

Research Article

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Corresponding author:

Richard Adu Amoah;
Email: richardadu2005@gmail.com

Analysis of agro-morphological variability and inter-trait relationships in Ghanaian groundnut (*Arachis hypogaea* L.) accessions

Richard Adu Amoah¹ , Charles Nelimor² , Bright Adu Gyamafi¹, Richard Boampong¹, Collins Yeboah Osei¹, Abraham Yeboah¹, Victoria Sackey¹, Eric Osafo Ansa¹, Samuel Awuah¹, Abednego Opoku Mensah¹, Yaw Kwateng¹ and Lawrence Misa Aboagye¹

¹Council for Scientific and Industrial Research (CSIR) - Plant Genetic Resources Research Institute, Bunso, Ghana and ²Soybean Improvement Program, Council for Scientific and Industrial Research (CSIR)-Savanna Agricultural Research Institute, Nyankpala-Tamale, Ghana

Abstract

Germplasm characterization and evaluation are essential for the genetic improvement of crops. In this study, a collection of 204 groundnut accessions including 13 checks held by Plant Genetic Resources Research Institute, Ghana were evaluated under optimal conditions for 2 years. The objectives were to characterize the groundnut collection using 18 qualitative and 14 quantitative traits and to determine the relationships between the traits. Combined analysis of variance based on augmented design revealed significant differences ($P < 0.05$) among the accessions for majority of the traits. Results of principal component analysis showed that all the quantitative traits were relevant in discriminating the accessions. Primary seed colour was the most diverse qualitative trait based on Shannon diversity index ($n = 0.77$). Frequency distribution analysis showed predominance of decumbent growth habit and pale tan seeds. Cluster analysis using qualitative traits identified five major groups of accessions and three each based on quantitative traits and joint analysis of quantitative and qualitative traits. Number of main branches (NMB) and pod width (PW) appeared the most important traits with positive contribution to yield based on correlation and path coefficient analysis. Ten promising trait-specific accessions were identified for earliness along with desirable pod and seed traits. GH 9672 and GH 9665 were identified as promising for higher grain and fodder yield. Five accessions (GH 9833, GH 9829, GH 9830, GH 9835 and GH 9750) produced ~5–30% more grain yield than the best check. This study underscored ample phenotypic variation that would ultimately be exploited for genetic improvement of groundnut.

Introduction

Groundnut (*Arachis hypogaea* L.) is a multipurpose grain legume cultivated globally. In developing countries where it is grown in large volumes, groundnut is important in the livelihood of many households for its nutritional and economic contributions (Shilman *et al.*, 2011; Oteng-Frimpong *et al.*, 2017). The groundnut kernel is highly nutritious, containing edible oil (36–54%) and proteins (12–36%) vital for human health (Mondal and Bhuiyan, 2020). Aside from nutritional benefits, groundnut improves soil fertility through nitrogen fixation, which makes it a good partner in cropping systems for improved soils and hence reduced need for mineral fertilizers (Ajeigbe *et al.*, 2015). In sub-Saharan Africa (SSA), groundnut is predominantly cultivated under rain-fed conditions and constrained by a wide range of biotic and abiotic stresses. Consequently, yields on farmers' fields are abysmally low at less than 1.5 tons/ha (FAOSTAT, 2020). Interventions geared towards yield improvement are therefore needed to safeguard the food and nutritional security of millions of smallholder farmers who depend on groundnut farming for livelihood.

In crop improvement programmes, assessment of genetic variation and identification of trait-specific germplasm is important because it facilitates efficient use of genetic resources to achieve breeding objectives (Obeng-bio *et al.*, 2020). Phenotypic characterization has long been the first step for classification of germplasm resources to enable their judicious use in breeding programmes (Nelimor *et al.*, 2019). Even in this era, phenotypic descriptors are still being employed for diversity analysis of germplasm collections of different crops including maize (Nelimor *et al.*, 2019); millet (Kandel *et al.*, 2019); sorghum (Gueye *et al.*, 2016), cowpea (Dareus *et al.*, 2021) and bambara groundnut (Siwale *et al.*, 2022). Genetic improvement in qualitative and quantitative traits is a major breeding goal of groundnut breeding



programmes worldwide. To this end, both quantitative and qualitative attributes of agronomically important traits such as the pods (yield traits), stem, branches and leaflets have been widely used to assess, describe, classify and identify promising accessions of groundnut for use in breeding programmes (Garba *et al.*, 2015; Yol *et al.*, 2018; Banla *et al.*, 2020). Yol *et al.* (2018) evaluated 256 groundnut accessions from the Mediterranean Basin and reported wide genetic variation for eight quantitative and five qualitative traits. In a similar study, Banla *et al.* (2020) phenotypically assessed 94 groundnut accessions from Togo and Senegal. Using Simpson index, the authors reported high diversity for primary seed colour (0.75), stem pigmentation (0.60) and growth habit (0.59).

