ISSN: 0975-833X

Available online at http://www.journalcra.com

International Journal of Current Research
Vol. 18, Issue, 06, pp.37637-37645, June, 2026
DOI: https://doi.org/10.24941/ijcr.50658.06.2026

INTERNATIONAL JOURNAL OF CURRENT RESEARCH

RESEARCH ARTICLE

TRAIT DECOUPLING AND PHENOTYPIC DIVERSITY IN FARMER-MANAGED BAMBARA GROUNDNUT ECOTYPES FROM NIGER

Abdel Kader Naino Jika[1*], Bassirou Hasane Djibo[1], Fourératou Ali Soumaila[2], Abdoulaye Djibo Ide[2] and Abdourahamane Tankari Dan Badjo[1]

[1]Faculty of Agronomy, University Abdou Moumouni of Niamey, Niger; [2]SWISSAID Niger, Niamey, Niger

ARTICLE INFO

Article History:
Received 27th March, 2026
Received in revised form
24th April, 2026
Accepted 25th May, 2026
Published online 30th June, 2026

Keywords:
Vigna subterranea; Bambara groundnut ;agromorphological diversity; phenotypic variability; trait decoupling; farmer-managed ecotypes; Niger.

**Corresponding author:*
Abdel Kader Naino Jika

ABSTRACT

Bambara groundnut (*Vigna subterranea (L.) Verdc.*) is a drought-tolerant grain legume widely cultivated in low-input systems across sub-Saharan Africa, yet its phenotypic diversity remains incompletely characterized under farmer-managed conditions. This study evaluated 20 local ecotypes from the Dosso region, Niger, in a randomized complete block design during the 2023 rainy season. Fourteen agromorphological traits were recorded at plot and plant level. Friedman tests identified significant varietal differentiation for days to flowering (DF; $\chi^2 = 53.56$, df = 19, $p < 0.001$) and hundred-seed weight (HSW_g; $\chi^2 = 42.79$, df = 19, $p < 0.01$), while all other traits, including grain yield and all plant-level morphological traits, did not reach statistical significance under this conservative blocked design. Conover post-hoc tests with Holm correction identified 104 significant pairwise contrasts for days to flowering (DF) and 18 for hundred-seed weight (HSW_g). Spearman rank correlations on ecotype means revealed a strongly integrated biomass-yield axis (PTFg-GY_kgha: $\rho = 0.945$, $p < 0.001$ after BH-FDR correction), with days to flowering and hundred-seed weight operating as independent dimensions. Principal component analysis on all 14 standardized traits explained 40.0% and 20.3% of variance on PC1 and PC2, respectively. Ward clustering separated the 20 ecotypes into four preliminary phenotypic groups, though sensitivity analysis showed moderate cluster instability when V3 was excluded (Adjusted Rand Index = 0.536). Three ecotypes merit targeted follow-up: V4 for early flowering, V28 for structural architecture, and V18 for pod production. These results argue for multi-trait, multi-environment evaluation before any selection decision.

Citation: Abdel Kader Naino Jika, Bassirou Hasane Djibo, Fourératou Ali Soumaila, Abdoulaye Djibo Ide and Abdourahamane Tankari Dan Badjo. 2026. "Trait decoupling and phenotypic diversity in farmer-managed bambara groundnut ecotypes from Niger". ***International Journal of Current Research, 18, (06), 37637-37645.***

INTRODUCTION

Food and nutritional security remain a major constraint in sub-Saharan Africa, particularly in Sahelian environments characterized by irregular rainfall, low soil fertility, and increasing climatic variability (Sultan & Gaetani, 2016). In these systems, crop diversification is a key strategy for maintaining production under environmental stress. Grain legumes contribute to household nutrition and cropping system functioning through their protein content and biological nitrogen fixation capacity (Kermah *et al*., 2018; Olanrewaju *et al*., 2022). Among these legumes, Bambara groundnut (*Vigna subterranea* (L.) Verdc.) is widely cultivated across sub-Saharan Africa but remains poorly integrated into formal research and breeding programs (Mabhaudhi *et al*., 2018, Naino Jika *et al*., 2023). The species tolerates drought and produces under low-input conditions (Collinson *et al*., 1996). Its seeds contain 16-25% protein and provide a complementary amino acid profile to cereal-based diets (Hillocks *et al*., 2012; Brink *et al*., 2006). Biological nitrogen fixation has been estimated at 3 to 51 kg N ha^{-1} per cropping cycle (Kermah *et al*., 2018). Despite these attributes, Bambara groundnut remains an underutilized species. Production falls below its reported potential, and the crop receives limited support from formal seed systems and public breeding investment (Massawe *et al*., 2002; Naino Jika *et al*., 2023). Across West Africa, the conservation and circulation of bambaragroundnut diversity rely heavily on custodian farmers, informal seed exchange, and locally maintained landraces (Naino Jika *et al*., 2023). In Niger, similar farmer-managed dynamics have been documented in the Dosso region, where Bambara groundnut remains embedded in local production, utilization, conservation, and marketing practices (Ibrahim *et al*., 2018, Haoua *et al*., 2024). Such farmer-managed seed systems are not merely channels of seed supply; they are also social and biological mechanisms

through which crop genetic diversity is maintained, circulated, and reshaped on farm (Jarvis *et al*., 2005; Naino Jika *et al*., 2023). This lack of structured phenotypic information limits the integration of local genetic resources into breeding programs. Agromorphological characterization is a standard initial step for describing phenotypic variation, identifying discriminating traits, and structuring germplasm collections (Ceccarelli and Grando, 2007). It provides a basis for parent selection, definition of breeding targets, and assessment of varietal performance under local conditions. Agronomic traits are often functionally interrelated, and understanding their relationships help in interpreting phenotypic diversity. In particular, the degree to which morphological differentiation corresponds to agronomic performance differences remains unclear for many underutilized crops. In farmer-managed systems, traits may reflect multiple, sometimes independent, selection pressures, generating complex phenotypic structures that cannot be captured by single-trait evaluation. This analytical framework also supports ideotype construction. An ideotype can be defined as a combination of traits expected to confer superior performance under specific environmental and management conditions (Donald, 1968). In Sahelian systems, relevant production objectives include grain yield, phenological adaptation to short rainfall seasons, and biomass production for crop-livestock integration. This study aimed to characterize the agromorphological diversity of 20 local Bambara groundnut ecotypes evaluated under Sahelian conditions in Niger. The specific objectives were to: (i) quantify phenotypic variation among ecotypes; (ii) assess varietal differentiation across agronomic and morphological traits; and (iii) analyze trait relationships to identify potential decoupling patterns between morphological diversity and agronomic performance.

