



Research Article

GENETIC STUDY FOR YIELD AND YIELD ATTRIBUTING TRAITS IN NIGER GERMPLASM

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Abstract- The present investigation was carried out at Project Coordinating Unit (Sesame and Niger) Research Farm, JNKVV, Jabalpur (M.P.) during 2015-16 to determine the extent of genetic variation, association and their interrelationship of yield with yield attributing traits among 71 niger accessions. Results revealed that high magnitude of phenotypic and genotypic coefficient of variation was observed for seed yield per plant followed by Free fatty acid content (%), number of secondary branches per plant, number of primary branches per plant, number of capitula per plant, plant height and seed length while, all other characters showed low PCV and GCV. High heritability was recorded for almost all the characters except number of primary branches/plant which showed moderate heritability. High genetic advance was exhibited by seed yield/plant followed by free fatty acid content (%), number of secondary branches/plant, number of capitula/plant, seed length, number of primary branches/plant and plant height. Moderate genetic advance was recorded for oil content (%). High heritability coupled with high genetic advance was exhibited by seed yield/plant followed by free fatty acid content (%), number of secondary branches/plant, number of capitula/plant, seed length and plant height indicating lesser influence of environment and presence of additive gene action, hence amenable for simple selection. Correlation revealed that positive and highly significant association of seed yield/plant was exhibited by seed length, number of capitula/plant, 1000 seed weight, number of secondary branches/plant and days to 50% flowering. Path analysis showed the highest positive direct effect on seed yield/plant was exerted by seed length followed by number of capitula/plant, number of secondary branches/plant, 1000 seed weight and days to 50% flowering suggesting that these traits are good yield enhancing indices

Keywords- Genetic improvement, Variability, Correlation, Path analysis and Niger.

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Introduction

Niger (*Guizotia abyssinica* (L.f.) Cass.) belonging to family Asteraceae is a minor oilseed crop cultivated in Indian subcontinent and East African Countries [1]. Niger though a native to Tropical Africa, is wide spread and extensively cultivated in India since long [2]. India ranks first in area, production and export of niger in the world with an earning of more than Rs. 100 crores as foreign exchange [3] but it has very low productivity 372 kg/ha [4]. Niger is an annual dicotyledonous herb commonly grown for its seed and oil. It contributes about 50% of Ethiopian and 3% of Indian oilseed production. Niger oil is slow drying, used in foods, paints, soaps and as an illuminant, and the press cake from oil extraction is used for livestock feed. Niger seeds contain about 40% edible oil and fatty acid composed of 75-80% linoleic acid, 7-8% palmitic and stearic acids, and 5-8% oleic acid [5]. The Indian types niger contain 25% oleic and 55% linoleic acids [6]. However, keeping quality of niger is poor due to high content of unsaturated fatty acids. Moreover, consuming niger seed oil is beneficial from public health point of view because it contains very low amount of tocopherols, phospholipids and sterols which give protection against cardiovascular disorders and cancer [7]. In recent years, it has gained much economic importance in context of inadequate oilseed production and due to its high export potential on account of being free from pesticide residues [8]. Niger is a self-incompatible cross pollinated crop. An assessment of variability is, therefore, required to judge its potential as base material for genetic improvement. Genetic variability in a population is important for biodiversity because without variability, a population may fail to adapt to environmental changes and therefore, makes it more prone to extinction. The

study of genetic variability including the important yield and yield attributing traits in niger is of utmost importance to judge its potential as base material for genetic improvement. Further direct selection for complex traits like seed yield is not effective. Knowledge of association of the simply inherited traits, which are less influenced by environment, is required to have sound selection criteria. This study was, therefore, carried out to determine the extent of genetic variation, association and their interrelationship of yield attributing traits to yield among 71 niger accessions with the specific objective to use suitable genetic parameters.

Materials and Methods

The present experiment was conducted under Project Coordinating Unit (Sesame and Niger) Research Farm, JNKVV, Jabalpur (M.P.) during 2015-16. The soil of the experimental area is medium black with uniform topography and free from water logged conditions. Jabalpur has sub tropical and semi arid climate. The main features are hot and dry summer and cold winter with occasional showers. The experimental material consisted of 71 niger germplasm laid out in a Randomized Block Design replicated thrice. The distance between rows was maintained at 0.40 m and plant to plant 0.15 m. The crop was raised under recommended package of practices along with prophylactic protection measures. The observations were recorded on days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, number of capitula/plant, 1000 seed weight, seed length, oil content (%), free fatty acid content (%) and seed yield/plant (g). The data on yield and quality traits were statistically analyzed on the basis of model described by [9] for randomized

complete block design. The phenotypic and genotype coefficients of variability were computed according to the method suggested by [10]. Heritability (broad sense) and genetic advance were estimated as per [11]. Correlation coefficients were computed as suggested by [12] and path coefficient analysis was carried out with genotypic correlations following the method of [13].