The genebank at the Plant Genetic Resources Research Institute of the Council for Scientific and Industrial Research (CSIR-PGRRI) at Bunso, Ghana conserves several groundnut accessions that possibly harbour genetic variation for viable groundnut improvement. The majority of these accessions are indigenous to Ghana and are under-characterized and hence grossly underutilized in breeding programmes since their genetic value is unknown. Therefore, it is imperative to characterize the groundnut accessions held by the CSIR-PGRRI so that they can be promoted for mainstreaming into breeding pipelines. Additionally, understanding the interrelationship between the traits associated with superior genotypes and contribution of traits to yield is necessary to improve selection efficiency. This could, in turn, enhance their value as potential resources for improvement of farmers' livelihoods and for generation of genomic resources to fast-track groundnut breeding. Therefore, this study was conducted to (i) assess the agromorphological performance and relationships among a collection of groundnut accessions held by the CSIR-PGRRI, (ii) determine the inter-trait relationships among the groundnut accessions using sequential path coefficient analysis and (iii) identify trait-specific germplasm for use in groundnut breeding programmes.

Materials and methods

Planting materials, study area and experimental procedure

The groundnut germplasm used for this study consisted of 204 accessions and 13 improved varieties used as checks (Table S1). The checks were specifically bred for increased grain and fodder yield potential along with resistance/tolerance to both early and late leaf spot diseases of groundnut. The 204 accessions originated (collection sites) from three agroecological zones in Ghana (Fig. 1) (Table S1) and were retrieved from the gene bank at CSIR-PGRRI where they are held under long-term storage.

The accessions were evaluated at the research field of CSIR-PGRRI, Bunso (latitude. 6° 17' 42.6" N, longitude. 0° 27' 38.5" W, 149 m above sea level), Ghana, during the major raining seasons of 2021 and 2022. The experiments were arranged using an augmented design with four blocks of 64 accessions, each including the 13 checks which were replicated. Plot size consisted of single rows, each being 2 m in length with 0.4 and 0.2 m inter and intra-row spacing, respectively. Observed pests and diseases were controlled using Lambda Super 2.5 EC at a rate of 0.4–0.8 L/ha and Mancozeb 640 g + metalaxyl 80 g/kg at a rate of 1.25 kg/ha respectively. Weeds were manually controlled using hoe as and when necessary.

Trait measurement

Data were recorded for 32 agro-morphological descriptors following the guidelines of International Board for Plant Genetic Resources (IBPGR) (IBPGR, 1992) (Table S2). Among the 32 descriptors used, 18 were qualitative and the remaining were quantitative.

Data analyses

Combined analysis of variance (ANOVA) was performed based on augmented design to determine differences among accessions for the various quantitative traits. Effects due to accession by environment interaction (AEIs) were estimated using adjusted means of the checks based on the difference in the mean value of each check used in each block and the overall plot. The AEI was calculated following the proposed equation by You *et al.* (2013);

$$Y_{ij} = \mu + \tau_i + v_j + (\tau v)_{ij} + \varepsilon_{ij}$$

where Y_{ij} : adjustment value of the i th accession in j th year; μ : average of trait; τ_i : effect of the i th accession; v_j : effect of the j th year; $(\tau v)_{ij}$: interactions effect of the i th accession in j th year, and ε_{ij} : combined error.

Broad sense heritability of each trait was estimated using the formula as suggested by Falconer and Mackay (1996)

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2/nloc + \sigma_e^2}$$

where h^2 , σ_g^2 , σ_e^2 , $nloc$ are broad sense heritability, the genotype variance, error variance and number of locations, respectively.