MATERIALS AND METHODS

Study site and plant material: The trial was conducted during the 2023 rainy season at the SWISSAID experimental site in Guri Bani Koara, a village located 7 km from the rural municipality of Kankandi in the Dosso region, Niger (12°49′24″ N, 2°57′18″ E). The site lies within the Sahelian agroclimatic zone, where annual rainfall typically ranges from 300 to 800 mm. The plant material consisted of seeds from 20 Bambara groundnut (*Vigna subterranea* (L.) Verdc.) ecotypes collected from farmers in the departments of Dogondoutchi and Tibiri, Dosso region, Niger. Each accession was identified by a numeric code. Seed color patterns were diverse and included red, cream, black, striped cream, white, yellow with brown streaks and black eye, and brown types. The accessions were treated as distinct local ecotypes throughout the analysis.

Experimental design and crop management: The experiment used a randomized complete block design (RCBD) with three replications, for a total of 60 elementary plots (20 varieties × 3 blocks). Each elementary plot measured 10 m² and comprised five rows of 34 planting hills, with a row spacing of 40 cm and a hill spacing of 15 cm. The total experimental area was 925 m². Inter-block spacing was 2 m. Sowing was performed on 2 July 2023 under rainfed conditions, at a depth of 4 to 5 cm with one seed per hill. Crop management was conducted manually by a team of nine local farmers. The first weeding was performed 30 days after sowing. A second operation combining hoeing and compost application followed, with 20 kg of compost applied per elementary plot on 7 August 2023. Ridging was carried out on 27 August 2023.

Data collection: Fourteen quantitative traits were recorded following the descriptor manual for ambara groundnut (IPGRI/IITA/BAMNET, 2000). Plant-level measurements were conducted on five randomly selected plants from the inner rows of each elementary plot, generating 300 individual observations (5 plants x 3 replications x 20 varieties). Plot-level agronomic traits were recorded across all 60 experimental units. The recorded traits, their abbreviations, measurement levels, and definitions are detailed in Table 1.

Statistical analysis: Data were entered into Microsoft Excel and all statistical analyses were performed using R software (version 4.3.3). Descriptive statistics (mean, standard deviation, median, interquartile range, minimum, maximum, and coefficient of variation) were computed for each trait at both plot and plant level. Plant-level traits were measured on five plants per plot; to avoid pseudoreplication, the five individual observations were first averaged at plot level before any inferential analysis, so that the experimental unit remained the plot (n = 60) for all tests. Because the experiment followed a randomized complete block design (RCBD) with three blocks and the assumptions of parametric models were not retained for small samples with likely non-normal distributions, varietal differentiation was assessed using Friedman tests, with ecotype as treatment factor and block as the blocking factor. This design-aware non-parametric test is the appropriate equivalent of a two-way ANOVA when assumptions are violated; with 20 treatments and only 3 blocks, the test is conservative and should be interpreted accordingly. When the Friedman test was significant, pairwise comparisons among ecotypes were conducted using Conover post-hoc tests for blocked designs with Holm adjustment for multiple comparisons. Monotonic associations among plot-level traits were assessed using Spearman rank correlations computed on ecotype-level means (n = 20), with Benjamini-Hochberg false discovery rate (BH-FDR) correction applied to the upper triangle of the p-value matrix. Correlations marked with a cross (×) were non-significant after FDR correction (adjusted $p \geq 0.05$). Multivariate structure was explored by principal component analysis (PCA) applied to standardized ecotype means for all 14 traits, and by Ward hierarchical clustering on Euclidean distances computed from the same standardized matrix. The optimal number of clusters was evaluated by silhouette analysis for k = 2 to 6. Because ecotype V3 displayed an extreme hundred-seed weight value in one replicate, PCA and Ward clustering were repeated after excluding V3; cluster stability was quantified using the Adjusted Rand Index (ARI; adjustedRandIndex, mclust package).

RESULTS

Phenotypic variability across plot-level and plant-level traits: Descriptive statistics revealed substantial and uneven phenotypic variability among the 20 ecotypes (Table 2). At the plot level, days to flowering (DF) was the most stable trait, with observations ranging from 29 to 39 days and a coefficient of variation of 6.1%. By contrast, biomass and yield components showed wide variation: total fresh pod weight (PTFg) ranged from 0.075 to 5.42 kg plot^{-1} (CV = 59.0%), total fresh biomass (BFT) from 0.16 to 5.77 kg plot^{-1}

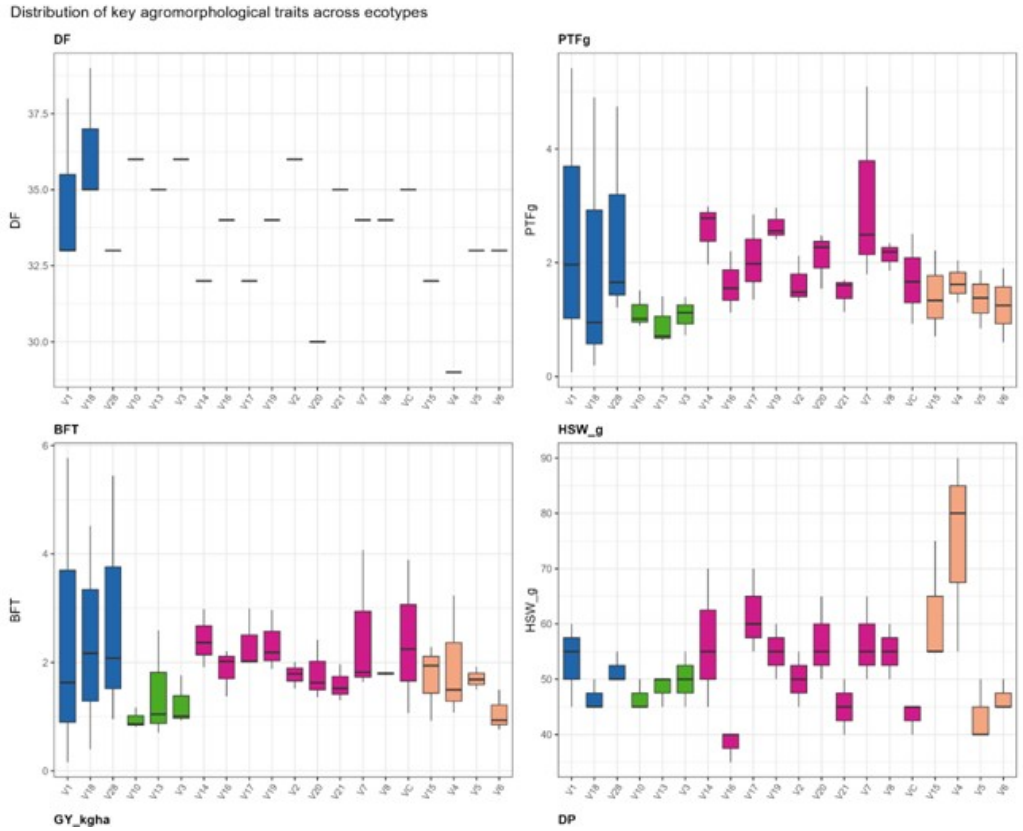
Table 1. Traits recorded, their abbreviations, measurement level, and definitions

