



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

Swati Saraswat ^a, Rajani Bisen ^{b*} and Vinod Kumar ^b

^a Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, Madhya Pradesh, India.

^b Project Coordinating Unit (Sesame & Niger), JNKVV Campus, Jabalpur, Madhya Pradesh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The experiment was conducted during Kharif 2020 and 2021 at Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, Madhya Pradesh, India. A total of 103 accessions including 03 checks were assessed and observations were recorded for ten traits viz., days to flower initiation, days to 50 % flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capitula per plant, number of seeds per capitula, 1000 seed weight (g) and seed yield per plant (g). REML analysis discovered significant differences among the 103 accessions for all the traits. It indicates a satisfactory amount of genetic variability among the accessions for yield and yield-attributing traits. Values of phenotypic coefficients of variation were higher than the value of genotypic coefficients of variation in this study. High heritability was noted for all the traits under the experiment. Genetic advance as a percentage of mean recorded high for seed yield per plant followed by number of capitula per plant, number of seeds per capitula, number of primary branches per plant, number of secondary branches per

*Corresponding author: E-mail: rajanitomar20@gmail.com;

plant, 1000-seed weight whereas, trait days to 50% flowering, days to flower initiation and days to maturity exhibited low magnitude. These results indicate the dominance of the additive gene effect, which will aid in selection in an early segregating generation.

Keywords: Niger; genetic variability; heritability; genetic advance; phenotypic; genotypic; coefficient.

ABBREVIATION

REML : Restricted Maximum Likelihood

1. INTRODUCTION

Niger; a member of Asteraceae family is an important oilseed crop having Ethiopian centre of origin [1] and is considered as a lifeline of tribal economy as it is grown mostly in tribal expanse of India. It is considered as an orphan but significant crop as it is likely to give sustainable yield under rainfed conditions [2]. Niger being a potential soil conservator, can be used as a biofertilizer and for land rehabilitation thus the crop succeeding niger is always good [3]. Flowering phenology of this crop is extremely responsive to cross pollination with honeybees being the major pollinator of niger flowers [4].

Niger seed is consumed by mixing with baked cereals, pulses and flour to make sugary cakes. The oil is used in culinary, soap, paint and as an illuminant. Also, it is utilized to cure burns and stipulate protection against cardio-vascular ailments and cancer [5], reported as a potential source of biodiesel [6] and bird-feed in North America [7].

Niger seed oil has a fatty acid profiling characteristic for seed oils of the Asteraceae family particularly sunflower and safflower having linoleic acid as the chief fatty acid [8]. "The oil content of niger is 30-50% and consists of four major fatty acids which comprises of two main unsaturated fatty acids viz., linoleic acid (18:2) and oleic acid (18:1); and two major saturated fatty acids viz., palmitic acid (16:0) and stearic acid (18:0)" [9].

"Any breeding program's success is dependent on the genetic diversity present in the breeding stock. Effective selection requires the evaluation of several factors, such as the phenotypic and genotypic coefficients of variation, heritability in broad sense and genetic advance as a percentage of the mean" [10]. Hence the present study was conducted to assess the genetic variability in niger accessions.

2. MATERIALS AND METHODS

The investigational research was laid out in un-replicated augmented block design evaluating 103 Niger accessions along with three checks (JNS-9, JNS-30 and JNS-28) procured from Project Coordinating Unit, AICRP on Sesame & Niger, JNKVV Campus, Jabalpur, Madhya Pradesh, India during two *kharif* seasons 2020 and 2021. Spacing between row to row and plant to plant was kept 45 cm and 15 cm respectively. Five randomly chosen competitive plants of each genotype were selected and tagged and observations were recorded on ten traits viz., days to flower initiation, days to fifty percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capitula per plant, number of seeds per capitula, 1000 seed weight (g) and seed yield per plant (g). These traits were used to assess genetic parameters of variability viz., mean, range, phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance as percentage of mean. The PCV and GCV were evaluated by the formulae according to Burton [11]. GCV and PCV were categorized into Low-less than 10%; moderate-10-20% and high-More than 20%. Heritability in broad sense was computed by the formulae given by Hanson [12]. The range of heritability was categorized as low (below 50%), moderate (50-70%) and high (above 70%). Genetic advance as percentage of mean was estimated according to the formulae given by Johnson [13]. GA was categorized into < 10% as low, 10- 20% as moderate and >20% as high.