Principal component analysis (PCA) and biplot analysis were performed to determine the contribution of each trait in differentiating the accessions. Phylogenetic trees were constructed to classify the accessions into dissimilar groups. The PCA, biplot and phylogenetic tree analyses were performed using SAS-based JMP software version 14 pro (SAS Institute, 2017). Also, correlation among the different quantitative variables was performed using the R software and result was displayed as heatmap (R Development Core Team, 2013). Shannon–Weaver diversity index (H') was estimated to determine the extent of genetic variability among the qualitative traits (Shannon and Weaver, 1949) using the equation below;

$$H' = \frac{[\sum (\frac{n}{N} \times \{\log_2 (\frac{n}{N}) \times (-1)\})}{\log_{2k}}$$

where H' : standardized Shannon–Weaver diversity index; k : number of phenotypic classes for a trait; n : number of observations in the phenotypic class of the trait and N : the total number of observations for the trait.

Results

Variance and frequency distribution analyses

Results of combined ANOVA across the 2 years (Table 1), showed that the year had a significant effect on the majority (eight) of the traits. Highly significant differences ($P < 0.01$) were observed among accessions for all of the measured traits except leaf

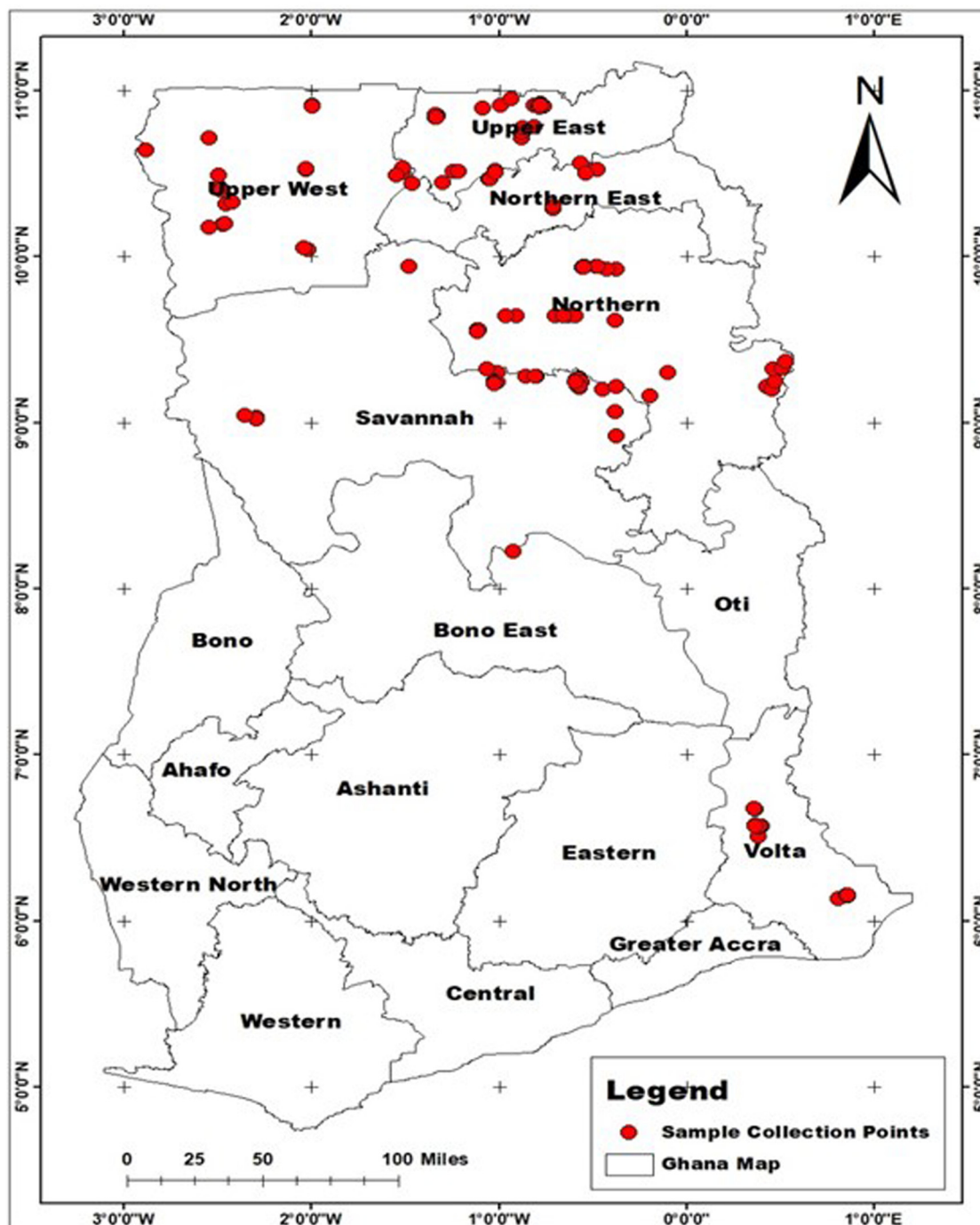


Figure 1. Map of Ghana showing the collection points of the groundnut accessions analysed in this study.

width (LW) and seed length (SL) (Table 1). The interaction of the accessions with year was also significant for number of pods per plant (NP), days to emergence (DE), first flowering (DF) and maturity (DM), pod size (PS), and hundred seed weight (HSW). Broad sense heritability values of the measured traits ranged from 0.21 for LW to 0.99 for NP. Mean comparison of the measured traits revealed that majority of the accessions on the average, emerged within 6 days after planting, and flowered at 26 days after planting (Table 1). The mean number of days from planting to maturity (DM) was 102. Among the genotypes,