Level	Abbreviation	Full name	Description	Unit / Derivation
Plot	DF	Days to flowering	Days from sowing to appearance of first flower	days
Plot	PTFg	Total freshpodweight	Fresh weight of all pods harvested per plot	kg
Plot	BFT	Total freshbiomass	Fresh weight of total aerial biomass per plot	kg
Plot	PTSg	Dry podweight	Dry weight of pods per plot	kg
Plot	PTG	Total grain weight	Dry weight of shelled grains per plot	kg
Plot	HSW_g	Hundred-seedweight	Weight of 100 randomly selected seeds	g
Plot	GY_kgha	Grain yield	PTG extrapolated to kg ha^{-1} from plot area	kg ha^{-1}
Plant	HP	Plant height	Distance from soil surface to terminal leaflet at maximum vegetative development	cm
Plant	DP	Plant diameter	Lateral spread diameter at maximum vegetative development	cm
Plant	LFT	Leaflet length	Length of the largest central leaflet	cm
Plant	lft	Leaflet width	Width of the largest central leaflet	cm
Plant	NT	Number of stems	Count of primary stems per plant	count
Plant	NF	Number of leaves	Count of functional leaves per plant at measurement date	count
Plant	NG	Number of pods	Count of pods per plant at harvest	count

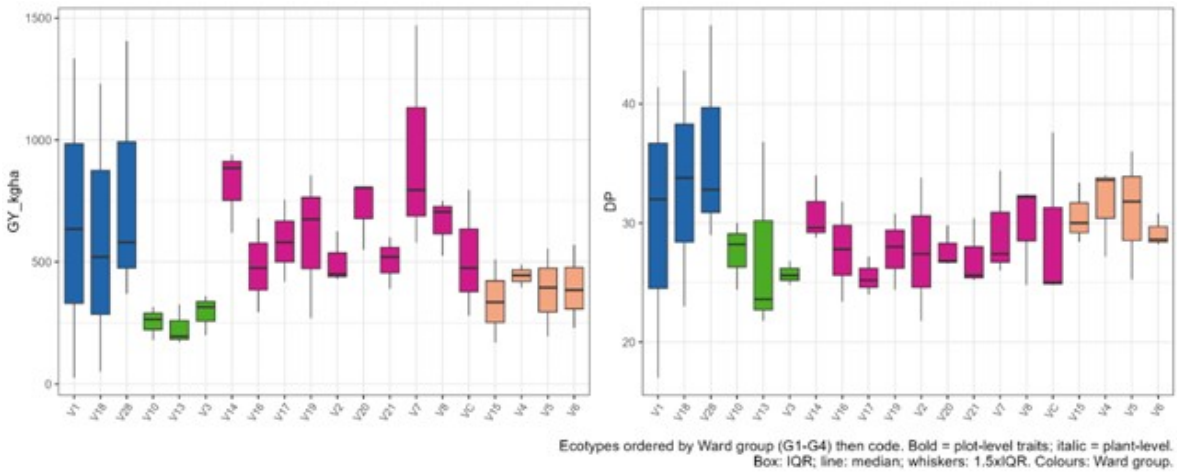
Table 2. Descriptive statistics of agromorphological traits

Level	*Trait*	*N*	*Mean*	*SD*	*Median*	*IQR*	*Min*	*Max*	*CV (%)*
Plot-level	*DF*	*60*	*33.70*	*2.07*	*34.00*	*2.25*	*29.0*	*39.0*	*6.1*
	PTFg	*60*	*1.847*	*1.090*	*1.638*	*1.037*	*0.075*	*5.420*	*59.0*
	BFT	*60*	*1.930*	*1.084*	*1.790*	*0.919*	*0.160*	*5.770*	*56.2*
	PTSg	*60*	*0.763*	*0.445*	*0.720*	*0.457*	*0.035*	*2.065*	*58.3*
	PTG	*60*	*0.536*	*0.308*	*0.500*	*0.354*	*0.025*	*1.470*	*57.4*
	HSW_g	*60*	*52.08*	*10.10*	*50.00*	*10.00*	*35.0*	*90.0*	*19.4*
	GY_kgha	*60*	***535.8***	***307.7***	***500***	***353.8***	*25.0*	*1470.0*	***57.4***
Plant-level	*HP*	*60*	*14.51*	*3.02*	*14.40*	*2.50*	*7.2*	*23.0*	*20.8*
	DP	*60*	*29.24*	*5.30*	*28.30*	*7.01*	*17.0*	*46.6*	*18.1*
	LFT	*60*	*6.058*	*0.785*	*6.100*	*1.050*	*4.2*	*7.8*	*13.0*
	lft	*60*	*2.479*	*0.373*	*2.450*	*0.525*	*1.7*	*3.3*	*15.0*
	NT	*60*	*56.75*	*23.27*	*50.30*	*27.65*	*15.8*	*122.2*	*41.0*
	NF	*60*	*172.5*	*71.55*	*151.2*	*82.20*	*47.4*	*363.0*	*41.5*
	NG	*60*	*32.20*	*10.46*	*31.30*	*12.80*	*11.0*	*70.0*	*32.5*

Statistics computed on plot-level means (n = 60 plots). For plant-level traits (shaded rows), individual measurements on five plants per plot were averaged before computing descriptive statistics. IQR: interquartile range; CV: coefficient of variation. DF: days to flowering; PTFg: total fresh pod weight (kg plot^{-1}); BFT: total fresh biomass (kg plot^{-1}); PTSg: dry pod weight (kg plot^{-1}); PTG: total grain weight (kg plot^{-1}); HSW_g: hundred-seed weight (g); GY_kgha: grain yield (kg ha^{-1}); HP: plant height (cm); DP: plant diameter (cm); LFT: leaflet length (cm); lft: leaflet width (cm); NT: number of stems; NF: number of leaves; NG: number of pods per plant.



