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## Assessment of Genetic Diversity among Bambara Groundnut (*Vigna subteranea*) Cultivars using Morphological Traits in the Sudan Savannah Ecological Zone of Nigeria

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### Abstract

*Bambara groundnut is an underutilized neglected leguminous crop with less research attention. This study was conducted to evaluate morphological traits, estimate heritability, and assess genetic variability through genotypic and phenotypic variance of 22 Bambara groundnut cultivars in the Sudan Savannah of Nigeria; using a wide range of morphological traits such as: days to germination, number of leaves, number of branches, canopy height, days to 50% flowering, days to 50% pods, leaf area index, seed color, eye color, pod texture, seed length, grain yield and yield components. The cultivars were collected from Kano State, Plateau State and IITA (Minna). The experiment was conducted at two different locations, the Teaching and Research farm of Bayero University Kano, and the Teaching and Research farm of Aliko Dangote University of Science and Technology Gaya during the rainy season of 2024. The treatments were laid out in randomized complete block design (RCBD) with 3 replications. The result from the analysis of variance (ANOVA) and principal component analysis (PCA) showed substantial genetic variation among the genotypes. The principal component analysis extracted five principal components explaining 75.51% of total phenotypic variation at BUK with PC1 (23.99%) and PC2 (20.65%) contributing the most, high heritability ( $h^2b=0.60-0.67$ ) with Genetic advance ( $GAM<40\%$ ). Whereas at GAYA, PC1 accounted for (49.9%), driven by early vegetative traits, broad sense heritability was highest for 100 seed weight ( $h^2b=0.82$ ), indicating strong genetic control and Genetic advance of (46.92%). High phenotypic and genotypic coefficients of variation were recorded for yield, 100 seed weight and number of seed per pod. Broad sense heritability was high for 100-seed weight (0.67 at BUK, 0.82 at GAYA), pod length (0.51-0.58), and single seed weight (0.62-0.59). The PCA vector revealed those with longer vectors in BUK (pod width, seed weight, seed yield kg/ha, pod length, number of seed per pod), and at GAYA (pod length, pod width, single seed weight, number of seed per pod, 100 seed weight) as more contributing to*

*the total variations observed. The analysis revealed significant variation among the cultivars across most traits indicating a broad genetic base. Traits such as 100 seed weight, single seed weight, and number of seeds per pod exhibited high heritability and genetic advance making them reliable targets for selection. These findings highlight the potential for effective selection of superior parental lines for Bambara groundnut improvement.*

**Key words:** Bambara groundnut; Genetic diversity; Morphological traits

## 1.0 Introduction

Bambara groundnut (*Vigna subteranea* (L.) Verdc) is a legume belonging to the family and subfamily Fabaceae and Faboidea, respectively (Ibny *et al.*, 2019). Bambara groundnut is a legume indigenous to Africa and it is believed that its origin is between west and central Africa (Temagne *et al.*, 2018). It grows in the wild in northern Nigeria and eastwards to southern Sudan and is currently grown across tropical Africa and to a smaller range in tropical portions of America, Asia, and Australia (Adeleke *et al.*, 2018). It ranks as the third most important legume in sub-Saharan Africa after groundnut (*Arachis hypogaea*) and cowpea (*Vigna hypogea*), valued for its nutritional richness, drought resilience, and adaptability to low fertility soils (Majola *et al.*, 2021; Muhammad *et al.*, 2020). It requires an average rainfall of about 600–700 mm during the growing season to maximize yield, though later research has estimated the minimum rainfall requirement of the crop to be around 300 mm (Majola *et al.*, 2021). Plant response to drought involves avoidance, escape or tolerance (Mayes *et al.*, 2019) and all the three mechanisms have been observed in BGN to varying levels (Chai *et al.*, 2016). Excessive rainfall especially during maturity and/or harvest potentially causes waterlogging and affects the underground grain causing yield losses. To avoid water logging, BGN crops are planted on mounds or ridges (Gulu, 2018).

The productivity of bambara groundnut remains low compared with other leguminous crops. Mostly in Africa, locally adapted landraces of bambara groundnut are the most widely cultivated, in the absence of improved or released varieties (Muhammad *et al.*, 2020). Annual world Bambara groundnut production is estimated at approximately 0.3 million tons, of which 0.2 million tons were produced in Africa (FAOSTAT, 2020). It is also noteworthy that some factors such as rainfall, temperature, humidity, agro-pedology, and abiotic/biotic cause differences in agronomic performance, especially yield stability and yield quality of the crops as a way of responding to different environment (Oladosu *et al.*, 2016). Several benefits (nutritional and economic) of Bambara groundnut, its production in areas of cultivation is still low because of the unavailability of improved varieties (Muhammad *et al.*, 2020). This has made the prospect of the crop at commercial or international level low and has led to production restricted to subsistence farmers or women in the rural areas. More so, the renewed interest in orphan crops like Bambara groundnut call for actions towards creating high yielding, drought resistant, disease resistant and high nutritional value genotypes with application of molecular techniques. Several studies have documented morphological and genetic diversity in Bambara groundnut across different African regions. For instance, Khan *et al.* (2021) reported significant variation in qualitative and quantitative traits among landraces in West Africa, while Olanrewaju *et al.* (2021) demonstrated that environmental factors strongly influence growth and yield parameters. In addition, molecular studies using SSR and SNP markers have further elucidated genetic structure and relationships among germplasm collections (Majola *et al.*, 2021).

Despite these advances, most previous studies have either focused on broad regional evaluations or employed molecular techniques to assess, genetic diversity in Bambara

groundnut (Khan *et al.*, 2021; Majola *et al.*, 2021). While these approaches have provided valuable insights into genetic structure and variability, they often overlook the importance of location-specific morphological evaluation under distinct agro ecological conditions (Olanrewaju *et al.*, 2021). In particular, there is limited information on the morphological diversity and genetic parameters of Bambara groundnut cultivars adapted to the Sudan Savannah Ecological Zone of Nigeria. Given that environmental factors such as rainfall, temperature, and soil conditions strongly influence the expression of morphological traits, the performance of genotypes may vary significantly across locations (Oladosu *et al.*, 2016). Although molecular techniques are powerful, morphological characterization remains a fundamental, accessible, and cost-effective approach for initial germplasm evaluation, especially in resource-limited settings where advanced tools may not be readily available (Olerewaju *et al.*, 2021). Therefore, evaluating these accessions under specific local conditions is essential for identifying stable, high performing and adaptable genotypes. Therefore, this study was designed to address this gap by evaluating morphological traits, estimating heritability, and assessing genetic variability among Bambara groundnut cultivars adapted to the Sudan Savannah Ecological Zone of Nigeria, with the aim of providing baseline information for effective selection and genetic improvement.

