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RESEARCH PAPER

Agromorphological characterization of six promising bambara groundnut [*Vigna subterranea* (L.) Verdc.] genotypes under selection in Burkina Faso

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ABSTRACT

Bambara groundnut (*Vigna subterranea* (L.) Verdc.) is a legume crop with high nutritional and economic potential but remains underutilized in Burkina Faso. The main objective of this study was to evaluate the agromorphological variability of six Bambara groundnut genotypes in comparison with two released varieties in order to identify discriminant traits for possible varietal registration. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Collected parameters were subjected to descriptive statistics, analysis of variance (ANOVA), principal component analysis (PCA), and hierarchical cluster analysis (HCA) to explore variability patterns. Results revealed significant phenotypic variability among the genotypes, particularly for seed width, growth cycle, 100-seed weight, and grain yield. Three distinct genotype clusters were identified based on maturity cycle and productivity. A clear differentiation was observed between the six genotypes and the released varieties, mainly according to maturity duration and yield potential. Genotypes KVS246C and KVS17C, characterized by short cycles and high productivity, appear promising candidates for varietal release and for production in short-rainfall zones, whereas KVS235C, KVS105bC, and KVS62C displayed moderate yields suitable for more favorable environments. These findings highlight exploitable diversity for selecting high-performing genotypes adapted to local agroecological conditions.

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INTRODUCTION

Increasing the production not only of staple crops such as cereals (sorghum, millet, maize), but also of so-called secondary or underutilized crops such as fonio, fabirama, and Bambara groundnut, has become a top priority to ensure sustainable food and nutritional security for vulnerable populations in the current context of climate change. Indeed, an underexploited crop like Bambara groundnut (*Vigna subterranea* (L.) Verdcourt), also known as earth pea or Bambara bean, is one of the most important food legumes consumed by many rural and urban populations in Burkina Faso (Ouédraogo *et al.*, 2008; Ouoba *et al.*, 2016). It is cultivated across all agroecological zones of Burkina Faso, ranging from the arid northern regions (300 mm isohyet) to the humid southern areas (1200 mm isohyet) (Ouédraogo *et al.*, 2012). The crop also serves as an income source, mainly for women farmers who grow it in nearly all production zones (Ouoba *et al.*, 2016).

Its highly nutritious seeds contain lysine and methionine, two essential amino acids, with concentrations of 80.2 mg/g and 6.4 mg/g, respectively (Halimi *et al.*, 2019). It also contains antioxidants and trace elements such as iron (Fe), magnesium (Mg), phosphorus (P), potassium (K), zinc (Zn), and copper (Cu) (Mkandawire, 2007; FAO, 2016). This balanced composition makes it a complete food, positioning Bambara groundnut as a key crop in strategies aimed at enhancing resilience to food and nutritional insecurity (Bamshaiye *et al.*, 2011).

Despite its potential, Bambara groundnut has long been neglected by research and agricultural development programs, receiving little breeding attention to improve productivity and quality. However, during the past decade, renewed interest has led to the release of three improved varieties listed in the *National Catalogue of Crop Species and Varieties of Burkina Faso* (CNS, 2014). Nevertheless, these released varieties remain insufficient to meet the needs of local seed systems, underscoring the necessity of selecting new varieties to strengthen production and valorization of this species. Given the urgent demand for improved varieties to boost Bambara groundnut production in Burkina Faso, genetic evaluation of genotypes compared to released varieties represents an essential step toward identifying promising candidates for varietal improvement. The present study aimed to assess the agromorphological variability of six Bambara groundnut genotypes in comparison with two released varieties, with the objective of identifying discriminant traits for potential varietal registration.

MATERIAL AND METHODS

Experimental Site

The study was conducted in Pamtaga, a village located in the rural commune of Dapélogo, Burkina Faso. The site is geographically situated at latitude 12.66868° N and longitude 1.50727° W (Fig. 1). The climate of the area is of the Sudanian-Sahelian type, characterized by two distinct seasons: a rainy season and a dry season. Rainfall in the commune is generally low and shows strong spatial and temporal variability from year to year. During the 2023–2024 cropping season, total rainfall recorded by the Dapélogo meteorological station was approximately 721.6 mm. The soils of Dapélogo are diverse, comprising sandy-gravelly, sandy-clay, clay-sandy, and clayey types.