3. RESULTS AND DISCUSSION

In present experiment, 103 niger accessions were evaluated to assess their genetic potential. The REML analysis revealed that significant differences are present among the niger accessions (Table 1 and Fig. 1) for all the traits under study indicating high magnitude of variability in the accessions. Mean, range, heritability, GCV, PCV and genetic advance as % of mean are presented in Table 2.

Days to flower initiation ranged from 36.00 to 46.00 with a mean value of 41.29 days. Days to 50% flowering exhibited a mean value of 43.95 days and varied from 38.00 to 50.00 days. Days to maturity showed mean value of 97.37 and varied from 87.00 to 105.00 days. Plant height was observed in a range from 36.00 cm to 117.90 cm with a mean of 90.77 cm. Number of primary branches per plant varied from 3.00 to 15.67 with a mean of 8.68. Number of secondary branches per plant ranged from 4.14 to 21.58 with an average value of 13.24. Number of capitula per plant varied from 24.75 to 104.3 with a mean value of 60.32. Number of seeds per capitula was observed within range from 16.06 to 51.18 with an average value of 32.49. 1000-seed weight ranged from 2.93 g to 5.95 g with mean value of 4.89 g and seed yield per plant ranged from 1.50 g to 15.26 g with an average value of 6.60 g.

“Coefficient of variation provides a relative measure of variance among the different traits” [14]. Results revealed that the values of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the traits in pooled over environments. High genotypic and phenotypic coefficients of variation were observed for the traits, such as seed yield per plant (44.44% and 47.06%) followed by number of capitula per plant (27.99% and 28.88%) and number of seeds per capitula (26.53% and 27.80%). These results are in conformity with the findings of Amsalu (10) for seed yield per plant, Bhoite et al. [15] for number of branches per plant, number of capitula per plant and number of seeds per capitula, Bhoite et al. [16] for number of capitula per plant and number of seeds per capitula, Baghel et al. [17] for seed yield per plant and number of capitula, Suryanarayana et al. [18] for number of capitula per plant, Kumar and Bisen [14] for seed yield per plant and number of capitula per plant, Ahmad et al. [19] for number of capitula per plant and Pradhan et al. [20] for number of seeds per capitula.

Moderate genotypic and phenotypic coefficients of variation were observed for the traits, such as number of secondary branches per plant (18.08% and 18.87%) followed by plant height (15.79% and 16.37%) and 1000-seed weight (12.81% and 13.64%). Similar findings have been reported by Bhoite et al. [15,16] for plant height, Gururaja et al. [21] for 1000-seed weight, Suryanarayana et al. [18] for plant height and

number of branches per plant and Baghel et al. [17] and Tiwari et al. [22] for plant height.

Whereas low genotypic and phenotypic coefficients of variation were observed for the traits, such as days to 50% flowering (4.99% and 5.13%), days to flower initiation (4.49% and 4.76%) and days to maturity (2.64% and 2.78%). These results agree with the findings of, Gururaja et al. [21] for days to 50% flowering, Bhoite et al. [16] for days to maturity, Baghel et al. [17], Suryanarayana et al. (18), Bhoite et al. [15] and Tiwari et al. [22] for days to 50% flowering and days to maturity.

