

MORPHO-AGRONOMIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE STUDIES IN SESAME (*SESAMUM INDICUM* L.) IN NIGERIA

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Abstract

The study explored morpho-agronomic and biochemical traits to assess variability level and the degree of genetic diversity in 15 Sesame accessions. Data were subjected to analysis of variance, multivariate analyses, and genetic parameters were estimated. Significant differences ($P < 0.05$) existed among the accessions in all the characters. Four components with a cumulative variation of 85.7% were extracted. Substantial broad sense heritability estimates and high genetic gain were observed in secondary branches (97.8, 719.4%), primary branches (96.1, 142.5%), capsules per plant (97.8, 141.1%), single plant seed yield (86.87, 46.03%), capsule length (99.16, 32%), and 500 seed weight (95.15, 34.12%). It may be inferred that a considerable level of variability existed among the accessions studied and characters like branching habit, capsules per plant, capsule length and single plant seed yield could be considered for selection in breeding for superior genotypes.

Introduction

Sesame (*Sesamum indicum* L.) also known as Til is of great value because its seeds contain protein and edible oil that is rich in unsaturated fatty acids (Kumar and Yadav, 2010). It is oldest and ancient Oil seed crops known to man. Owing to the availability of antioxidants, micronutrients, and minerals, its oil is extremely stable when compared to other edible oils (Hassan *et al.* 2018). Nigeria is ranked 6th among the major sesame producers in the world between the year 2009-2019 (FAOSTAT 2021). The crop is gaining recognition in the Nigerian agricultural system as the number of production areas has increased in the last ten years, yet without a complementary increase in seed yield. According to FAOSTAT (2021), there was a gradual decrease in the yield of sesame in Nigeria from 2012 till date. Sesame low seed yield had been attributed to numerous factors, varying from susceptibility to infections, shattering nature and uneven ripening of the capsule, through water logging, poor crop stand establishment, low harvest index, to indefinite growth habit, and drought (Tripathy *et al.* 2016). In order to increase sesame yield, there is need for the development of varieties with good agronomic traits as well as biochemical attributes. The varieties must also show resistance to major pests and diseases. However, the breeding of such varieties is dependent on the available genetic variability upon which selection for good traits could be made. In Nigeria, sesame is typically not improved, and many collections are made up of landrace varieties with scanty genetic information that may be used in breeding programs. A thorough understanding of the current genetic variation is essential for the development of high-yielding cultivars. The present study was undertaken to assess the genetic variability and divergence existing in 15 accessions of sesame in Nigeria using agromorphological and biochemical characteristics

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Materials and Methods

The present study was conducted at the research field, Department of Pure and Applied Biology, LAUTECH, Ogbomoso in 2016. The area is on latitude: 8° 8' 31.7940" N, and longitude: 4° 14' 42.6696" E. Experimental materials consisted of 15 Sesame accessions. A complete Randomized Block Design was employed and seeds were sown in 50 cm diameter, 15-liter capacity planting pots filled with well-homogenized humus soil. Each accession was replicated 10 times (10 planting pots). Seedlings were thinned down to 2 plant stands per pot after two weeks of planting. Quantitative data were taken on both agronomic and biochemical characters and subjected to Analysis of Variance (ANOVA) using SPSS statistical software package (version 25) and sample means were separated using Duncan's Multiple Range Test (DRMT) at 0.05 probability level. The contribution of each character to genetic diversity was assessed using principal component analysis (PCA), and the total variance was estimated using the sum of extracted Eigenvalues. Genetic parameters [Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Broad sense Heritability (Hbs), Genetic Advance (GA), and Genetic Gain (GG)] were estimated according to Meena *et al.* (2017).

Results and Discussion

Analysis of variance revealed significant differences among the accessions for all the vegetative, yield, and biochemical characteristics studied. Mean plant height varied between 60.52 and 113.45 cm (Table 1a). NGB00942 was the accession with the highest (113.45) value for plant height while Bogoro was the shortest among the accessions. However, Bogoro had the highest number of primary branches (12.33) showing that it was a highly branched accession. Similar trend was observed in secondary branches. Days to flowering ranged between 33 and 56 days among the accessions. Maximum number of capsules per plant was produced by Bogoro, followed by Igboora and Igboho-black (Table 1b). Among the accessions, Kenan 4 produced the longest capsule (3.4cm), while Bogoro had the shortest capsule (1.5 cm). Bogoro had the highest seed yield per plant (16.07 g) and close to this were NGB00960 (15.89 g) and Igboora (15.43g). The percentage oil and protein content in the accessions ranged from 40.2 to 44.6 % and 16.6 - 17.9%, respectively. The oil content was at variance with the report of Azeez and Morakinyo (2010), who reported seed oil content ranging from 52.2 - 55.1% (cultivated sesame accessions) and 53.4 - 58.6% (wild relatives). However, this outcome is in agreement with the findings of Kadvani *et al.* (2020) where oil content ranged from 32 to 48% among 45 sesame genotypes. Zahran *et al.* (2020) also reported oil content ranging from 39.6 to 54.6% among six Egyptian sesame genotypes. While oil content as low as 25% was reported by Mohanty *et al.* (2020). Differences in oil content reported by different authors could be attributed to differences in genetic makeup as well as the differences in the geographical location. Seed oil content is a polygenic trait that is greatly influenced not only by genes but also by the environment.