Fig. 1. Geographical location of the study site

Plant material

The plant material consists of eight accessions of Bambara Groundnut, including six genotypes currently undergoing selection and two approved varieties used as controls (Table 1). This material comes from the INERA gene bank.

Table 1. List of studied genotypes

No	Codes	Status
1	KVS115H	Released variety (H)
2	KVS259H	Released variety (H)
3	KVS62aC	Genotype under selection (C)
4	KVS17C	Genotype under selection (C)
5	KVS114C	Genotype under selection (C)
6	KVS105bC	Genotype under selection (C)
7	KVS235C	Genotype under selection (C)
8	KVS246C	Genotype under selection (C)

Experimental design and trial management

A Fisher's randomized complete block design (RCBD) with three replications was used for this study. Each replication corresponded to one block, and each block consisted of sowing rows representing the elementary plots. The planting density within each block was 0.4 m × 0.2 m. Each block was 2 m wide and 10.4 m long, containing eight sowing rows with eleven planting holes per row. The spacing between adjacent blocks (replications) was 1 m.

The field experiment was established during the 2023 cropping season. Land preparation consisted of manual flat tillage followed by hand ridging to clearly delineate the sowing rows. Blocks were then demarcated and elementary plots labeled. One seed was sown per hole in all plots. Basal fertilization was applied using composted poultry manure at a rate of 6000 kg/ha. Three manual weedings were performed as needed to ensure good crop development. Earthing-up was carried out at 49 days after sowing (DAS). Harvesting was done at pod maturity, and post-harvest measurements were taken after sun-drying the pods for two weeks.

Data collection

A total of six quantitative traits and one qualitative trait (seed coat color) were observed or measured during plant development and after harvest, following the *Bambara Groundnut (Vigna subterranea [L.] Verdc.) Descriptor List* established by the International Plant Genetic Resources Institute (IPGRI and Bennett, 2000). The measured parameters included the main phenological, morphological, and agronomic traits of the studied genotypes. Phenological traits included the number of days to 50% flowering (FLOW50) and days to 50% physiological maturity (MAT50), which were used to evaluate genotype growth cycles. Morphological traits, such as seed length (SEEDL) and seed width (SEEDW), characterized seed morphology. Yield components included 100-seed weight (100SDW), number of pods per plant (NPodP), and grain yield per hectare (YIELD). These traits were selected as they are among the most decisive for assessing plant development, morphology, and agronomic performance in Bambara groundnut. Phenological parameters such as FLOW50 and MAT50 indicate earliness or lateness of the genotypes, a key factor for adaptation to variable climatic conditions and the constraints of the growing season. Morphological characteristics such as SEEDL and SEEDW serve as important indicators of seed quality and selection potential, as seed size affects consumer preference, processing ease, and market value. Yield-related traits—100SDW, NPodP, and YIELD—are directly associated with crop productivity and profitability, making them major criteria in varietal improvement programs. Finally, the qualitative trait (seed coat color) has significant socioeconomic and commercial importance since it influences product acceptability in local and regional markets. Altogether, these traits provide a comprehensive and integrated basis for evaluating the agronomic, economic, and adaptive value of Bambara groundnut genotypes.

Data analysis

The data collected were entered into Microsoft Excel 2016 and then analyzed using XLSTAT 2019 software. The analyses focused on descriptive statistics to highlight the variation between traits, an analysis of variance (ANOVA) to identify discriminating traits and compare the performance of genotypes under selection with that of already registered varieties, principal component analysis (PCA) to assess the relationships between traits and between genotypes and traits, and finally ascending hierarchical classification (AHC) to group the selected genotypes and control varieties according to their maturity cycle and yield. All analyses of variance were performed at a significance level of 5%, and the separation of means was performed using the Newman–Keuls test at the same significance level.

RESULTS

Seed Coat Color Characteristics of the Genotypes

The studied genotypes exhibited notable diversity in seed coat color and pattern (Fig. 2).

Fig. 2. Seed coat coloration of the different genotypes studied

Legend: KVS: Kamboinsé *Vigna subterranea*; C: genotype under selection; H: released variety

The two released varieties, KVS115H and KVS259H, served as reference standards for comparison. The variety KVS115H was distinguished by a black seed coat with a gray butterfly-shaped eye, whereas KVS259H showed a uniform cream color without any eye.

