Genetic variability and character association studies among the yield and yield attributing traits in niger (*Guizotia abyssinica* (L. f.) Cass.)

Abstract

Niger is a minor oil seed crop mostly cultivated in high altitude and tribal zones of India with relatively lower productivity. Development of varieties with higher yielding ability needs keen observations and scientific studies on the genetic variability and character association studies among the available germplasm or in the breeding material. Analysis of heritability$_{(bs)}$ and genetic advance as percent of mean revealed that four characters *viz*., plant height, number of branches plant^{-1}, number of capitula plant^{-1} and seed yield plant^{-1} are governed by additive gene action, which can be improved further by simple selection methods. Majority of the characters under study are having a significant positive association with seed yield ha^{-1} which helps in indirect selection for higher yield by using these character combinations.

Keywords : Niger, Genetic Variability, Character Association, Additive Gene Action.

Introduction

Niger (*Guizotia abyssinica* (L. f.) Cass.) is an important minor oil seed crop that is majorly cultivated for its edible oil seeds in cooler tropical parts of Ethiopia and in sub-tropical regions of India (Bhoite *et al*., 2021), mostly in high altitude and tribal regions. It is highly cross pollinated crop due to the presence of sporophytic self-incompatibilityand pollinated majorly by insects like honey bees (Kumar *et al*., 2006). It belongs to the family of Asteraceae with a diploid chromosome complement of 2n = 2x = 30. Although it is considered as a minor oilseed crop, is important in terms of its 32 to 40% content ofquality oil with 18 – 24 % protein in the seed with good keeping quality (Thorat *et al*., 2022) and contain about 40% edible oil with fatty acid composition of 75-80% linoleic acid, 7-8% palmitic and stearic acids and 5-8% oleic acid and it is free from any toxins (Suryanarayana *et al*., 2018). The oil is considered good for health. Niger oil is slow drying, used in food, paint, soap and as anilluminant. It is used as a substitute for olive oil, can be adultrated with rapeseed, sesame and linseed oil. It is used as green manure in the pre-flowering stage.Niger oil is pale yellow, with a nutty taste and a pleasant odour. It is mostly used for cooking, as well as in paints and for the extraction of perfume from flowers. It is an important crop in high altitude and tribal zones which is mostly suitable for agro-eco tourism during flowering stage.

Even though India ranks first in area, production and export of niger, is contributes about only 3% of Indian oilseed production (Getinet and Sharma, 1996). This is mainly due to lack of improved or high yielding varieties and mostly it is cultivated under input starved conditions without proper management practices. Development of high yielding varieties is one of the utmost important breeding objectives to increase its productivity, thereby increase in production and export. Hence it is important to know the extent of genetic variability present in the available germplasm or in the breeding material for their further utilization in varietal development. Understanding the extent of genetic variability along with the character association studies will help us in guiding the selection of superior varieties or lines with higher yielding ability. Hence, the present investigation was carried out with a main objective to estimate the extent of genetic variability and to ascertain the information on character association with respect to yield and yield component traits in niger.

Materials and Methods

Thirty five genotypes of niger were collected from different niger stations and sown in *rabi*, 2022 in a randomized block design in Regional Agricultural Research Station, High Altitude and Tribal Zone, Chintapalle, ANGRAU. Each genotype was sown in two rows of 3 m length with a spacing of 30 x 10 cm in between rows and plants respectively. All necessary cultural practices along with proper plant protection measures were taken to control insect pests and diseases.Observations were recorded for thirty five advanced breeding lines separately on randomly chosen five competitive plants in each line in each replication for plant height, number of branches plant^{-1}, number of capitula plant^{-1}, test weight and seed yield plant^{-1}. Days to 50 % flowering, days to maturity and seed yield ha^{-1} were recorded on plot basis.

The significance of data was examined using the analysis of variance technique as described by Panse and Sukhatme (1961), genotypic and phenotypic coefficient of variations were calculated according to Burton (1952) and categorized as low (< 10 %), medium (11– 20 %) and high (> 20 %), broad sense heritability (h_{bs}) was calculated based on the formula given by Allard (1960) and categorized as low (< 30 %), medium (30 – 60 %) and high (> 60 %) as suggested by Johnson *et al*. (1955), genetic advance as percent of mean was estimated and classified as low (10 %), medium (10 – 20 %) and high (> 20 %) based on Johnson *et al*.(1955) and finally genotypic and phenotypic correlation coefficients were calculated based on method given by Johnson *et al*. (1955). All the statistical analysis was carried out by using INDOSTAT Version 9.2.

Results and Discussion

Analysis of variance revealed significant differences for all the characters among all the genotypes (Table 1), which is an indicative of presence of ample amount of genetic variability in the experimental material which can be exploited for further crop improvement. PCV was slightly higher than GCV estimates for all the characters indicating that the expression of all the characters under study were slightly influenced by the environment. Higher PCV and GCV estimates were recorded for plant height, number of capitula plant^{-1}, seed yield plant^{-1} and seed yield ha^{-1} (Table 2) indicating that these characters can be further improved by selecting the genotypes based on these characters alone. These results were in accordance with the scientific findings of Suryanarayana*et al*. (2018). Whereas lower PCV and GCV estimates were recorded for days to 50 % flowering, days to maturity and test weight (Table 2). Similar results were reported by Bhoite *et al*. (2021) for number of capitula plant^{-1} and days to 50 % flowering.