## 2.0 Materials and Methods

### 2.1 Study Area

The experiment was conducted at two different locations, the Teaching and Research farm of Bayero University Kano (BUK) located at 11°59' 47"N, 8°31'00" 472m above sea level and the Teaching and Research farm of Aliko Dangote University of Science and Technology Gaya, located at 11°52'N, 9°00'E, 430m above sea level during the 2024 rainy season. Kano state lies on the geographical coordinates of 11°59' 47"N, 8°31'0"E. The soil at BUK was sandy loam, while the soil at Gaya soil was loamy soil.

### 2.2 Experimental Materials

The experimental material consisted of 22 Bambara groundnut accessions which were collected from Kano State (Badume market, Dawanau market, Kurna market, and Yankaba market), Plateau State (from a farm), and International Institute of Tropical Agriculture IITA Minna. The cultivars were selected based on their adaptations to local agroecological conditions such as temperature, soil type, rainfall, etc. The Sudan Savannah is characterized by a unimodal rainfall pattern ranging from 600 to 1000mm annually, with a rainy season typically lasting from May to October. Average daily temperatures range from 26°C to 34°C. The soils in both locations are classified as sandy loam, moderately well-drained, and low in organic matter and nitrogen, which makes them typical representatives of the savannah soils used for crop production in Northern Nigeria. The seeds were carefully sorted and thoroughly screened to remove foreign materials and undesirable ones before planting.

### 2.3 Experimental Design and Layout and Cultural Practices

The treatments were laid out in a randomized complete block design (RCBD) with three replications at each location. The total experimental area covered was 630m<sup>2</sup>.

The land was cleared of unwanted debris, ploughed and harrowed for easy planting. Poultry manure was incorporated into the soil at the rate of 3.2 t ha<sup>-1</sup> prior to planting. The seeds were subjected to preliminary analysis to ensure they were good quality seeds with uniform size, the seeds were sown by hand to a depth of 2-3cm, 1 seed per accession on each plot in each replication, due to limited number of accessions. Irrigation was carried out when there was no

enough rainfall. Weeding was carried out manually by the use of hoes and hand pulling. Harvesting was done at physiological maturity when the plant showed signs of senescence including leaf yellowing and drying.

#### 2.4 Data Collection

Data was collected on morphological and agronomic traits such as days to germination, canopy height at 3, 6, 9 weeks after sowing (WAS), number of leaves at 3, 6, 9 WAS, Leaf area index (LAI) (Length\*Breadth\*Correction factor/Ground area), at 8 WAS. The days to 50% flowering, days to 50% podding, days to maturity, pod length, pod width, single seed weight, 100 seed weight, seed yield per hectare. Qualitative traits such as seed colour, eye colour, and pod texture were also recorded. The data were collected from five randomly tagged plants per plot. The experimental material consisted of 22 Bambara groundnut accessions; 5 plants from each plot were chosen and tagged for accurate data taking, and the average measurements of the tagged plants were recorded.

#### 2.5 Data Analysis

The data was collected and subjected to analysis of variance (ANOVA), means were separated using the Turkey's honest significant difference (HSD) Test. The cluster and principal component analysis were performed using Factoextra and FactorMineR R packages. GCV, PCV, GA and GAM were estimated using the variability package in R. Genotypic variance (GV), Phenotypic variance (PV), and Environmental variance were estimated using the mean square values from ANOVA. GCV, and PCV were calculated following standard procedures. Broad-sense heritability ( $H^2$ ) was estimated as the ratio of genotypic variance to phenotypic variance. Genetic advance (GA) and Genetic advance as a percentage of mean (GAM) were computed assuming a selection intensity of 5%.

### 3.0 Results and Discussion

This study assessed the genetic diversity among Bambara groundnut (*Vigna subterranea*) cultivars using key morphological traits. Significant variability was observed across traits such as plant height, days to germination, canopy height, number of leaves, leaf area index, days to maturity, and 100-seed weight (Table 3.1 and Table 3.2) indicating a broad genetic base within the evaluated germplasm.

The genetic variability analysis conducted on Bambara Groundnut (BGN) genotypes in Gaya during the 2024 rainy season revealed considerable differences among the traits studied, suggesting the existence of exploitable genetic diversity. The phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) across all traits, indicating the influence of environmental factors on trait expression. However, traits such as 100 seed weight (GCV: 25.10%, PCV: 27.66%) and days to germination (GCV: 20.54%, PCV: 32.91%) showed relatively close values, suggesting that these traits are less influenced by the environment and more governed by genetic factors (Table 3.1). This is similar to the findings of Sarkar and Obilana (2020) who reported high phenotypic and genotypic coefficients of variation (PCV and GCV) for traits like number of pod per plant, seed yield, and days to maturity, indicating a significant portion of high phenotypic variation due to environmental effect. Furthermore, high heritability estimates for certain traits indicate that genetic factors play a predominant role in their expression, which is beneficial for breeders targeting these traits.

**Table 2.1 Description of the Bambara Groundnut Accessions used for Diversity Study**

| ACCESSIONS   | ORIGIN  | DESCRIPTION                      | MATURITY<br>(DAYS) | YIELD KG/HA |
|--------------|---------|----------------------------------|--------------------|-------------|
| KBN-24-8     | KANO    | Peachy brown +black dots ash eye | 104                | 124.06      |
| KBN-24-16    | KANO    | Reddish brown no eye             | 106                | 78.26       |
| KBN-24-13    | KANO    | Cream+ brown dots brown eye      | 107                | 112.87      |
| PBN-24-19    | PLATEAU | Cream no eye                     | 107                | 120.61      |
| KBN-24-22    | KANO    | Black+ cream patches ash eye     | 108                | 118.10      |
| KBN-24-10    | KANO    | Cream+ brown dots ash eye        | 106                | 68.15       |
| OTUKPO-2-2   | IITA    | Cream no eye                     | 107                | 61.74       |
| OTUKPO-3a-3  | IITA    | Cream black eye                  | 108                | 87.18       |
| KBN-24-24    | KANO    | Peach no eye                     | 108                | 108.52      |
| KBN-24-12    | KANO    | Reddish brown + coffee no eye    | 108                | 68.62       |
| KBN-24-14    | KANO    | Maroon + stripe no eye           | 106                | 79.00       |
| KBN-24-20    | KANO    | Black no eye                     | 105                | 46.00       |
| OTUKPO -3b-4 | IITA    | Ash+ cream patches coffee eye    | 107                | 87.20       |
| OTUKPO-1-5   | IITA    | Peachy brown no eye              | 111                | 89.78       |
| KBN-24-7     | KANO    | Purple + stripe black eye        | 107                | 94.38       |
| KWANDE-2-6   | IITA    | Black no eye                     | 107                | 102.00      |
| KBN-24-15    | KANO    | Cream pale purple eye            | 107                | 117.3       |
| KBN-24-11    | KANO    | Cream+ purple dots ash eye       | 107                | 131.90      |
| KBN-24-9     | KANO    | Cream + coffee stripe ash eye    | 105                | 92.50       |
| KBN-24-17    | KANO    | Black no eye                     | 105                | 127.80      |
| KWANDE-1-1   | IITA    | Light brown brown eye            | 106                | 68.73       |
| KBN-24-21    | KANO    | Cream+ purple stripe black eye   | 107                | 69.70       |

