Mysore J. Agric. Sci., 59 (3) : 12-21 (2025)

Unlocking Genetic Potential: Morphological Insights and Genetic Diversity Assessment in Bambara Groundnut (*Vigna subterranea* L. Verdc.) Accessions Imported from IITA, Ibadan, Nigeria

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Received : January 2025
Accepted : Feburary 2025

ABSTRACT

Bambara groundnut (*Vigna subterranea* [L.] Verdc.) is a nutrient-dense legume native to Africa. Known for its drought resilience, it thrives in low-input and marginal agricultural systems across both Africa and Asia. The present study aims to analyse the genetic diversity and potential for crop improvement among 84 Bambara groundnut genotypes for 24 quantitative traits using an augmented design. The analysis of variance (ANOVA) revealed substantial differences among genotypes for certain quantitative traits revealing considerable genetic variability. Days to germination ranged from 6 to 11 days and days to first flowering spanned between 40 to 60 days indicating both early- and late-flowering types. Wide variability was observed in pod count (1 to 54 pods per plant) and seed yield (0.6g to 185g per plant) showing a wide spectrum of diversity indicating potential pathways for breeding. The 84 genotypes were categorized into eight clusters utilizing K means clustering and notably no single cluster possessed all desired traits, reinforcing the necessity of crossbreeding to achieve optimal trait combinations. Average intra- and inter-cluster distances calculated revealed that the inter-cluster distances exceeded intra-cluster distances thus indicating a substantial level of genetic variation among the genotypes. Days to maturity was the largest contributor to genetic divergence (19.25%) followed by number of leaves and shelling percentage. Contribution was less from traits like number of seeds/pods and pod thickness. The findings reveal that Bambara groundnut holds valuable genetic resources for crop improvement with hybridization across diverse clusters offering a promising route for developing high-yielding, adaptable varieties. This genetic diversity in Bambara groundnut could contribute significantly to food security especially in regions where it is an underutilized crop.

Keywords : Bambara groundnut, Genotypes, Cluster analysis, Genetic diversity

BAMBARA groundnut (*Vigna subterranea* L. Verdc., 2n=2x=22) is predominantly cultivated by small-scale farmers in sub-Saharan Africa and serves as a secondary food crop. Its origins can be traced back to West Africa. The name 'Bambara' is derived from the Bambara ethinic group near Timbuktu in Central Mali, West Africa. The term 'groundnut' reflects its underground development of the pod, hence the common name 'Bambara groundnut'. This leguminous crop ranks as the third most important source of food and revenue after peanut and cowpea among the African nations where it is grown. Women predominantly participate in its cultivation, sale, and processing, rendering it especially significant for female subsistence. It is an annual crop with similarities to groundnut (*Arachis hypogaea*) in terms of cultivation and appearance. It is a legume and is commonly planted independently or alongside drought-tolerant crops like millet. Bambara groundnut can thrive at elevations of up to 1600 m above sea level. The crop thrives well in temperatures ranging from 20 p C to 28 p C during day time. The crop also thrives in poor soil with low nutrient content. As per Wrigley (1981), this plant usually thrives in soil with a pH range of 5.0 to 6.5 and places receiving an annual rainfall between 600 to 1200 mm, it can also withstand high temperatures and is also capable of enduring varying levels of rainfall (Wrigley, 1981 and Dakora & Muofhe, 1996). Therefore, the crop is not highly susceptible to complete crop failure, particularly in regions with low and unpredictable rainfall. In many parts of Africa, it plays a significant role in providing good quantity of protein in the diets of a large portion of the population. The average yield is 650 to 850 kg/ha and depending on the environment and landrace, the crop requires a growth period of 110 to 150 days to mature (Rachie & Roberts, 1974 and Rachie, 1979). It is high in essential amino acids like leucine (102.1mg/g crude protein), lysine (80.2mg/g crude protein), cysteine (24.1mg/100g crude protein) and low in methionine (6.41mg/g crude protein). Its seeds have a higher gross energy value compared to other commonly consumed pulses like cowpea, lentil and pigeon pea. In essence, the kind and extent of genetic variability in the crop determines the effectiveness of any crop improvement procedure. Understanding the nature and extent of genetic variability is crucial for designing an effective breeding program that would increase the genotypes' potential yield. As a result, any morphological feature that is associated with and significantly contributes to higher seed yield would be advantageous for increasing overall yield. The main objective of the research was focused on the study of genetic diversity among the 84 Bambara groundnut accessions to identify the genotypes to be included in hybridisation to improve yield.

