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RESEARCH ARTICLE

PHENOTYPIC DIVERSITY AMONG SOME COWPEA (VIGNAUNGUICULATA(L.) WALP) AND SESAME (SESAMUMSPP) ACCESSIONS CONSERVED AT GENETIC RESOURCES RESEARCH INSTITUTE(GERRI) IN KENYA

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Abstract

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Cowpea (Vignaunguiculata(L.) Walp) and sesame (SesamumindicumL.) are both adapted to the dry and infertilearid and semi-arid environments (ASALs). These crops are rich sources of high quality protein and essential oils, respectively. Consequently, the two crops are ideal food and nutritionalsecurity commodities for the vulnerable communities who live in these fragile environments.The Genetics Resources Research Institute (GeRRI)'s genebankhas amassed 972 and 2491 accessions of cowpea and sesame,respectively. However,utilization of these genetic resources has remained generally low largely due to limited characterization and evaluation data. As one of the measures to mitigate this problem, 123 accessions of cowpeaand 203 of sesame werephenotypically characterized at KALRO- Kiboko field.Five quantitative and nineteen qualitative traits were used to characterize the cowpea accessions whilethree quantitative and twenty one qualitative traits were used to characterize the sesame accessions.According to principal component analysis (PCA), 10 factors accounted for 65% of the total variability among the cowpea accessions while 10 factors accounted for 68% of the total variability among the sesame accessions.Hierarchical clustering generated five similarity clusters (groups) for cowpeas and twomain clusters (groups) for sesame. The hierarchical clusters observed for the crops could be attributed to the regions from which the accessions were collected or donated. Passport data held at the genebank indicate that majority of the cowpea accessions were collected from the Eastern, Western and Coast regions of Kenya or donated from ICRISAT and IITA. Similarly, majority of sesame accessions were collected from Kenya or donated from othercountries such as Israel, Greece, Turkey, Egypt, Somalia, Mexico, Mozambique, Vietnam, South Korea and USA.The diversity in these accessions can be exploited in breeding better varieties of these crops.

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Introduction:-

Cowpea (Vignaunguiculata(L.) Walp) and sesame (SesamumindicumL.) are both adapted to the dry and infertile arid and semi-arid environments (ASALs). These crops are rich sources of high quality protein and essential oils, respectively. Consequently, the two crops are ideal food and nutritional security commodities for the vulnerable communities who live in these fragile environments. Cowpea is a member of Leguminosae family and is considered a native of Africa. It is one of the most important legume crops in the world, especially in the drought prone areas and it is a major source of proteins, essential amino acids (Márciaet al., 2017; Wamalwa et al., 2016; Ishiyaku and Habibu, 2013; Naima et al., 2009). Sesame is an erect annual herb commonly known as sesamum, benniseed, or simsim and a member of the Pedaliaceaefamily (Faisal et al., 2016). It is one of the oldest oilseed crops valued for its high-quality seed oil (Faisal et al., 2016); it is thought to have been first cultivated in Africa before its introduction in India (Weisskopf and Fuller, 2014).It is estimated that Asia and Africa produce more than 90 % of the global sesame output (FAOSTAT, 2022). In 2022, Asia produced 2.4 million tons of sesame accounting for 35.6% of the global output (WORLD DATA ATLAS, 2022).

Cowpea production in Kenya is concentrated in the dry former Eastern and Coast provinces (AFA, 2014) while sesame is largely grown in lower midlands in western region (former Western and Nyanza provinces) and coastal lowlands (former Coast province) (Ong'injo and Ayiecho, 2009). Over the years, the Genetics Resources Research Institute (GeRRI) has collected and conserved 972 and 2491 accessions of cowpea and sesame respectively. However, the distribution and utilization of this germplasm has remained low largely because of limited characterization and evaluation data (GeRRI, 2015).Actually, in many African gene banks, only a fraction of the conserved germplasm is actively being used because of similar reasons. For instance, Ishiyaku and Habibu (2013) reported that40% of the cowpea germplasm maintained at IITA has never been distributed because breeders seldom request the germplasm. Globally, breeders prefer genetic materials that have undergone pre-breeding analysis and whose characterization and evaluation data is available.

