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Research Article

Diversity Assessment of Some Sesame (*Sesamum indicum* L.) Genotypes Cultivated in Northern Ghana Using Morphological and Simple Sequence Repeat (SSR) Markers

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In Ghana, sesame is cultivated in some districts of northern Ghana. Genotypes cultivated are land races that are low yielding leading to decline in production. There is the need for improvement of these land races to generate high yielding cultivars. Characterization of genetic diversity of the sesame land races will be of great value in assisting in parental lines selection for sesame breeding programmes in Ghana. Twenty-five sesame land races were collected from five districts in northern Ghana noted for sesame cultivation. Seeds collected were planted in three replicates in randomized complete block design and were evaluated for a number of morphological characters. Data collected were subjected to Principal Component Analysis (PCA) and a dendrogram showing similarity between the accessions were drawn. Data on number of capsules per plant, number of seeds per capsule, and plant height at flowering were subjected to analysis of variance using GenStat Discovery Edition 4. Molecular genetic diversity was assessed by using thirty eight SSR markers widely distributed across sesame genome to characterize the materials. Twenty-one out of the 38 primers were polymorphic. Cluster analyses using the Euclidean similarity test and a complete link clustering method were used to make a dendrogram out of the morphological data. Analysis of variance showed that capsule number was significantly different; a range of 54.9 and 146.7 was produced. The number of seeds per capsule varied significantly and the variation between highest and lowest accession in seed production was 33%. Plant height was also significantly different ranging from 60.6 to 94.1 cm. Using morphological traits the accessions clustered into two major groups and two minor groups and variation among accessions were 10-61%. On the other hand, SSR marker-based dendrogram revealed five major and two minor groups. It showed that variation among the accessions was low, 10-20%. Heterozygosity was 0.52, total alleles produced were 410, and average allele per locus was 19.52. Six accessions, C3, C4, S5, W1, W3, and W5 fell in five different clusters in the SSR dendrogram and in six clusters in the morphomolecular based dendrogram. These accessions were noted for high capsule number per plant and seeds number per capsule and are recommended for consideration as potential parental lines for breeding programme for high yield.

1. Introduction

The plant *Sesamum indicum* is an important edible oil seed crop. It is commonly referred to as 'the queen of the oil seeds' by virtue of the excellent quality of oil it produces. Sesame seeds are considered to have the highest oil contents among major oilseed crops including peanut and soybean and rapeseed with 50 to 60% oil [1]. Sesame seed oil has diverse health benefits including reducing cholesterol levels and lowering blood pressure [2, 3]. Antimicrobial compounds have been reported to be present in sesame plant and seed [4, 5]. It is also rich in proteins, vitamins, and antioxidants such as sesamin and sesamolin [1]. The seeds are most commonly used in soups while the young leaves are used as a soup vegetable. Various parts of the plants are also used in native medicines. The stems are usually burned as fuel where firewood is scarce and the ash is commonly used for local soap production. The pressed cake remaining after

Table 1: Details of sesame accessions used for the studies.

Sample ID	District	Sample ID	District
C1	Chereponi	S4	Saboba
C2	Chereponi	S5	Saboba
C3	Chereponi	T1	Tatale
C4	Chereponi	T2	Tatale
C5	Chereponi	T3	Tatale
K1	Kassena Nankana	T4	Tatale
K2	Kassena Nankana	T5	Tatale
K3	Kassena Nankana	W1	West Mamprusi
K4	Kassena Nankana	W2	West Mamprusi
K5	Kassena Nankana	W3	West Mamprusi
S1	Saboba	W4	West Mamprusi
S2	Saboba	W5	West Mamprusi
S3	Saboba		

the oil is extracted is a rich source of protein for farm animals.

In Ghana, the crop is cultivated in some parts of northern Ghana but production has been declining due to low yields among other factors. The use of landraces which are of low yielding by farmers mainly accounts for this trend. In recent past, production is picking up through the promotion by SNV, Ghana (Netherlands Development Organization), an international NGO [6]. Improved yield depends on the use of improved genotypes. Genotypes in Ghana are low in yield ranging between 150 and 200 kg/ha. Improvement of sesame requires knowledge of the genetic diversity of germplasm as well as genetic relationships among accessions [7]. There is therefore the need for assembling genotypes and characterizing them to determine the similarity or differences that exists between them. Knowledge on this will help in the improvement of the crop for higher grain and oil yield. Morphological descriptors have over the years been used in characterization [8–12]. They permit easy identification and differentiation of accessions. Generally, these descriptors have high heritability, suggesting that they are expressed in different environments. They have played essential role in crop improvement since the beginning of modern breeding programme [13]. However, cultivar characterization when based on morphological descriptors alone can be subjected to errors from variations in environmental conditions.

