

Diversity Study of Some Common Bean Collection (*Phaseolus vulgaris* L.) from varied Environments

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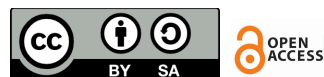
Abstract

Common bean (*Phaseolus vulgaris* L.), popularly known as Green bean, is still underutilized in Nigeria going by its anti-nutritional properties, longer cooking time, and limited germplasms, with no known improved variety. A total of 54 accessions were sourced International Center for Tropical Agriculture (CIAT), Uganda; International Institute of Tropical Agriculture (IITA) Nigeria, and from open markets in Jos, Abuja and Abeokuta, all in Nigeria; and evaluated to assess their level of diversity and adaptation to the southwest zone. The study was conducted at Ilora out-station of the Institute of Agricultural Research and Training (IAR&T) in 2022. The experiment was laid out in a Randomized Complete Block Design (RCBD) in two replications. Parameters on which data were collected are agronomic traits and yield, disease and pests damage. Data were subjected to Principal component analysis (PCA) and cluster analysis. Some accessions like Michigan Red, ADP -65 and TPV -205 performed well showing good sign of adaptability. Eight PCs with Eigen values >1 accounted for 99.86 % of the variations observed. PC1 alone accounted for 66.5 % of the variation with days to 50 % flowering and podding being most important. PC 2 and 3 accounted for 24.5 % and 6.75 % respectively, with pod weight/plot and 100 seed weight as the most significant traits, respectively. At 1/3 distance of the dendrogram, five major groups were formed. Group 3 had the largest number of accessions with a lot of sub-groups. The result revealed a broad genetic base in the pool for selection for further improvement.

Keywords: Adaptability, cluster analysis, crop improvement, principal component analysis, under-utilized legumes

Introduction

Common bean (*Phaseolus vulgaris* L.), also known as green bean, is a vegetable legume of high nutritional value. It has high dietary fibre which can help to lower high body cholesterol according to Hayat et al. [1]. It is rich in iron, and contains important vitamins and minerals thereby making it a potential key component in addressing nutritional security in Nigeria as reported by Boye et al. [2]. Despite its importance, common bean is still underutilized in Nigeria, where its potential has not been fully exploited to contribute to nutritional security. Adesoye and Ojobo [3] opine that Majority of the common beans consumed in the southwest are grown in Northern part of Nigeria. This shows that the environment plays a crucial role in shaping the diversity of common beans. Development of varieties adapted to the southwest will create more gene pool of the bean for



research purposes and increase its production and utilization in the zone, hence improving the health status of the populace.

There has been limited research on the extent and nature of genetic diversity among common bean accessions in Nigeria, leaving a significant gap in knowledge that this study aims to fill. This geographic and environmental diversity has resulted in significant phenotypic and genotypic variations, making this crop an important subject of study for understanding genetic diversity and its implications for agriculture according to Sher et al. [4]. According to Szilagyi et al. [5], diversity studies are crucial for identifying traits that can enhance crop performance, such as disease resistance, drought tolerance, and improved nutritional content. In Nigeria, where agriculture is central to the economy and food security, understanding the diversity of common beans is not just important but necessary for sustainable agricultural development. The need for studying the diversity of common bean collections from various environments is rooted in the need to improve the crop's productivity. Furthermore, not only will this study contribute to the global understanding of bean diversity, it will also provide critical insights for improving bean production in Nigeria. The objective of this study therefore is to assess the level of diversity among selected common bean accessions using agronomic traits.

Materials and Methods

A total of 54 accessions comprising of Snap bean, Navy bean, Kidney bean and Green pea were sourced from the International Centre for Tropical Agriculture (CIAT), Uganda, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria and from open markets in Jos, Abuja and Abeokuta (Table 1). The study was conducted at the Ilora out-station (Transition zone) of the Institute of Agricultural Research and Training (IAR&T), Ibadan in April, 2022.