Therefore, a study was carried atKenya Agricultural and Livestock Research Organization (KALRO)'s field station atKibokoto undertake phenotypiccharacterization as well as regeneratingof selected cowpea and sesame accessions conserved at the Kenyan genebank.

Materials and Methods:-

Study site

The study was conducted at the KALRO-Kiboko experimental farm which is located on latitude 2^0 21'14''S and longitude 37^0 71'68''E at about 975 meters above sea level. The area is hot and dry with rain-fed crop production being difficult (Jaetzold and Schmidt, 1982) The annual mean rainfall is estimated at 530mm and the mean annual temperature is between 21^0C and 24^0C(Jaetzold and Schmidt, 1982).The soils are developed from undifferentiated Basement System rocks and are well drained, deep to very deep, dark red to strong brown, friable, sandy clay to clay (rhodic and orthic FERRALSOLS) and described to be of low to moderately low fertility(UNESCO, 1977).

Crop management

The land was ploughed and harrowed to a fine tilth and planting was done inMarch, 2017. Cowpea accessions were planted on plots consisting of two rows measuring 4.4 meterslong with intra-row spacing of 30cm giving a total of 30 plants per plot. Sesame accessions were planted on four rows measuring 2.7 meters with intra-raw spacing of 30cm. Water was supplied throughout the season using overhead irrigation. Control of weeds, pests and diseases was done as and when required.

Data collection and Analysis

Agro-morphological characters (both qualitative and quantitative traits) during crop development and post-harvest processing were captured using a descriptor list customized from the International Board on Plant Genetic Resources (IBPGR) (IBPGR, 2004).For cowpeas, the following characters were captured:Growth Habit, Growth Pattern, Twinning Tendency, Average of Number of Main branches, Average of Number of Nodes on main stem, Plant pigmentation, Terminal Leaflet shape, Leaf Marking, Leaf Colour Leaf Texture Flower Colour, Flowering Pigmentation Pattern, Raceme Position, Pod Attachment to Peduncle, Immature Pod Pigmentation, Pod Colour, Pod Curvature, Pod Length, the Number of locules per Pod, Seed Shape, Testa Texture, Eye Pattern, Eye Colour, and 100 seed weight. For sesame, the following characters were recorded: Plant Growth Type, Plant Growth Habit, Stem Hairiness, Hair Shape, Stem Branching, Branch Pattern, Leaf Arrangement,Leaf Colour,Leaf Hairiness, Leaf Shape, Basal Leaf Pattern, Lobe Incision of Basel Leaf, Leaf Angle to Main Stem, Petiole Colour, Petiole Hairiness, Calyx Hairiness, Corolla Hairiness, Exterior Corolla Colour, Interior Corolla Colour, Corolla Interior Pigmentation, Lower Lip Colour, Plant Height, Number of Flowers per Leaf Axil, and Number of Nodes to First Flower.

Data were then entered in excel and analyzed using the SPSS Statistical software (SPSS Inc. 1999). The Principal Component Analysis (PCA) and correlation matrices were used to explore the links between the quantitative traits, identify, and define the main characteristics of groups of accessions. Descriptive statistics and correlation coefficients analysis were computed. The hierarchical classification tree by unweighted pair group method with arithmetic mean (UPGMA)automatically created groups of accessions according to the importance of the variables. Clustering was done using Euclidean distance nearest-neighbourmethod.

Results and Discussions:-

Cowpea

Principal Component Analysis (PCA) indicated that 10 factors accounted for 65% of the total variability among these accessions (Table 1).Each of the 10 Principal Components generated showed fairly strong to strong negative or positive correlation to the characters studied (Table 2). Principal Component (PC) 1 showed strong positive correlation (0.767) to leaf colour and strong negative correlation (-0.844) to leaf texture. A similar contrast can be seen for PC 2 which show fairly strong negative correlation (-0.690) to twinning tendency and strong positive correlation (0.708) to flowering pigmentation pattern. Strong positive correlation between the PCs and any of the studied characters means an increase in that specific component will result in positive increase in the relevant character of the plant. Conversely, negative strong correlation means an increase in a certain component results in a decrease in some specific character of the plant.