Molecular markers have been widely used for checking the identity and purity of cultivars and for assessing their genetic variability in different crops. In sesame, the genetic diversity has been detected using markers such as amplified fragment length polymorphism (AFLP), sequence-related amplified polymorphisms (SRAP), random amplified polymorphic DNA (RAPD), and intersimple sequence repeat (ISSR). Characterization of sesame genotypes using molecular markers is of great value in assisting parental line and breeding strategy design selection [14]. Simple sequence repeats (SSRs) that enable exploration of the sesame genome have also been reported in many studies [15–19]. Considering the importance of the crop, it is anticipated that varieties which are more productive than those currently grown by farmers can be developed. It is therefore necessary that sesame germplasm in Ghana is collected and characterized. The objective of this study was to determine the genetic variability among sesame accessions cultivated in selected districts of northern Ghana using morphological and SSR markers.

2. Materials and Methods

2.1. Morphological Characterization. Five districts in Northern Ghana situated in semiarid ecological zone where sesame is predominantly cultivated were selected for the study. Subsequently, five farmers per district were selected using the snow ball method and sesame seeds were collected from each farmer. A total of twenty five sesame accessions were collected for the study (Table 1). They were grown in the experimental field of the University for Development Studies, Nyankpala campus, in a randomized complete block design with three replicates. Evaluation was carried out on all the accessions according to a set of morphological descriptors for sesame [20]. Data for morphological characterization were taken at three, six, and nine weeks after planting and at harvest. Morphological characterization of accessions was based on eleven qualitative and quantitative traits. Some of the morphological characters evaluated were stem hairiness, leaf hairiness, number of flowers/axil, height at flower initiation, and branching pattern. Others include number of branches per plant, length of first capsule, capsule hairiness, carpels/capsule, number of capsule/plant, and seeds per capsule.

2.2. Molecular Characterization. Molecular characterization was conducted at the CSIR-Crops Research Institute, Fumesua, in the Ashanti Region. The twenty-five sesame accessions were established in a screen-house. Young apical leaves about 200 mg per sample were harvested and genomic DNA extracted using CTAB Protocol.

Table 2: List of 21 SSR primers used for the study.

Primer	Annealing temp (°C)	Expected band size	Primer	Annealing temp (°C)	Expected band size
BU668385	52	185 - 240	BU670264	51	350 - 400
BU668626	53	290 - 310	BU669462	51	182 - 228
BU667505	53	230 - 250	BU669409	51	160 - 190
BU670690	52	220 - 240	BU669908	51	181 - 199
BU668961	51	181 - 223	BU668438	51	187 - 224
BU670450	52	185 - 232	BU670516	55	210 - 260
BU670128	52	120 - 160	BU669957	49	220 - 240
BU668318	52	140 - 170	BU670003	54	170 - 240
BU669684	50	280 - 320	BU670334	52	480 - 510
BU667382	50	184 - 196	HQ236490	53	290 - 310
BU667375	50	222 - 236			

2.3. Genomic DNA Extraction. Samples were grinded to fine powder with liquid nitrogen and one ml of freshly prepared CTAB buffer was added to each tube. Precipitation of nucleic acids was performed using Phenol Chloroform isoamyl alcohol and then washed with 70% ethanol. Further precipitation of DNA was done using low salt TE (1X) buffer. RNAase was added to degrade the RNA and, finally, purification of DNA was carried out. DNA pellet was dissolved in low salt TE (1X) buffer. Quality check was carried out on 0.8% agarose gel and quantification of genomic DNA conducted using Nanaodrop 2000c Spectrophotometer.

2.4. Genotyping Using Simple Sequence Repeat (SSR) Markers. A total of 38 primers were used to genotype the sesame accessions to determine polymorphic primers that would produce scorable bands at the expected band size. Twenty-one out of the 38 primers were polymorphic (Table 2) and produced scorable bands. Subsequently, the 21 SSR primers were used to screen the 25 accessions using SeeAMP™ PCR thermal cycler. DNA amplification was performed in a reaction volume of 10 μL containing 50 ng of DNA template, 1X PCR reaction buffer (15 mM Tris-HCl), 2 mM dNTPs, 1 U of Taq DNA polymerase, 10 μM of forward and reverse primers, and sterile distilled water. The PCR conditions were programmed for an initial denaturation step of 94°C for 5 min, followed by 35 cycles of denaturation at 94°C for 45 s, annealing temperature (depending on the primer) for 45 s, extension at 72°C for 1 min, and then a final extension of 72°C for 10 min. The PCR products were run on 6% PAGE gels after which they were stained with ethidium bromide and visualized using Alpha-Imager HP system. Data was scored using the Alpha-View software inbuilt within the Alpha-Imager HP system.