the average plant height was 43.38 cm, whereas the average number of pods recorded was 80.14 per plant. The mean weight of 100 seeds per genotype was 54.56 g (Table 1).

Results of the frequency distribution of the various qualitative traits indicated variations in the description of most of the traits with the exception of inflorescence and flower traits (Table 2). Evaluating the gross morphology of the accessions revealed that annual was the frequent life form among the accessions. With respect to the growth habit (GH), decumbent-3 was the most frequent (70.37%) character among the accessions while

Table 1. Mean sum of squares from combined analysis of variance of 204 groundnut accessions including 13 checks assessed during the major growing seasons of 2021 and 2022 at Bunso, Ghana

Source	DE (days)	DFF (days)	LL (cm)	LW (cm)	PH (cm)	PS (cm)	NMB	NP	PL (cm)	PW (cm)	SL (cm)	SW (cm)	DM (days)	HSW (g)
Year	7.94*	42.8**	8.05*	5.85*	7.47	152.56**	6.02	220.48**	1.21	1.87	83.49	11.32*	6.85	24.67*
Accession	8.566**	5.85**	7.14**	1.29	234.41**	1045.68**	73.26**	4367.83**	116.31**	13.18**	91.25	8.2**	186.69*8	1163.61**
Accession × year	5.7**	6.38**	0.18	0.15	0.1	64.07**	1.1	652.51**	2.01	0.24	59.37	0.45	231.96**	1077.39**
Residual	1.93	2.02	1.87	1.59	3.21	7.84	1.98	11.14	2.27	1.92	2.13	2.02	2.81	3.84
Grand Mean	6.14	25.95	6.93	3.54	48.38	98.79	9.14	80.14	25.34	11.98	13.53	7.53	102.45	54.56
Heritability	0.49	0.44	0.31	0.21	0.89	0.96	0.53	0.99	0.81	0.4	0.71	0.41	0.93	0.92

Notes: *, **, Significant at 0.5 and 0.01 probability levels, respectively; DE, days to 50% emergence; DFF, days to 50% flowering; LL, leaf length; LW, leaf width; PH, plant height; PS, plant spread; NMB, number of main branches; NP, number of pods per plant; PL, pod length; PW, pod width; SL, seed length; SW, seed width; DM, days to maturity; HSW, hundred seed weight.

Table 2. Frequency distribution and Shannon–Weaver diversity index (H') of the measured qualitative traits of the 217 groundnut accessions