Continue …



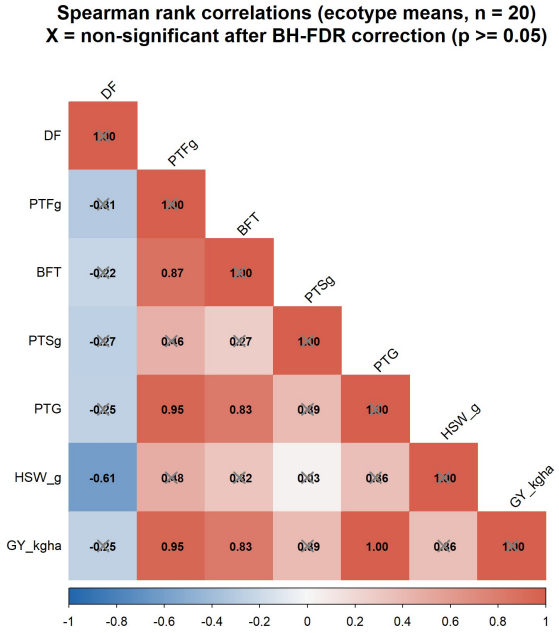


Figure 2. Spearman rank correlation matrix among plot-level agromorphological traits, computed on ecotype means (n = 20 ecotypes). Benjamini-Hochberg FDR correction was applied across all pairwise tests. Crosses (×) indicate correlations that did not survive FDR correction (adjusted p ≥ 0.05). Colour intensity reflects the magnitude of the Spearman coefficient (ρ). Trait abbreviations as in Table 1

(CV = 56.2%), and grain yield (GY_kgha) from 25 to 1470 kg ha^{-1} (CV = 57.4%). Hundred-seed weight (HSW_g) showed moderate variability overall (mean = 52.08 g, SD = 10.10, CV = 19.4%), but one replicate of V3 reached 90 g, which is substantially above the collection mean. At the plant level, plant-level means per plot showed narrower variability than the raw individual observations, reflecting partial averaging of within-plot variation. Number of stems (NT, CV = 41.0%), number of leaves (NF, CV = 41.5%), and pod number (NG, CV = 32.5%) were the most variable. Plant height (HP, CV = 20.8%), plant diameter (DP, CV = 18.1%), leaflet length (LFT, CV = 13.0%), and leaflet width (lft, CV = 15.0%) were comparatively stable across plots.

Varietal differentiation: Flowering time and seed size: Friedman tests, which account for the block structure of the RCBD, revealed a more conservative pattern of varietal differentiation than univariate tests ignoring block effects would suggest (Table 3). At the plot level, significant varietal differentiation was detected only for days to flowering (DF; χ^2 = 53.56, df = 19, p < 0.001) and hundred-seed weight (HSW_g; χ^2 = 42.79, df = 19, p = 0.001).

No significant varietal differences were detected for grain yield (GY_kgha; χ^2 = 29.351, p = 0.061), total grain weight (PTG; χ^2 = 29.351, p = 0.061), total fresh pod weight (PTFg; χ^2 = 25.31, p = 0.151), total fresh biomass (BFT; χ^2 = 19.59, p = 0.420), or dry pod weight (PTSg; χ^2 = 18.88, p = 0.465). At the plant level, none of the seven morphological and reproductive traits reached statistical significance after accounting for block effects: plant height (HP; χ^2 = 13.12, p = 0.832), plant diameter (DP; χ^2 = 17.11, p = 0.583), leaflet length (LFT; χ^2 = 16.21, p = 0.644), leaflet width (lft; χ^2 = 12.81, p = 0.848), number of stems (NT; χ^2 = 15.38, p = 0.698), number of leaves (NF; χ^2 = 15.89, p = 0.664), and number of pods (NG; χ^2 = 19.11, p = 0.450). These non-significant results reflect the conservative nature of the Friedman test with only three blocks, rather than an absence of biological differentiation among ecotypes.

Post- hoc contrasts identify specific ecotypes for phenology and seed size: Conover post-hoc tests with Holm correction identified 122 significant pairwise contrasts across the two significant traits (Table 4). For flowering time, 104 contrasts were significant, structuring ecotypes into two broad phenological groups: early-flowering ecotypes (V4, V20, V28, V5, V6 with DF = 29-33 days) and intermediate-to-late

Table 4. Selected significant pairwise contrasts from Conover post-hoc tests with Holm correction for days to flowering (DF) and hundred-seed weight (HSW_g), Bambara groundnut ecotypes, Dosso region, Niger, 2023

Trait	Ecotype 1	Ecotype 2	p_adj	Significance
DF	V4	V1	< 0.001	***
	V20	V1	< 0.001	***
	V4	V10	< 0.001	***
	V20	V10	< 0.001	***
	V4	V13	< 0.001	***
	V18	V14	< 0.001	***
	V4	V18	< 0.001	***
	V20	V18	< 0.001	***
	V3	V20	< 0.001	***
	V4	V28	0.008	**
	V18	V1	0.029	*
HSW_g	V4	V16	< 0.001	***
	VC	V4	< 0.001	***
	V17	V16	0.001	***
	V16	V15	0.001	**
	V5	V4	0.001	**
	V4	V21	0.006	**
	V4	V10	0.010	*
	V4	V18	0.020	*

Only contrasts significant after Holm correction (p_adj< 0.05) are shown. A total of 104 significant contrasts were identified for DF and 18 for HSW_g; representative contrasts involving the most phenologically or agronomically distinct ecotypes are presented here. The complete table is available as supplementary material. Shaded rows separate the two traits. Significance codes: *, p < 0.05; **, p < 0.01; ***, p < 0.001.