2.5. Data Analysis. Data on morphological traits were subjected to Principal Component Analysis (PCA) and a dendrogram showing similarity between the accessions was constructed. Yield and plant height data, namely, number of capsules per plant, number of seeds per capsule, and plant height at flowering, were subjected to analysis of variance using GenStat Discovery Edition 4.

Cluster analyses were carried out using the Euclidean similarity test and a complete link clustering method. The genetic analysis package (PowerMarker version 3.0 [21]) was used to generate the following statistics: number of alleles per locus, major allele frequency, observed heterozygosity (H_O), expected heterozygosity (H_E), and polymorphic information content (PIC) [22]. Dendrogram was constructed using DarWIN 6 software. The morphological and molecular Euclidean distance were combined to construct circular dendrogram using the R software.

3. Results

3.1. Morphological Characterization

3.1.1. Number of Capsules Formed per Plant and Number of Seeds per Capsule. Capsules formed per plant varied significantly (*P=0.001*) among the accessions (Table 3). Most of the Tatale accessions, with the exception of T1, produced similar number of capsules per plant (83.7-95.4). Three of the Saboba accessions (S3, S4 and S5) produced more than 100 capsules per plant. Three of the accessions from Chereponi (C1, C3 and C4) and West Mamprusi (W2, W3, and W5) also produced more than 100 capsules per plant (Table 3).

The number of seeds per capsule varied significantly (*P=0.001*) among the accessions. The number of seeds per capsule followed the same pattern as the number of capsule per plant (Table 3). Three of the five accessions that produced the least number of capsules (S1, K1 and T1) were also among the five accessions that produced the least number of seeds per capsule. West Mamprusi accessions (W3 and W5) produced the highest number of seeds per capsule as well as top capsule producers. The variation between the highest and the least seed producer was about 33%.

3.1.2. Plant Height at Flowering. There was significant difference among the accessions (*P=0.001*) in terms of plant

Table 3: Number of capsules per plant and seeds per capsule.

Accession	Capsule/plant	DMRT	Accession	seed/capsule	DMRT∗
SI	54.9	a	SI	52.2	a
T1	59.5	ab	T1	60.0	b
K3	61	ab	C5	62.9	bc
K1	62.2	ab	K1	63.3	bc
C2	69.9	abc	S2	64.0	bc
S2	71.0	abcd	K3	64.7	bc
C5	74.8	abcde	W4	67.3	cd
W4	80.9	abcdef	C2	68.0	cde
K5	81.8	abcdef	T2	70.3	def
T5	83.7	abcdef	K5	71.9	defg
T4	83.8	abcdef	K2	72.7	efgh
T2	84.2	abcdef	T4	73.0	efghi
K2	94.1	abcdefg	W2	73.9	fghi
T3	95.4	abcdefg	T5	74.8	fghij
C3	98.6	bcdefgh	C1	75.0	fghij
S3	102.9	bcdefghi	C4	75.0	fghij
K4	109.2	cdefghi	S3	75.0	fghij
C1	111.6	cdefghi	K4	76.0	ghij
W2	115.9	defghi	T3	76.0	ghij
S4	118.3	efghi	W1	76.33	ghij
C4	123.0	fghi	S4	77.0	ghij
W1	135.0	ghi	C3	77.9	hij
S5	140.4	hi	S5	78.0	hij
W3	140.7	hi	W5	78.5	ij
W5	146.7	i	W3	80.0	j

∗Duncan multiple range test.

height at flowering (Figure 1). The height ranges from 60.6 to 94.1 cm. Each district had accession that was below 70 cm in height. The Kassena Nankana accessions were relatively shorter while those of Chereponi were taller and the tallest accession (C3) was found in that district.

