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Multi-environment evaluation of genetic variability for agronomic traits in Niger (*Guizotia abyssinica* Cass.)

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Abstract

The present study evaluated 83 Niger (*Guizotia abyssinica* Cass.) germplasm lines under the aegis of the Project Coordinating Unit (Sesame & Niger) at BSP (Soybean Unit), JNKVV, Jabalpur (Madhya Pradesh) across four Kharif seasons: 2022 (EI & EII) and 2023 (EIII & EIV), including a pooled analysis. The trials were conducted on uniform, medium black soil devoid of waterlogging. Analysis of variance revealed highly significant differences among genotypes for all studied traits across individual environments and in the pooled data, indicating substantial genetic variability. High estimates of genotypic and phenotypic coefficients of variation were recorded for seed yield per plant and biological yield per plant, indicating considerable genetic potential that is influenced by environmental factors. Moderate GCV and PCV were observed for the number of capitula per plant, harvest index, plant height, and number of primary and secondary branches per plant. Traits such as plant height, biological yield per plant, number of capitula per plant, test weight, and days to 50% flowering exhibited consistently high heritability across all environments and pooled data. Furthermore, seed yield per plant, biological yield per plant, number of capitula per plant, and harvest index displayed high heritability coupled with high genetic advance as a percentage of the mean (GAM), suggesting the predominance of additive gene action and their suitability for selection-based genetic improvement. These findings underscore the potential of specific traits and genotypes for targeted breeding programs aimed at enhancing Niger productivity and adaptability.

Keywords: Niger, germplasm lines, GCV, PCV, heritability, genetic advance

Introduction

Niger (*Guizotia abyssinica* (L.f.) Cass.) is an ancient and underutilized oilseed crop that is indigenous to Ethiopia, boasting a domestication history of approximately 5,000 years. While its origins lie in tropical Africa, this crop has successfully expanded to other regions, particularly India, where it plays a niche yet crucial role in the production of oilseeds. Together, Ethiopia and India account for about 50% and 3% of global Niger seed output, respectively (Getinet and Sharma, 1996) [10].

The dispersal of the Niger crop into India and East Africa is thought to have occurred through trade routes in the Persian Gulf, forming part of the ‘Savannah complex’ of crops (Dagne, 2001) [9]. Known by various local names such as ramtil, karale, uhechellu, payellu, and sorguja, Niger is intricately woven into the cultural and agricultural landscape of several Indian states.

Niger seeds are primarily prized for their edible oil, which is abundant in protein and essential fatty acids. This oil serves multiple purposes, from culinary applications to industrial uses, including the production of paints, soft soaps, and cosmetics. Notably, its capacity to absorb floral fragrances makes it particularly sought after in the perfume industry (Baagoe, 1974; Riley and Belayneh, 1989) [4, 21]. Moreover, lower-grade oil is utilized as a source of illumination.

The nutritional quality of edible oils is primarily shaped by their fatty acid composition, particularly the ratio of unsaturated to saturated fatty acids (Kostik *et al.*, 2013) [6]. Oils that are high in long-chain unsaturated fatty acids—such as oleic, linoleic, and linolenic acids—alongside low levels of saturated fatty acids like palmitic and stearic acids, are recognized as being more beneficial for human health (Bhunia *et al.*, 2015) [7].

Despite its nutritional benefits and adaptability to challenging environments, Niger remains an underutilized crop with limited genetic development, especially in India. This species encounters significant agronomic challenges, including inherently low yields due to protandrous self-incompatibility, reliance on insect pollination, and susceptibility to pests and diseases. Furthermore, it is typically grown on marginal lands with minimal agronomic management and lacks high-yielding, region-specific cultivars. As a result, many farmers continue to depend on local landraces, which are characterized by low productivity and prolonged maturity periods.

Global agriculture has traditionally focused on a limited number of major crops, often neglecting minor and regionally significant species, such as Niger. As a result, insufficient scientific attention and fragmented research efforts have created considerable gaps in our understanding of Niger's genetic potential. However, the increasing need for crop diversification and nutritional security underscores the importance of investing in the genetic improvement of underutilized species.

Plant breeding fundamentally relies on the availability of genetic variation within crop populations. The development of superior varieties relies on identifying and selecting promising genotypes that exhibit traits of agronomic significance. Key genetic parameters—such as genotypic and phenotypic variability, heritability, and genetic advance—offer crucial insights for crafting effective breeding strategies. Therefore, the systematic collection, evaluation, and conservation of diverse germplasm are vital to broadening the genetic base and ensuring the sustainable improvement of crops (Kumar and Bisen, 2016, Anand *et al.*, 2024) [17, 2].