In comparison, the genotypes under selection displayed more varied color and pattern combinations. The genotype KVS17C showed dark brown speckles on a cream background, with a brown butterfly-shaped eye, resembling the butterfly pattern of KVS115H but with a lighter shade. The genotype KVS246C was characterized by black rhomboid spots on a cream background with a gray butterfly-shaped eye, similar to KVS115H in the presence of the butterfly pattern but with a more pronounced texture. Genotype KVS105bC exhibited a uniform light red seed coat without an eye, resembling KVS259H in the absence of the eye but with stronger pigmentation.

The genotype KVS114C displayed dark brown rhomboid spots on a cream background with a brown butterfly-shaped eye, combining characteristics of both released varieties—the strong contrast of KVS115H and the softer tone of KVS259H. Genotype KVS62C was uniformly black without an eye, differing from KVS115H by the absence of the eye despite similar pigmentation. Finally, genotype KVS235C presented a uniform cream color without an eye, very similar to KVS259H both in hue and in the absence of pattern.

Variation in quantitative traits and genotype performance

Descriptive and variance analyses revealed differentiated phenotypic variability among the studied traits (Table 2). Phenological parameters generally showed low dispersion, indicating relative homogeneity of the plant material regarding flowering.

Table 2. Results of descriptive and variance analysis of the studied traits

Variables	Minimum	Maximum	Mean	Standard deviation	F value
FLOW50	32.000	38.000	35.042	1.574	0.073Ns
MAT50	78.000	95.000	85.208	5.225	0.006**
NPodP	12.200	36.667	23.149	7.417	0.270Ns
SEEDL	8.844	12.820	10.746	0.858	0.313Ns
SEEDW	7.489	9.712	8.590	0.511	0.045**
100SDWH	38.000	63.000	50.333	7.938	0.000**
YIELD	1008.150	3360.500	2128.161	675.498	0.001**

Legend: FLOW50: Number of days to 50% flowering; MAT50: 50% plant maturity; SEEDL: Seed length; SEEDW: Seed width; 100SDW: 100-seed weight; YIELD: Grain yield (kg/ha); NPodP: Number of pods per plant. **Highly significant ; Ns : Not significant.

The number of days to 50% flowering (FLOW50) ranged from 32 to 38 days after sowing, with a mean of 35.04 days and a standard deviation of 1.57; the analysis of variance revealed no significant difference ($p > 0.05$). In contrast, the number of days to 50% maturity (MAT50) exhibited greater variability (78 to 95 days, mean of 85.21 days, standard deviation of 5.23) and a highly significant difference ($p = 0.006$).

This result highlights the coexistence of early- and late-maturing genotypes, indicating an interesting potential for selection according to growth cycle duration. Yield component traits confirmed this pattern of contrasted variability. The number of pods per plant (NPodP) showed a wide range (12.2 to 36.7 pods, standard deviation of 7.42) but without significant difference ($p > 0.05$), suggesting that, despite observed variability, this trait was not strongly influenced by experimental factors. Conversely, seed width (SEEDW, $p = 0.045$), 100-seed weight (100SDW, $p = 0.000$), and grain yield per hectare (YIELD, $p = 0.001$) displayed highly significant differences, supported by high standard deviations (7.94 g for 100SDW and 743.29 kg/ha for yield).

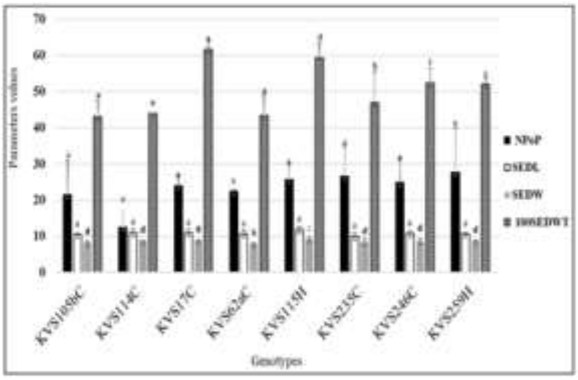

Fig. 3. Performance of genotypes in number of pods per plant, seed length and width, and 100-seed weight.