High heritability was observed for all the traits viz., days to 50% flowering (94.74%), number of capitula per plant (93.02%), plant height (93.02%), number of secondary branches per plant (91.80%), number of seeds per capitula (91.10%), days to maturity (90.02%), seed yield per plant (89.18%), days to flower initiation (88.63%), 1000-seed weight (88.17%) and number of primary branches per plant (85.00%). These results are in accordance with Gururaja et al. [21] for the trait plant height (cm), primary branches, secondary branches, days to 50% flowering and seed yield per plant (g), Amsalu [10] for seed yield per plant, Baghel et al. [17] for trait days to maturity, days to 50% flowering, plant height (cm), capitula per plant, seed yield per plant (g), seeds per capitula and primary branches per plant, Kumar and Bisen [14] for all the traits except number of branches per plant, Tiwari et al. [22] for days to maturity, days to 50% flowering, seed yield and plant height.

Genetic advance as percentage of mean was observed highest for seed yield per plant (86.45%) followed by number of capitula per plant (55.87%), number of seeds per capitula (52.17%), number of primary branches per plant (39.28%), number of secondary branches per plant (35.68%), plant height (31.67%) and 1000-seed weight (24.78%). The outcomes aligned with the work of Bhoite et al. [15] for number of branches per plant, number of capitula per plant and number seeds per capitula, Gururaja et al. [21] for the trait primary branches per plant, secondary branches per plant and seed yield per plant, Amsalu [10] for seed yield per plant, Baghel et al. [17] for number of capitula per plant, seed yield per plant (g), seeds per capitula, primary branches per plant, plant height (cm), Kumar and Bisen [14] for seed yield/plant, number of secondary branches per plant,

Table 1. Variance components due to genotypes

Traits	Pooled over environments			
	σ^2_g	SE	σ^2_{gXe}	SE
Days to flower initiation	3.4375**	0.5154	0.7316**	0.0634
Days to 50% flowering	4.8116**	0.7274	0.2821**	0.0998
Days to maturity	6.5857**	0.9682	1.2695**	0.0922
Plant height (cm)	205.4506**	28.884	30.25**	0.135
Number of primary branches per plant	3.2197**	0.4683	1.02**	0.0236
Number of secondary branches per plant	5.7293**	0.9048	0.547*	0.2922
Number of capitula per plant	284.994**	40.048	30.11**	0.175
Number of seeds per capitula	74.3151**	10.4689	12.35**	0.1122
1000-seed weight (g)	0.3926**	0.0557	0.10**	0.0006
Seed yield per plant (g)	8.6029**	1.21457	2.05**	0.0140

*Significant at $P \leq 0.05$, ** significant at $P \leq 0.01$ **Table 2. Genetic parameters of variability for yield and its attributing traits**

Traits	Range			GCV (%)	PCV (%)	h^2 (bs) %	GA as % of mean
	G. Mean	Min	Max				
Days to flower initiation	41.29	36.00	46.00	4.49	4.76	88.83	8.72
Days to 50% flowering	43.95	38.00	50.00	4.99	5.13	94.74	10.01
Days to maturity	97.37	87.00	105.00	2.64	2.78	90.02	5.15
Plant height (cm)	90.77	36.00	117.9	15.79	16.37	93.02	31.37
Number of primary branches per plant	8.68	3.00	15.67	20.68	22.43	85.00	39.28
Number of secondary branches per plant	13.24	4.14	21.58	18.08	18.87	91.80	35.68
Number of capitula per plant	60.32	24.75	104.3	27.99	28.88	93.90	55.87
Number of seeds per capitula	32.49	16.06	51.18	26.53	27.80	91.10	52.17
1000-seed weight (g)	4.892	2.93	5.950	12.81	13.64	88.17	24.78
Seed yield per plant (g)	6.60	1.50	15.26	44.44	47.06	89.18	86.45