MATERIAL AND METHODS

Experimental Material : The present study comprised of 84 germplasm accessions of Bambara groundnut imported from IITA, Nigeria (Table 1) through NBPGR, Delhi.

Evaluation of Experimental Material : The research was conducted at Zonal Agricultural Research Station, V.C. Farm, Mandya, University of Agricultural Sciences, Bangalore during the *kharif* of 2023.

TABLE 1

List of Bambara groundnut accessions used for the study

Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
1	TVSu-5	29	TVSu-536	57	TVSu-1108
2	TVSu-6	30	TVSu-545	58	TVSu-1123
3	TVSu-11	31	TVSu-574	59	TVSu-1252
4	TVSu-97	32	TVSu-592	60	TVSu-1260
5	TVSu-106	33	TVSu-597	61	TVSu-1272
6	TVSu-138	34	TVSu-598	62	TVSu-1321
7	TVSu-158	35	TVSu-611	63	TVSu-1379
8	TVSu-217	36	TVSu-612	64	TVSu-1388
9	TVSu-235	37	TVSu-627	65	TVSu-1394
10	TVSu-262	38	TVSu-633	66	TVSu-1403
11	TVSu-270	39	TVSu-640	67	TVSu-1408
12	TVSu-275	40	TVSu-691	68	TVSu-1431
13	TVSu-283	41	TVSu-698	69	TVSu-1451
14	TVSu-287	42	TVSu-702	70	TVSu-1459
15	TVSu-302	43	TVSu-723	71	TVSu-1603
16	TVSu-303	44	TVSu-740	72	TVSu-1614
17	TVSu-328	45	TVSu-878	73	TVSu-1620
18	TVSu-329	46	TVSu-884	74	TVSu-1641
19	TVSu-330	47	TVSu-885	75	TVSu-1658
20	TVSu-334	48	TVSu-926	76	TVSu-1662
21	TVSu-367	49	TVSu-975	77	TVSu-1684
22	TVSu-442	50	TVSu-989	78	TVSu-1693
23	TVSu-445	51	TVSu-1034	79	TVSu-1721
24	TVSu-455	52	TVSu-1038	80	TVSu-1829
25	TVSu-458	53	TVSu-1049	81	TVSu-1833
26	TVSu-505	54	TVSu-1051	82	TVSu-1887
27	TVSu-513	55	TVSu-1068	83	TVSu-1940
28	TVSu-527	56	TVSu-1069	84	TVSu-1972

TABLE 2

Analysis of variance (ANOVA) for twenty-four traits in 84 Bambara groundnut (*Vigna subterranea* L. Verdc.) accessions

Source	df	DG	DFF	DFT	NFPP	BL	PL	NOS	NL	TLL	TLW	PETL	PLSP
	1	2	3	4	5	6	7	8	9	10	11	12	13
Treatment (ignoring Blocks)	85	1.18 ns	18.25 **	38.89 **	0.08 ns	2.12 ns	27.72 *	31.71 *	2467.92 **	164.48 ns	30.04 ns	7.98 ns	40.22 ns
Treatment: Check	1	0.50 ns	46.72 **	29.39 **	0.06 ns	12.50 **	2.35 ns	156.06 **	1624.50 *	7.22 ns	41.10 ns	15.31 ns	9.83 ns
Treatment: Test	83	1.20 ns	13.94 **	25.83 **	0.08 ns	1.93 ns	27.79 *	28.09 *	2449.95 **	159.25 ns	30.20 ns	7.98 ns	41.04 ns
Treatment: Test vs. Check	1	0.24 ns	347.43 **	1132.87 **	0.00 ns	7.07 *	47.33 *	207.57 **	4802.82 **	755.71 *	5.59 ns	0.82 ns	2.31 ns
Block (eliminating Treatments)	8	0.93 ns	2.60 ns	2.43 ns	0.06 ns	1.37 ns	2.94 ns	14.47 ns	345.00 ns	32.49 ns	21.23 ns	2.93 ns	25.67 ns
Residuals	8	0.87	1.60	1.51	0.06	0.88	6.47	8.56	219.00	118.07	51.21	4.27	48.42

Continued....