A hierarchical clustering analysis for cowpea generated a dendrogram using a final partition of five similarity clusters (groups) (**Error! Reference source not found.**). Among the clusters, the first one is the largest (91 accessions) comprising of twenty three main branches out of which four are single-leafed. The single-leafed branches are represented by accessions GB-005173, GBK-013120, GBK-003962, and GBK-051357. There are also many sub-branches within cluster 1 that gave rise to one, two or three leaves (accessions). The second and fourth clusters were composed of six and five main branches respectively. The smallest is the fifth cluster with a single branch represented by GBK-005182 and GBK-027028. The similarity groups observed could be attributed to the specific regions from which the accessions were collected or donated. The passport data held at the Kenyan genebank indicate that majority of the cowpea accessions were collected from the main growing areas of Eastern, Western and Coast regions of Kenya or donated from ICRISAT and IITA. For instance, the passport data indicate that GBK-051357 which liesat the extreme end of cluster 1 was collected from Tharaka-Nithi, while GBK-003694, GBK-004313 and GBK-003740 positioned at the extremities of cluster 2, 3 and 4 respectively were all collected from Machakos. It therefore means most of the accessions in the groups were collected from Eastern Kenya and that may explain the close similarity among them as seen in the dendrogram.

Sesame

For sesame, Principal Component Analysis indicated that 10 factors accounted for 68% of the total variability among the accessions (Table 1).Each of the 10 Principal Components generated showed fairly strong to strong negative or positive correlation to the characters studied. For instance, Principal Component (PC) 1 showed strong negative or positive correlation to five characters while PC 7 and PC 10 showed strong negative or positive correlation to three characters each. PC5 showed strong positive (0.806) only to one character (branch pattern) while the other remaining PCs showed strong negative or positive correlation. PC 1 showed strong positive correlation (0.783) to Basal leaf pattern and strong negative correlation (-0.518) to Plant Growth type. PC 2 and PC 3 show very strong correlation to hairiness in Sesame (Table 3). PC 2 showed very strong positive correlation to Stem Hairiness and Hair Shape of 0.818 and 0.891 respectively while PC 3 exhibited strong correlation to Hairiness in Calyx (0.804) and Corolla (0.795).

As in cowpea the strong positive correlation between the PCs and any of the studied characters means an increase in that specific component will result in positive increase in the relevant character of the plant. Conversely, negative strong correlation means an increase in a certain component results in a decrease in some specific character of the plant.

The hierarchical clustering analysis for sesame generated a dendrogram comprising of two main similarity clusters (groups) (**Error! Reference source not found.**2). The first one consisting of a total of 35 accessions has five (5) main branches while cluster 2 is the largest consisting of 94 accessions constituting Eighteen (18) main branches. The largest branch in cluster 1 has a total of 14 accessions represented by GBK-031494 to GBK-040683 and the largest branch in cluster 2 has 30 accessions represented by accessions GB-031379 to GBK-040829 (Figure 2).

The passport data held at the Kenyan genebank indicate that majority of the sesame accessions were collected from Kenya or donated from a number of countries that include, Israel, Greece, Turkey, Egypt, Somalia, Mexico, Mozambique, Vietnam, South Korea and USA among others. Actuallythe Kenya Gene Bank is a global repository for sesame.

Therefore, the many distinct branches consisting of many accessions as observed in both clusters could be attributed to the specific regions from which the accessions were collected or donated.

For Kenya, the main sesame growing areas are in Western and coastal lowlands and therefore most of the accessions would have been collected in these regions.

Conclusions:-

The Genetics Resources Research Institute (GeRRI)'s genebank has amassed 972 and 2491 accessions of cowpea and sesame, respectively. However,utilization of these genetic resources has remained generally low largely due to limited characterization and evaluation data. Phenotypic characterization of 123 accessions of cowpeaand 203 of sesameshowed wide diversity among the accessions. This diversity could be exploited in breeding better varieties of these crops.