3.1.3. Clustering Sesame Accessions by Morphological Traits. The average linkage grouping method identified by Principal Clustering Analysis produced four clusters (Figure 2). Individuals within any cluster were more closely related than individuals in different clusters. The dendrogram shows that there was some level of variation among the accessions, 38.8-90% similarity. The accessions were grouped into two major clusters A and B, and two minor ones, clusters C and D that have fewer number of accessions (Figure 2). Cluster B was the largest with 14 accessions. This cluster consisted of accessions from all the five districts: two accessions from Chereponi district C2 and C5, four of the five accessions from Kassena Nankana district K1, K2, K3, and K5, all the accessions from Tatale district T1-T5, W1 and W4 from West Mamprusi district, and one from Saboba district, S2. The second largest cluster, A, was related to cluster B at similarity index of (58.0%). It contained nine genotypes and they include the rest of the accessions from Chereponi, Kassena Nankana, and West Mamprusi districts, C1, C3. C4, K4, W2, W3, and W5. The Saboba accessions were diverse; they were found in all the four clusters. Two accessions, S4 and S5, were part of Cluster A. Cluster C having only accession S3 was related to Cluster B at similarity index of (56.0%) and Cluster D containing only accession S1 was distantly related to the rest of the 24 accessions at similarity index of 38.8%.

3.2. Molecular Characterization

3.2.1. Genetic Diversity. A total of 410 alleles with an average of 19.5 alleles per locus were observed in the accessions (Table 4). The highest number of alleles was detected by primer BU668318 which also produced the lowest major allele frequency. Primer BU667375 which produced the least numbers of allele showed more diversity in the form of genotype number, gene diversity, heterozygosity, and PIC (Table 4). The major allele frequency ranged between 0.08 and 0.28 with an average for the population being 0.17. The genotype number was analogous to the allele number with a total of 395 and average of 18.81 per locus. The average gene diversity among the samples was 0.91 which was similar to the polymorphic information content (PIC). PIC ranges from 0.80 to 0.96. Heterozygosity among the accessions ranged from 0.04 to 1.00 with an average of 0.56 (Table 4).

Table 4: Summary statistics of genetic variation among sesame accessions using SSR markers.

Marker	No. of Allele	Major Allele Frequency	Genotype No	Gene Diversity	Heterozygosity	PIC
BU667375	7.00	0.24	8.00	0.82	0.04	0.80
BU667382	18.00	0.24	15.00	0.88	1.00	0.87
BU667505	18.00	0.12	18.00	0.92	0.28	0.92
BU668318	33.00	0.08	24.00	0.96	1.00	0.96
BU668385	25.00	0.20	22.00	0.92	0.52	0.92
BU668438	24.00	0.16	23.00	0.94	0.92	0.93
BU668626	14.00	0.12	17.00	0.92	0.16	0.91
BU668961	26.00	0.12	23.00	0.94	0.80	0.94
BU669409	22.00	0.14	21.00	0.93	0.92	0.93
BU669462	14.00	0.20	18.00	0.90	0.32	0.89
BU669684	17.00	0.16	17.00	0.91	0.36	0.90
BU669908	21.00	0.12	22.00	0.93	0.88	0.92
BU670128	13.00	0.28	12.00	0.85	0.12	0.84
BU670264	21.00	0.16	20.00	0.93	0.32	0.93
BU670334	24.00	0.10	25.00	0.95	0.56	0.94
BU670516	18.00	0.20	18.00	0.91	0.40	0.90
BU670690	26.00	0.08	24.00	0.95	0.80	0.95
BU670450	9.00	0.28	8.00	0.82	0.04	0.80
BU669957	22.00	0.20	17.00	0.92	1.00	0.91
BU670003	20.00	0.14	19.00	0.93	0.64	0.92
HQ236490	18.00	0.14	24.00	0.92	0.68	0.92
Mean	**19.52**	**0.17**	**18.81**	**0.91**	**0.56**	**0.91**