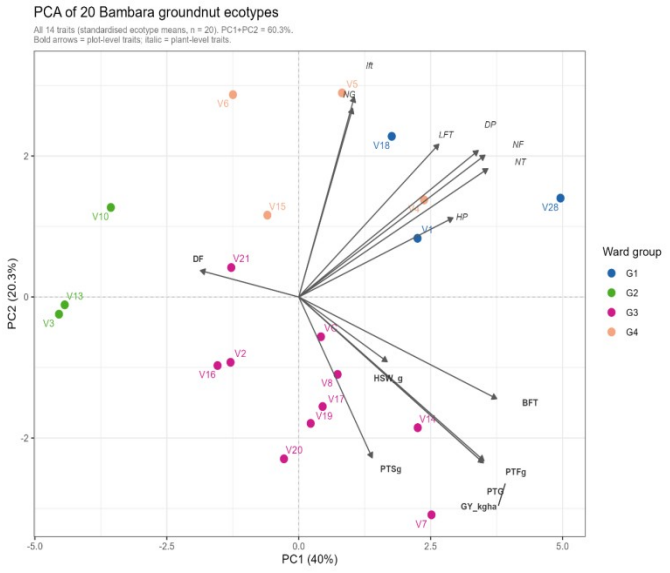


Figure 3. PCA projection of phenotypic groups based on all 14 standardized agromorphological traits

ecotypes (V14, V15, V17, DF = 32-35 days; and V18, V2, V21, V3, VC with DF = 35-39 days). V4 was the earliest-flowering ecotype and differed significantly from the large majority of the collection (p_adj< 0.001 for most contrasts). V20 showed a similarly early phenology (DF = 30 days) with equally broad differentiation. V18 was consistently late-flowering and differed from most early-cycle ecotypes (p_adj ≤ 0.029).

For hundred-seed weight, 18 significant contrasts were identified. V4 had significantly lower hundred-seed weight than most of the collection and differed from V16 (p_adj< 0.001), V5, V17, V15, V20, V7, V8, V21, V10, V18, and V6 (all p_adj ≤ 0.029). VC showed higher hundred-seed weight than V4 (p_adj< 0.001) and also differed from V17 and V15. No significant pairwise contrasts were retained for any yield-related trait after Holm correction.

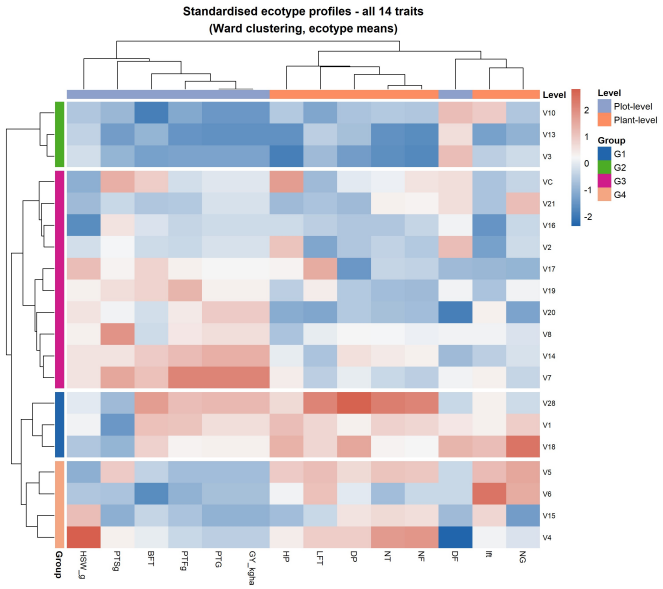


Figure 4. Heatmap of standardized trait profiles across ecotypes, grouped by Ward cluster

Correlation structure: an integrated biomass-yield axis: Spearman rank correlation analysis on ecotype means (n = 20) with BH-FDR correction confirmed a strongly integrated productivity axis, with phenology and seed size operating as independent dimensions (Figure 2). The strongest associations were found between total fresh pod weight (PTFg) and total grain weight (PTG; ρ = 0.945, p_adj< 0.001), PTFg and grain yield (GY_kgha; ρ = 0.945, p_adj< 0.001), and BFT and GY_kgha (ρ = 0.827, p_adj< 0.001). These associations indicate that fresh biomass, pod weight, total grain weight, and grain yield form a tightly co-varying productivity complex. Note that GY_kgha was derived directly from PTG by unit conversion; their Spearman correlation is therefore 1.000 by construction and is not shown as an independent association.

Days to flowering showed weak, non-significant correlations with all productivity traits after FDR correction (ρ ranging from −0.31 to −0.26, all p_adj ≥ 0.308). Hundred-seed weight (HSW_g) was similarly independent from grain yield (ρ = 0.364, p_adj = 0.186) and from most biomass-related traits, though it showed a moderate negative association with DF (ρ = −0.609, p_adj = 0.013). Dry pod weight (PTSg) showed weaker associations with the productivity axis (ρ = 0.392 with PTG and GY_kgha, p_adj ≥ 0.167), suggesting it captures a partially distinct dimension of seed-filling efficiency.

Multivariate analysis identifies four preliminary phenotypic groups: Principal component analysis on all 14 standardized traits captured 40.0% (PC1) and 20.3% (PC2) of total variation, for a cumulative 60.3% on the first two axes (Figure 3). PC1 was primarily associated with agronomic productivity traits (BFT: loading = 0.833; NT: 0.796; NF: 0.784; PTFg: 0.779; DP: 0.755) and opposed these to days to flowering (DF: −0.414). PC2 contrasted leaflet width (lft: 0.630), pod number per plant (NG: 0.594), and plant diameter (DP: 0.461) against pod and grain weight traits (GY_kgha: −0.522; PTFg: −0.516; PTG: −0.522). HSW_g loaded primarily on PC3 (−0.775), confirming its independence from both productivity and morphological dimensions.

Table 5. Mean plot-level trait profiles of four preliminary phenotypic groups derived from Ward hierarchical clustering on all 14 standardized agromorphological traits

Group	n	Ecotypes	DF	PTFg	BFT	PTSg	PTG	HSW_g	GY_kgha
G1	3	V1, V18, V28	34.667	2.346	2.57	0.487	0.683	50.556	683.333
G2	3	V10, V13, V3	35.667	1.047	1.21	0.488	0.258	48.333	258.333
G3	10	V14, V16, V17, V19, V2, V20, V21, V7, V8, VC	33.6	2.108	2.084	0.94	0.633	51.833	633.333
G4	4	V15, V4, V5, V6	31.75	1.421	1.605	0.735	0.39	56.667	389.583

Values are group means computed from ecotype-level means. Group sizes correspond to the number of ecotypes per cluster (n = 3 to 10 ecotypes). DF in days; PTFg, BFT, PTSg, PTG in kg plot^{-1}; HSW_g in g; GY_kgha in kg ha^{-1}. PCA and Ward clustering were performed on all 14 standardized traits; only plot-level means are shown for concision.