Source	df	PH	DM	NOPP	POD	POW	PODT	SP	NOSP	SEL	SW	Y	TW
	14	15	16	17	18	19	20	21	22	23	24	25	26
Treatment (ignoring Blocks)	85	5.80 ^{ns}	75.05 **	157.26 ^{ns}	11.73 ^{ns}	3.50 ^{ns}	0.06 **	65.51 **	0.18 ^{ns}	2.30 *	1.33 ^{ns}	851.17 **	241.10 **
Treatment: Check	1	12.33 ^{ns}	329.39 **	2.00 ^{ns}	9.53 ^{ns}	38.14 **	0.02 ^{ns}	213.56 **	0.22 ^{ns}	0.25 ^{ns}	0.22 ^{ns}	2652.35 **	833.68 **
Treatment: Test	83	5.79 ^{ns}	39.69 **	137.51 ^{ns}	11.85 ^{ns}	3.12 ^{ns}	0.06 **	36.62 *	0.18 ^{ns}	2.32 *	1.36 ^{ns}	811.49 **	197.93 **
Treatment: Test vs. Check	1	0.39 ^{ns}	2755.86 **	1952.30 **	4.58 ^{ns}	0.11 ^{ns}	0.03 ^{ns}	2315.74 **	0.20 ^{ns}	2.65 ^{ns}	0.37 ^{ns}	2343.52 **	3231.82 **
Block (eliminating Treatments)	8	3.11 ^{ns}	20.56 *	26.75 ^{ns}	13.57 ^{ns}	4.28 ^{ns}	0.04 *	27.75 ^{ns}	0.10 ^{ns}	1.96 ^{ns}	0.69 ^{ns}	24.73 ^{ns}	175.16 **
Residuals	8	3.62	5.89	68.75	8.21	1.57	0.01	9.06	0.10	0.69	0.98	53.68	8.48

*Significant at p=5% ,**Significant at p=1%

DG = Days to germination, DFF = Days to first flowering, DFT = Days to fifty percent flowering,
NFPP = Number of flowers/peduncle, BL = Banner length, PL = Peduncle length, NOS = No of stems, NL = Number of leaves,
TLL = Terminal leaflet length, TLW = Terminal leaflet width, PETL= Petiole Length, PLSP = Plant spread, PH = Plant height,
DM = Days to maturity, NOPP = Number of pods/plant, POD = Pod length, POW = Pod width, PODT = Pod thickness, SP = Shelling %,
NOSP = Number of seeds/pods, SEL = Seed length, SW = Seed width, Y = Seed Yield, TW = Test weight

The accessions were grown in augmented design and planted at a spacing of 45cm x 15cm. All essential agronomic practices were carried out in accordance with the crop production guide. Observations on all quantitative traits were recorded using the descriptors outlined by IPGRI (2000). Data collection was conducted on five randomly selected plants to assess agro-morphological and seed traits at different growth stages. In total, 24 quantitative traits were evaluated in the study.

Statistical Analysis : The R statistical software (version 3.3.2) was utilized to classify 84 Bambara groundnut genotypes into distinct clusters based on genetic diversity. The same was also employed to calculate intra- and inter-cluster distances and to construct a dendrogram

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) showed highly significant differences among the genotypes for twelve traits *viz.,* days to first flowering, days to fifty per cent flowering, banner length (uppermost petal is referred to as the banner), plant length, number of stem, number of leaves, terminal leaf length, days to maturity, number of pods/plant, shelling percent, yield and test weight, out of the twenty four quantitative traits examined indicating a substantial amount of genetic variability among them (Table 2). Karikari (2000) reported that the high genetic variability observed in Bambara groundnut landraces lends itself to high potential for crop improvement. The trait means, range, standard deviation and coefficient of variance for all the twenty-four quantitative traits are presented in Table 3. Days to germination ranged from 6 days (TVSu-513, TVSu-1603) to 11 days (TVSu-302, TVSu-545, TVSu-574) with mean value of 8.07 days while the days to first flowering ranged between 40 days (TVSu-283, TVSu-458, TVSu-740, TVSu-1662) to 60 days (TVSu-287, TVSu-329) after sowing (DAS) with mean of 46.45 indicating wide variation for days to flowering.