Table 1:- Cowpea and sesame variances as explained by principal components.

Principal Component	Initial Eigenvalues			Extraction Sums of Squared Loadings			Rotation Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
Cowpea									
1	2.102	8.757	8.757	2.102	8.757	8.757	1.809	7.539	7.539
2	2.064	8.601	17.358	2.064	8.601	17.358	1.770	7.376	14.915
3	1.837	7.652	25.011	1.837	7.652	25.011	1.714	7.140	22.055
4	1.713	7.136	32.147	1.713	7.136	32.147	1.653	6.887	28.942
5	1.601	6.671	38.818	1.601	6.671	38.818	1.631	6.798	35.740
6	1.539	6.413	45.231	1.539	6.413	45.231	1.577	6.571	42.311
7	1.387	5.781	51.012	1.387	5.781	51.012	1.435	5.981	48.292
8	1.285	5.355	56.367	1.285	5.355	56.367	1.432	5.966	54.258
9	1.085	4.520	60.887	1.085	4.520	60.887	1.385	5.772	60.031
10	1.011	4.211	65.099	1.011	4.211	65.099	1.216	5.068	65.099
Sesame									
1	2.709	11.289	11.289	2.709	11.289	11.289	2.467	10.277	10.277
2	2.479	10.327	21.617	2.479	10.327	21.617	1.955	8.148	18.425
3	1.863	7.761	29.377	1.863	7.761	29.377	1.774	7.394	25.819
4	1.723	7.177	36.555	1.723	7.177	36.555	1.656	6.900	32.719
5	1.525	6.356	42.910	1.525	6.356	42.910	1.528	6.368	39.086
6	1.370	5.709	48.619	1.370	5.709	48.619	1.450	6.043	45.129
7	1.259	5.245	53.864	1.259	5.245	53.864	1.426	5.940	51.070
8	1.214	5.057	58.920	1.214	5.057	58.920	1.391	5.795	56.865
9	1.169	4.872	63.792	1.169	4.872	63.792	1.378	5.742	62.607
10	1.080	4.501	68.293	1.080	4.501	68.293	1.365	5.686	68.293

Table 2:- Correlation coefficients of principal components with cowpea qualitative and quantitative characters generated from Varimax with Kaiser normalization rotation method.

Phenotypic Characters	**Principal Component**									
	1	2	3	4	5	6	7	8	9	10
Growth Habit	**0.363**	0.045	0.206	-0.092	0.011	0.003	0.166	0.626	-0.252	-0.165
Growth Pattern	0.029	0.417	-0.058	-0.124	-0.222	-0.019	**-0.521**	0.316	0.250	-0.155
Twinning Tendency	0.074	**-0.690**	0.158	0.053	-0.021	-0.070	-0.078	0.092	0.162	0.176
Plant Pigmentation	0.200	0.147	-0.081	-0.040	0.005	**0.459**	0.012	0.281	0.310	-0.257
Terminal Leaflet Shape	-0.129	-0.078	0.009	0.184	0.089	-0.107	**0.652**	0.199	0.091	-0.205
Raceme Position	0.175	0.115	-0.016	-0.176	0.074	0.034	-0.032	**-0.633**	-0.118	-0.148
Pod Attachment to Peduncle	0.061	0.443	-0.010	-0.151	-0.010	0.167	**0.547**	-0.091	0.182	0.091