High heritability estimates were observed in traits like 100 seed weight (82%), single seed weight (59%), and pod length (58%), implying strong genetic control and suggesting that these traits are reliable for selection. In addition, these traits also recorded high genetic advance as a percentage of the mean (GAM), with values of 46.92%, 35.47%, and 27.52%, respectively. This combination of high heritability and high GAM suggests that these traits are largely governed by additive gene action and can be effectively improved through selection. Conversely, traits such as canopy height at 6 weeks after sowing (WAS), number of branches at 3 WAS, and days to 50% flowering exhibited low heritability and genetic advance, indicating that selection for these traits may be less effective due to the greater influence of environmental factors (Table 3.1).

At BUK Genetic advance as a percentage of the mean (GAM) provides insight into the effectiveness of selection. High GAM in number of seeds per pod (44.90%), single seed weight (44.47%), and 100 seed weight (41.50%) suggests the predominance of additive gene

action, making selection for these traits more efficient. In contrast, traits like days to 50% flowering and days to maturity exhibited low heritability and GAM, suggesting they are more environmentally influenced and less responsive to selection. Genotypic (GV), phenotypic (PV), and environmental (EV), variances revealed significant variability among BGN genotypes. PV consistently exceeded GV, suggesting considerable environmental influence. Traits such as yield (PV=4446.0), number of leaves at 9WAS (PV=9806.0), and number of branches at 9WAS (PV=1176.7) exhibiting high phenotypic variation. Moderate to high genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for yield (20.05%, 69.79%), 100 seed weight (24.56%, 29.94%), and number of seeds per pod (22.52%, 35.92%), indicating substantial genetic variability. Broad sense heritability estimate exhibited a wide range from very low for traits such as yield (0.08), and canopy height at 3 weeks after sowing (CH3WAS) (0.08) to moderate for traits such as 100 seed weight (0.67), single seed weight (0.62), and number of seeds per pod (0.60), suggesting these traits are largely under genetic control. The high genetic advance (GA), and genetic advance as percentage of mean (GAM) in these traits support the presence of additive gene action (Table 3.2) in BUK. The observed genetic variability among Bambara groundnut (BGN) genotypes suggests significant potential for genetic improvement. Phenotypic variance (PV) exceeded genotypic variance (GV) for all traits, which aligns with previous findings in legume crops, indicating substantial environmental influence on phenotypic expression (Falconer & Mackay, 1996; Johnson *et al.*, 1955). Khan *et al.*, (2021) reported a similar findings in which the phenotypic variances were significantly higher than the corresponding genotypic variances.

The cluster analysis (Figure 3.1) grouped the genotypes to 5 clusters based on closely related clusters. The purple cluster considered as cluster 1 has accessions such as: OTUKPO3a-3, KBN-24-13, OTUKPO2-2, KBN-24-14, KBN-24-22, KBN-24-17, KBN-24-16, KBN-24-15, and KBN-24-11. The blue cluster as cluster 2 with accessions such as KWANDE 1-1, KBN-24-24, KBN-24-12 and OTUKPO 1-5, the green cluster which is cluster 3 contains accessions such as PBN-24-19 and KBN-24-10, the brown cluster which is cluster 4 contains accessions such as OTUKPO 3b-4, KBN-24-7, KBN-24-7, KBN-24-21, KBN-24-9, and the red cluster which is cluster 5 contains only KBN-24-8. Crossing between the genotypes in cluster 1 won't give a hybrid vigor because they are closely related indicating a high level of genetic similarity, but hybridization between genotype in cluster 1 and 5 or 1 and 3, or 1 and any other cluster will provide better recombinant for the exploitation of heterosis for the development of hybrid in Bambara nut. These clusters likely reflect differences in geographical origin or selection history (Figure 3.1). The presence of closely related accessions within clusters, particularly in cluster I, suggests a narrow genetic base among some groups, which may result from historical seed exchanges, common ancestry, or similar environmental adaptation (Massawe *et al.*, 2005). Conversely, the wide genetic distances observed between accessions in different clusters, especially in Cluster III, highlight the existence of broad genetic variability, which is critical for the genetic improvement of Bambara nut. Akinyosoye *et al.* (2023) reported similar clustering patterns and emphasized its value in identifying heterotic groups for cross-breeding, which can enhance genetic gains in breeding programs.

In the BUK trial, the first 5 principal components accounted for 75.5% of the total variation observed among the measured traits (Table 3.3). PC1 (23.99% variance) was influenced by traits such as NB3WAS (10.69), NB6WAS (8.84), NL3WAS (10.53), NL6WAS (8.50), days to podding (6.09), days to maturity(6.09). PC1 showed variations in early vegetative vigor. PC2 (20.65%) was associated with pod weight (PW) (13.89), number of branches at 9 weeks after sowing (NB9WAS) (9.37), number of leaves at 9 weeks after sowing (NL9WAS)

(8.16). Therefore, PC2 showed variations in late season vegetative growth and yield. PC3 (14.93% variance) was contributed by traits such as CH6WAS, LAI, N P/P, and Days to 50% flowering. PC4 (9.11% variance) has strongest positive variance for traits such as canopy height at 3 weeks after sowing CH3WAS (14.51), and number of seed per pod (NS/P) (14.39). PC4 represent a variation with yield component and early seedling vigor. PC5 (6.83% variance) which was driven by traits such as days to germination, CH9WAS, and seed weight. (Table 3.3). This followed the approach used in Bambara groundnut studies by Olanrewaju *et al.*, (2021), where traits with the highest absolute values within each component were considered the primary contributors to that axis of variation.

In the GAYA trial, PC1 had high loadings on traits like Days to germination (7.00), CH9WAS (5.73), NB9WAS (3.54), NL9WAS (8.76) and yield/ha (0.59) which contributed strongly to DIM1. PC2 was contributed by traits such as CH6WAS (2.16), NB6WAS (5.85), NL6WAS (1.38), and yield/ha (9.54). PC3 was contributed by traits such as D to G (11.35), CH6WAS (14.93), and LAI (15.86). PC4 and PC5 showed different patterns with some traits like CH9WAS (22.81), and yield/ha (13.91) loading strongly on PC5 (Table 3.4). This follows with the description by Khan *et al.* (2021), where with traits having the highest possible eigenvector values were considered major contributors to each component. The cumulative variance of 100% indicates that all measured morphological variation was captured by the first five components.