The experimental layout is a Randomized Complete Block Design in two replications. A 2-row plot of 3 m long was used and seeds were sown at 1 seed per hole spaced at 60 cm apart. All plots were hoe weeded and insects were controlled using Cypermethrin 30g/L + Dimethoate 250 g/L EC when the need arises.

The accessions were evaluated for traits such as pod length (PL) in cm was measured from the average of 10 randomly selected pods among the harvested pods/plot, number of seeds per pod (SPP) was estimated by getting the average number of seeds in 10 selected pods, 100 seed weight (100SW) in g, seed weight per plot (SWP) in g, seed length (SL) in cm, seed width (SW) in mm, leaf damage (LD) was done by visual observation and rating done on a scale of 1-5 (1 for no damage and 5 for severe damage), virus incidence (VI), virus severity (VS) was done by visual observation and rating done on a scale of 1-5 (1 for no symptom and 5 for high severity), days to first flowering (DFF), days to 50% flowering (DPF) determined by counting the number of days from emergence to when 50% of the plants in a plot had flowered, days to first pod (DFP) determined by counting the number of days from emergence to when a pod first emerged, and days to 50% podding (DPP) determined by counting the number of days from emergence to when 50% of the plants had developed pods.

Data collected from these traits were analyzed using SAS version 9.0. Mean, CV and ranges were estimated. Principal component analysis (PCA) and cluster analysis were also conducted using PAST software.

Results and Discussion

Performance of Common Bean Accessions

Table 2 presents the top-performing common bean accessions using a 20% selection intensity based on various agronomic traits. The accessions 13, 15, and 3 (Michigan Red, ADP-655 and TPV-205) were particularly notable for their high performance for several traits. Accession 13, for instance, exhibited a high 100 seed weight (33.73 g), seed length (13.92 mm), and relatively early days to first flowering (32.00 days). Accession 15 also showed a high number of seed per pod (3.87), moderate pod length (11.56 cm), and early flowering (31.67 days). Some of the accessions evaluated did not survive at all, while some performed poorly, probably due to poor adaptability

of those accessions. This variability indicates a broad range of performance among the accessions, which could be exploited for improvement and breeding purposes.

Table 1: List of the 54 accessions and their sources evaluated in 2022

Accession Number	Accession Name	Location
1	TPV -84	IITA, Ibadan
2	TPV -131	IITA, Ibadan
3	TPV -205	IITA, Ibadan
4	TPV -694	IITA, Ibadan
5	TPV -757	IITA, Ibadan
6	TPV -917	IITA, Ibadan
7	TPV -923	IITA, Ibadan
8	TPV -929	IITA, Ibadan
9	TPV -938	IITA, Ibadan
10	TPV -950	IITA, Ibadan
11	Abeo 2020	Abeokuta
12	MONT-CALM	CIAT, Uganda
13	MICHIGAN RED	CIAT, Uganda
14	ADP-654	CIAT, Uganda
15	ADP-655	CIAT, Uganda
16	ADP-670	CIAT, Uganda
17	ADP-94	CIAT, Uganda
18	ADP-610	CIAT, Uganda
19	DAB 41	CIAT, Uganda
20	DAB 613	CIAT, Uganda
21	DAB 540	CIAT, Uganda
22	DAB 3	CIAT, Uganda
23	MBC 34	CIAT, Uganda
24	AWASH MELKA	CIAT, Uganda
25	AWASH -1	CIAT, Uganda
26	RAZ 42	CIAT, Uganda
27	NABE 6	CIAT, Uganda
28	RWV 3006	CIAT, Uganda
29	CAB 2	CIAT, Uganda
30	RANJANOMBY	CIAT, Uganda
31	MEXICO 142	CIAT, Uganda
32	SELLian 9	CIAT, Uganda
33	SELLian 10	CIAT, Uganda
34	SELLian 11	CIAT, Uganda
35	HAB 404	CIAT, Uganda
36	KSB-08-07	CIAT, Uganda
37	KSB-08-3	CIAT, Uganda
38	HAV 130	CIAT, Uganda
39	Tarrot	CIAT, Uganda
40	HAV 134	CIAT, Uganda
41	VAriet Local	CIAT, Uganda
42	HAB 449	CIAT, Uganda
43	PYramidae	CIAT, Uganda
44	LOIRET NOIR	CIAT, Uganda
45	Oxinel	CIAT, Uganda
46	HAB 406	CIAT, Uganda
47	KSB-08-11	CIAT, Uganda
48	HAB 423	CIAT, Uganda
49	HAB 173	CIAT, Uganda
50	AC Jos	Jos
51	AC Jos P1	Jos
52	AC Jos P2	Jos
53	AC ABJ	Abuja
54	Turtle bean	Abuja