TABLE 3

Summary statistics of various quantitative traits evaluated in 84 Bambara groundnut (*Vigna subterranea* L. Verdc.) germplasm accessions

Trait	Mean	Std. Error	Range		Std. Deviation	CV
			Min	Max		
DG	8.04	0.12	6	11	1.09	11.62
DFF	46.23	0.407	40	60	3.73	2.77
DFT	56.52	0.554	48	74	5.08	2.23
NFPP	1.94	0.03	1	2	0.27	12.14
BL	5.83	0.152	3	9	1.39	16.31
PL	19.06	0.575	7.6	41.2	5.27	13.54
NOS	14.02	0.578	4	28	5.3	20.13
NL	110.75	5.401	24	249	49.49	13.06
TLL	33.80	1.377	16.8	71.6	12.62	33.65
TLW	17.57	0.6	8.7	30.9	5.49	41.67
PETL	15.21	0.308	10.2	25.6	2.82	13.61
PLSP	27.34	0.699	16.5	43.9	6.4	25.67
PH	19.34	0.262	14.7	27.4	2.4	9.88
DM	135.33	0.687	124	147	6.29	1.82
NOPP	12.31	1.279	1	54	11.73	58.33

Continued....

Table 3 Continued....

Trait Mean		Stand. Error	Range		Std.Deviation	CV
			Min	Max		
POD	18.33	0.376	11	29.5	3.44	15.59
POW	11.89	0.193	7.3	16.6	1.77	10.38
PODT	1.04	0.027	0.54	1.64	0.24	10.03
SP	63.45	0.66	47.6	77.9	6.05	4.6
NOSP	1.22	0.048	1	2	0.44	25.86
SEL	10.76	0.166	6.3	13.5	1.53	7.85
SW	8.13	0.127	5.1	11	1.17	12.15
Y	22.67	3.108	0.6	185	28.49	29.87
TW	43.18	1.535	14.3	81.6	14.07	7.03

Number of pods per plant showed broad range of variation from 1 (TVSu-97, TVSu-442, TVSu-611, TVSu-612, TVSu-627) to 54 (TVSu-691) with an average of 12.19 pods per plant. These findings were in alignment with the studies carried out by Chibudu (1997). Number of seeds per pod showed least variation and varied between 1 to 2 while the seed yield showed the maximum variation and ranged between 0.6g/plant (TVSu-1068) to 185g/plant (TVSu-1321) with a mean of 22.31g/plant. Similar research by Goli *et al*. (1997) on Bambara groundnut collections at IITA highlighted substantial agro-morphological diversity, which could be leveraged for crop improvement. However, this agro-morphological diversity should be validated through molecular and genetic studies.

Based on the K means cluster analysis of the morphological traits studied, the 84 genotypes were grouped into eight clusters (cluster I - VIII).