Immature Pod Pigmentation	-0.127	-0.103	0.145	0.145	-0.298	**0.600**	-0.032	-0.161	-0.053	-0.140
Pod Curveture	-0.060	-0.022	-0.156	0.004	0.165	0.200	-0.412	-0.156	0.258	**-0.419**
Seed Shape	0.055	0.122	-0.133	0.048	-0.107	0.031	-0.037	0.028	**-0.768**	0.097
Testa Texture	0.321	-0.090	-0.001	-0.205	-0.104	-0.419	0.085	**-0.442**	0.126	-0.134
Eye Pattern	-0.030	-0.021	-0.001	0.088	**0.709**	0.033	-0.063	-0.192	0.222	0.027
Eye colour	0.052	0.030	-0.026	-0.105	**0.792**	-0.083	0.153	0.133	-0.115	0.008
Leaf Colour	**0.767**	-0.162	0.012	-0.185	0.035	0.091	-0.171	-0.101	-0.137	0.005
Leaf Marking	-0.025	-0.010	0.096	-0.007	0.081	-0.099	-0.061	0.026	-0.035	**0.796**
Leaf Texture	**-0.844**	0.000	0.049	-0.093	0.002	-0.047	-0.060	-0.028	-0.086	-0.004
Flowering Pigmentation Pattern	-0.142	**0.708**	0.039	-0.003	0.059	-0.035	-0.085	0.082	-0.089	0.109
Flower Colour	-0.245	**-0.542**	-0.156	-0.376	0.107	0.087	0.021	0.167	-0.325	-0.074
Pod Colour	0.179	0.025	-0.054	-0.006	0.071	**0.816**	-0.007	0.019	-0.016	-0.033
Pod Length	0.108	0.014	**-0.444**	-0.096	-0.294	0.092	0.320	0.168	0.398	0.289
Number of locules per Pod	0.049	-0.123	-0.063	**0.787**	-0.347	-0.038	0.200	0.067	-0.071	-0.113
Number of Main Branches	0.031	-0.058	**0.840**	0.114	-0.045	-0.010	-0.010	0.053	-0.024	0.079
Number of Nodes on Main Stem	-0.049	0.008	**0.791**	-0.194	-0.014	0.036	0.099	0.073	0.194	0.110
100 Seed Weight	-0.142	0.064	-0.001	**0.768**	0.249	0.175	-0.040	0.123	-0.030	0.072

Table 3:- Correlation coefficients of principal components with sesame qualitative and quantitative characters generated from Varimax with Kaiser normalization rotation method.

Phenotypic Characters	**Principal Component**									
	1	2	3	4	5	6	7	8	9	10
Plant Growth Type	**-0.518**	-0.151	-0.127	-0.282	0.251	-0.034	0.257	0.142	0.359	0.101
Plant growth Habit	-0.088	0.005	-0.071	**0.728**	-0.004	-0.103	0.040	-0.116	0.105	0.125
Stem Hairiness	-0.027	**0.898**	0.159	0.043	0.044	0.036	0.068	0.057	0.063	0.028
Hair Shape	-0.010	**0.891**	0.133	-0.007	-0.031	0.051	-0.055	-0.144	0.069	-0.010
Stem Branching	0.149	-0.001	0.051	0.372	-0.116	0.084	-0.164	0.041	0.112	**0.600**
Branch Pattern	-0.032	0.022	0.078	0.061	**0.806**	0.057	0.002	-0.004	0.079	0.011
Leaf Arrangement	0.140	0.035	-0.272	0.393	-0.103	-0.260	**0.579**	-0.042	0.003	-0.059
Leaf Colour	0.071	0.256	-0.153	-0.233	-0.091	**0.684**	0.042	-0.014	-0.200	0.116
Leaf Hairiness	0.000	-0.069	0.269	-0.065	0.141	0.122	**0.742**	-0.010	-0.022	-0.040
Leaf Shape	0.120	0.104	0.136	-0.132	0.026	-0.267	0.349	0.334	-0.309	**0.433**
Basal Leaf Pattern	**0.783**	-0.106	-0.117	-0.115	0.090	-0.130	-0.036	0.030	0.230	0.118
Lobe Incision of Basel Leaf	**0.744**	-0.095	-0.061	-0.356	-0.020	0.028	0.120	-0.001	0.141	0.006
Leaf Angle to Main Stem	-0.087	-0.003	0.019	-0.026	0.085	-0.018	0.005	-0.045	0.015	**0.808**
Petiole Colour	0.274	0.145	-0.206	-0.140	0.031	0.316	-0.168	**0.618**	-0.080	0.062
Petiole Hairiness	-0.325	0.215	0.139	-0.038	-0.365	0.160	**0.493**	-0.108	0.140	-0.014
Calyx Hairiness	-0.046	0.192	**0.804**	-0.063	-0.019	-0.025	0.084	-0.108	0.107	-0.112
Corolla Hairiness	0.027	0.121	**0.795**	-0.036	0.016	-0.011	0.115	0.124	-0.086	0.237
Exterior Corolla Colour	-0.038	-0.086	0.096	0.047	0.105	**0.731**	0.036	0.010	0.307	-0.098
Interior Corolla Colour	-0.044	-0.180	0.107	-0.005	-0.036	-0.109	0.028	**0.821**	0.129	-0.026
Corolla Interior Pigmentation	0.092	-0.008	0.087	-0.560	-0.414	-0.019	-0.025	-0.046	**0.406**	0.017
Lower Lip Colour	0.055	0.143	0.032	0.058	0.013	0.077	0.005	0.064	**0.775**	0.041
Plant Height	**0.671**	0.031	0.105	0.179	-0.187	0.309	-0.007	0.049	-0.267	-0.039
Number of Flowers per Leaf Axil	-0.040	0.059	0.336	**0.380**	-0.477	0.034	-0.071	0.211	0.063	-0.102
Number of Nodes to First Flower	**0.549**	0.215	0.054	0.095	0.404	-0.098	-0.006	0.262	-0.077	-0.088