Principal Component Analysis

Table 3 showed the principal component analysis (PCA) results for the traits assessed among the 54 common bean accessions evaluated in 2022. The first five principal components (PCs) are presented, with PC1 accounting for 66.5% of the total variation, followed by PC2 with 24.51%, PC3 with 6.75%, PC4 with 0.83%, and PC5 with 0.60%. The analysis further showed that days to 50% flowering (D50F) and days to 50% podding (D50P) contribute significantly to the first principal component, indicating that these traits are major determinants of variation among the accessions. The first principal component (PC1) accounts for 66.5% of the total variation, this highlights importance of reproductive stage traits such as days to 50% flowering (D50F) and days to 50% podding (D50P). These traits are crucial because they are directly associated with earliness, a highly desirable characteristic in breeding programs aimed at developing crops capable of escaping adverse climatic conditions like drought according to Labastida et al. [6]. Earliness can also help mitigate the risk of yield loss due to unexpected environmental stressors, allowing crops to complete their lifecycle before such events occur as reported by Xiong et al. [7].

Pod weight per plot (PWP) and 100 seed weight (100SW) contribute significantly to PC2 and PC3 respectively. The significance of pod weight per plot (PWP) in PC2, which explains 24.51% of the variance, highlights its role as a critical determinant of yield performance. The fourth and fifth principal components are less influential, with seed weight per plot (SWP) showing a significant negative loading on PC5. These findings suggest that traits related to the reproductive stage, particularly flowering and podding times, are critical in differentiating the accessions as also suggested by Chauhan et al. [8]. This information could guide selection in breeding programs, particularly when targeting earliness and yield traits.

Table 2. The top performing common bean accessions using 20% selection intensity

Acc	PL(cm)	SPP	100SW(g)	SL(mm)	SW(mm)	LD	VI	VS	DFF	DPF	DFF	DPP
13	11.41	3.40	33.73	13.92	7.09	2.33	4.18	3.00	32.00	36.00	34.33	38.67
15	11.56	3.87	27.03	12.23	6.47	2.33	4.18	2.67	31.67	36.00	36.33	40.67
17	10.43	3.13	31.37	13.86	6.99	2.00	13.68	2.00	31.33	36.00	35.67	40.33
20	10.27	3.00	30.13	13.35	6.93	2.50	1.59	1.33	32.33	37.00	37.33	43.00
21	10.15	3.13	30.10	14.07	7.41	3.50	3.94	2.33	31.33	36.00	35.67	41.33
14	11.04	3.13	33.97	15.07	6.96	2.00	9.01	3.33	32.33	37.00	36.00	42.67
18	10.96	3.20	25.53	14.37	7.72	2.33	5.36	2.83	31.33	35.67	36.00	41.67
30	11.61	2.80	31.53	13.17	6.27	3.00	6.78	1.67	31.33	35.67	36.00	40.00
3	11.93	4.60	22.83	12.74	6.67	2.33	4.74	2.00	33.67	39.67	37.33	43.67
12	11.05	3.80	27.03	10.69	6.22	2.00	7.84	2.67	31.67	36.33	37.00	42.33
16	11.46	3.00	40.40	14.31	7.03	2.00	6.25	2.00	33.33	37.00	37.00	48.00
Mean	9.88	3.25	23.50	10.90	5.89	2.70	5.16	1.88	38.52	43.30	44.07	50.54
S.E	0.25	0.14	0.73	0.33	0.17	0.07	0.56	0.09	1.42	1.43	1.55	1.59
CV(%)	23.04	42.03	23.05	30.40	28.70	27.72	133.00	56.20	37.01	32.86	32.30	29.00
Range	0-16.36	0-6.6	6.4- 53	0- 16	0-9.26	1-5	0- 33	1-5	29-144	31- 148	33- 147	37- 152