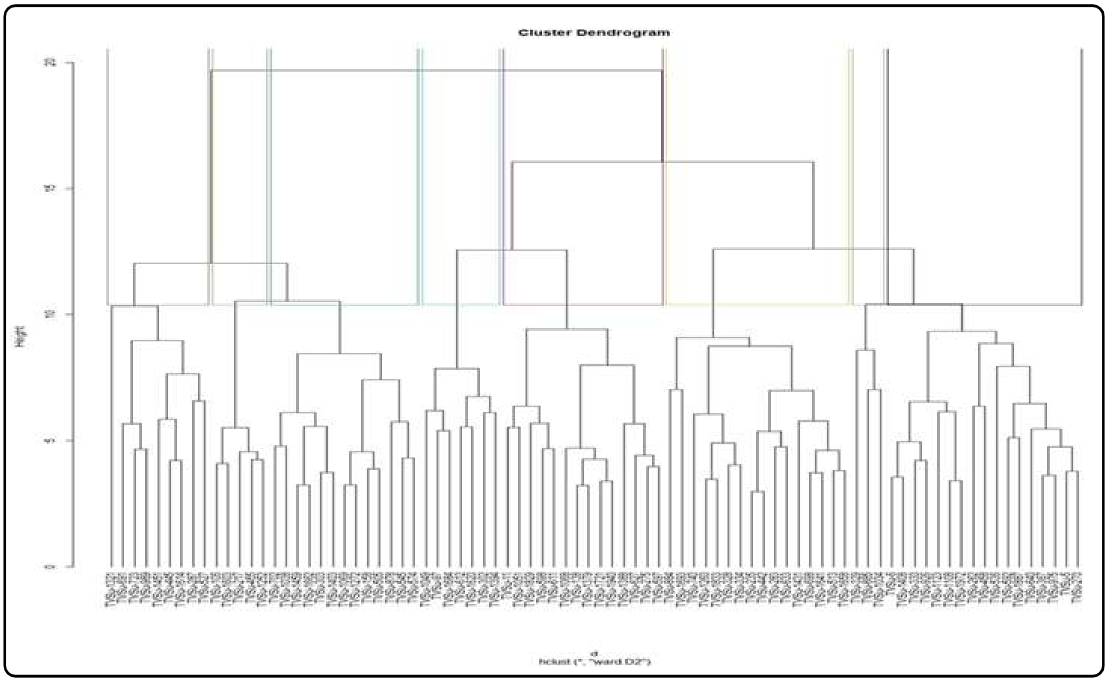

Fig. 1 : Hierarchical clustering pattern of 84 Bambara groundnut (*Vigna subterranea* L. Verdc.) germplasm accessions

TABLE 4

Distribution of 84 Bambara groundnut (*Vigna subterranea* L. Verdc.) into different clusters based on genetic divergence (Hierarchical clustering)

Cluster No.	Number of Genotypes in cluster	Genotypes included in the cluster
I	9	TVSu-1321, TVSu-691, TVSu-723, TVSu-989, TVSu-1451, TVSu-445, TVSu-1614, TVSu-287, TVSu-527
II	5	TVSu-106, TVSu-1603, TVSu-217, TVSu-455, TVSu-1252
III	13	TVSu-702, TVSu-1038, TVSu-1459, TVSu-1662, TVSu-303, TVSu-1403, TVSu-1069, TVSu-1272, TVSu-158, TVSu-505, TVSu-878, TVSu-545, TVSu-574
IV	7	TVSu-1049, TVSu-97, TVSu-1684, TVSu-612, TVSu-1620, TVSu-302, TVSu-1394
V	14	TVSu-11, TVSu-1051, TVSu-1829, TVSu-598, TVSu-611, TVSu-1068, TVSu-138, TVSu-1379, TVSu-1721, TVSu-1940, TVSu-1388, TVSu-627, TVSu-275, TVSu-597
VI	16	TVSu-884, TVSu-1693, TVSu-740, TVSu-1260, TVSu-1833, TVSu-328, TVSu-334, TVSu-235, TVSu-442, TVSu-283, TVSu-633, TVSu-1431, TVSu-698, TVSu-1641, TVSu-513, TVSu-1658
VII	3	TVSu-329, TVSu-885, TVSu-1034
VIII	17	TVSu-6, TVSu-1408, TVSu-330, TVSu-926, TVSu-1123, TVSu-1108, TVSu-1972, TVSu-262, TVSu-458, TVSu-536, TVSu-592, TVSu-1887, TVSu-640, TVSu-367, TVSu-975, TVSu-5, TVSu-270

Fig. 1 represents the hierarchical clustering pattern of 84 Bambara groundnut germplasm accessions. The clustering pattern (Table 4) showed that the cluster VIII was the largest containing 17 genotypes, followed by cluster VI with 16 genotypes, cluster V with 14 genotypes, and cluster III with 13 genotypes. Cluster I included 9 genotypes, while cluster IV and cluster II had 7 and 5 genotypes, respectively. The smallest cluster was cluster VII with only 3 genotypes. Average intra and inter-cluster distances were computed from divergence analysis (Table 5). The inter-cluster distances were larger than the intra-cluster distances, indicating a significant degree of genetic variation across different clusters. The intra-cluster distance reflects the variation among genotypes within a cluster, while the inter-cluster distance represents the diversity between different clusters (Suresh and Savithramma, 2015).

The highest intra-cluster distance was recorded in Cluster IV (3.148) followed by Cluster II (2.530), while Clusters III, V and VII had the lowest intra-cluster distance (0.00) indicating no variation among the genotypes within these clusters. The maximum inter-cluster distance was observed between Clusters III and VIII (11.829) followed by Clusters VI and VIII (11.103) suggesting a high level of genetic diversity among the genotypes in these clusters. Consequently, elite genotypes from these diverse clusters can be selected as parent lines for hybridization to produce high-yielding individuals with favourable yield-related traits in future generations. Such crosses will create variability for desired traits facilitating the selection of superior recombinants for trait improvement. Similar findings were reported by Saini *et al*. (2020) in groundnut wherein recombinant inbred lines (RILs) were