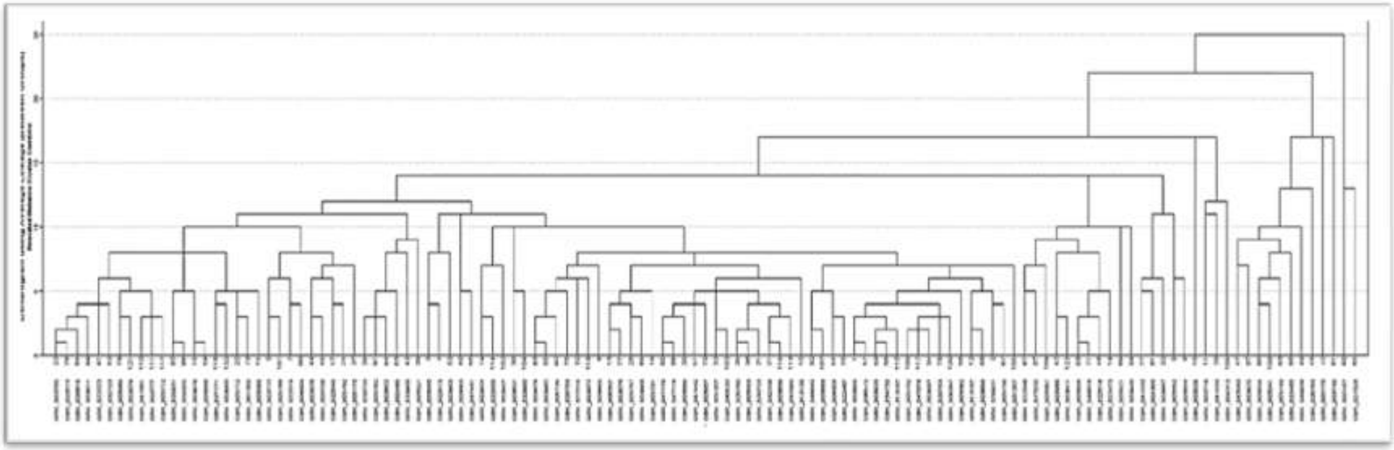

Figure 1:- Genetic relationship among 123 cowpea accessions generated by unweighted pair group method with arithmetic mean (UPGMA).