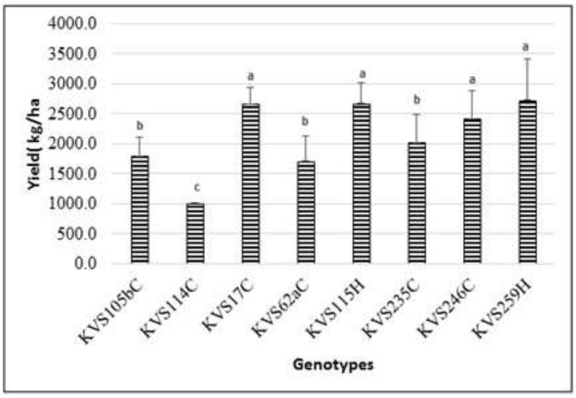

Fig. 4. Grain yield performance of genotypes (kg/ha)

These findings indicate a strong influence of genetic potential and/or environmental conditions on the productive performance of the genotypes (Fig. 3&4). Seed length (SEEDL) showed low variability (standard deviation ≈ 0.86) and no significant difference among genotypes, suggesting morphological stability for this trait. Overall, the combined analyses revealed that traits related to maturity and yield were the most discriminant variables.

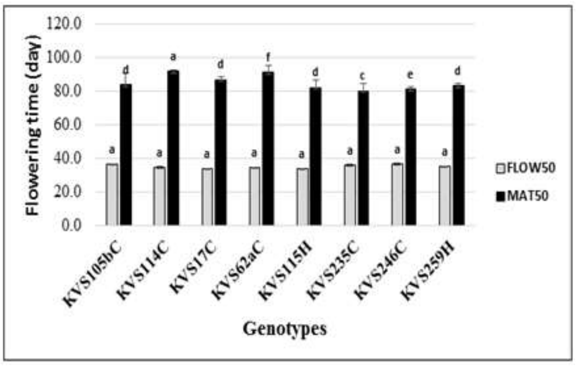

Fig. 5. Results of mean separation analysis

Mean separation tests (Fig. 5) showed that genotypes KVS114C and KVS62C were the latest maturing (92 and 91.33 days, respectively), while KVS235C was the earliest (80.33 days). Grain yield, the main trait of interest, exhibited significant differences, ranging from 1008.15 kg/ha for genotype KVS114C to 2676.18 kg/ha for the released variety KVS115H. The reference variety KVS115H maintained its high-yielding status (2676.2 kg/ha), but genotype KVS17C also appeared promising, showing a competitive yield (2615.08 kg/ha) combined with a higher 100-seed weight (61.67 g). In contrast, genotypes KVS114C and KVS105bC were less productive, with yields below 1700 kg/ha and 100-seed weights under 44 g.

Relationship between the studied traits and genotypes

Table 3 and Fig.6 summarize the results of the Principal Component Analysis (PCA), highlighting the relationships between variables and factors as well as the distribution of variables and genotypes along the axes. The PCA biplot (Fig. 6) shows that the first two factorial axes (F1 and F2) together explain 85.86% of the total variance, indicating an excellent representation of the variability observed among the genotypes and the studied traits.

Table 3. Correlations between variables and factors

Traits	F1	F2
FLOW50	-0.448	-0.755
MAT50	-0.485	0.793
NPodP	0.617	-0.694
SEEDL	0.599	0.690
SEEDW	0.838	0.344
100SDW	0.957	0.110
YIELD	0.890	-0.374

Legend: FLOW50: Number of days to 50% flowering; MAT50: 50% plant maturity; SEEDL: Seed length; SEEDW: Seed width; 100SDW: 100-seed weight; YIELD: Grain yield (kg/ha); NPodP: Number of pods per plant

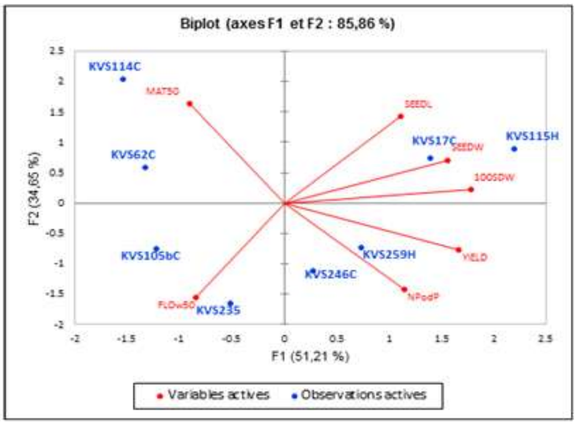

Fig. 6. Biplot representation of Bambara groundnut genotypes and agronomic variables based on the first two principal component axes (PCA)

