17.14	67.38	8.81	28.99	A	20.51	17.27	70.96	8.60	29.98	A
4.	NSBPP	28.18	25.63	82.71	7.66	48.02	A	18.24	14.35	61.94	4.67	23.27	A	19.61	16.08	67.19	4.38	27.14	A
5.	NCPP	30.20	28.75	90.58	22.38	56.36	A	17.54	13.05	55.31	7.49	19.99	A	19.78	17.69	79.97	13.35	32.59	A
6.	CD (cm)	9.20	8.27	80.82	0.16	15.31	NA	9.93	7.90	63.30	0.14	12.94	NA	9.75	8.00	67.39	0.15	13.54	NA
7.	NSPC	13.83	9.95	51.79	4.92	14.75	A	13.12	9.46	52.04	4.27	14.06	A	13.90	10.27	54.65	5.06	15.64	A
8.	1000 SW (g)	6.53	3.81	33.95	6.12	4.57	A	6.71	4.43	43.62	10.15	6.03	A	8.81	5.75	42.56	10.20	7.73	A
9.	SYPp (g)	13.37	8.45	39.90	10.30	10.99	A	12.02	8.41	48.93	10.34	12.12	A	11.00	6.97	40.13	10.32	9.09	A

10.	SYPP (g)	10.11	6.40	40.11	19.01	8.35	A	10.54	6.98	43.82	21.75	9.51	A	13.41	7.24	49.14	18.75	8.05	A
11.	DM	4.56	4.08	79.85	6.34	7.50	A	3.98	3.18	63.70	4.32	5.22	A	5.67	4.07	51.50	4.85	6.02	A
12.	OC (%)	6.98	3.62	26.93	1.42	3.87	NA	5.72	3.07	28.78	1.29	3.39	NA	5.10	2.72	28.55	1.18	3.00	NA
13.	PC (%)	6.74	5.13	57.88	1.49	8.04	NA	7.55	4.65	37.96	1.14	5.90	NA	5.70	3.99	49.15	1.16	5.77	NA

PCV: Phenotypic Coefficient of Variation
GCV: Genotypic Coefficient of Variation
H2b: Heritability (Broad Sense)
GA: Genetic Advance
GAM: Genetic Advance Per cent Mean
Ga: Gene Action
NA: Non-Additive
A: Additive
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 S
W: Seed weight
SYPp: Seed yield plant-1
SYPP: Seed yield plot-1
DM: Days to maturity
OC: Oil content
PC: Protein content

Table 4: Table Contd…

Sr. No.	Characters	RARS, Karjat (E4)						ARS, Palghar (E5)					
		PCV	GCV	H^2b	GA	GAM	Ga	PCV	GCV	H^2b	GA	GAM	Ga
1.	DFPF	7.21	6.63	84.60	6.49	12.56	A	7.32	6.70	83.78	6.10	12.64	A
2.	PH (cm)	5.18	3.27	39.83	5.84	4.25	A	6.27	4.28	46.51	8.28	6.01	A
3.	NPBPP	27.91	25.70	84.80	8.76	48.75	A	23.66	20.67	76.31	8.37	37.20	A
4.	NSBPP	23.54	20.80	78.06	5.43	37.85	A	21.51	17.87	69.02	5.12	30.58	A
5.	NCPP	18.20	15.97	77.00	10.58	28.87	A	18.35	16.05	76.53	10.38	28.93	A
6.	CD (cm)	9.00	5.90	42.91	0.08	7.96	NA	10.05	7.99	63.30	0.13	13.10	NA
7.	NSPC	12.52	7.50	35.88	5.94	9.25	A	16.32	10.81	43.82	3.67	14.74	A
8.	1000 SW (g)	11.59	5.98	36.64	10.15	6.36	A	10.01	4.59	38.07	10.11	4.34	A
9.	SYPp (g)	10.32	6.53	40.08	10.20	8.52	A	12.48	6.68	38.63	10.19	7.36	A
10.	SYPP (g)	9.42	5.19	38.35	11.57	5.89	A	11.89	6.40	39.00	15.43	7.10	A
11.	DM	3.50	2.63	56.46	3.55	4.07	A	5.30	4.33	66.75	6.05	7.29	A
12.	OC (%)	5.54	3.88	49.09	2.07	5.60	NA	5.57	3.32	35.47	1.52	4.07	NA
13.	PC (%)	7.50	4.54	36.74	1.09	5.67	NA	7.09	4.20	35.02	0.97	5.11	NA

PCV: Phenotypic Coefficient of Variation
GCV: Genotypic Coefficient of Variation
H2b: Heritability (Broad Sense)
GA: Genetic Advance
GAM: Genetic Advance per cent Mean
Ga: Gene Action
NA: Non-Additive
A: Additive
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 yield is controlled by both GCV and PCV also to use appropriate selection procedure for improvement of the characters in general and yield in particular since high heritability with high genetic advance was indicated the influence of additive gene action. The heritability provides the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful for selection than the heritability alone. This study helps in the selection of genetically superior parents for their exploitation in hybridization programmes. Therefore, improvement in these traits would be more efficiently done by selection method in the present materials. Depending upon the variability, heritability and genetic advance estimates, it could be predicted that improvement by selection was possible in niger for traits like days to 50 per cent flowering, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capitula plant^{-1}, total number of seeds capitulum^{-1}, 1000 seed weight, seed yield plant^{-1}, seed yield plot^{-1} and days to maturity.

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