Trait	Description	Frequency, %	H'
Gross morphology			
Growth habit (GH)	Decumbent-1	0.93	0.37
	Decumbent-2	14.81	
	Decumbent-3	70.37	
	Erect	13.89	
Stem			
Branching pattern (BP)	Irregular without flowers on main stem	49.31	0.30
	Sequential	50.69	
Leaf			
Leaf colour (LC)	Dark green	84.33	0.19
	Light green	15.67	
Leaflet shape (LS)	Dark green	0.46	0.25
	Oblong-elliptic	76.04	
	Obovate	23.50	
Fruit			
Pod beak (PB)	Absent	5.07	0.39
	Moderate	72.35	
	Prominent	8.29	
	Slight	13.36	
	Very prominent	0.92	
Pod constriction (PC)	Deep	3.23	0.50
	Moderate	17.51	
	None	24.42	
	Slight	53.46	
	Very deep	1.38	
Pod reticulation (PR)	Moderate	44.24	0.54
	None	2.30	
	Prominent	35.02	
	Slight	12.44	
	Very prominent	5.99	
Seed colour (SC)	One Colour	92.17	0.12
	Variegated	7.83	
Primary seed colour (PSC)	Dark red	7.83	0.77
	Dark tan	21.20	
	Light red	5.99	
	Light tan	13.82	
	Off-white	3.23	
	Pale tan	35.94	
	Purplish red/reddish purple	0.46	
	Tan	10.14	
	Very pale	1.38	

decumbent-1 recorded the lowest frequency of 0.93%. Based on stem traits, variation was only observed for branching patterns (BP) with 50.69% of them being sequential. Morphological characterization of the accessions according to their fruit traits indicated variations among all the fruit traits. Seed colour (SC) varied between one colour and variegated. Primary seed colour (PSC) recorded the maximum number of varying characters or descriptions (Table 2). There were a total of nine descriptions among which pale tan recorded the highest frequency of 35.94% followed by dark tan with a frequency of 21.2%. A few of the accessions had purplish red/reddish purple as their primary seed colour representing the lowest frequency of 0.46% among all the primary seed colour (PSC) characters.

Assessment of the contribution of individual traits to the genetic diversity of the accessions using the Shannon–Weaver diversity index revealed that traits such as branching pattern (BP), leaf colour (LC), leaflet shape (LS) and seed colour (SC) recorded low diversity indexes of 0.3, 0.19, 0.25 and 0.12, respectively (Table 2). Traits such as growth habit, pod beak, pod constriction and pod reticulation recorded intermediate diversity indexes of 0.37, 0.39, 0.50 and 0.54, respectively. Primary seed colour (PC) was the only trait that recorded a higher diversity index of 0.77 indicating that this trait contributed to most of the genetic diversity among the accessions evaluated in this study (Table 2).

Principal component and accession by trait biplot analyses

Principal component analyses based on the quantitative traits showed four principal components that accounted for more than half (~68%) of the overall variability among the accessions (Table S3). In particular, PC1 explained ~26% of total variation, where SW, LW, HSW, LL, SL and PW appeared the most discriminant traits. PC2 accounted for ~21% of the total variation with traits such as DM, DFF, PH and LL as the major contributors. The PC3 explained ~11% of the total variation with the main contribution coming from five variables (NMB, DE, NP, PL and

HSW). In the PC4 where ~9% of the total variation was explained, PS, NP and DE were the principal contributory traits. Based on the contribution of each of the measured traits to the most informative principal components, all the 14 quantitative traits were found to be relevant in discriminating the groundnut accessions (Table S3). Combined data across quantitative and qualitative traits revealed seven principal components with Eigen values >1 capturing ~68% of the total variation (Table S4). PC1 and PC2 together accounted for ~37% of the total variation while the remaining four principal components each contributed <10% to total variation (Table S4).

The accession-by-trait biplot analysis revealed that the first two PCs were able to distinguish the groundnut accessions according to their major contributing traits by capturing nearly 50% of the total variation (Fig. 2). The biplot diagram supports the earlier clustering results that generally, the accessions in cluster III (represented by red colour) were associated with increased values for the various quantitative traits measured. In addition, the biplot diagram depicted the association/closeness of the different traits, where positively associated traits were in acute angle (e.g. LL and LW, LW and SW, SL and HSW, etc.) (Fig. 2).

Phylogenetic tree analyses

Phylogenetic tree constructed based on the quantitative traits classified the groundnut accessions into three distinct clusters (Fig. 3a). Each cluster was further divided into two or more sub-clusters. The first major cluster contained 78 accessions that were early to emerge, flower and mature but with reduced pod size and small and light weighted seeds. Cluster II consisted of 73 dwarfed accessions with delayed emergence, narrow and short leaves, and late maturity (Table S5). Cluster III, which was the most distinct, had 66 accessions characterized by wide and long leaves, and increased plant height, and numerous branches, as well as increased pod and seed-related traits. Based on the qualitative traits, five major groups of groundnut accessions were revealed