TABLE 5

Average intra- and inter-cluster distance (diagonal) among 8 clusters in 84 genotypes of Bambara groundnut

	1	2	3	4	5	6	7	8
1	**1.993747**	3.175108	5.802835	4.373375	5.790632	6.692659	6.504179	7.253118
2		**2.530019**	4.396772	3.568092	6.060871	5.956659	5.487579	8.828770
3			**0**	4.421305	7.602493	5.678631	5.021850	11.829463
4				**3.148112**	6.852870	4.264871	4.109961	9.638346
5					**0**	9.370121	8.987428	7.239146
6						**2.372181**	3.634499	11.103514
7							**0**	11.472202
8								**1.254202**

(Bold figures indicate intra-cluster distance)

grouped into 15 clusters using Tocher's method highlighting substantial diversity. The minimum inter-cluster distance was noted between Clusters I and II (3.175) indicating close genetic relationships, which suggests that selecting parents from within the same cluster may not be effective for hybridization programs. The findings in the present study are in line with the results reported by Preethi *et al*. (2022) in blackgram where the most promising genotypes from divergent clusters may be used as parents directly in future hybridization programs. An analysis of cluster means for 24 quantitative traits (Table 6) indicated significant differences across different clusters for all traits underscoring that each cluster encompasses genotypes with distinct phenotypic characteristics. Lowest cluster mean values for days to germination was observed in cluster VII (7.50 days) and highest mean values (8.56 days) in cluster I. The mean days to first flowering was lowest (43.21 days) in cluster VII and was highest (50.80) in cluster VIII while the mean days to fifty percent flowering was found to be lowest (51.86 days) in cluster VII and maximum (62.20) in cluster VIII. The mean banner length was maximum (6.60) in cluster IV while minimum in cluster VIII (4.40). Peduncle length was maximum (23.35) in cluster III while minimum (15.43) in cluster V. The mean number of stems was found to be maximum (19.27) in cluster II and minimum (8.90) in cluster VI while mean number of leaves was maximum (168.63) in cluster V and lowest (59.30) in cluster VI. The mean days to maturity was lowest in cluster II at 132.00 days while it was highest (142.38 days) in cluster V. The mean number of pods per plant was lowest (3.00) in cluster III and maximum (43.40) in cluster VIII. The mean shelling percentage was maximum in cluster III at 71.05 per cent while it was minimum at 61.09 per cent in cluster VI. The mean number of seeds/pods was lowest (1.00) in both clusters I and II while maximum (1.80) in cluster VIII. The seed yield per plant was high (90.94g/plant) in cluster VIII while it was minimum in cluster I at 3.27g/ plant. The maximum mean test weight of 52.48 g was recorded in cluster VI while it was lowest (34.13g) in cluster V. Baswana *et al.* (1980) previously observed a similar pattern of diversity in the germplasm evaluation studies in Dolichos beans.

Organizing a large collection of germplasm accessions into a smaller number of homogeneous clusters simplifies the process of selecting diverse parents for breeding programs. This study highlighted the presence of substantial genetic variability within the evaluated material. These findings indicate that none of the clusters contained genotypes possessing all desirable traits for direct selection and use. Consequently, hybridizing genotypes from different

Table 6

Cluster mean values of twenty-four quantitative traits in 84 genotypes of Bambara groundnut (*Vigna subterranea* L. Verdc.) accessions

Cluster	DG	DFF	DFT	NFPP	BL	PL	NOS	NL	TLL	TLW	PETL	PLSP
	1	2	3	4	5	6	7	8	9	10	11	12
1	8.56	47.00	58.00	1.78	6.56	17.57	12.89	99.22	37.47	21.56	16.92	31.14
2	7.93	45.40	55.80	1.93	6.20	17.78	19.27	154.27	43.95	21.09	13.33	30.04
3	8.50	48.00	59.13	1.63	5.38	23.35	11.00	100.63	26.93	15.29	15.18	23.68
4	8.40	45.13	54.73	2.00	6.60	19.81	11.73	91.73	22.90	11.37	16.66	21.86
5	8.00	48.25	59.63	2.00	5.75	15.43	17.88	168.63	49.15	22.94	14.28	32.09
6	7.90	49.20	60.40	2.00	6.30	18.05	8.90	59.30	22.50	13.53	15.30	23.23
7	7.50	43.21	51.86	1.93	4.79	21.46	15.07	110.50	37.81	19.43	14.64	30.03
8	8.00	50.80	62.20	2.00	4.40	18.32	10.60	75.40	23.06	11.52	16.42	22.82

Continued....