Ward hierarchical clustering on standardized ecotype means for all 14 traits separated the 20 ecotypes into four phenotypic groups (Table 5, Figure 4). Silhouette analysis across k = 2 to 6 yielded uniformly low scores (range 0.206–0.264), indicating the absence of strongly defined cluster structure in these data. A partition into four groups was retained as an organizational framework for describing ecotype diversity, not as evidence of discrete phenotypic classes. Group G1 (n = 3: V1, V18, V28) showed the highest mean values for PTFg (2.346 kg), BFT (2.570 kg), and GY_kgha (683.3 kg ha^{-1}), and was associated with the positive end of the morphological axis (Figure 3). Group G2 (n = 3: V10, V13, V3) had the lowest plot-level performance values (PTFg = 1.047 kg, GY_kgha = 258.3 kg ha^{-1}) and was positioned on the negative end of PC1. Group G3 (n = 10: V14, V16, V17, V19, V2, V20, V21, V7, V8, VC) was the largest group and displayed mean grain yield of 633.3 kg ha^{-1}, highest dry pod weight (PTSg = 0.940 kg). Group G4 (n = 4: V15, V4, V5, V6) showed the lowest mean grain yield (GY_kgha = 389.6 kg ha^{-1}), lowest PTFg (1.421 kg), and occupied a central-to-negative position on both PCA axes. A sensitivity analysis excluding V3 showed moderate cluster instability (ARI = 0.536). Four of 19 ecotypes changed group assignment when V3 was removed (V16, V2, V21, VC, all moving from G3 to G2). This result indicates that the four-group structure is sensitive to the presence of V3 and should be treated as a preliminary phenotypic organization rather than a stable classification. Ecotypes remaining stable across both analyses (V1, V18, V28, V10, V13, V14, V17, V19, V20, V7, V8, V15, V4, V5, V6) can be considered more reliably assigned to their respective groups (Figure S2).

DISCUSSION

Constrained phenology and wide variability in productive and structural traits: The narrow phenological window observed in this collection is biologically coherent under Sahelian rainfall regimes. Terminal drought strongly penalizes late-cycle crops, and the low coefficient of variation for days to flowering (6.1%) suggests stabilizing selection around flowering schedules compatible with short rainy seasons. Despite this low dispersion, the Friedman test detected highly significant varietal differentiation for DF ($\chi^2 = 53.56$, df = 19, $p < 0.001$), with V4 and V20 consistently earlier than the large majority of the collection, and V18 occupying the latest phenological position. This indicates that meaningful, albeit bounded, phenological variation is present and should be treated as a selection target rather than dismissed as negligible. The high variability recorded for biomass, vegetative architecture, yield components, and seed size presents a more complex interpretation. Although Bambara groundnut is classified as a predominantly autogamous, cleistogamous species, local landraces frequently exhibit substantial within-ecotype variation (Massawe *et al*., 2002). This pattern may reflect low but historically continuous cross-pollination events, seed-lot mixing across generations, or high phenotypic plasticity within genetically heterogeneous traditional materials. In the farmer-managed systems of the Dosso region, multi-use selection pressures combining grain production, vegetative biomass value for livestock fodder, soil cover, and specific seed morphotype preferences appear to maintain wide structural variation even when phenological norms are strictly conserved. Hundred-seed weight deserves particular attention. The collection mean was 52.08 g (SD = 10.10 g, CV = 19.4%), with values ranging from 35 to 90 g at the plot level. This moderate variability is consistent with the significant varietal differentiation detected by the Friedman test ($\chi^2 = 42.79$, p = 0.001). One replicate of V3 reached 90 g, substantially above the collection mean; while this value is biologically plausible for a large-seeded Bambara groundnut morphotype, seed mixture, within-ecotype segregation, or isolated outlier plants are equally plausible explanations. V3 should be treated as a priority accession for verification through seed purification and progeny testing before any conclusion about large-seeded morphotype differentiation can be made.

Dissociation between morphological and yield differentiation: The Friedman test, which accounts for the block structure of the RCBD, revealed a more conservative pattern of varietal differentiation than univariate tests ignoring block effects would suggest. Only DF and HSW_g reached statistical significance at the plot level. None of the seven plant-level morphological traits were significant. This result reflects a genuine methodological constraint: with only three blocks and 20 ecotypes, the Friedman test has limited power to detect moderate varietal effects in the presence of block-by-ecotype interactions or high within-ecotype variability, both of which are expected in farmer-managed heterogeneous seed lots. The non-significant results for plant-level traits and yield components should therefore not be interpreted as the absence of biological differentiation, but as the inability of the current design to confirm it statistically (Esan *et al*., 2023). The wide numerical ranges and the PCA ordination (Figure 3) both document that morphological differentiation exists; it is not captured at conventional significance thresholds under this conservative blocked design. The absence of significant varietal differentiation for grain yield despite its wide numerical range (25 to 1470 kg ha^{-1}) is an important finding that should not be interpreted as an absence of varietal potential. In low-input rainfed systems, grain yield is highly sensitive to micro-environmental variation including soil heterogeneity, plant establishment, and local rainfall distribution. Such environmental noise can mask genuine varietal differences, particularly when the tested materials are heterogeneous farmer-managed ecotypes rather than genetically stabilized lines (Esan *et al*., 2023). The post-hoc structure for DF is informative despite this conservatism. With 104 significant pairwise contrasts after Holm correction, the Conover test confirms that phenological diversity in this collection is real and wide, structuring ecotypes across a gradient from V4 (DF = 29 days) to V18 (DF ≥ 35 days). For

hundred-seed weight, 18 significant contrasts were identified, pointing to V4 as consistently small-seeded relative to much of the collection, and VC as relatively large-seeded. These profiles are analytically distinct, which makes them useful candidates for targeted multi-environment evaluation. However, none of these morphological advantages translated into statistically confirmed yield superiority under the present conditions.