Legend: FLOW50: Number of days to 50% flowering; MAT50: 50% plant maturity; SEEDL: Seed length; SEEDW: Seed width; 100SDW: 100-seed weight; YIELD: Grain yield (kg/ha); NPodP: Number of pods per plant

The first axis (F1), which accounts for 51.21% of the variance, is mainly and positively associated with yield-related traits, notably seed width (SEEDW), 100-seed weight (100SDWH), grain yield (YIELD), and number of pods per plant (NPodP). Conversely, 50% flowering (FLOW50) is negatively correlated with this axis. Thus, genotypes located on the right side of the plane—such as KVS115H, KVS17C, and KVS259H—are distinguished by high agronomic performance, while those positioned on the left (KVS62C, KVS105bC, KVS235) are characterized by early flowering and lower yields. The second axis (F2), explaining 34.65% of the variance, is strongly and positively correlated with 50% maturity (MAT50), while negatively correlated with flowering (FLOW50) and number of pods per plant (NPodP). This axis illustrates a gradient of earliness and vegetative development. Genotypes located in the upper part of the plane, such as KVS114C, exhibit late maturity, whereas those in the lower part (KVS235, KVS246C) are earlier. Observation of genotype groupings allows three main clusters to be distinguished: (i) a high-yielding group (KVS115H, KVS17C, KVS259H) characterized by high yields and heavy seeds; (ii) an early-maturing group (KVS62C, KVS105bC, KVS235) with rapid flowering and maturity but moderate productivity; and (iii) a late-maturing group (KVS114C) with a long growth cycle. The correlations observed among pod length (PODL), seed width (SEEDW), 100-seed weight (100SDWH), grain yield (YIELD), and number of pods per plant (NPodP) indicate interdependence between pod size, seed weight, and overall productivity. Conversely, the strong opposition between earliness traits (FLOW50, MAT50) and yield traits suggests that early genotypes tend to produce less than late ones. In summary, this PCA reveals two main profiles: high-performing but late genotypes, adapted to long-season environments, and early-maturing genotypes with moderate yield, better suited to areas with water constraints or short growing cycles.

Distribution of genotypes according to maturity cycle and grain yield

The hierarchical cluster analysis (HCA), based on the parameters of 50% maturity (MAT50) and grain yield (YIELD, kg/ha), allowed the distinction of three distinct groups of genotypes. These groups reflect marked differences in crop cycle duration and production potential (Fig. 7). Group 1 consists of early-maturing and high-yielding genotypes, including KVS246C, KVS17C, KVS259H, and KVS115H. They are characterized by a short growth cycle (81–87 days) and high yields ranging from 2414 to 2728 kg/ha. The two registered varieties, KVS115H and KVS259H, belong to this group. Their coexistence with KVS246C suggests that this latter genotype exhibits agronomic performances comparable to those of the commercial reference varieties. Therefore, KVS246C can be considered a *promising genotype*, displaying similar behavior to the registered varieties in terms of both earliness and yield. Group 2 includes *intermediate genotypes with moderate yields*, namely KVS235C, KVS105bC, and KVS62C. These genotypes have a relatively longer maturity cycle (84–91 days) with variable yields ranging from 1710 to 2027.5 kg/ha.

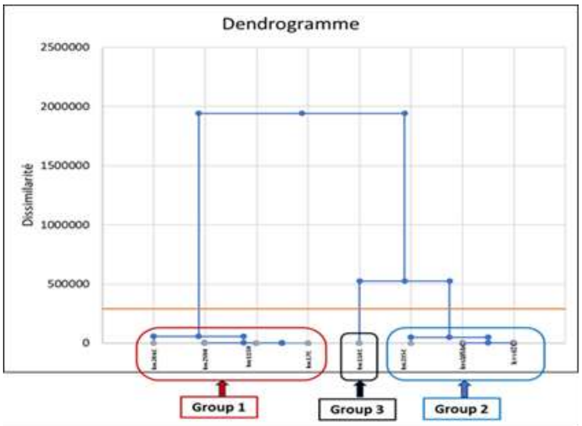

Fig. 7. Distribution of genotypes based on maturity cycle and grain yield using hierarchical ascending classification

This group represents intermediate to late genotypes that offer a compromise between crop duration and productivity. Such profiles may be suitable for areas with well-distributed rainfall or medium-cycle production systems, although their average yield remains lower than that of the registered reference varieties. Group 3 comprises a single late and low-yielding genotype, KVS114C. This genotype forms an isolated group, indicating strong dissimilarity from the others. With a long maturity cycle (92 days) and low yield (1008 kg/ha), it demonstrates limited resource-use efficiency over its growth period. Despite its lower productivity, KVS114C may still hold specific genetic interest (e.g., tolerance to abiotic stress or robustness), making it potentially valuable for targeted breeding programs.