Results and Discussions

The analysis of variance revealed highly significant differences among the genotypes for all the eleven characters studied, thus indicating the existence of sufficient genetic variability among the existing collection and scope for further improvement.

Coefficient of variation provides a relative measure of variance among the different traits. The value of phenotypic coefficient of variation was found to be higher than genotypic coefficient of variation for characters viz., seed yield/plant followed by FFA content (%), number of secondary branches/plant, number of primary branches/plant, number of capitula/plant, plant height and seed length while all other characters showed low PCV and GCV [Table-1]. Similar results have been obtained by [14-17, 3] for seed yield/plant, [14] for plant height, [15] for days to maturity, [3] for oil content (%), 1000 seed weight, days to 50% flowering and days to maturity.

High heritability was recorded for almost all the characters except number of primary branches/plant, which showed moderate heritability [Table-1]. Similar results have been obtained by [18] as they observed high heritability for all the characters examined except number of primary and secondary branches/plant, [15] for days to 50% flowering and 1000-seed weight, [19] for days to 50% flowering, plant height and number of capitula/plant, [20] for days to 50% flowering and days to maturity, [17] for plant height, seed yield/plant and oil content (%), [3] for seed yield/plant, days to maturity and number of capitula/plant. Whereas, contradictory results were reported by [15] for plant height and [20] for number of primary branches/plant. The highest genetic advance as percentage of mean was recorded for seed yield/plant, free fatty acid content (%), number of secondary branches/plant, number of capitula/plant, seed length, number of primary branches/plant and plant height. Moderate genetic advance was recorded for oil content (%). Low genetic advance was recorded for 1000 seed weight, days to 50% flowering and days to maturity [Table-1]. Heritability combined with genetic advance is a more reliable index for selections of traits [21]. High heritability coupled with high genetic advance for seed yield/plant, free fatty acid content (%), number of secondary branches/plant, number of capitula/plant, seed length and plant height, while high heritability coupled with moderate genetic advance was observed for oil content (%) indicating lesser influence of environment in expression of these characters and presence of additive gene action, hence amenable for simple selection and useful in further population improvement. Similar results have been reported by [14] for plant height, [15] for number of capitula/plant and [3] for seed yield/plant and number of capitula/plant. Similarly, high heritability coupled with low genetic advance was obtained for 1000 seed weight, days to 50% flowering and days to maturity. It indicates that non-additive genes play major role in the inheritance of these characters, thus, the direct selection based on these characters will not be appropriate and reliable. These

results are in conformity with the findings of [15] for 1000 seed weight.

Table-1 Parameters of genetic variability for yield and yield related traits in niger germplasm

Characters	GCV	PCV	h^2_b	GA as % of Mean
Days to 50% flowering	3.09	3.41	0.82	5.75
Plant height	12.75	13.65	0.87	24.56
No. of primary branches/plant	15.47	19.78	0.61	24.91
No. of secondary branches/plant	17.99	19.95	0.81	33.40
No. of capitula/plant	15.48	15.77	0.96	31.31
Days to maturity	1.22	1.37	0.79	2.24
1000 seed weight	3.39	3.45	0.97	6.86
Seed length	13.17	13.40	0.97	26.68
Oil content (%)	7.91	8.09	0.96	15.92
Free Fatty Acid content (%)	28.73	28.78	0.99	59.07
Seed yield/plant	35.38	35.58	0.99	72.46

Results of correlation studies revealed that positive and highly significant association of seed yield/plant was exhibited by seed length, number of capitula/plant, 1000 seed weight, number of secondary branches/plant and days to 50% flowering [Table-2]. This suggests that while selecting for improvement in seed yield these characters should be kept in mind provided the characters also show high heritability. The present findings are in agreement with those of [22] for number of secondary branches/plant, number of capitula/plant and 1000 seed weight, [18] for number of secondary branches/plant, number of capitula/plant and 1000 seed weight, [23] for 1000 seed weight and number of secondary branches/plant, [19] for days to 50% flowering and number of capitula/plant, [20] for days to 50% flowering and 1000 seed weight, [24] for days to 50% flowering, number of capitula/plant and 1000 seed weight and [3] for 1000 seed weight and number of secondary branches/plant.

Path coefficient analysis revealed the results of direct and indirect effects of various interrelated components of a complex trait. Path analysis showed that the highest positive direct effect on seed yield was exerted by seed length followed by number of capitula/plant, number of secondary branches/plant, 1000 seed weight and days to 50% flowering. Therefore, these traits may be considered as the principal traits while selecting for seed yield and selection indices may be formed by considering all these characters for improvement of seed yield [Table-3]. Negative direct effect on seed yield/plant was recorded by number of primary branches/plant, oil content (%) and plant height. Similar results have been obtained by [22, 25] for number of capitula/plant; [19] for number of secondary branches/plant, [3] for number of capitula/plant and number of secondary branches/plant. Number of primary branches/plant exhibited significant positive indirect association via oil content (%) while negative indirect effect was observed for number of secondary branches/plant and number of capitula/plant. Number of secondary branches/plant exhibited indirect positive effect via number of capitula/plant. Number of capitula/plant recorded significant positive indirect effect via seed length and 1000 seed weight. Seed length showed significant negative indirect effect via free fatty acid content (%) [Table-3].