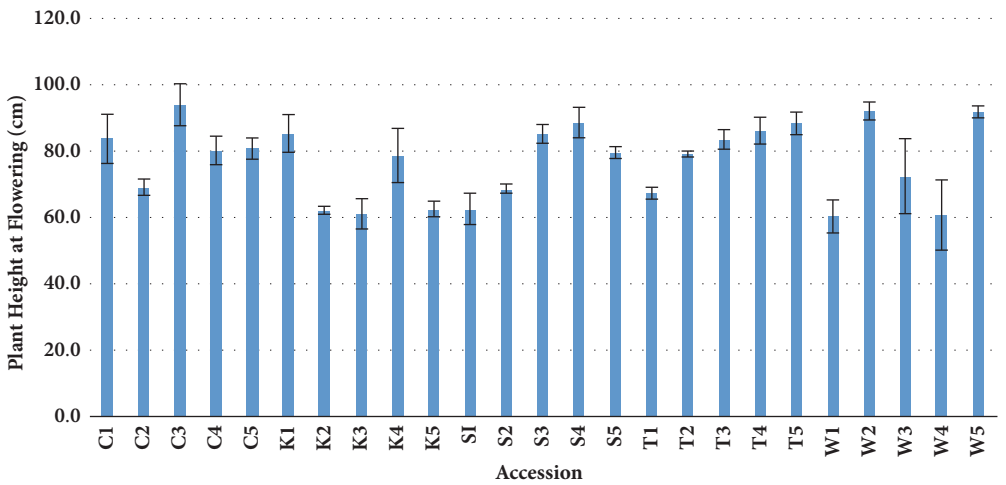

Figure 1: Plant height of sesame accessions collected from some districts in northern Ghana. Error bars represent standard error of means.

3.2.2. Dendrogram Analysis. The dendrogram generated is presented in Figure 3. The molecular analysis showed that variation among the accessions was low 10-20%. The dendrogram revealed two main clusters, A and B, at similarity index of 80%. Cluster A was subdivided into four subclusters, I-IV. Cluster B was also subclustered into three, V-VII. Subcluster I consisted of three accessions from West Mamprusi, W1, W2, and W3. Another West Mamprusi accession, W4, lonely in cluster II, was related to Subcluster I accessions at similarity index of 83.5%. Subcluster III consists of all accessions from Tatale together with accession W5 from West Mamprusi. Saboba accessions were split into 3 subclusters. Accession S1 stood alone in subcluster IV. Two other accessions from Saboba, S2 and S3, were in close association with two accessions from Chereponi, C4 and C5, together forming subcluster V. Saboba and Chereponi used to be one district and it is probable that the same materials were distributed among the farmers. Subcluster VI consists of the other three accessions from Chereponi, C1, C2, and C3, and one accession collected from Kassena Nankana, K5. The other four accessions from Kassena Nankana have similarity with the two remaining accessions from Saboba and they together

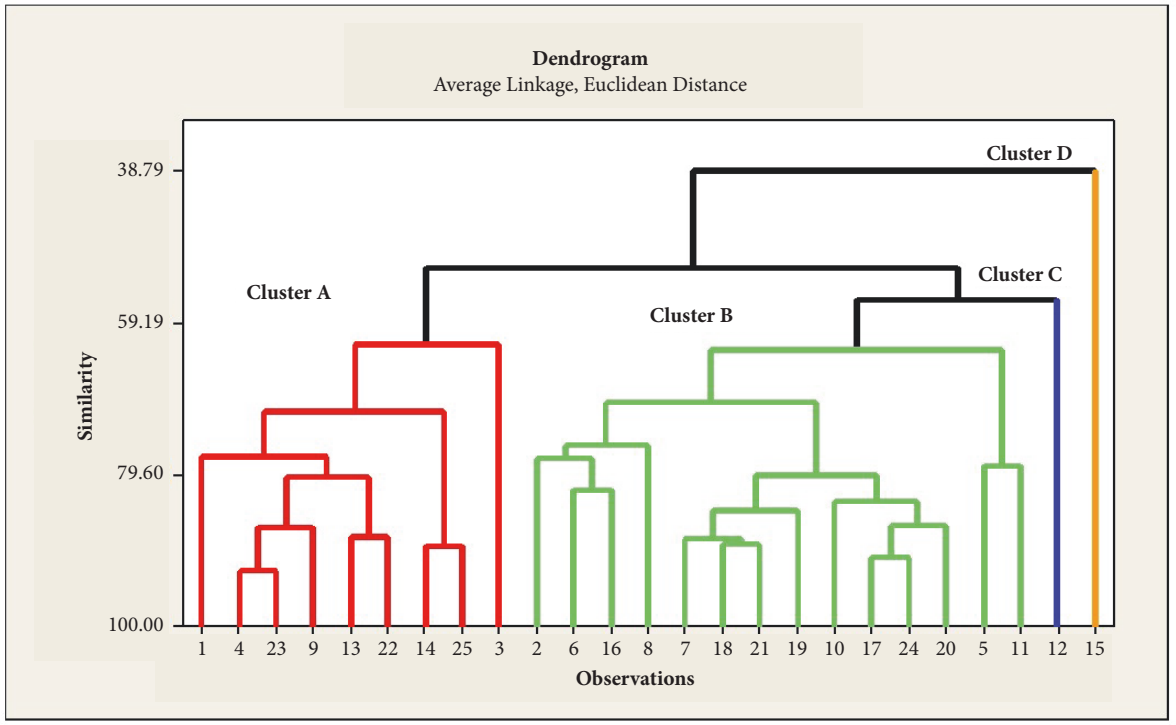

Figure 2: Average linkage-based dendrogram showing hierarchical grouping patterns of 25 sesame accessions (C1-W5) in four clusters based on 11 major quantitative and qualitative morphophysiological traits. 1=C1, 2=C2, 3=C3, 4=C4, 5=C5, 6=K1, 7=K2, 8=K3, 9=K4, 10=K5, 11=S2, 12=S3, 13=S4, 14=S5, 15=S1. 16=T1, 17=T2, 18=T3, 19=T4, 20=T5, 21=W1, 22=W2, 23=W3, 24=W4, 25=W5.