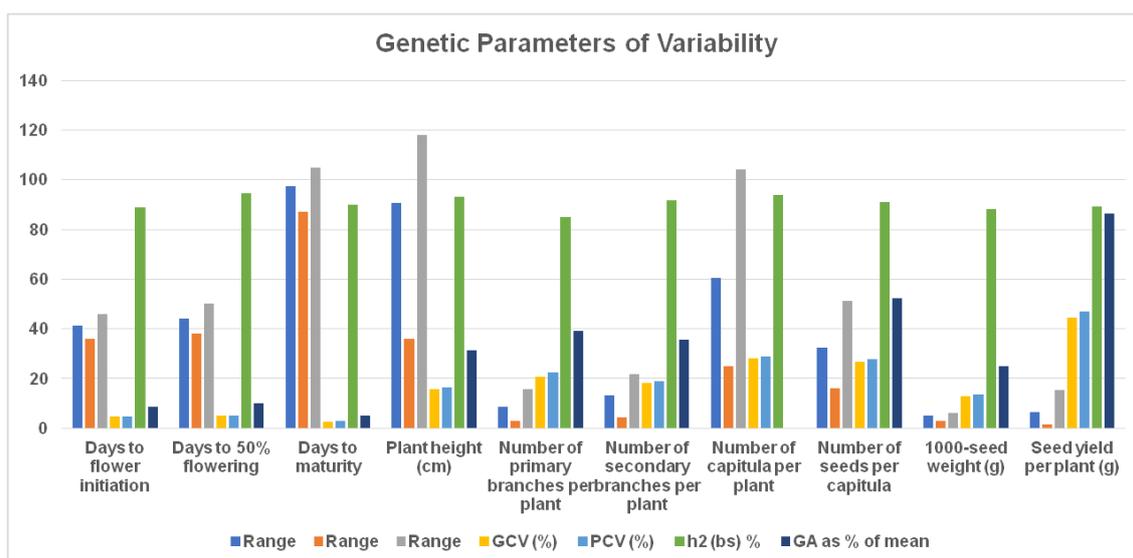


Fig. 1. Genetic parameters of variability for yield and its attributing traits

number of capitula per plant, number of primary branches per plant and plant height. While traits, days to 50% flowering (10.01%), days to flower initiation (8.72%) and days to maturity (5.15%) exhibited low magnitude of genetic advance as a percentage of mean. Similar results were recorded by Kumar and Bisen [14] for days to 50% flowering and days to maturity.

High heritability coupled with high genetic advance recorded for seed yield per plant, number of capitula per plant, number of seeds per capitula, number of secondary branches per plant, 1000-seed weight, plant height and number of primary branches per plant. The result were in accordance with the findings of Bhoite et al. [16] for number of branches per plant, number of capitula per plant and number of seeds per capitula, Suryanarayana et al. [18] for number of capitula per plant, number of seeds per capitula and seed yield per plant, Baghel et al. [17] for number of capitula per plant, seed yield per plant (g) number of seeds per capitula, primary branches per plant and plant height (cm). Kumar and Bisen [14] for seed yield per plant, number of secondary branches per plant, number of capitula per plant and plant height, Tiwari et al. [22] for plant height, Ahmad et al. [19] for number of capitula per plant, number of secondary branches per plant and number of seeds per capitula, Bisen et al. [23] for seed yield per plant, Thakur and Reddy [24] for number of capitula per plant and Rani et al. [25] for plant height. High heritability coupled with low genetic advance recorded for days to fifty percent flowering, days to flower initiation and days to maturity which

goes similar with the findings of Suryanarayana et al. [18] for days to maturity, days to flower initiation and days to 50% flowering, Tiwari et al. [22] for days to maturity and days to 50% flowering.

4. CONCLUSION

In the present investigation, 103 accessions were evaluated for genetic variability. REML analysis exhibited highly significant differences among accessions for the ten traits under study that indicated presence of extensive genetic variation in the accessions. High heritability exhibited for all the traits. Phenological traits recorded low magnitude of genetic advance as percentage of mean and rest of the traits were recorded high in magnitude. Heritability coupled with genetic advance provides a virtuous idea regarding the efficacy of selection for improving the traits. High heritability coupled with genetic advance recorded for seed yield per plant. The experimental results discovered substantial variations among the accessions. As a result, there is great chance of utilizing these genotypes in diverse breeding programmes for expanding the crop yield.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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