There was a slight difference in the phenotypic and genotypic coefficient of variation (PCV and GCV) estimates for all the characters, indicating little influence of the environment on the expression of these characters, as the PCV was slightly greater than GCV (Table 2). This is similar to the results reported by Abate and Mekbib (2015), Kiruthika *et al.* (2018) and Mohanty *et al.* (2020). Number of secondary branches registered the highest GCV and PCV, while the lowest GCV (2.56) and PCV (2.58) values were recorded for percentage protein content. The amount of a character's genotypic coefficient of variation has a significant impact on how reliably it can be chosen for improvement in a breeding program. Higher ratio of GCV to PCV indicates the presence of significant variability and is desirable in breeding programs, a lower value of GCV often implies little variability among the tested samples (Bello *et al.* 2012) and the selection of

characters with a higher GCV: PCV ratio will be effective. The accessions showed highest genetic variability for number of secondary branches, since this character had the maximum value for the genotypic coefficient of variation. Other characters with high genetic variability include number of primary branches, number of leaf nodes per plant, number of capsules per plant, and number of

Table 1a. Mean, range and SE values of morpho-agronomic characters in sesame accessions.

Accessions	PHM (cm)	NPB	NSB	INL (cm)	DFF	DM	LFR
Bogoro	60.52 ^g	12 ^a	11 ^a	3.65 ^e	40 ^c	94 ^{de}	41.95 ^e
Exsudana	68.78 ^{fg}	2 ^c	0	6.72 ^c	330 ^g	104 ^c	41.28 ^e
E8	83.38 ^{ef}	3 ^c	0	6.77 ^c	35 ^{e-g}	96 ^{de}	58.97 ^{a-d}
Kenana 4	81.70 ^{ef}	2 ^c	0	8.97 ^b	34 ^{fg}	90 ^{fg}	47.95 ^{c-e}
Igboora	91.08 ^{de}	10 ^b	1 ^b	3.77 ^e	56 ^a	116 ^a	56.42 ^{a-d}
Igboho Black	92.83 ^{c-d}	9 ^b	0	5.08 ^d	51 ^b	111 ^b	53.67 ^{b-d}
Igboho cream	110.93 ^{ab}	4 ^c	0	8.73 ^b	36.83 ^{ab}	89 ^g	70.82 ^a
NCRI 01M	102.42 ^{a-d}	3 ^c	0	9.57 ^{ab}	37.17 ^d	97 ^{de}	60.55 ^{a-c}
NCRI 02M	111.58 ^{ab}	3 ^c	0	10.63 ^a	34.67 ^{e-g}	99 ^{de}	63.30 ^{ab}
NGB00932	106.93 ^{a-c}	4 ^c	0	10.67 ^a	35.33 ^{d-f}	86 ^g	66.82 ^{ab}
NGB00935	101.68 ^{a-d}	3 ^c	0	8.93 ^b	36.17 ^{d-f}	98 ^{de}	62.65 ^{ab}
NGB00942	113.45 ^a	3 ^c	0	9.95 ^{ab}	34.83 ^{e-g}	100 ^{cd}	65.22 ^{ab}
NGB00959	97.17 ^{b-e}	3 ^c	0	10.48 ^a	36.50 ^{de}	89 ^g	60.67 ^{a-c}
NGB00960	100.63 ^{a-d}	4 ^c	0	10.32 ^a	34.83 ^{e-g}	94 ^{ef}	56.95 ^{a-d}
NGB00963	83.12 ^{ef}	3 ^c	0	8.87 ^b	34.83 ^{e-g}	96 ^{de}	45.23 ^{de}
Maximum	142.50	16	17	12.70	60.00	125.00	90.00
Mean	93.75	4.89	0.78	8.21	37.97	97.12	56.83
Minimum	50.50	1.00	0.00	3.30	32.00	79.00	30.00
SE	1.99	0.35	0.30	0.27	0.68	0.93	1.39
F-Value	10.425*	25.631*	44.965*	36.301*	94.655*	25.402*	4.406*

Means followed by the same superscript along the column are not statistically different at $p < 0.05$.