Trait decoupling and implications for selection: Spearman rank correlations on ecotype means, with BH-FDR correction, confirmed a strongly integrated biomass-yield axis with phenology and seed size operating as independent dimensions. The tight correlations among PTFg, BFT, PTG, and GY_kgha (ρ = 0.827 to 0.945, all p_adj< 0.001) suggest that productive capacity in this collection was primarily determined by the ability of plants to accumulate biomass and convert it into pod and grain mass. This is biologically coherent for Bambara groundnut, where pods develop underground as high-priority sinks and their formation depends on the integration of vegetative biomass accumulation and reproductive allocation (Kendabie *et al*., 2020; Khan *et al*., 2022).

Days to flowering did not show significant correlations with any productivity trait after FDR correction (ρ ranging from -0.31 to -0.26, all p_adj $\geq$ 0.308), despite its highly significant varietal differentiation in the Friedman test. This dissociation is consistent with the interpretation that earliness functions as an adaptive threshold under Sahelian conditions: ecotypes must flower within the available rainfall window to escape terminal drought, but small differences within that window do not produce proportional yield differences. Phenological adaptation and numeric yield performance thus appear to be subject to distinct selection pressures in local germplasm (Bonny *et al*., 2019). The independence of seed size from grain yield is equally important for selection. The negative association between DF and HSW_g ($\rho = -0.609$, p_adj = 0.013) is the only significant correlation involving either of these traits after FDR correction, suggesting that early-flowering ecotypes tend to have larger seeds on average, possibly through a compensatory allocation strategy. V3's extreme hundred-seed weight did not confer a yield advantage; its grain yield was among the lowest in the collection. This decoupling indicates that large seed size in farmer-managed ecotypes may reflect selection for culinary preference, market identity, or household storage value rather than agronomic productivity. Treating seed size and grain yield as independent selection criteria, each evaluated on its own merit against farmer priorities, is therefore more appropriate than using one as a proxy for the other.

Phenotypic groups as preliminary selection profiles: The four Ward clusters, derived from all 14 standardized traits, integrate both agronomic and morphological dimensions of phenotypic variation and thus provide a more complete picture of ecotype diversity than clustering on plot-level traits alone would offer. Group G3 (V14, V16, V17, V19, V2, V20, V21, V7, V8, VC) emerged as the largest group and displayed the highest mean grain yield (633.3 kg ha^{-1}) and dry pod weight (0.940 kg). Group G1 (V1, V18, V28) showed the highest mean fresh biomass (2.570 kg) and grain yield (683.3 kg ha^{-1}), and was associated with the positive end of the morphological axis in the PCA. Group G2 (V10, V13, V3) was consistently the lowest-performing group across most agronomic traits (GY_kgha = 258.3 kg ha^{-1}). Group G4 (V15, V4, V5, V6) showed the lowest mean productivity overall (GY_kgha = 389.6 kg ha^{-1}). These tendencies do not represent statistically confirmed yield superiority; they reflect correlated patterns across replications (Aliyu *et al*., 2016).

The moderate cluster instability (ARI = 0.536 when V3 is excluded) is a critical caveat. Four of 19 ecotypes changed group assignment in the sensitivity analysis (V16, V2, V21, and VC moved from G3 to G2), indicating that the four-group structure is sensitive to V3's extreme seed-size value. This confirms that multivariate distances can be dominated by extreme individual traits even after standardization. Ecotypes with stable assignments across both analyses (V1, V18, V28, V10, V13, V14, V17, V19, V20, V7, V8, V15, V4, V5, V6) are the most reliable candidates for targeted phenotyping in follow-up trials. These clusters serve to guide hypothesis formation and to structure candidate sets for farmer evaluation, not to replace multi-environment validation.

Implications for breeding and genetic resource management: The observed trait structure argues for a multi-trait, multi-environment breeding strategy. Grain yield alone was not a reliable discriminator in this trial, whereas phenological differentiation and seed-size contrasts revealed clear and biologically interpretable varietal structure. In a Bambara groundnut improvement program for the Dosso region, complementary selection dimensions should include: phenological adaptation for climate-risk management; vegetative architecture and pod production for biomass and food security; and seed morphotype for farmer and market acceptability (Aliyu *et al*., 2016). For participatory selection, the most appropriate candidate sets are those expressing stable and contextually relevant trait combinations, not those with the highest yield in a single season. V28, V4, and V18 represent phenotypically distinct and potentially complementary materials for further farmer-led evaluation (Ceccarelli and Grando, 2007). For genetic resource management, conservation should not narrow the collection based on preliminary agronomic performance. The combination of constrained phenology and wide structural diversity suggests that different ecotypes may carry distinct adaptive mechanisms and user-value attributes that warrant preservation and further characterization (Ibrahim *et al*., 2018).

Limitations and perspectives: The interpretation of this study is constrained by its single-site, single-season design. One season under rainfed Sahelian conditions cannot adequately capture the variability in rainfall distribution, soil heterogeneity, and terminal drought scenarios that determine Bambara groundnut performance over time (Khan *et al*., 2022). The non-significant varietal differentiation for yield should therefore be read as insufficient evidence for stable yield ranking, not as proof that the ecotypes do not differ in productive potential. A second methodological limitation must be stated explicitly. The Friedman test with 20 treatments and only 3 blocks is conservative: its power to detect moderate varietal effects is low, particularly when within-ecotype variability is high. The non-significant results for plant-level

morphological traits and yield-related components do not exclude biologically meaningful differences among ecotypes; they reflect the limits of the current design. Increasing the number of replications in future trials would substantially improve discriminating power. The block effect was explicitly modeled in the non-parametric Friedman framework, which corrects a limitation of the earlier analysis. The farmer-managed nature of the materials introduces a further level of uncertainty.

These accessions are better treated as heterogeneous seed lots than as genetically fixed varieties. Within-ecotype variability may have inflated trait dispersion, particularly for seed size and reproductive traits. The moderate ARI value (0.536) reinforces the exploratory status of the Ward groups: V3, whose extreme seed-size value remains unexplained, had a measurable effect on cluster boundaries. Future work should prioritize multi-environment trials across contrasting sites and seasons, combined with formal participatory evaluation by farmers from the Dosso region. Candidate materials identified here should be re-assessed for yield stability, biomass value, phenological behavior, and seed traits under diverse management conditions. Molecular characterization would complement phenotypic data by distinguishing true genetic differentiation from seed-lot admixture and environmentally induced plasticity (Esan *et al*., 2023).

CONCLUSION

This study documented substantial but structurally uneven phenotypic diversity among 20 farmer-managed bambaragroundnut ecotypes from the Dosso region, Niger. Days to flowering was constrained within a narrow but significantly differentiated range, while biomass, plant architecture, pod production, grain yield, and seed size varied widely. Statistical discrimination was confirmed for days to flowering and hundred-seed weight, while morphological, reproductive, and yield-related traits showed wide numerical variability without reaching significance under the conservative Friedman test.