Cluster	PH	DM	NOPP	POD	POW	PODT	SP	NOSP	SEL	SW	Y	TW
	13	14	15	16	17	18	19	20	21	22	23	24
1	19.42	133.67	4.11	14.79	9.56	0.89	63.76	1.00	10.34	8.06	3.27	41.84
2	20.04	132.00	11.40	18.93	12.48	1.00	63.11	1.00	9.10	7.26	20.41	51.07
3	18.45	138.38	3.00	15.74	11.25	1.05	71.05	1.38	9.13	6.56	4.69	41.26
4	17.69	135.47	10.33	20.78	12.74	1.22	63.01	1.53	10.85	8.13	21.05	45.43
5	19.90	142.38	20.38	18.09	12.00	1.21	61.14	1.25	12.18	9.09	35.49	34.13
6	18.32	137.50	12.40	17.05	12.06	0.84	61.09	1.30	11.61	8.18	12.70	52.48
7	20.73	135.14	9.50	19.24	12.84	1.03	61.14	1.07	11.68	9.09	22.84	37.34
8	20.08	134.00	43.40	19.32	12.08	1.07	63.22	1.80	10.66	8.70	90.94	44.50

clusters is essential to develop genotypes with the desired traits. The results of the present study are in line with studies by Mohammed *et al*. (2016), Atoyebi *et al*. (2017a) and Gbaguidi *et al*. (2018) who reported about high genetic variability in Bambara groundnut accessions.

The study also examined the percentage contribution of 24 traits to total genetic divergence and is presented in Table 7. The findings showed that days to maturity contributed the most (19.25%) to total genetic divergence, highlighting its importance in differentiating among the genotypes. Other traits with substantial contributions included number of leaves (15.20%) and shelling percentage (8.98%) while moderate to low contribution was exhibited by days to fifty percent flowering (8.17%), days to first flowering (6.67%), test weight (6.16%) and yield (3.74%). The lowest per cent contribution was shown by banner length (0.81%), number of flowers/ peduncle (0.27%), number of seeds/pod (0.18%) and pod thickness (0.15%).

TABLE 7

Percent contribution of the traits towards total genetic divergence in Bambara groundnut (*Vigna subterranea* L. Verdc.) accessions

Traits	Contribution to the Traits (%)
Days to germination	1.15
Days to first flowering	6.67
Days to fifty percent flowering	8.17
Number of flowers/peduncle	0.27
Banner length	0.81
Peduncle length	2.68
No of stems	1.90
Number of leaves	15.20
Terminal leaflet length	4.66
Terminal leaflet width	2.42
Petiole Length	2.17
Plant spread	3.80
Plant height	2.73
Days to maturity	19.25
Number of pods/plant	2.03
Pod length	2.55
Pod width	1.68
Pod thickness	0.15
Shelling %	8.98
Number of seeds/pods	0.18
Seed length	1.51
Seed width	1.14
Yield	3.74
Test weight	6.16
Total	100.00

The study underscores significant genetic variability among Bambara groundnut accessions, as revealed by ANOVA, cluster and divergence analyses. High genetic diversity was evident across multiple traits, with days to maturity contributing the most to genetic divergence. The clustering of accessions into eight groups highlights diversity among the genotypes offering a rich resource for selecting parent lines in breeding programs. These findings provide a foundation for future breeding efforts to exploit the genetic potential of Bambara groundnut.

Future Line of Work

The findings emphasize the need to validate agro-morphological diversity using molecular markers (e.g., SSRs, SNPs) to confirm genetic relationships among clusters and accessions and also thorough testing of germplasm accessions across multiple years and locations to identify stable, genetically diverse genotypes in Bambara groundnut. Breeding for yield optimization by focusing on genotypes with exceptional yield potential to optimize seed production and thereby improving nutritional food security should be given top most priority.

Acknowledgement : The author gratefully acknowledges Council of Scientific and Industrial Research (CSIR), New Delhi, India for providing Junior Research Fellowship (JRF) for pursuing Ph.D. degree program at UAS, Bangalore, India.

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