The PCA biplot showed which trait contributed more; those with longer vectors are more contributing to the total variation observed, out of the total variation, those with light blue recorded high trait performance. Traits such as pod length, pod width, 1 seed weight, and number of seed per pod have a longer vector which shows they are major contributors to the observed variability among accessions (figure 3.6). This is in line with the work of Khan *et al.*, (2021) which stated that accessions located near these vectors exhibited superior performance for those traits, indicating their potential as parents for selection.

The PCA biplot shows which trait contributes more; those with longer vectors are more contributing to the total variation observed, out of the total variation, those with light blue recorded high trait performance. Traits such as pod width, seed weight, seed yield and others have longer pointing towards the positive direction suggesting they are major contributors to the observed variability among accessions .traits that are close together like pod width and pod length, and seed weight are correlated , such that improving one may likely enhance the other (Figure 3.3). This agrees with findings of Crista *et al.*, 2024, who reported that traits with high contributions (long vectors or loadings) play major roles in explaining variability among crop genotypes.

The cluster plot in GAYA trial (Figure 3.5) shows results of inter and intra distance of the clusters. It shows the actual distance between the two. The blue cluster contains accessions such as: OTUKPO3a-3, OYUKPO1-5, KBN-24-24, the red cluster contains KBN-24-16, PBN-24-19, OTUKPO3b-4, KBN-24-12, KBN-24-17, KBN-24-13, KBN-24-15, KBN-24-14, KBN-24-10, OTUKPO2-2, and the brown cluster contains KBN-24-11, KBN-24-7, KBN-24-9, KBN-24-8, KBN-24-21, KBN-24-22, and the purple contains KWANDE2-6 and KWANDE1-1, and the green contains only KBN-24-20. E.g accessions in cluster blue and cluster brown if you cross between them, you will get a better hybrid because of the distance. Like OTUKPO1-5 and KBN-24-22 (figure. 3.5). This findings agrees with recent studies which reported that high inter-cluster distances are indicative of wider genetic divergence, while low intra-distance reflect genetic similarity among genotypes (Kumar *et al.*, 2024).

**Table 3.1: Genetic Variability Analysis of BGN Genotypes in GAYA during the 2024 Rainy Season**

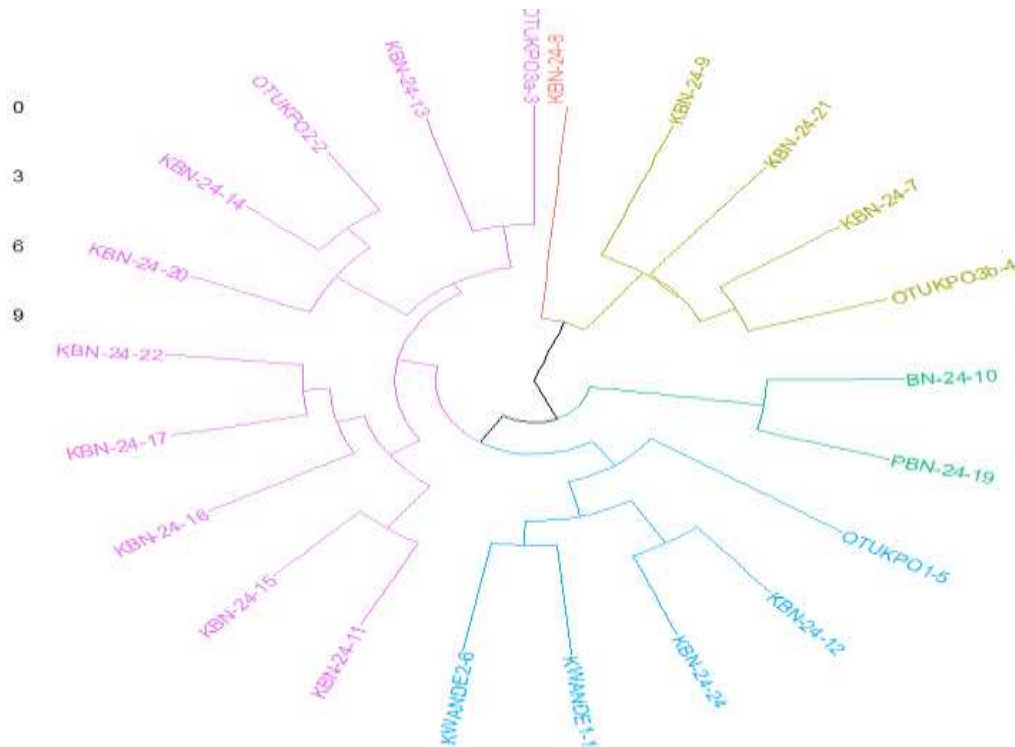
| Traits      | GV     | PV     | EV     | GCV   | PCV   | ECV   | H <sub>b</sub> | GA    | GAM   |
|-------------|--------|--------|--------|-------|-------|-------|----------------|-------|-------|
| Day to G    | 175.89 | 451.65 | 275.76 | 20.54 | 32.91 | 25.72 | 0.38           | 17.04 | 26.40 |
| CH 3WAS     | 0.37   | 2.28   | 1.90   | 5.63  | 13.94 | 12.74 | 0.16           | 0.50  | 4.70  |
| CH 6WAS     | 0.22   | 1.75   | 1.53   | 3.57  | 10.03 | 9.37  | 0.12           | 0.34  | 2.62  |
| CH 9WAS     | 0.66   | 4.00   | 3.33   | 5.14  | 12.59 | 11.49 | 0.16           | 0.68  | 4.32  |
| NB 3WAS     | 0.21   | 1.50   | 1.28   | 7.12  | 18.64 | 17.23 | 0.14           | 0.36  | 5.60  |
| NB 6WAS     | 32.15  | 66.25  | 34.09  | 19.50 | 27.99 | 20.08 | 0.48           | 8.13  | 27.98 |
| NB 9WAS     | 154.07 | 242.09 | 88.02  | 20.35 | 25.51 | 15.38 | 0.63           | 20.38 | 33.44 |
| NL 3WAS     | 3.74   | 19.31  | 15.57  | 9.55  | 21.71 | 19.49 | 0.19           | 1.75  | 8.66  |
| NL 6WAS     | 327.69 | 811.23 | 483.54 | 20.77 | 32.69 | 25.24 | 0.40           | 23.70 | 27.20 |
| NL 9WAS     | 1338.6 | 2195.3 | 856.7  | 20.43 | 26.17 | 16.35 | 0.60           | 58.85 | 32.87 |
| D to 50% F  | 1.80   | 6.63   | 4.83   | 2.74  | 5.26  | 4.49  | 0.27           | 1.44  | 2.95  |
| D to 50% P  | 1.46   | 7.33   | 5.86   | 1.89  | 4.22  | 3.78  | 0.20           | 1.11  | 1.74  |
| LAI         | 0.09   | 0.20   | 0.10   | 18.93 | 27.07 | 19.35 | 0.48           | 0.45  | 27.28 |
| D to M      | 1.46   | 7.33   | 5.86   | 1.12  | 2.50  | 2.24  | 0.20           | 1.11  | 1.03  |
| N P/P       | 8.46   | 59.81  | 51.35  | 16.20 | 43.07 | 39.91 | 0.14           | 2.25  | 12.55 |
| P LENGTH    | 13.25  | 22.77  | 9.51   | 17.50 | 22.94 | 14.83 | 0.58           | 5.72  | 27.52 |
| P WIDTH     | 3.67   | 10.39  | 6.72   | 11.61 | 19.53 | 15.70 | 0.35           | 2.34  | 14.21 |
| N S/P       | 0.04   | 0.13   | 0.09   | 17.60 | 31.46 | 26.07 | 0.31           | 0.23  | 20.29 |
| 1 S W       | 0.04   | 0.08   | 0.03   | 22.29 | 28.86 | 18.32 | 0.59           | 0.35  | 35.47 |
| 100 S W     | 436.96 | 530.72 | 93.76  | 25.10 | 17.66 | 11.62 | 0.82           | 39.07 | 46.92 |
| YIELD kg/ha | 470.54 | 2704.9 | 2234.4 | 23.96 | 57.43 | 52.21 | 0.17           | 18.63 | 20.59 |