*Significant at 0.05 probability level.

PHM = Plant height at maturity, NPB = Number of primary branches, NSB = Number of secondary branches, LNP = leaf nodes per plant, INL = Internodal length, DFF = Days to first flowering, DM = Days to maturity, LFR = Length of fruiting region.

seeds per plant. This finding is similar to the findings of Kiruthika *et al.* (2018), whereas number of days to maturity, percentage oil content, and protein content exhibited low genetic variability. Moderate variabilities were observed in other characters. In selection process, characters with high and moderate variability might be relied upon (Teklu *et al.* 2021). Kiruthika *et al.* (2018) opined that the extent of variability is revealed by simple measures of variability such as mean and coefficient of variation, however, the heritable portion of the total variability cannot be revealed by these simple measures. Therefore, an estimate of heritability for each character is needed to ascertain the heritable portion of the total variation. All the characters studied showed very high broad sense heritability (greater than 80%), except the length of the fruiting region. Genetic advance varied from 0.13 to 125 and Genetic advance over mean (Genetic Gain) ranged from 5.22 % (percentage protein content) to 719.4 % (number of secondary branches). Oil content had the highest heritability estimate (99.76%). This observation is in agreement the findings of Mohanty

et al. (2020). High heritability for single plant seed yield in the present study run contrary to low heritability estimated for same trait by Kiruthika *et al.* (2018), and moderate heritability reported by Rani and Kumar (2013). However, heritability estimates alone might not be adequate in choosing characters based on their phenotypes because heritability is also influenced by the environment (Nahak *et al.* 2018). Therefore, the combination of heritability estimates and genetic gain is of paramount importance in making selections for improvement. The genetic gain is important because a high value denotes additive gene effect, which is the only genetic variance that responds to the selection and it also provides information about the projected gain in a character from one cycle of selection (Dutta *et al.* 2013). Percentage of oil and protein content exhibited high heritability but low genetic gain, hence these characteristics may be controlled by non-additive gene effect and simple selection may not be effective in their improvement. Other traits like the number of capsules produced per plant, seed yield produced by a single plant, height of the plant, the number of primary, and number of secondary branches showed very high heritability with high genetic gain, indicating little environmental influence and the predominance of additive gene activities in the inheritance of these traits.

Table 1b. Mean, range and SE values of yield parameters in 15 sesame accessions.

Accession	NCP	NSC	CL (cm)	CB (cm)	500SWT	SPSY(g)	NCPM	POC	PPC
Bogoro	172a	39h	1.50g	0.58ef	1.20i	16.07a	21b-d	41.40i	17.97ab
Exsudana	39de	66f	3.03bc	0.72ab	1.82cd	9.35c-e	25b	44.67a	17.17f
E8	35e	76c-e	3.07b	0.72ab	2.07ab	11.22b-d	18de	43.37f	17.57de
Kenan 4	34e	81ab	3.40a	0.60d-f	1.65d-f	9.46c-e	24bc	43.80cd	17.13f
Igbo Ora	97b	57g	2.45f	0.52g	1.42gh	15.43a	40a	40.2j	18.07a
Igboho Black	80c	68f	2.52f	0.56fg	1.150i	13.00ab	26b	40.23j	17.71cd
Igboho Cream	56d	84a	3.30a	0.77a	1.33hi	12.03bc	23b-d	42.57g	17.13f
NCRI01M	37e	75de	2.95b-d	0.62c-e	1.70c-f	9.40c-e	19c-e	41.83h	18.10a
NCRI02M	35e	78b-d	3.05b	0.60d-f	1.80c-e	9.89b-e	20 de	43.97c	16.90g
NGN00932	33e	73e	2.83de	0.60d-f	1.52f-h	7.16e	20b-d	42.63g	17.63d
NGN00935	31e	79b-d	2.95b-d	0.60d-f	1.75c-e	8.86c-e	18de	43.64de	16.57h
NGN00942	40de	80a-c	3.02b-d	0.60d-f	1.90bc	12.21bc	18de	40.17j	17.87bc
NGN00959	34e	73e	2.80e	0.67bc	1.60e-g	7.86de	15e	44.37b	17.47e
NGN00960	49de	78b-d	2.98b-d	0.65cd	2.12a	15.89a	19c-e	43.63de	17.30f
NGN00963	35e	76c-e	2.90c-e	0.60d-f	1.75c-e	9.62c-e	19c-e	43.50ef	17.17f
Max	227	88	3.50	0.80	2.70	21.87	46.00	44.81	18.22
Mean	53.73	72.07	2.85	0.63	1.65	11.66	21.00	42.66	17.45
Min	21	36	1.40	0.50	1.10	5.04	12.00	39.72	16.42
SE	4.09	1.22	0.05	0.01	0.03	0.38	0.72	0.16	0.05
F-Value	43.125*	54.738*	106.788*	14.441*	20.383*	7.624*	12.607*	425.956*	65.169*

Means followed by the same alphabet along the column are not statistically different at p 0.05

*Significant 0.05 probability level.