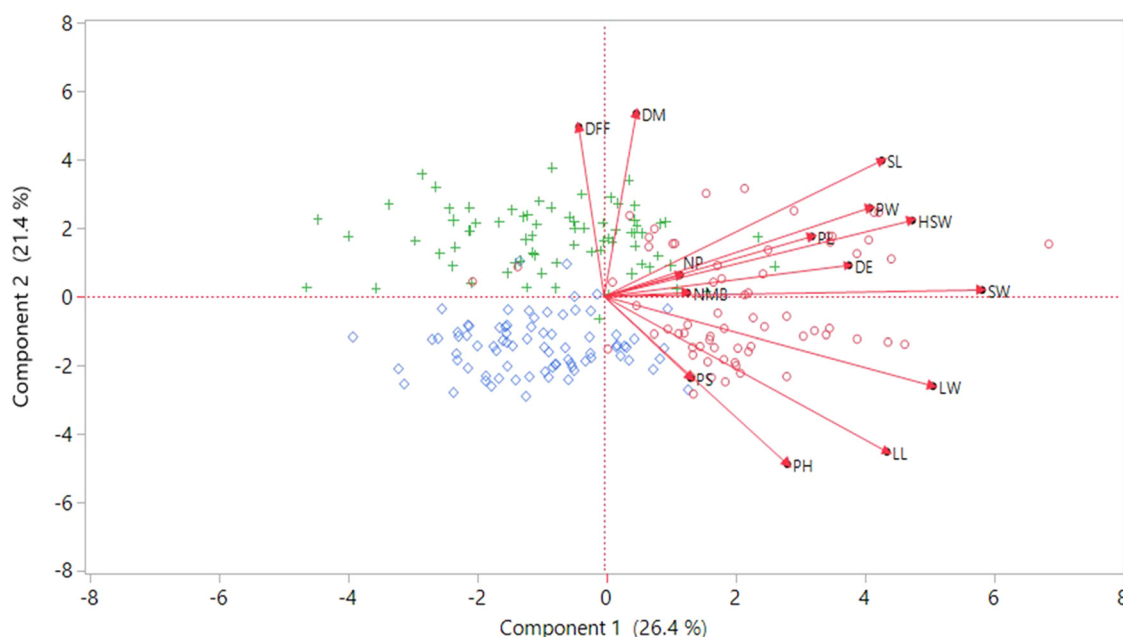


Figure 2. Genotype by trait biplot analysis of 217 groundnut accessions for two principal components.

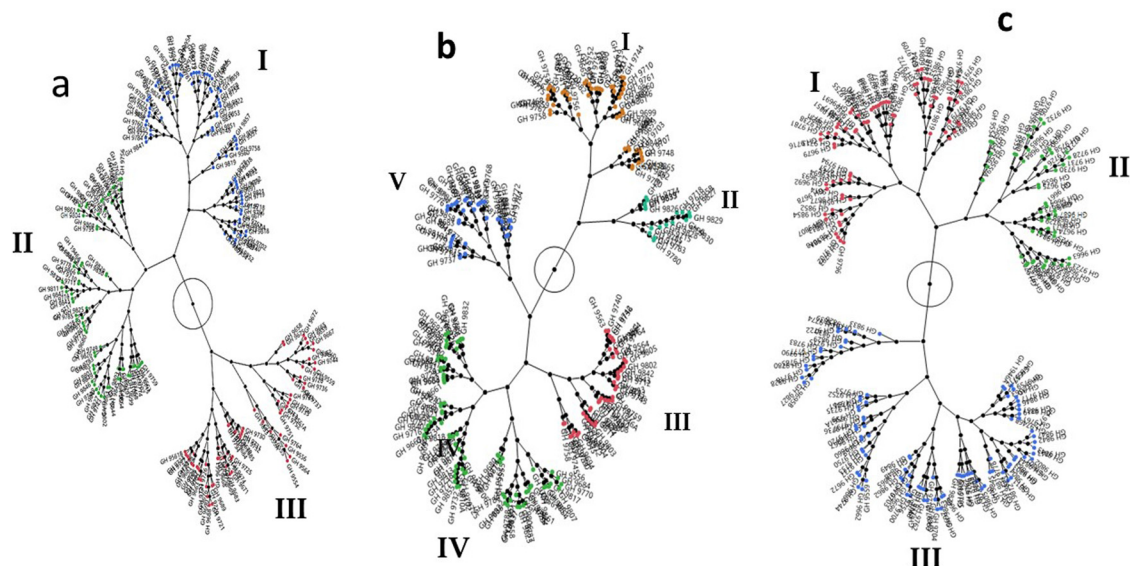


Figure 3. Phylogenetic constellation plot displaying genetic relatedness among 217 groundnut accessions based on hierarchical cluster analysis. (a) Quantitative traits, (b) Qualitative traits and (c) Across quantitative and qualitative traits.