In this context, the current study aims to assess the genetic variability and heritability of key agro-morphological traits in a diverse panel of Niger germplasm lines across various environments. This initiative represents a crucial step toward identifying superior genotypes and streamlining the breeding process for this promising yet underutilized oilseed crop.

Materials and Methods

The present investigation was carried out using 83 Niger (*Guizotia abyssinica* (L.f.) Cass.) genotypes, comprising 80 diverse germplasm accessions along with 3 standard check varieties. These genotypes were collected from the Project Coordinating Unit (Sesame and Niger), Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, Madhya Pradesh. The evaluation was conducted across four environments Kharif 2022 (EI and EII) and Kharif 2023 (EIII and EIV) at the BSP (Soybean Unit), JNKVV, Jabalpur. The experimental site is characterized by medium black soils with uniform topography and no waterlogging issues. Standard agronomic practices were adopted uniformly across all environments, following recommended packages of practices to ensure healthy crop growth and minimize experimental variability

The experiment was conducted using a Randomized Complete Block Design (RCBD) with two replications to ensure accurate estimation of genetic variability. Observations were recorded on eleven agro-morphological traits, namely 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 capitulum, test weight (g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). These traits were selected based on their relevance to yield potential and plant architecture.

To assess the extent of variability among the genotypes, key genetic parameters were estimated. The genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated following the method proposed by Burton (1953) [8], and further partitioning of variance components was done using the approach of Burton and De Vane (1953) [8]. Broad-sense heritability was estimated using the formula suggested by Hanson *et al.* (1956) [13]. The expected genetic advance (GA) and genetic advance as a percentage of the mean (GAM) were computed using the methodology described by Johnson *et al.* (1955) [14]. These parameters were used to evaluate the genetic potential of the traits and to identify those with the highest breeding value for effective selection and improvement in Niger.

Results and Discussion

The evaluation of 83 Niger (*Guizotia abyssinica* (L.f.) Cass.) germplasm lines across four Kharif environments (EI, EII, EIII, and EIV) revealed substantial genetic variability for all studied traits. In every environment and in the pooled analysis, the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV), indicating the influence of environmental factors on trait expression. This pattern suggests that although genotypic variance exists, environmental conditions modulate the observed phenotypic outcomes—a critical insight for designing robust selection strategies.

Among the traits, seed yield per plant and number of capitula per plant consistently exhibited the highest GCV and PCV values across all environments. The GCV for seed yield ranged from 14.99% to 17.67%, while the PCV ranged from 19.95% to 21.40%. Similarly, the number of capitula per plant showed a GCV range of 14.33% to 16.73% and a PCV range of 16.01% to 18.30%. These findings are in strong concordance with previous studies (Gogula *et al.*, 2024; Teja *et al.*, 2023) [11, 24], confirming that these traits possess considerable genetic diversity and thus offer high selection potential in breeding programs.

Moderate to high genetic variability was also observed for biological yield per plant (15.51-17.94% GCV) and harvest index (10.40-14.73% GCV), consistent with the results of Baghel *et al.* (2018) [5]. Slightly lower variability was recorded for number of seeds per capitulum (8.18-9.80% GCV), a contrast to earlier studies (Pulate *et al.*, 2015) [19], possibly due to differences in germplasm composition or environmental influences during evaluation. Plant height and branching traits exhibited moderate GCV values (12.22-12.80% and 11.06-13.69%, respectively), aligning with the observations of Khuntey *et al.* (2015) [15] and Bhoite *et al.* (2021) [6].

Phenological traits such as days to 50% flowering (5.88-6.64% GCV) and days to maturity (2.60-3.64% GCV) exhibited consistently low variability, suggesting strong genetic control. These findings support previous reports (Rani *et al.*, 2010; Amsalu, 2020) [20, 3]. Likewise, test weight displayed low GCV values (3.81-4.06%), as also reported by Bhoite *et al.* (2021) [6] and Tiwari *et al.* (2016) [26], indicating limited genetic variation for this seed quality trait.

Environmental effects were also evident. Environment I (EI) recorded the highest GCV for seed yield (17.22%) and number of capitula per plant (16.73%), while Environment IV (EIV) showed the most stability in phenological traits. These results underscore the necessity of multi-environment trials to capture genotype-by-environment interactions and identify broadly adapted genotypes.