formed subcluster VII (K1-K4, S4 and S5). Accessions from a district that are found in one cluster may be more closely related to that particular cluster mates than the district members outside that cluster.

3.3. Morphological and Molecular Cluster Analysis. When morphological and molecular Euclidean distance values were combined the accessions clustered into fifteen groups (Figure 4). The Chereponi accessions were found in four clusters (B, L, J, and G). The Kassena Nankana accessions fell into five different clusters (C, E, J, M, and O) The Saboba accessions also clustered into five groups (A, B, D, F, and K). Accession S1 consistently separated out into a solitary cluster (A) showing that it is different from its cohort and other accessions. The Tatale accessions grouped into five different accessions (D, E, G, N, and O). The West Mamprusi accessions were not widely dispersed as they fell into three accessions that were not far apart (E, H, and I).

4. Discussion

Capsule number was diverse, a range of 54.9 and 146.7. It has been reported that in a row planting in a Mediterranean environment the number of capsules formed were between 43.0 and 47.2 [23]. Another study also reported that the capsules formed per plant among different accessions taken from six countries in two continents were in the range of 78 and 232 [24].Variation in capsule number reported among 129 accessions by [7] ranged between 21.0–197 capsules per plant among. This study produced capsules higher than that reported by [23] but similar to that of [7, 24].

The numbers of seeds recorded by the current study were higher than what was reported by [23]. They reported 47. 1-50.4 seeds per capsule. Reference [24] obtained much higher seed number in their study of fifteen accessions from six countries (88-138 seeds per capsule). In a study in Turkey [7], seeds per capsule were in the range of 34.0–84.0 which is similar to what was obtained in this study. The variation in seed number may be influenced by seed size. Plants that produce plenty seeds tend to have smaller seed size. The number of capsules and seeds per plant and 1000 seed weight of sesame have been reported to have strong correlation with yield [25]. Sesame genotypes express diverse plant height. References [23, 24] reported higher plant height of sesame in Vietnam and Mediterranean environment (126.4–161.6 cm and 99.3 and 139.9 cm, respectively). These were quite higher than height observed in the Ghanaian accessions used in this study. The height obtained in this study was however closer to that observed by [7]. According to [7] shorter accessions may be more resistant to lodging than taller ones. They observed some accessions that combined shortness with higher capsule and seed numbers. Therefore, accessions that are short and produce many capsules and seeds need to be selected for breeding. In our study, the shortest accession W1 was among the top six accessions that produced higher capsule per plant and seeds per capsule and would be a potential candidate for parental line selection