Acc: Accession; PL: Pod length ; SPP: Seed per pod; 100SW: 100 Seed weight; SL: Seed length; SW: Seed width; LD: Leaf damage (1-5) 1 for no damage, 5 for severe damage; VI: Virus incidence (%); VS: Virus severity (1-5) 1 for no symptom, 5 for high severity; DFF: Days to first flowering; DPF: Days to 50% flowering; DFP: Days to first pod; DPP: Days to 50% podding

Genetic Relatedness among Common Bean Accessions Using Dendrogram

The dendrogram in Figure 1 illustrates the genetic relatedness among the common bean accessions, as derived from the cluster analysis. The dendrogram reveals distinct clusters, indicating varying degrees of genetic

similarity among the accessions. Therefore, at 1/3 distance of the dendrogram, five major groups were formed. Cluster 3 had the largest number of accessions with a lot of sub-groups. Accessions such as 51, 53, and 52 form a closely related cluster which suggests that the accessions share a closer genetic makeup, which could be indicative of similar agronomic traits or breeding history, whereas accessions like 1, 34, and 18 are more distantly related. The identification of these clusters provides valuable insights for breeding programs aiming to combine desirable traits from genetically diverse accessions to enhance crop performance under varying environmental conditions.

Table 3: Principal component analysis for the traits assessed among the 54 common bean accessions evaluated in 2022.

Traits	PC1	PC2	PC3	PC4	PC5
PL	0.00	0.07	0.25	0.48	0.12
PW	0.00	0.08	0.23	0.23	0.21
PWP	0.01	0.89*	-0.35	-0.11	0.26
SPP	0.00	0.04	0.02	0.25	0.17
100SW	0.00	0.32	0.80*	-0.46	-0.18
SWP	0.01	0.29	-0.08	0.38	-0.86*
SL	0.00	0.12	0.29	0.42	0.25
SW	0.00	0.06	0.14	0.24	0.11
LD	0.01	0.01	0.03	0.08	0.00
VSV	0.00	0.02	0.04	-0.02	-0.01
D50F	0.70*	-0.03	-0.06	-0.15	0.01
D50P	0.71*	0.01	0.07	0.14	-0.01
Eigen value	785.91	289.60	79.76	9.79	7.12
% variance	66.5	24.51	6.75	0.83	0.60
Cumulative variance %	66.5	91.01	97.76	98.59	99.19

The clustering patterns observed in the dendrogram align with previous studies, which have showed the usefulness of genetic diversity in improving crop performance. For instance, FAO [9] reported that mung bean accessions with greater genetic diversity were more likely to exhibit superior performance under stress conditions. This finding supports the notion that genetically diverse germplasms are crucial for breeding climate-resilient crops capable of thriving in variable environments.

In conclusion, the study represents a preliminary step in evaluation of common bean to test their adaptability and understand its diversity for further improvement. The study established high genetic variation in the common bean accessions, most especially for traits such as Days to 50% flowering and Days to 50% podding which constitute major determinants of variation among the accessions. By harnessing the genetic diversity within common bean collections, we can ensure the continued productivity and resilience of this important crop for future generations.

Authors' contribution

Adewumi A.D: Literature review, Data interpretation, original draft, writing and editing. **Oloyede-Kamiyo Q.O:** Conceptualization, Supervision, experiment planning, Data analysis, and Review. **Adewumi A.D., Oladipo M.S., Oloyede-Kamiyo Q.O, Ukachukwu P.C.:** Carried out the experiments. **Ukachukwu P.C and Oladipo M.S.:** Reviewing and Editing. **Kareem K.T., Oduwaye O.F., Olayinka R.B.:** Technical Expertise and guidance on insect and disease data.