Table-2 Correlation analysis for yield and yield related traits in niger germplasm

Character	DFF	PH	PB	SB	CP	DM	TSW	SL	Oil %	FFA %	SY/P
DFF	1	0.0356	0.2449	0.2415	0.3978**	0.5966**	0.1566	0.3116*	-0.0925	-0.049	0.3955**
PH		1	0.4596**	0.3173*	0.3599**	0.1911	0.1154	0.1666	-0.1828	0.1126	0.0607
PB			1	0.7449**	0.4802**	0.165	0.1265	0.1738	-0.2627	0.1826	0.1987
SB				1	0.5336**	0.1838	0.2743*	0.3727**	-0.18	-0.05	0.4522**
CP					1	0.2622	0.3688**	0.5455**	-0.062	-0.1754	0.6227**
DM						1	-0.0209	0.2059	-0.1372	0.0684	0.205
TSW							1	0.6728**	0.2267	-0.3438*	0.5642**
SL								1	0.1558	-0.4241**	0.7323**
Oil %									1	-0.3835**	-0.0012
FFA %										1	-0.3874**
SY/P											1

Significant Levels 0.05 0.01
If correlation $r = 0.2732$ 0.3541

Table-3 Path coefficient analysis showing direct and indirect effects for yield and yield related traits in niger germplasm

	DFF	PH	PB	SB	CP	DM	TSW	SL	Oil %	FFA %	SY/P
DFF	0.139	-0.0012	0.0314	0.0318	0.0601	0.0787	0.0205	0.0469	-0.016	-0.0067	0.4298
PH	0.001	-0.119	-0.0421	-0.0261	-0.0392	-0.022	-0.008	-0.0157	0.0285	-0.0162	0.034
PB	-0.0538	-0.0843	-0.2385	-0.1721	-0.1206	-0.0304	-0.0094	-0.0289	0.1027	-0.0638	0.1896
SB	0.0602	0.0575	0.1896	0.2628	0.1393	0.0475	0.0623	0.0946	-0.0661	-0.0093	0.4655
CP	0.1363	0.104	0.1595	0.1672	0.3154	0.0909	0.1115	0.1703	-0.0263	-0.0541	0.6208
DM	-0.0195	-0.0064	-0.0044	-0.0062	-0.0099	-0.0345	0.0016	-0.0077	0.0056	-0.0028	0.2234
TSW	0.0207	0.0094	0.0056	0.0333	0.0496	-0.0065	0.1404	0.0944	0.0299	-0.048	0.5616
SL	0.1232	0.0481	0.0442	0.1315	0.1973	0.0813	0.2456	0.3654	0.0531	-0.1555	0.7349
Oil %	0.0184	0.0382	0.0686	0.04	0.0133	0.026	-0.0339	-0.0232	-0.1593	0.0617	-0.0127
FFA %	0.0044	-0.0123	-0.0243	0.0032	0.0156	-0.0074	0.0311	0.0387	0.0352	-0.0909	-0.3857

R² = 0.7054

Residual Effect = 0.5428

Note: Diagonal bold figure are the direct effect and the off diagonals are indirect effects.

Abbreviations: DFF: Days to 50% flowering, PH: Plant height, PB: No. of primary branches/plant, SB: No. of secondary branches/plant, CP: No. of capitula/plant, DM: Days to maturity, TSW: 1000 seed weight, SL: Seed length (cm), FFA %: Free fatty acid (%), SY/P: Seed yield/plant

Conclusion

Considerable genetic variation has been exhibited by genotypes involved in present investigation. Highest PCV and GCV were recorded for seed yield per plant followed by free fatty acid (%), number of secondary branches per plant, number of primary branches per plant, number of capitula per plant, plant height and seed length. High heritability coupled with high genetic advance was observed for seed yield per plant, free fatty acid content (%), number of secondary branches per plant, number of capitula per plant, seed length and plant height, indicating that heritability may be due to additive gene action and selection based on these characters may be effective. On the basis of correlation and path analysis, it could be concluded that seed length, number of capitula/plant, 1000 seed weight, number of secondary branches/plant and days to 50% flowering were the major yield components. Therefore, direct selection through these traits would be effective.

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Author Contributions

The research work is a M.Sc (Ag) thesis work and both the author and co-author have contributed equally to the analytical methods used for the research concept and the experiment design.

Abbreviations

DFF: Days to 50% flowering, PH: Plant height, PB: No. of primary branches/plant, SB: No. of secondary branches/plant, CP: No. of capitula/plant, DM: Days to maturity, TSW: 1000 seed weight, SL: Seed length (cm), FFA %: Free fatty acid (%), SY/P: Seed yield/plant

Conflict of Interest: None declared

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