DISCUSSION

In studies of the genetic diversity of *Vigna subterranea* (bambara groundnut), seed coat color occupies a particular place due to its importance in local food, sociocultural, and economic practices. This trait, far from being trivial, plays a decisive role not only in the identification and distinction of local cultivated varieties but also in determining consumer and market preferences regarding visual appearance and product presentation (Ouoba *et al.*, 2016). Moreover, seed coat color is recognized as an essential differentiating criterion between hard-seeded and soft-seeded varieties in other legumes such as *Vicia sativa* (Büyükkartal *et al.*, 2013). The results of this study confirm the importance of this trait by revealing marked phenotypic variability among *Vigna subterranea* genotypes in terms of seed coat coloration and pattern. The genotypes analyzed displayed diverse combinations of colors (black, cream, light red, brown) and patterns (uniform, spotted, butterfly-shaped, rhombic), demonstrating substantial intraspecific diversity. In comparison, the two registered reference varieties, KVS115H and KVS259H, exhibited respectively a black coat with a gray butterfly eye and a uniform cream color, positioning the new genotypes between these two morphological extremes. These findings are consistent with those of Ouoba *et al.* (2018), who also reported wide variability in seed coat coloration, though their study included a larger number of accessions (300). However, this pronounced variability in seed coat color contrasts with the limited phenotypic variability observed in pod traits by Kambou *et al.* (2020), suggesting that seed coat color is a more stable and discriminant character for genotype differentiation. A high proportion of cream-colored seeds was also observed, consistent with the results of Ouoba *et al.* (2016), who attributed this predominance to consumer preference for this color, perceived as more aesthetically pleasing and commercially valuable. Similarly, in Ghana, Abu and Buah (2011) found that cream-colored varieties were most sought after by producers and consumers due to their genetic stability and better marketability. Therefore, seed coat color emerges as a key morphological, genetic, and economic trait in bambara groundnut breeding. According to Yang *et al.* (2010), it represents a decisive criterion of quality and commercial value in many legumes, while Tiryaki *et al.* (2016) highlighted its potential as a selection indicator when correlated with other agronomic traits such as yield, resistance, or nutritional quality. These observations underscore the importance of this character in breeding programs aimed at exploiting the genetic diversity of *Vigna subterranea* in Burkina Faso and West Africa.

Regarding the quantitative traits, this study also revealed significant variability among genotypes, reflecting appreciable genetic diversity. Indeed, the analysis of variance showed that, apart from the number of days to 50% flowering, seed length, and number of pods per plant, most traits significantly discriminated among genotypes at the 5% level. These results are in line with those of Ouédraogo *et al.* (2008) and Kambou *et al.* (2020), who also observed variability in quantitative traits among local bambara groundnut accessions in Burkina Faso. The yield components—particularly 100-seed weight and grain yield per hectare—showed highly significant differences, highlighting the combined influence of genetic potential and environmental conditions. The registered reference variety KVS115H maintained its superiority with a yield of 2676.2 kg/ha, but the genotype KVS17C also showed competitive performance (2615.08 kg/ha) and a high 100-seed weight (61.67 g). Conversely, genotypes KVS114C and KVS105bC were less productive, possibly due to unfavorable genotype–environment interactions or reduced assimilate allocation to seeds. Principal component analysis (PCA) revealed that the first two axes (F1 and F2) explained 85.86% of the total variability among the evaluated *Vigna subterranea* genotypes. In comparison, in the study by Kambou *et al.* (2020), the first two factors explained only 47.38% of the total variance. This difference may be attributed to the smaller number of traits considered in the present study, which increased the proportion of variance explained by the first axis. The distribution of variables on the correlation circle identified two main groups of traits determining agronomic performance. The first group, composed of seed length (SEEDL), seed width (SEEDW), 100-seed weight (100SDW), yield (YIELD), and number of pods per plant (NPodP), was positively correlated with axis F1, representing overall productivity. Genotypes located along this axis displayed greater vegetative vigor and higher pod production. The second group, consisting of 50% flowering (FLOW50) and 50% maturity (MAT50), was negatively associated with F1, reflecting earliness. Axis F2 represented a secondary dimension associated with vegetative cycle duration. This structuring indicates that productive genotypes can be contrasted with early-maturing ones—two key agronomic criteria in breeding programs. Hierarchical cluster analysis (HCA), based on maturity duration (MAT50) and grain yield (YIELD), revealed clear differentiation among the studied genotypes. Three distinct groups emerged, reflecting strong genetic heterogeneity similar to that reported by Kambou *et al.* (2020) in their agro-morphological characterization of bambara groundnut accessions in Burkina Faso.