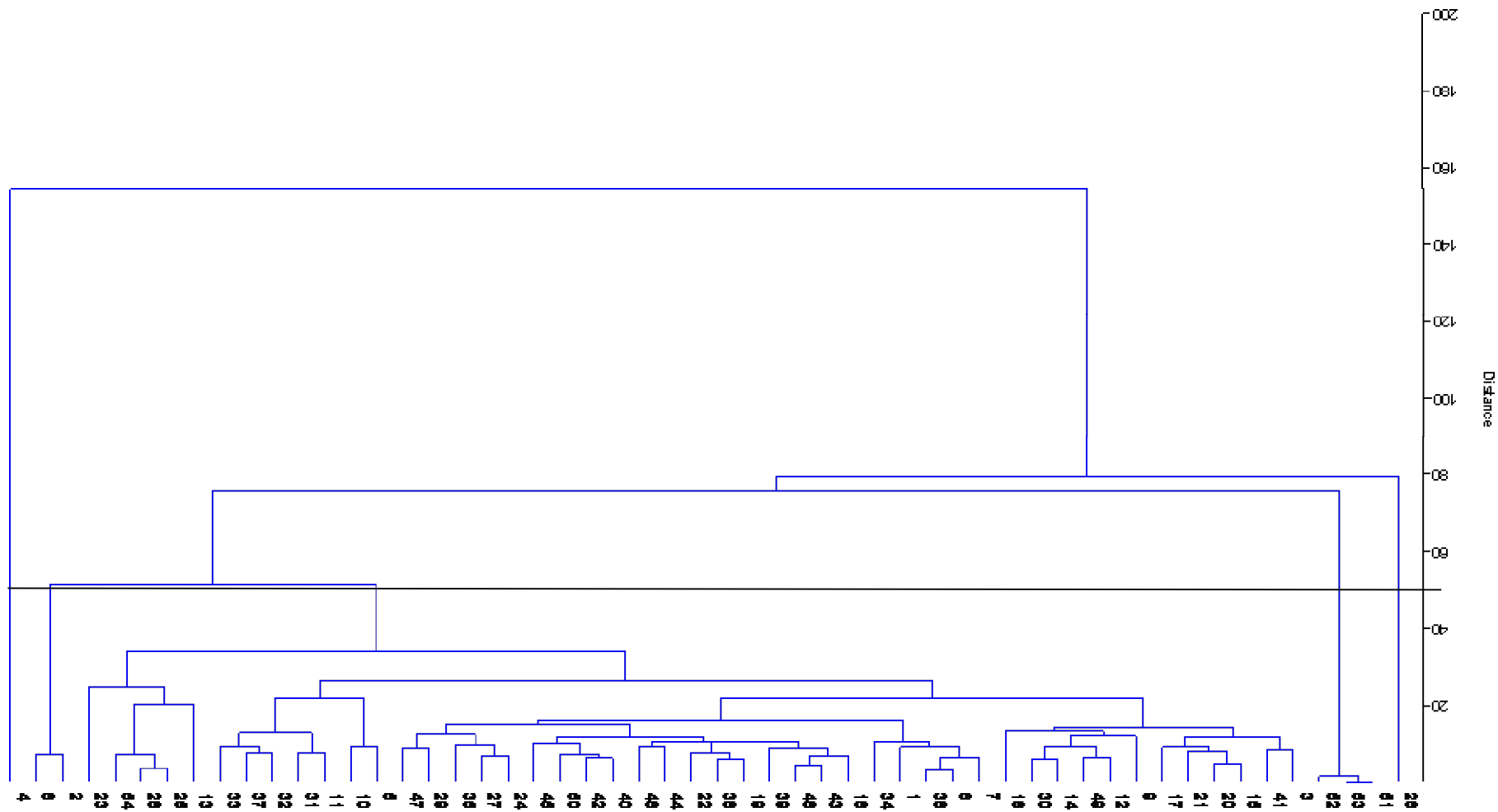


Figure 1: Dendrogram showing the genetic relatedness among the common bean accessions derived from cluster analysis

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Declaration of Competing Interest

There is no conflict of interests

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