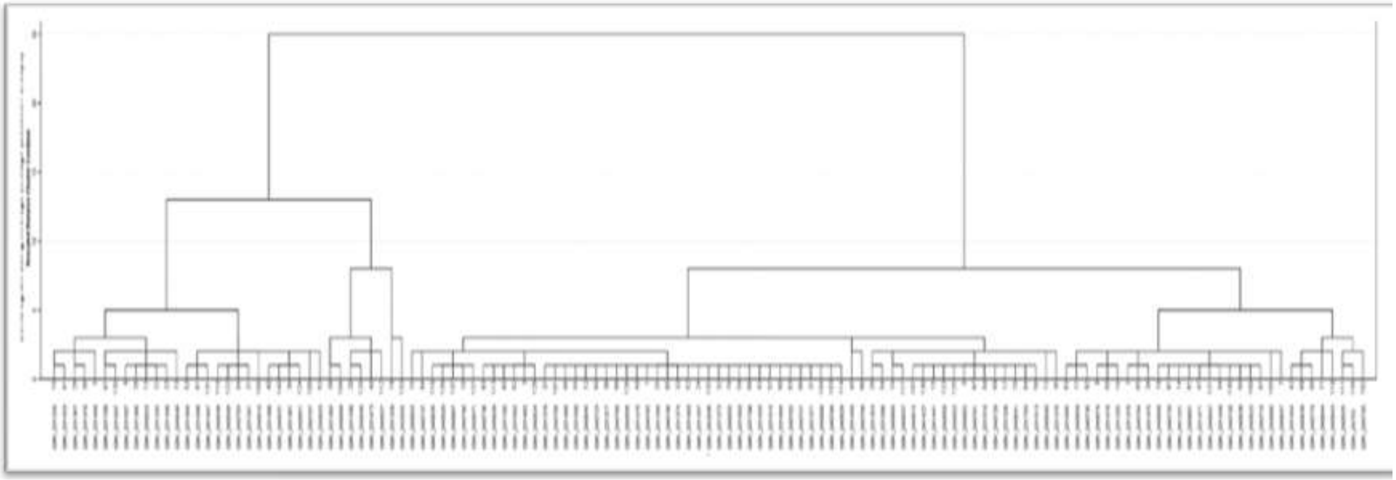

Figure 2:- Genetic relationship among 129 sesame accessions generated by unweighted pair group method with arithmetic mean (UPGMA).

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References:-

1. WORLD DATA ATLAS (2022) SESAME PRODUCTION IN THE WORLD AVAILABLE AT HTTPS://KNOEMA.COM/DATA/AGRICULTURE-INDICATORS-PRODUCTION+SESAME
2. FAOSTAT. 2022.Food and Agriculture Organization Statistics, Statistical data on crops, sesame seeds, area, production quantity of Tanzania, Africa and the world, Available online at, http://www.fao.org, 2022. (Accessed 20 December 2022).
3. AFA. (2014). Agriculture and Food Authority Year book of Statistics.http://www.agricultureauthority.go.ke/wp-content/uploads/2016/03/AFFA-Year-Book-of-Statistics-2014.pdf. Downloaded 4/25/2018 4.13 PM
4. Olajide, A.A. and C. O. Ilori. 2017. Effects of drought on morphological traits in some cowpea genotypes by

evaluating their combining abilities. Advances in Agriculture Volume 2017, Article ID 7265726, 10 pages https://doi.org/10.1155/2017/7265726.