Heritability estimates provides information on how the characters under study were passed from the parents to their offsprings. The breeders can successfully select for desirable traits and can generate most of the genetic gain under selection with the least amount of work and resources by estimating the heritability of a particular trait (Gangireddy *et al*., 2023). Higher estimates of broad sense heritability coupled with genetic advance as percent of mean is a good indicaton for selection and advancement of lines or genotypes to improve a particular character in a crop species as such characters are governed by additive gene action which is heritable and fixable in nature. In this present investigation, plant height, number of branches plant^{-1}, number of capitula plant^{-1} and seed yield plant^{-1} were recorded with higher estimates of heritability coupled with higher genetic advance as percent of mean (Table 2) indicating that these characters can be improved further by selecting based on their performance alone.These results were in accordance with Vinod and Rajni *et al.* (2016) and Bhoite *et al*., 2021.

Character association studies will reveal the strength and direction of association between any two characters, there by helps in selecting superior genotypes or lines based on the character combinations (Killada *et al*., 2023). In this present investigation, significant and positive association was observed among seed yield plant^{-1} with all the characters except with number of branches plant^{-1}(Table 3) indicates that selection based on these character combinations will ultimately results in higher productivity per unit area. Similarly, days to 50 % flowering have significant and positive association with days to maturity, plant height and number of capitula plant^{-1}; days to maturity with plant height, number of capitula plant^{-1} (Table 3) and test weight indicates that selection of lines or genotypes based on maturity duration will results in high seed yield due to the increased number of capitula plant^{-1} and test weight. Similarly, plant height have a significant and positive association with number of capitula plant^{-1} and number of capitula plant^{-1} with test weight (Table 3). Similar results were reported by Patil *et al.* (2013). Hence, further advancement of lines or genotypes can be done based on these character combinations will definitely leads to the development of superior variety with higher yielding ability.

Conclusion

Presence of genetic variability in any crop species for any traits of interest is of prima facie important by which we can able to improve that particular character in that crop by implementing any breeding method or tools. Any character having high heritability along with high genetic advance as percent of mean indicates that it is governed by additive gene action which is heritable and fixable in nature. In this current investigation, the characters *viz*., plant height, number of branches plant^{-1}, number of capitula plant^{-1} and seed yield plant^{-1} can be improved by simple selection efforts as they are governed by additive gene action. Almost all the characters showed significant and positive association with seed yield plant^{-1} which helps in indirect selection of genotypes for improved yielding ability.

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Table 1. Analysis of Variance for yield and yield attributing traits in 35 genotypes of niger

Character	Mean Sum of Squares		
	Replications (df : 1)	Genotypes (df : 34)	Error (df : 34)
Days to 50 % flowering	4.62	20.04**	3.33
Days to maturity	7.56	98.87**	7.62
Plant height	2.76	508.77**	3.55
Number of branches/plant	0.37	1.58**	0.1
Number of capitula/plant	0.58	113.84**	0.81
Test weight	0.0003	0.24**	0.01
Seed Yield Plant^{-1}	1.39	24.76**	0.37
Seed yield ha^{-1}	142.25	21770.4**	71.73

**Significant at 1 % level

Table 2. Genetic parameters for yield and yield attributing traits in 35 genotypes of niger

S. No	Characters	Mean	Range		GCV %	PCV %	Heritability	Genetic Advance as % of mean
			Max.	Min.				
1	Days to 50 % flowering	43.49	54	39.5	6.65	7.86	71.47	11.57
2	Days to maturity	86.1	106.5	76	7.85	8.48	85.69	14.96
3	Plant height	58.18	107.62	44.83	27.32	27.51	98.61	55.88
4	Number of branches/plant	5.49	7.31	3.64	15.66	16.7	87.88	30.24
5	Number of capitula/plant	16.89	39.68	16.28	44.5	44.82	98.58	91.01
6	Test weight	3.8	4.5	3.25	8.93	9.42	89.8	17.42
7	Seed Yield Plant^{-1}	8.05	17.16	4.11	43.4	44.05	97.07	88.09
8	Seed yield ha^{-1}	429.81	830.29	275.22	24.23	24.31	99.34	49.75

Table 3. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among the yield and yield attributing traits in 35 genotypes of niger

Character		DM	PH	NBPP	NCPP	TW	SYPP	SYPH
DFF	r_p	0.697^{**}	0.669^{**}	-0.199^{NS}	0.693^{**}	0.186^{NS}	0.485^{**}	-0.002^{NS}
	rg	0.890^{**}	0.802^{**}	-0.243^{*}	0.849^{**}	0.208^{NS}	0.610^{**}	0.007^{NS}
DM	r_p		0.809^{**}	-0.056^{NS}	0.802^{**}	0.288^{*}	0.554^{**}	0.100^{NS}
	rg		0.886^{**}	-0.044^{NS}	0.875^{**}	0.316^{**}	0.621^{**}	0.117^{NS}
PH	r_p			0.046^{NS}	0.907^{**}	0.208^{NS}	0.573^{**}	0.146^{NS}
	rg			0.050^{NS}	0.919^{**}	0.226^{NS}	0.586^{**}	0.147^{NS}
NBPP	r_p				0.116^{NS}	0.053^{NS}	0.128^{NS}	0.175^{NS}
	rg				0.132^{NS}	0.039^{NS}	0.157^{NS}	0.178^{NS}
NCPP	r_p					0.271^{*}	0.721^{**}	0.252^{*}
	rg					0.303^{*}	0.733^{**}	0.255^{*}
TW	r_p						0.320^{**}	0.325^{**}
	rg						0.357^{**}	0.339^{**}
SYPP	r_p							0.600^{**}
	rg							0.609^{**}

DFF : Days to 50 % flowering **DM :** Days to Maturity **PH :** Plant Height

NBPP : Number of Branches Plant^{-1} **NCPP :** Number of Capitula Plant^{-1} **TW :** Test Weight

SYPP : Seed Yield Plant^{-1} **SYHP :** Seed Yield ha^{-1}