A strongly integrated biomass-pod-grain axis was identified, while flowering time and seed size behaved as independent phenotypic dimensions. Three ecotypes stand out for targeted follow-up: V4 for early flowering and contrasting seed-size profile, V28 for structural architecture and biomass-related performance, and V18 for late phenology and its contribution to the high-productivity G1 profile. V3 requires verification for seed-lot purity and trait stability before any conclusion regarding large-seeded morphotype differentiation can be drawn. Multi-environment, multi-season evaluation is required before any varietal ranking or breeding recommendation can be made.

Acknowledgements

This work was conducted within the framework of the CROPS4HD project, implemented in Niger by SWISSAID Niger. The authors gratefully acknowledge the support of SWISSAID Niger, Regional Centre for Specialised Agricultural Education (CRESA), the Faculty of Agronomy of Abdou Moumouni University, and the farmers and field staff from Dosso involved in the evaluation.

Conflict of interest: The authors declare that they have no conflict of interest.

REFERENCES

Aliyu, S., Massawe, F., & Mayes, S. (2016). Genetic diversity and population structure of Bambara groundnut (Vigna subterranea (L.) Verdc.): synopsis of the past two decades of analysis and implications for crop improvement programmes. Genetic Resources and Crop Evolution, 63(6), 925-943.

Bonny, B. S., Adjoumani, K., Seka, D., Koffi, K. G., Kouonon, L. C., Koffi, K. K., & Bi, I. A. Z. (2019). Agromorphological divergence among four agro-ecological populations of Bambara groundnut (Vigna subterranea (L.) Verdc.) in Côte d'Ivoire. Annals of Agricultural Sciences, 64(1), 103-111.

Brink, M., Ramolemana, G. M., &Sibuga, K. P. (2006). Vigna subterranea (L.) Verdc. Plant Resources of Tropical African, 1, 213-218.

Ceccarelli, S., & Grando, S. (2007). Decentralized-participatory plant breeding: an example of demand driven research. Euphytica, 155(3), 349-360.

Collinson, S. T., Azam-Ali, S. N., Chavula, K. M., & Hodson, D. A. (1996). Growth, development and yield of bambaragroundnut (Vigna subterranea) in response to soil moisture. The Journal of Agricultural Science, 126(3), 307-318.

Donald, C. M. (1968). The breeding of crop ideotypes. Euphytica, 17(3), 385-403.

Esan, V. I., Oke, G. O., &Ogunbode, T. O. (2023). Genetic variation and characterization of Bambara groundnut [Vigna subterranea (L.) verdc.] accessions under multi-environments considering yield and yield components performance. Scientific Reports, 13(1), 1498.

Haoua, B., Abdel Kader, N. J., Rahila, M. M. N., Hamissou, A. M., Rabiou, H. S. M., Iro, D. G., &Toudou, A. (2024). Caractérisation agronomique de six (6) morphotypes de voandzou (Vignasubterranea L. verdc) cultivés au Niger. European Scientific Journal, ESJ, 30, 465.

Hillocks, R. J., Bennett, C., & Mponda, O. M. (2012). Bambara nut: A review of utilisation, market potential and crop improvement. AfricanCrop Science Journal, 20(1).

Ibrahim, A. R., Dansi, A., Salifou, M., Ousmane, A., Alzouma, A., & Alou, W. (2018). Farmers' practices, utilization, conservation and marketing of Bambara groundnut (Vigna subterranea (L.) Verdc.) in Dosso Region, Western Niger. Genetic Resources and crop evolution, 65(7), 1907-1914.

Jarvis, D. I., & Hodgkin, T. (2005). Seed systems and crop genetic diversity on-farm. In D. I. Jarvis, R. Sevilla-Panizo, J.-L. Chávez-Servia, & T. Hodgkin (Eds.), *Seed Systems and Crop Genetic Diversity On-Farm: Proceedings of a Workshop, 16–20 September 2003, Pucallpa, Peru* (pp. 1–4). International Plant Genetic Resources Institute.

Kendabie, P., Jørgensen, S. T., Massawe, F., Fernandez, J., Azam-Ali, S., & Mayes, S. (2020). Photoperiod control of yield and sink capacity in Bambara groundnut (Vigna subterranea) genotypes. Food and Energy Security, 9(4), e240.

Kermah, M., Franke, A. C., Adjei-Nsiah, S., Ahiabor, B. D. K., Abaidoo, R. C., & Giller, K. E. (2018). N2-fixation and N contribution by grain legumes under different soil fertility status and cropping systems in the Guinea savanna of

northern Ghana. Agriculture, ecosystems & environment, 261, 201-210.

Khan, M. M. H., Rafii, M. Y., Ramlee, S. I., Jusoh, M., & Al Mamun, M. (2022). Hereditary analysis and genotype× environment interaction effects on growth and yield components of Bambara groundnut (Vigna subterranea (L.) Verdc.) over multi-environments. Scientific reports, 12(1), 15658.

Mabhaudhi, T., Chibarabada, T. P., Chimonyo, V. G. P., Murugani, V. G., Pereira, L. M., Sobratee, N., & Modi, A. T. (2018). Mainstreaming underutilized indigenous and traditional crops into food systems: A South African perspective. Sustainability, 11(1), 172.

Massawe, F. J., Dickinson, M., Roberts, J. A., & Azam-Ali, S. N. (2002). Genetic diversity in bambaragroundnut (Vigna subterranea (L.) Verdc) landraces revealed by AFLP markers. Genome, 45(6), 1175-1180.

Naino Jika, A. K., Kiebre, Z., Ba, M., Banazaro, P., Grazioli, F., & El Bilali, H. (2023). Custodian farmers of Bambara groundnut and sorrel seeds in Mossi area of Burkina Faso: Profile, diversity and conservation methods. AGROFOR International Journal, 77.

Olanrewaju, O. S., Oyatomi, O., Babalola, O. O., & Abberton, M. (2022). Breeding potentials of Bambara groundnut for food and nutrition security in the face of climate change. Frontiers in Plant Science, 12, 798993.

Sultan, B., & Gaetani, M. (2016). Agriculture in West Africa in the twenty-first century: climate change and impacts scenarios, and potential for adaptation. Frontiers in plant science, 7, 1262.

****