5. Mohammed B.and G.A. Hamidu. 2018. Growth and yield performance of sesame (SesamumindicumL.) varieties at varying levels of inter-row spacing in northern part of Sokoto, Nigeria. Asian Journal of Research in Crop Science1 (2): 1-14.
6. Wamalwa,E.N., J. Muoma, and C.Wekesa. 2016. Genetic diversity of cowpea (Vignaunguiculata(L.) Walp.) accession in Kenya genebankbased on simple sequence repeat markers. International Journal of Genomics Volume 2016, Article ID 8956412, 5 pages http://dx.doi.org/10.1155/2016/8956412.
7. Ong'injoE.O. and P.O. Ayiecho.2009.Genotypic variability in sesame mutant lines in Kenya.African Crop Science Journal 17 (2): 101 – 107.
8. Faisal I., R. A. Gill, B. Ali, M. A. Farooq, L. Xu, U.Najeeb and W. Zhou.2016. Sesame.p.135-147. In S. K.Gupta (ed) Breeding oilseed crops forsustainable production. Opportunities and Constraints. Elsevier Academic PressAnsterdam. Boston. Heldelberg. London. New York. Oxford. Paris. San Diego. San Franscisco. Singapore. Sydney. Tokyo.
9. Jaetzold, R. and H. Schmidt.1982. Farm Management Handbook of Kenya.Natural Conditions and Farm Management Information. Vol. II/C. East Kenya. (Eastern and Coast Provinces). Ministry of Agriculture, Nairobi, Kenya.
10. Pele,F. D., A.Yeboah, M. S. Buari and E. J. Kofi. 2016.Morpho-physiological parameters used in selecting drought tolerant cowpea varieties using drought index. African Journal of Agriculture 3 (1): 125-134.
11. GeRRI (2015) Kenya national strategy on genetic resources within the context of climate change 2016-2020, Genetic Resources Research Institute (GeRRI), Kenya Agricultural and Livestock Research Organization (KALRO), Kenya.
12. Olubunmi, I. D. 2015.Genetic analysis of drought tolerance in cowpea [vignaunguiculata(l.) Walp. PhD Dissertation. http://ugspace.ug.edu.gh/bitstream/handle/123456789/8616. downloaded 3/27/2018 4.18PM
13. Kramer, P.J. 1980. Drought stress and the origin of adaptations. p.7-20.In N.C. Turner and Kramer (ed) Adaptation of plants to water and high temperature stress. Wiley interscience publication. New York.
14. Pungulani, L. L. M., J.P. Millner, and W.M. Williams. 2012. Screening cowpea (Vignaunguiculata) germplasm for canopy maintenance under water stress. Agronomy New Zealand 42: 23-32.
15. Pungulani, L. L. M., J.P. Millner, W. M. Williams, and M. Banda. 2013. Improvement of leaf wilting scoring system in cowpea (Vignaunguiculata(L) Walp.): From qualitative scale to quantitative index. Australian Journal of Crop Science 7(9):1262-1269.
16. Márcia C., T.Lino-Neto, E. Rosa, and V.Carnide. 2017. Cowpea: a legume crop for a challenging environment. Journal of the Science of Food and Agriculture97: 4273–4284.
17. Ishiyaku, M. F. and A. Habibu. 2013. Field evaluation of cowpea genotypes for drought tolerance and strigaresistance in the dry savanna of North-West Nigeria. International Journal of Plant Breeding and Genetics 7 (1):47-56.
18. Mwale, S.E., Ochwo-Ssemakula, M., Sadik, K., Achola, E., Okul, V., Gibson, P., Edema, R.,Singini, W. and Rubaihayo, P. 2017. Response of cowpea genotypes to drought stress in Uganda. American Journal of Plant Sciences 8: 720-733.
19. Naima G., M. Malice, J.M. Jacquemin,S.M. Ounane, L.Mekliche, and J.P.Baudoin. 2009. Morphological and molecular diversity within Algerian cowpea (Vignaunguiculata (L.) Walp.) landraces. Genet Resources and Crop Evolution 57:371–386.
20. Karuma, R.W., O. Kiplagat, E. Ateka, and G.Owuoche. 2008. Genetic diversity of Kenyan cowpea accessions based on morphological and microsatellite markers. East African Agricultural andForestry Journal76: 3–4.
21. Satoshi L., K. Y. Shinozaki, T. Urao, T.Terao, and K. Shinozaki. 1996. Novel drought-inducible genes in the highly drought-tolerant cowpea: Cloning of cDNAs and analysis of the expression of the corresponding genes. Plant CellPhysiology37(8): 1073-1082.
22. SPSS. (1999). SPSS for Windows, Standard Version, SPSS Inc.
23. Weisskopf, A. and D.Q. Fuller. 2014. Sesame: Origins and Development. In: Smith, C. (ed) Encyclopedia of Global Archaeology. Springer, New York.
24. UNESCO (1977) FAO-UNESCO Soil Map of the World. Vol. VI. Africa. UNESCO, Paris, France.