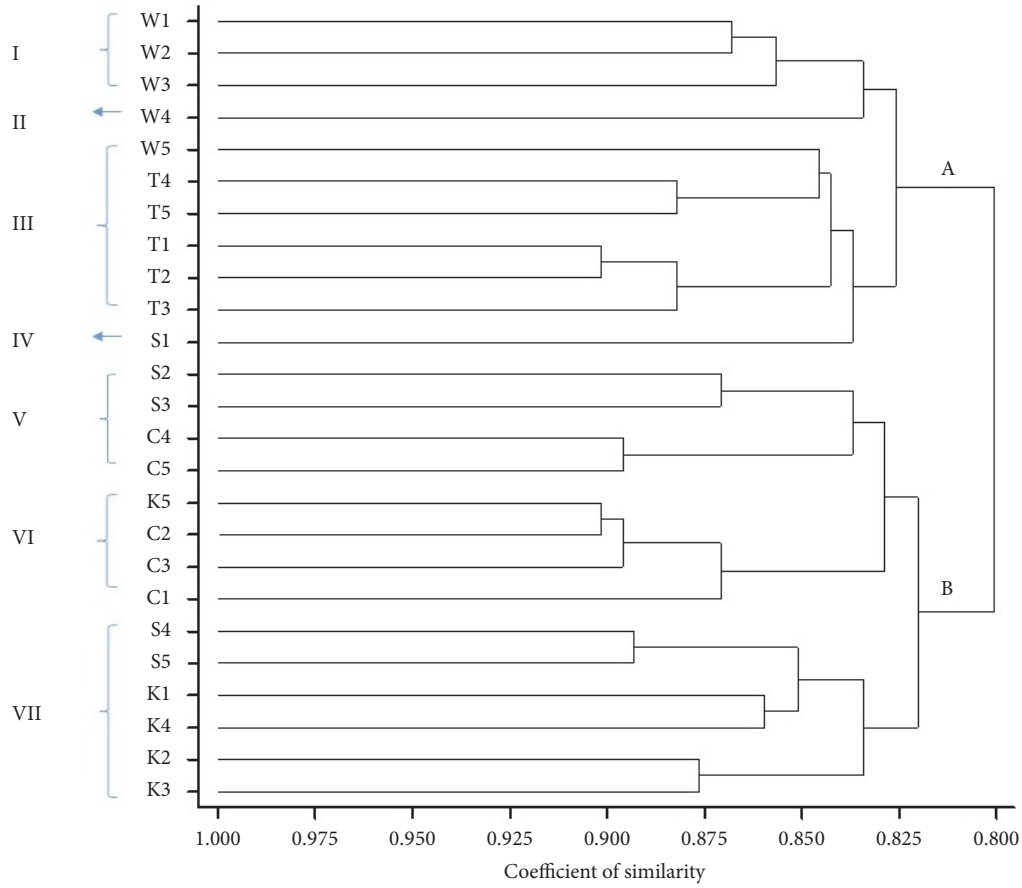

Figure 3: Dendrogram of 25 sesame accessions screened with 21 SSR markers using complete link Euclidean cluster method.

Diversity of genotypes from different origin can be studied by either morphological traits, geographical origin, or using molecular marker techniques like SSR markers. These markers are considered a powerful tool to investigate variability in plants [26–28]. Sesame has been cultivated in northern Ghana over the years and genotypes used are normally landraces that have spread among the farmers. There has not been any breeding program in Ghana where these landraces have been improved for some of the economically important traits and subsequently released to farmers. Based on the morphological characterization, variation observed among the accessions was high, 10-61.2%. The two main clusters obtained in morphological dendrogram had accessions from each of the districts. Studies by [29] revealed that sesame genotypes from different geographical origin clustered together. It appears that sesame accessions cultivated in northern Ghana are similar and that it is these same materials that are exchanged between farmers. All the accessions from Tatale district and four from Kassena Nankana district are grouped together with other accessions from the three remaining districts in one cluster. This shows that it is the same genotype that the farmers cultivate in the districts. Could it be domestication that has narrowed genetic basis of this cultivated sesame as suggested by [14]?

The SSR markers used in this study revealed higher number of alleles as compared with other studies [15, 28]. The PIC demonstrates the informativeness of the markers with values ranging from 0 to 1 and locus having PIC values near to 1 are more desirable [28]. The average PIC value for all the 21 SSR marker loci was 0.91 which was higher than the 0.56 obtained when 44 sesame cultivars were studied by [28]. Quantitatively the degree of polymorphism can also be measured by heterozygosity which is unbiased estimator of variance [30]. The values of heterozygosity indicate the diversity level of the molecular marker. When the value is high, the molecular marker's diversity is high too. The average heterozygosity obtained in the Ghanaian accessions was 0.52 which was comparable with the 0.59 obtained by [28].

SSR's dendrogram clustering was better in revealing the true diversity in the accessions than that observed by the morphological clustering. Diversity revealed by the SSR markers showed that variation among the accessions was lower than revealed by morphological, 10.0-20.0% as compared to the 10.0-61.2% recorded by morphological characterization. This could be due to the fact that the environment has so much effect on the phenotype as with morphological traits whereas the environment does not have any effect on the SSR markers. SSR markers are reported to give a good discrimination between closely related individuals [31]. The SSR markers used for this study gave more subgroups than the morphological data but the variation among the groups were low.