df = Degrees of freedom, D to E: Days to Emergence, CH3WAS: Canopy height at 3 weeks after sowing, CH6WAS: Canopy height at 6 weeks after sowing, CH9WAS: Canopy height at 9 weeks after sowing, NB3WAS: Number of branches at 3 weeks after sowing, NB6WAS: Number of branches at 6 weeks after sowing, NB9WAS: Number of branches at 9 weeks after sowing, NL3WAS: Number of Leaves at 3 weeks after sowing, NL6WAS: Number of Leaves at 6 weeks after sowing, NL9WAS: Number of Leaves at 9 weeks after sowing, D to 50% F: Days to 50% flowering, D to 50% P: Days to 50% Podding, LAI: Leaf area index, D to M: Days to Maturity, N P/P: Number of pod per plant, PL: Pod length, PW: Pod width, N S/P: Number of seed per plant, 1 SW: 1 Seed weight, 100 SW: 100 Sees weight, YIELD/KG: Yield kg per plot, YIELD KG/HA: Yield kg per hectare.

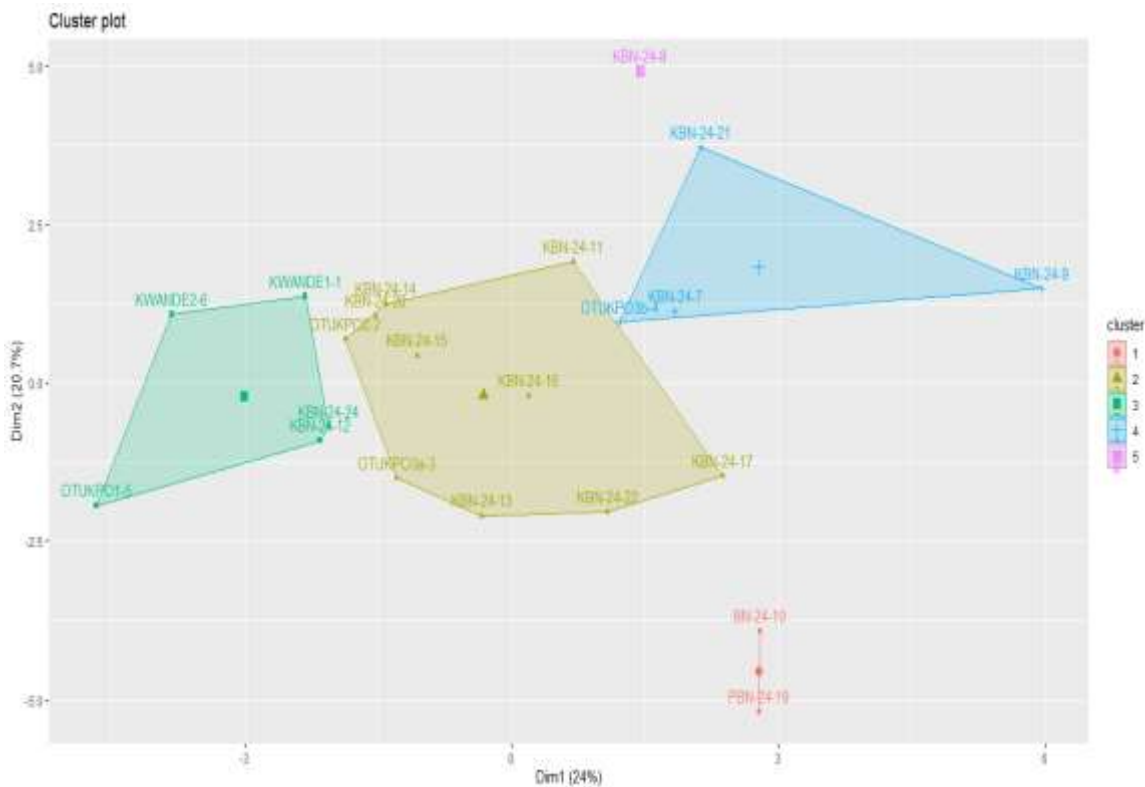
**Table 3.2: Genetic Variability Analysis of BGN Genotypes in BUK during the 2024 Raining Season**