Group 1, composed of genotypes KVS246C, KVS17C, KVS259H, and KVS115H, included *early-maturing, high-yielding* types with short cycles (81–87 days) and high yields (2414–2728 kg/ha). These results are comparable to those of high-potential accessions described by Unigwé *et al.* (2016), characterized by early flowering, high pod production, and large seed size. The presence of the registered varieties KVS115H and KVS259H in this group validates the classification and suggests that KVS246C may be a promising breeding candidate combining earliness and productivity—traits particularly valuable in short rainy-season areas where early-maturing varieties are an effective adaptation strategy to climatic variability (Doku and Karikari, 1971; Sadiki and Jarvis, 2005). Group 2, including KVS235C, KVS105bC, and KVS62C, exhibited *intermediate maturity cycles* (84–91 days) and *moderate yields* (1710–2027.5 kg/ha), representing a balance between crop duration and productivity. This group resembles that described by Kambou *et al.* (2020), composed of accessions with intermediate morpho-productive values. These genotypes may be suitable for areas with well-distributed rainfall, although their lower yield compared to reference varieties suggests the need for targeted selection to improve their resource-use efficiency. Group 3 included a single late-maturing genotype, KVS114C, with a long cycle (92 days) and low yield (1008 kg/ha). Its isolated position in the classification reflects strong dissimilarity with other genotypes, similar to the low-yield group reported by Kambou *et al.* (2020). Despite its low agronomic performance, KVS114C may represent a valuable genetic reservoir for traits such as drought tolerance, hardiness, or adaptation to marginal environments. Such genotypes are important in breeding programs as complementary parents to broaden the genetic base of cultivated varieties. Overall, the HCA results confirm that the observed variability among genotypes is largely structured by yield- and phenology-related traits, as also reported by Kambou *et al.* (2020) and Touré *et al.* (2013). These parameters are discriminant and reflect the differential adaptation of genotypes to agroecological conditions. Therefore, the diversity identified in this study offers promising opportunities for breeding and varietal improvement aimed at developing high-yielding, early, and stable cultivars suited to the short rainy seasons of the Sudano-Sahelian zones.

CONCLUSION

This study provided a comparative analysis of the agromorphological characteristics and performance of six *Vigna subterranea* genotypes relative to two registered varieties (KVS115H and KVS259H), highlighting clear differentiation mainly based on maturity cycle and yield potential. Genotypes KVS246C and KVS17C exhibited short growth cycles and high yields, with agronomic performances comparable to those of the reference varieties. These results underscore their potential for breeding programs targeting the development of early and productive cultivars adapted to the short rainy seasons of Burkina Faso, making them strong candidates for official registration to strengthen the sector with high-performing varieties. Genotypes KVS235C, KVS105bC, and KVS62C displayed intermediate profiles, with longer maturity cycles and moderate yields, suggesting adaptation to environments with more favorable rainfall distribution. The late genotype KVS114C, despite its low productivity, could serve as a valuable genetic source for the introgression of stress-tolerance or resilience traits in improvement programs. Overall, the results demonstrate significant phenotypic variability within the evaluated material. This diversity provides a solid foundation for selecting genotypes that combine earliness, high yield, and stability-key features for sustainably improving bambara groundnut productivity in Burkina Faso's farming systems. Research prospects include evaluating the yield stability and phenotypic plasticity of promising genotypes (KVS246C and KVS17C) through multi-location and multi-year trials, as well as conducting additional studies on their tolerance to abiotic stresses (drought, water deficit) and biotic stresses (diseases, pests) in order to refine the selection of the most resilient genotypes. They also include analyzing the agronomic and socio-economic acceptability of these genotypes among producers, with a view to promoting their adoption in local production systems.

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