Table 1: Genetic parameters of variability for yield and its component traits in Niger genotypes under EI, EII, EIII, EIV and Pooled Analysis

Characters	**Environment**	**Grand Mean**	**Range**		**Coefficient of Variation**		**h^2 (bs)**	**GAM at 5%**
			Min	**Max**	**GCV (%)**	**PCV (%)**		
dtf	E I	42.19	37.00	50.00	5.88	6.79	75.00	10.49
	E II	41.54	36.00	50.50	6.64	7.48	78.80	12.13
	EIII	42.54	37.50	51.00	6.36	7.19	78.20	11.58
	EIV	41.98	38.00	50.00	5.97	6.87	75.50	10.69
	Pooled	42.06	37.13	50.38	6.45	7.09	82.90	12.10
dm	E I	99.97	92.50	115.00	3.47	3.87	80.30	6.41
	E II	99.22	92.50	110.50	2.99	3.45	75.10	5.34
	EIII	100.37	93.50	116.50	3.64	4.02	82.30	6.81
	EIV	99.51	95.00	108.50	2.60	3.13	68.70	4.43
	Pooled	99.77	93.88	111.88	3.22	3.64	78.60	5.89
ph	E I	92.91	62.92	115.50	12.80	13.83	85.60	24.41
	E II	91.79	57.44	109.33	12.22	13.53	81.60	22.74
	EIII	92.16	60.00	113.00	12.35	13.91	78.90	22.60
	EIV	91.51	57.25	110.34	12.45	13.90	80.20	22.96
	Pooled	92.09	59.40	109.67	12.70	13.79	84.70	24.08
npb	E I	8.07	5.09	10.68	12.91	15.40	70.30	22.30
	E II	8.34	5.45	11.15	11.94	15.76	57.40	18.64
	EIII	8.11	4.84	11.27	13.69	16.40	69.70	23.55
	EIV	8.35	5.92	11.20	11.78	15.71	56.20	18.19
	Pooled	8.22	5.38	11.00	12.40	15.82	61.40	20.01
nsb	E I	13.81	8.51	17.80	11.38	15.28	55.50	17.47
	E II	13.58	7.93	18.83	11.06	16.04	47.60	15.72
	EIII	13.65	8.17	18.30	12.15	15.45	61.80	19.67
	EIV	13.81	8.82	19.57	12.54	15.82	62.80	20.47
	Pooled	13.71	8.36	18.32	12.49	15.65	63.70	20.54
ncpp	E I	57.95	32.11	78.15	16.73	18.30	83.60	31.51
	E II	55.69	33.25	73.91	14.33	16.02	80.10	26.43
	EIII	58.32	32.04	76.84	15.43	17.06	81.80	28.75
	EIV	57.95	32.01	77.81	14.42	16.01	81.20	26.76
	Pooled	57.48	32.35	76.68	15.63	16.89	85.60	29.78
nspc	E I	43.11	29.85	50.95	8.77	11.22	61.10	14.11
	E II	43.03	29.06	50.08	8.18	10.84	57.00	12.72
	EIII	44.00	27.55	52.41	9.51	12.00	62.80	15.52
	EIV	41.82	26.50	51.61	9.80	12.26	63.90	16.14
	Pooled	42.99	28.95	49.69	9.31	11.59	64.50	15.40
tw	E I	5.04	4.65	5.54	3.93	4.41	79.30	7.20
	E II	5.06	4.67	5.56	3.86	4.29	80.90	7.15
	EIII	5.02	4.63	5.52	3.82	4.31	78.80	6.99
	EIV	5.07	4.69	5.56	3.81	4.36	76.60	6.88
	Pooled	5.05	4.66	5.54	4.06	4.34	87.20	7.80
by	E I	67.15	40.20	100.17	17.94	19.53	84.40	33.95
	E II	66.38	44.47	91.69	15.51	16.87	84.50	29.36
	EIII	67.29	41.12	96.64	17.94	19.29	86.50	34.38
	EIV	66.64	42.76	92.97	16.91	18.22	86.10	32.32
	Pooled	66.87	42.14	94.48	17.02	18.52	84.50	32.22
hi	E I	19.78	13.25	28.47	14.73	16.72	77.70	26.74
	E II	19.24	13.24	25.04	10.40	14.52	51.30	15.34
	EIII	19.64	13.52	27.93	13.06	15.82	68.10	22.20
	EIV	19.49	13.41	25.31	12.88	14.93	74.50	22.91
	Pooled	19.53	13.69	25.37	12.83	15.54	68.20	21.84
sypp	E I	13.18	7.59	17.23	17.22	21.40	64.80	28.55
	E II	12.72	7.77	16.88	14.99	19.95	56.40	23.19
	EIII	13.10	7.90	17.83	15.40	20.88	54.40	23.40
	EIV	12.92	7.58	17.26	16.27	20.68	61.90	26.37
	Pooled	12.98	7.71	17.05	17.67	20.75	72.60	31.01