| Traits             | GV      | PV      | EV     | GCV   | PCV   | ECV   | H <sub>b</sub> | GA    | GAM   |
|--------------------|---------|---------|--------|-------|-------|-------|----------------|-------|-------|
| <b>Day to G</b>    | 141.22  | 552.67  | 411.45 | 19.17 | 37.92 | 32.72 | 0.26           | 12.37 | 19.96 |
| <b>CH 3WAS</b>     | 0.15    | 1.74    | 1.59   | 1.12  | 12.02 | 10.88 | 0.08           | 0.23  | 0.52  |
| <b>CH 6WAS</b>     | 0.09    | 3.78    | 3.69   | 2.03  | 13.07 | 12.91 | 0.02           | 0.09  | 0.65  |
| <b>CH 9WAS</b>     | 1.55    | 5.62    | 4.07   | 5.68  | 10.82 | 9.20  | 0.27           | 1.34  | 6.15  |
| <b>NB 3WAS</b>     | 0.68    | 1.84    | 1.15   | 10.74 | 17.59 | 13.93 | 0.37           | 1.04  | 13.51 |
| <b>NB 6WAS</b>     | 39.31   | 118.65  | 79.33  | 15.29 | 26.57 | 21.73 | 0.33           | 7.43  | 18.14 |
| <b>NB 9WAS</b>     | 500.51  | 1176.70 | 676.25 | 28.75 | 44.09 | 33.42 | 0.42           | 30.05 | 38.63 |
| <b>NL 3WAS</b>     | 6.61    | 16.83   | 10.21  | 11.70 | 18.66 | 14.54 | 0.39           | 3.32  | 15.11 |
| <b>NL 6WAS</b>     | 357.69  | 1055.19 | 697.4  | 15.42 | 26.49 | 21.53 | 0.33           | 22.68 | 18.49 |
| <b>NL 9WAS</b>     | 3651.00 | 9806.00 | 6154.9 | 26.44 | 43.33 | 34.33 | 0.37           | 75.95 | 33.23 |
| <b>D to 50% F</b>  | 0.78    | 4.69    | 3.91   | 1.84  | 4.50  | 4.11  | 0.16           | 0.74  | 1.54  |
| <b>D to 50% P</b>  | 0.77    | 4.59    | 3.82   | 1.39  | 3.39  | 3.09  | 0.16           | 0.74  | 1.17  |
| <b>LAI</b>         | 0.008   | 0.04    | 0.03   | 7.68  | 17.15 | 15.34 | 0.20           | 0.08  | 7.08  |
| <b>D to M</b>      | 0.77    | 4.59    | 3.82   | 0.82  | 2.00  | 1.82  | 0.16           | 0.74  | 0.69  |
| <b>N P/P</b>       | 13.46   | 70.89   | 57.42  | 17.67 | 40.56 | 36.50 | 0.18           | 3.29  | 15.86 |
| <b>P LENGTH</b>    | 7.69    | 14.82   | 7.12   | 12.06 | 16.74 | 11.61 | 0.51           | 4.11  | 17.90 |
| <b>P WIDTH</b>     | 1.84    | 6.61    | 4.76   | 7.66  | 14.50 | 12.31 | 0.27           | 1.47  | 8.34  |
| <b>N S/P</b>       | 0.13    | 0.22    | 0.09   | 22.52 | 35.92 | 22.52 | 0.60           | 0.59  | 44.90 |
| <b>1 S W</b>       | 0.07    | 0.12    | 0.04   | 27.41 | 34.80 | 21.45 | 0.62           | 0.45  | 44.47 |
| <b>100 S W</b>     | 413.88  | 615.14  | 201.25 | 24.56 | 29.94 | 17.12 | 0.67           | 34.37 | 41.50 |
| <b>YIELD kg/ha</b> | 367.20  | 4446.0  | 4078.8 | 20.05 | 69.79 | 66.85 | 0.08           | 11.34 | 11.87 |

df = Degrees of freedom, D to E: Days to Emergence, CH3WAS: Canopy height at 3weeks after sowing, CH6WAS: Canopy height at 6 weeks after sowing, CH9WAS: Canopy height at 9 weeks after sowing, NB3WAS: Number of branches at 3 weeks after sowing, NB6WAS: Number of branches at 6 weeks after sowing, NB9WAS: Number of branches at 9 weeks after sowing, NL3WAS: Number of Leaves at 3 weeks after sowing, NL6WAS: Number of Leaves at 6 weeks after sowing, NL9WAS: Number of Leaves at 9 weeks after sowing, D to 50% F: Days to 50% flowering, D to 50% P: Days to 50% Podding, LAI: Leaf area index, D to M: Days to Maturity, N P/P: Number of pod per plant, PL: Pod length, PW: Pod width, N S/P: Number of seed per plant, 1 SW: 1 Seed weight, 100 SW: 100 Sees weight, YIELD/KG: Yield kg per plot, YIELD KG/HA: Yield kg per hectare.



**Figure 3.1. BUK cluster analysis-** The genotypes are grouped into 5 clusters based on closely related clusters. The purple cluster is cluster 1, the blue cluster is cluster 2, the green cluster is cluster 3, the brown cluster is cluster 4 and the red cluster is cluster 5.



**Figure 3.2: Bayero University Kano (BUK) cluster plot for 22 Bambara groundnut accessions**

**Table 3.3: Principal components and loadings associated with yield and yield contributing traits of the Bambara groundnut genotypes evaluated at BUK during the 2024 rainy season**

|                     | PC1   | PC2   | PC3   | PC4   | PC5   |
|---------------------|-------|-------|-------|-------|-------|
| DTG                 | 0.03  | 0.43  | 0.52  | 2.42  | 21.95 |
| CH3WAS              | 1.05  | 1.64  | 0.86  | 14.51 | 2.54  |
| CH6WAS              | 0.21  | 0.15  | 0.64  | 0.02  | 3.63  |
| CH9WAS              | 0.11  | 2.21  | 0.08  | 0.36  | 14.05 |
| NB3WAS              | 10.69 | 0.66  | 0.36  | 0.41  | 2.70  |
| NB6WAS              | 8.84  | 0.66  | 1.49  | 0.49  | 0.96  |
| NB9WAS              | 1.69  | 9.37  | 1.92  | 2.81  | 1.48  |
| NL3WAS              | 10.53 | 0.49  | 0.49  | 0.12  | 2.99  |
| NL6WAS              | 8.50  | 0.77  | 1.72  | 0.51  | 0.97  |
| NL9WAS              | 1.78  | 8.16  | 1.80  | 4.59  | 0.12  |
| D to F              | 6.41  | 2.47  | 1.79  | 12.31 | 1.66  |
| D to P              | 6.09  | 2.96  | 1.68  | 11.84 | 2.10  |
| LAI                 | 1.15  | 2.29  | 0.70  | 0.38  | 14.42 |
| D to M              | 6.09  | 2.96  | 1.68  | 11.84 | 2.10  |
| N P/P               | 2.70  | 8.67  | 4.06  | 2.30  | 0.22  |
| PL                  | 5.15  | 5.64  | 2.20  | 4.09  | 0.07  |
| PW                  | 5.12  | 3.65  | 1.49  | 1.34  | 8.29  |
| 100 SW              | 10.54 | 0.16  | 2.27  | 1.77  | 0.18  |
| 1 SW                | 8.48  | 0.30  | 3.55  | 3.50  | 4.76  |
| YIELD/PLOT          | 0.02  | 1.13  | 20.72 | 2.02  | 2.26  |
| YIELD/HA            | 0.21  | 0.45  | 22.58 | 2.47  | 0.56  |
| Eigen value         | 6.24  | 5.37  | 3.88  | 2.37  | 1.78  |
| Variance (%)        | 23.99 | 20.65 | 14.92 | 9.11  | 6.83  |
| Cumulative variance | 23.99 | 44.64 | 59.57 | 68.68 | 75.51 |