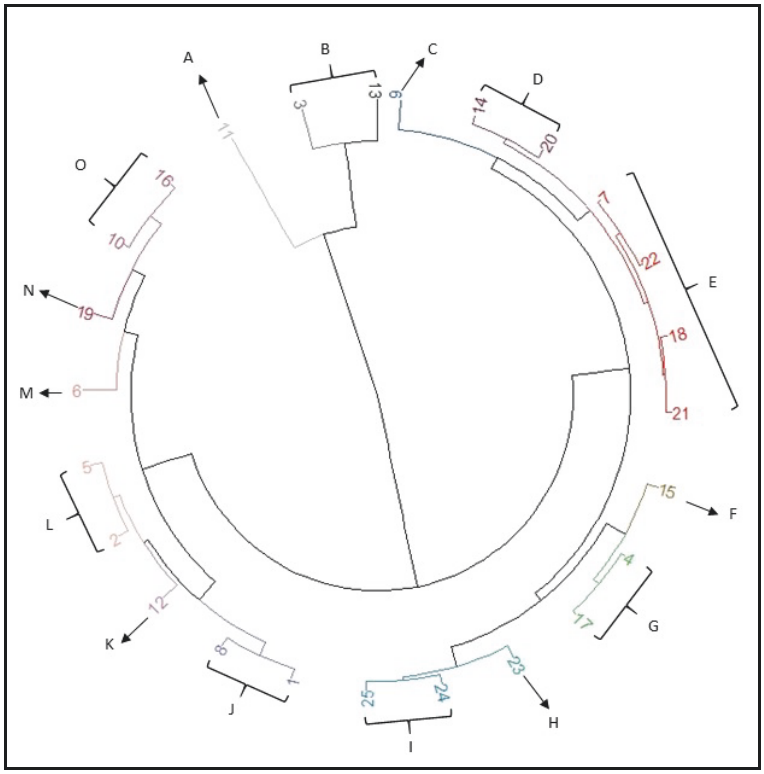

Figure 4: Associations among 25 sesame accessions revealed by circular clustering analysis on the basis of combined morphological and molecular Euclidean distance values. 1=C1, 2=C2, 3=C3, 4=C4, 5=C5, 6=K1, 7=K2, 8=K3, 9=K4, 10=K5, 11=S1, 12=S2, 13=S3, 14=S4, 15=S5. 16=T1, 17=T2, 18=T3, 19=T4, 20=T5, 21=W1, 22=W2, 23=W3, 24=W4, 25=W5.

Reference [32] observed that no relationship existed between genetic diversity and origin of accessions in composition of clusters; however, they found that some Iranian sesame genotypes have the tendency to cluster together. In this study the Tatale and some Kassena-Nankana accessions grouped together like the way the Iranian genotypes behaved in the study [32]. Our study agrees with other studies by [29, 33] where clustering of genotypes did not indicate any clear division based on their geographical origin.

The analysis of variance revealed that the top five capsule producing accessions were C4, W1, S5, W3, and W5 while the top five accessions that produced higher number of seeds per capsule were S4, C3, S5, W5, and W3. The dendrogram constructed with molecular data shows that, for the top five capsule producers, C4 belongs to Cluster V, W1 and W3 belong to Cluster I, and W5 and S5 belong to Clusters III and VII, respectively. In the case of the top five seed producer accessions, the molecular based dendrogram put them in four clusters. S4 and S5 were grouped into Cluster VII, C3 in Cluster VI, and W5 and W3 were found in Clusters III and I, respectively. S4 and S5 are closely related; they fell into Cluster VII. Based on position of capsule and seed production S5 will be selected over S4 for consideration as potential parental line. W1 and W3 are found in one cluster, I. W1 combines shortness of plant height with profuse capsule formation while W3 is the highest seed producing genotype. W3 is selected over W1 but, due to shortness and prolific capsule development, W1 will also be selected as a potential parental line. C4 is selected on the basis of being the fifth highest capsule producing genotype while C3 is also considered as a potential parental line because of being the fourth highest seed producing genotype. W5 is selected as a potential parental line because it is the highest capsule producing and the second highest seed producing genotype.

When morphological and molecular data were combined these top six accessions were found in different clusters in the resulting dendrogram showing that they exhibit some degree of variation and have the potential to be parental lines.

5. Conclusion

It can be concluded that the SSR markers revealed the true variation in the accessions better than the morphological markers. The accessions cultivated in the five districts are similar with diversity of 10-20% as revealed by the SSR markers. There were few accessions that produced more capsules and seeds that showed diversity. The combination of morphological and molecular data revealed more diversity among the accessions as they grouped into 15 clusters. It is recommended that the six accessions, C3, C4, S5, W1, W3, and W5 found in five different clusters and noted for their high capsule and seed production should be considered as potential parental lines for breeding programs to improve the sesame accessions.

Data Availability

The research data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that they do not have any conflicts of interest.

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Supplementary Materials

It is excel sheets (3) containing the morphological data collected, molecular similarity, and genetic variations used for the study. *(Supplementary Materials)*

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