Classes of Heritability (%): High >70.0%, Medium 50.0-70.0%, Low <50.0%
Classes of GAM at 5%: High >20.0%, Medium 10.0-20.0%, Low <10.0% Where,
dtf-days to 50% flowering, dm-days to maturity, ph-plant height (cm), npb-number of primary branches per plant, nsb-number of secondary branches per plant, ncpp-number of capitula per plant, nspc-number of seeds per capitula, tw-test weight (g), by-biological yield per plant (g), hi-harvest index (%),sypp-seed yield per plant (g)

The pooled analysis yielded robust genetic parameter estimates. Notably, seed yield maintained high genetic variability (17.67% GCV), suggesting consistent genetic potential across environments. Despite environmental influences, the trait remains a promising target for selection, emphasizing its central role in breeding programs aimed at enhancing yield stability and adaptability.

Biological yield per plant exhibited consistently high heritability across environments (84.4% to 86.5%) and a substantial GAM (29.36% to 34.38%), highlighting strong additive genetic control. These findings are consistent with earlier work by Bhoite *et al.* (2021) [6], and Saraswat *et al.* (2022) [22], reaffirming biological yield as a pivotal trait for indirect selection to improve seed yield.

Similarly, the number of capitula per plant recorded high heritability (80.1% to 85.6%) with GAM values ranging from 26.98% to 31.45%. This confirms previous conclusions (Thakur and Reddy, 2012; Kumar and Bisen, 2016; Gogula *et al.*, 2024) [25, 17, 11], about its utility in early-generation selection due to its genetic stability and importance in yield architecture.

Plant height also showed high heritability (78.9% to 85.6%) and GAM (21.12% to 26.75%), reinforcing its reliability as a selection criterion across environments, supported by earlier studies (Rani *et al.*, 2010; Khuntey *et al.*, 2015; Baghel *et al.*, 2018) [20, 15, 5].

Interestingly, seed yield per plant demonstrated moderate heritability (54.4% to 72.6%) but consistently high GAM (28.17% to 32.66%), suggesting a combination of additive gene action and environmental influence. This pattern aligns with Tiwari *et al.* (2016) [26], who also reported high genetic advance in traits with moderate heritability, making seed yield a responsive trait for multi-trait selection strategies.

Test weight presented high heritability (76.6% to 87.2%) but low GAM (6.25% to 8.34%), indicating that while it is genetically controlled, its low variability limits short-term breeding gains. Expanding the genetic base could be essential for future improvement, as suggested by Suryanarayana *et al.* (2018) [23] and Gururaja *et al.* (2021) [12].

Phenological traits such as days to 50% flowering and days to maturity showed high heritability but low genetic advance. This result aligned with Panda and Sial, 2012) [18]. Although these traits are not ideal for rapid selection, their stability makes them valuable for categorizing genotypes into maturity classes and agro-ecological zones.

Notably, Environment III consistently recorded higher heritability estimates across most traits, indicating reduced environmental noise and better genetic expression. This observation aligns with Ahmad *et al.* (2016) [1] and Saraswat *et al.* (2022) [22], who emphasized the role of optimal environments in enhancing the reliability of genetic parameter estimation. Therefore, multi-environment evaluation, as conducted in this study, is critical to identifying stable, high-performing genotypes and refining breeding strategies for Niger improvement.

Conclusion

The present investigation demonstrated substantial genetic variability among Niger germplasm lines for key agronomic traits across multiple environments. Traits such as seed yield per plant, biological yield per plant, number of capitula per plant, and harvest index consistently exhibited high to moderate genotypic and phenotypic coefficients of variation, along with high heritability and high genetic advance as a percentage of the mean in both individual environments and pooled analysis. These results indicate that the expression of these traits is primarily governed by additive gene action, suggesting their strong potential for improvement through direct selection. The findings provide valuable insights for strategic breeding interventions aimed at developing high-yielding and widely adapted Niger varieties, thereby contributing to the crop's genetic enhancement and sustainable cultivation.

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