D to G: Days to Germination, CH 3WAS: Canopy height at weeks after sowing, CH 6WAS: Canopy height at 6 weeks after sowing, CH 9WAS: Canopy height at 9 weeks after sowing, NB 3WAS: Number of branches at 3 weeks after sowing, NB 6WAS: Number of branches at 6 weeks after sowing, NB 9WAS: Number of branches at 9 weeks after sowing, NL 3WAS: Number of leaves at 3 weeks after sowing, NL 6WAS: Number of leaves at 6 weeks after sowing, NL 9WAS: Number of leaves at 9 weeks after sowing, D to 50% F: Days to 50% flowering, D to 50% P: Days to 50% podding, LAI: Leaf area index, D to M: days to maturity, N P/P: number of pod per plant, P L: Pod length, P W: Pod width, N S/P: number of seed per pod, 1 SW: 1 Seed weight, 100 SW: 100 Seed weight.

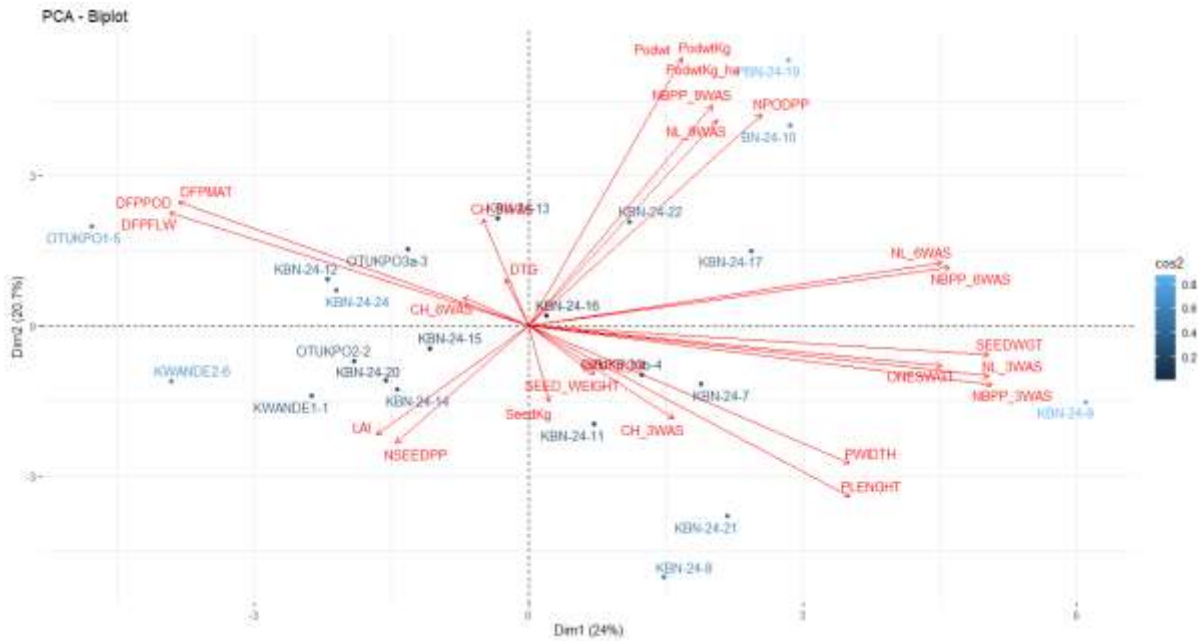


Figure 3.3 Bayero University Kano (BUK) PCA biplot for 22 Bambara groundnut accessions

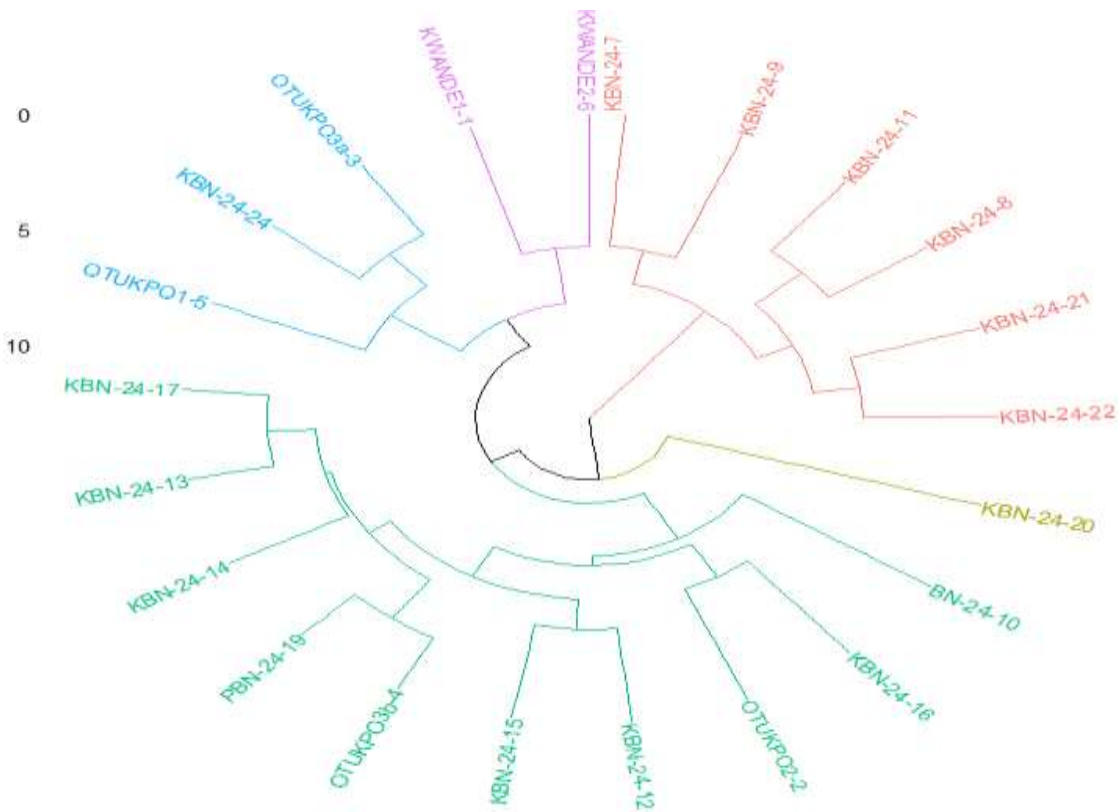
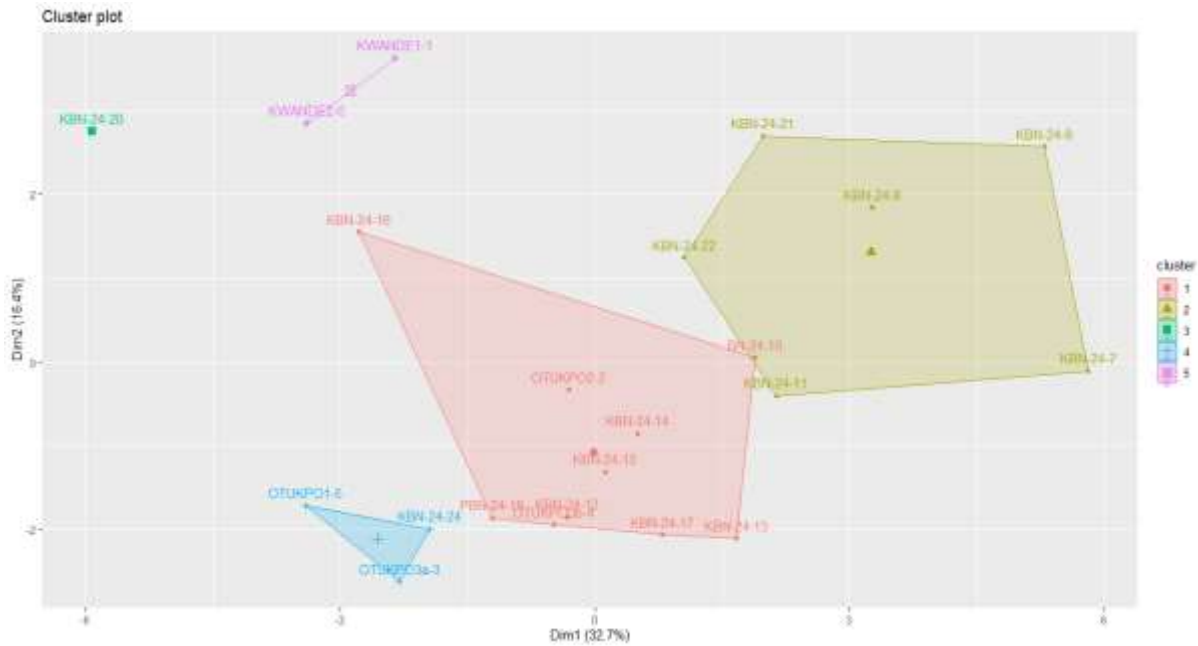