NCP=Number of capsules per plant, NSC=Number of seeds per capsule, CL=Capsule length.

CB=Capsule breadth, 500SW= Five hundred seed weight, SPSY= Single plant seed yield NCPM=Number of capsules per main stem, POC= Percentage oil content, PPC=Percentage protein content.

Table 2. Estimate of genetic variability, heritability, genetic advance and genetic gain in sesame.

Characters	Coefficient of variation		Hb (%)	GA	GG (%)
	GCV (%)	PCV (%)			
Plant height at maturity	15.97	16.80	90.40	29.33	31.28
Number of primary branches	70.56	71.98	96.10	6.24	142.50
Number of secondary branches	353.18	357.18	97.78	5.61	719.42
Inter-nodal length	29.21	29.62	97.24	4.87	59.34
Days to flowering	16.87	16.96	98.94	13.13	34.57
Days to fifty percent maturity	8.30	8.47	96.06	16.27	16.75
Length of fruiting region	14.09	16.02	77.31	14.50	25.52
Number of capsules per main stem	26.20	27.31	92.07	11.19	51.79
Number of capsules per plant	69.31	70.12	97.68	75.82	141.11
Capsule length	15.60	15.67	99.16	0.91	32.00
Capsule breadth	10.25	10.65	92.59	0.13	20.31
Number of seeds per capsule	15.66	15.81	98.17	23.04	31.96
500 seed weight	16.98	17.41	95.15	0.56	34.12
Single plant seed yield	3.97	25.72	86.87	5.14	46.03
Percentage Oil content	3.62	3.63	99.76	3.18	7.45
Percentage Protein content	2.56	2.58	98.43	0.91	5.22

GCV= Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation.

Hb= Heritability (Broad sense), GA= Genetic Advance, GG= Genetic gain.

Table 3. Eigen vectors and percentages variation by the first four components.

Characters	PC-1	PC-2	PC-3	PC-4
Number of Primary Branches	0.981	0.026	-0.131	-0.006
Number of Secondary Branches	0.708	-0.533	-0.436	-0.012
Inter nodal length	-0.877	0.155	-0.340	0.131
Leaf nodes per plant	0.968	0.082	-0.152	-0.055
Length of fruiting region	-0.385	0.702	-0.444	-0.029
Days to flowering	0.776	0.499	0.280	0.004
Days to fruit maturity	0.545	0.357	0.607	0.170
Number of capsules per main stem	0.609	0.381	0.518	-0.299
Number of capsules per plant	0.938	-0.206	-0.236	-0.104
Plant height at maturity	-0.470	0.783	-0.369	0.108
Capsule length	-0.866	0.279	0.237	-0.168
Capsule breadth	-0.504	-0.255	-0.076	-0.578
Number of seeds per capsule	-0.871	0.379	0.026	-0.007
Number of seeds per plant	0.922	0.092	-0.169	-0.194
500 seed weight	-0.660	-0.144	0.257	0.242
Single plant seed yield	0.737	0.101	-0.023	-0.081
Percentage Protein content	0.612	0.153	-0.074	0.331
Percentage Oil content	-0.691	-0.503	0.125	-0.347
Eigenvalue	12.106	4.758	2.346	1.363
Proportion (%)	50.444	19.823	9.773	5.678
Cumulative (%)	50.443	70.266	80.039	85.717

Four components with Eigen values greater than 1 accounted for 85.72% of the total variation present among the accessions (Table 3). This report is in agreement with the findings of Shim *et al.* (2016) but contrary to the report of Tesfaye *et al.* (2021) who retrieved 5 PCs which comprised 75.4% of the overall variation in 30 sesame genotypes. Many of the characters in the present study took their origin from the first two components. The proportion of total variance accounted for by the first PC and the characters that gave high positive loadings in the component revealed that branching habit, earliness, capsule yield, and seed yield are characters of great importance to be considered for selection in the improvement of these sesame accessions in breeding program.

The findings of this investigation showed that the sesame accessions studied are genetically diverse with respect to all the characters studied. Characters like branching habit (primary and secondary), capsules per plant, seed yield, and capsule length, are under the control of additive genes. These characters could be considered for selection in breeding for superior genotypes.

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