Figure 3.4 Gaya PCA and Cluster Analysis. The genotypes are grouped into 5 clusters based on closely related clusters. The purple cluster is cluster 1, the blue cluster is cluster 2, the green cluster is cluster 3, the brown cluster is cluster 4 and the red cluster is cluster 5.



**Figure 3.5 GAYA cluster plot for 22 Bambara groundnut accessions**

**Table 3.4: Principal components and loadings associated with yield and yield contributing traits of the Bambara groundnut genotypes evaluated at GAYA during the 2024 rainy season**

| Trait                   | PC1  | PC2  | PC3   | PC4  | PC5   |
|-------------------------|------|------|-------|------|-------|
| D to G                  | 0.10 | 7.00 | 11.35 | 4.46 | 0.59  |
| CH 3WAS                 | 2.34 | 1.14 | 7.59  | 8.62 | 4.47  |
| CH 6WAS                 | 0.96 | 2.16 | 14.93 | 1.05 | 13.62 |
| CH 9WAS                 | 1.15 | 1.28 | 9.13  | 1.22 | 22.81 |
| NB 3WAS                 | 7.24 | 2.47 | 0.20  | 2.07 | 0.96  |
| NB 6WAS                 | 5.73 | 5.85 | 2.47  | 1.90 | 0.05  |
| NB 9WAS                 | 3.54 | 3.13 | 1.30  | 1.11 | 0.01  |
| NL 3WAS                 | 8.76 | 1.38 | 0.38  | 1.20 | 2.03  |
| NL 6WAS                 | 4.13 | 5.66 | 2.19  | 1.96 | 0.64  |
| NL 9WAS                 | 3.02 | 3.02 | 2.17  | 9.39 | 0.04  |
| D to 50% F              | 6.17 | 2.55 | 3.24  | 1.04 | 0.66  |
| D to 50% P              | 5.55 | 1.26 | 2.74  | 1.36 | 0.78  |
| LAI                     | 0.28 | 1.39 | 15.86 | 1.13 | 9.57  |
| D to M                  | 5.55 | 1.26 | 2.27  | 1.36 | 0.78  |
| N P/P                   | 0.17 | 1.39 | 0.01  | 4.93 | 0.43  |
| P L                     | 1.89 | 1.10 | 4.98  | 1.92 | 3.56  |
| P W                     | 3.90 | 3.69 | 0.99  | 8.80 | 2.83  |
| No S/P                  | 0.04 | 7.14 | 4.92  | 2.64 | 1.39  |
| 100 S W                 | 9.04 | 3.05 | 0.02  | 6.49 | 0.10  |
| 1 S W                   | 9.46 | 3.37 | 0.11  | 4.79 | 0.09  |
| YIELD/PLOT              | 0.47 | 5.31 | 0.01  | 6.21 | 6.19  |
| YIELD/HA                | 0.59 | 9.54 | 6.25  | 3.23 | 13.91 |
| Eigen value             | 7.00 | 1.14 | 2.16  | 1.28 | 2.47  |
| Variance (%)            | 49.9 | 8.1  | 15.4  | 9.1  | 17.6  |
| Cumulative variance (%) | 49.9 | 58.0 | 73.4  | 82.5 | 100.0 |

D to G: Days to Germination, CH 3WAS: Canopy height at weeks after sowing, CH 6WAS: Canopy height at 6 weeks after sowing, CH 9WAS: Canopy height at 9 weeks after sowing, NB 3WAS: Number of branches at 3 weeks after sowing, NB 6WAS: Number of branches at 6 weeks after sowing, NB 9WAS: Number of branches at 9 weeks after sowing, NL 3WAS: Number of leaves at 3 weeks after sowing, NL 6WAS: Number of leaves at 6 weeks after sowing, NL 9WAS: Number of leaves at 9 weeks after sowing, D to 50% F: Days to 50% flowering, D to 50% P: Days to 50% podding, LAI: Leaf area index, D to M: days to maturity, N P/P: number of pod per plant, P L: Pod length, P W: Pod width, N S/P: number of seed per pod, 1 SW: 1 Seed weight, 100 SW: 100 Seed weight.



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