(Fig. 3b) while three groups were identified based on joint analyses of quantitative and qualitative traits (Fig. 3c).

Determination of inter-trait relationships

Sequential path analysis was performed to determine the relationship between yield (NP) and other measured traits of the studied accessions (Figure S1). Results showed that only number of main branches (NMB) and pod width (PW) had a significant direct effect on pod number/yield, accounting for 70% of the total variation in pod number/yield (Figure S1). Of these two first-order traits, number of NMB had the largest positive direct effect (0.212). Six traits, namely, LW, DFF, seed width (SW), seed length (SL), pod length (PL) and DM were identified as second-order traits (Figure S1). Of these, leaf LW and DFF contributed indirectly to yield through NMB, whereas the remaining second-order traits contributed indirectly to yield through PW. Traits categorized in the third order included leaf length (LL), DE, plant height (PH), HSW and plant spread (PS), each with an indirect contribution to yield through one or more second-order traits (Figure S1).

Correlation analysis revealed a highly significant ($P < 0.001$) and positive correlation between a majority of the measured traits (Fig. 3). Yield (NP) was significant and positively correlated with only number of NMB ($r = 0.25^{***}$) and PW ($r = 0.22^{**}$) supporting the sequential path analysis results. Leaf width (LW) showed a significant and positive correlation with leaf length (LL) ($r = 0.86^{***}$), seed width (SW) ($r = 0.81^{***}$), DE ($r = 0.67^{***}$), PW ($r = 0.51^{***}$), SL ($r = 0.40^{***}$), PH ($r = 0.38^{***}$) and NMB (0.33^{***}). Plant height showed significant and negative correlation with days to DFF and DM ($r = -0.49^{***}$). Similarly, DFF was significant and negatively correlated with LL (-0.39^{***}) and PS (-0.22^{**}) (Fig. 4).

Promising trait-specific accessions

Earliness, increased seed size and high grain yield are important agronomic traits for groundnut improvement. In the germplasm

set, 29 accessions were earlier (DFF < 25 days). However, after considering yield along with increased pod and seed traits (PL, SW and SL), as well as reduced days to emergence (DE) and maturity (DM), the top 10 accessions were (GH 9813, GH 9680, GH 9693, GH 9664, GH 9787, GH 9825, GH 9702, GH 9793, GH 9681 and GH 9676) (Table S6). For yield, which is represented by NP, 23 accessions were identified with increased NP (100–178) compared to the grand mean of ~80. The top five (GH 9833, GH 9829, GH 9830, GH 9835, and GH 9750) produced 4.5–30% more grain yields (NP) than the best check (GH 9559A with NP = 133). These high-yielding accessions matured in 97–120 days (Table S6). Accessions with increased values for both PH and NMB (above the trial means of 43 cm and 9.14, respectively) were considered promising for use as fodder. Based on this, 15 accessions were identified as desirable for fodder. Of the 15, two accessions (GH 9672 and GH 9665) recorded high grain yield while one accession (GH 9664) displayed earliness (Table S6).

Discussion

In this study, a collection of groundnut accessions from three agroecological zones of Ghana was investigated for variation in phenotypic attributes as a preliminary step to identify accessions that could be used in groundnut improvement programmes. The large significant variation observed for the majority of the traits measured in this study is an indication of ample phenotypic diversity in the groundnut accessions and thus increased the possibility of identifying promising or trait-specific-germplasm for genetic improvement of target traits. The significant interactions of accessions with year for NP and other agronomic traits suggest the influence of environments on the expression of these traits. Nonetheless, the heritability estimates of the traits were moderate to very high, suggesting that for this set of accessions, progress in genetic improvement could be achieved through selection for traits in the studied environment. These observations are concordant with the results of previous studies which reported considerable phenotypic variation in groundnut accessions (Yol

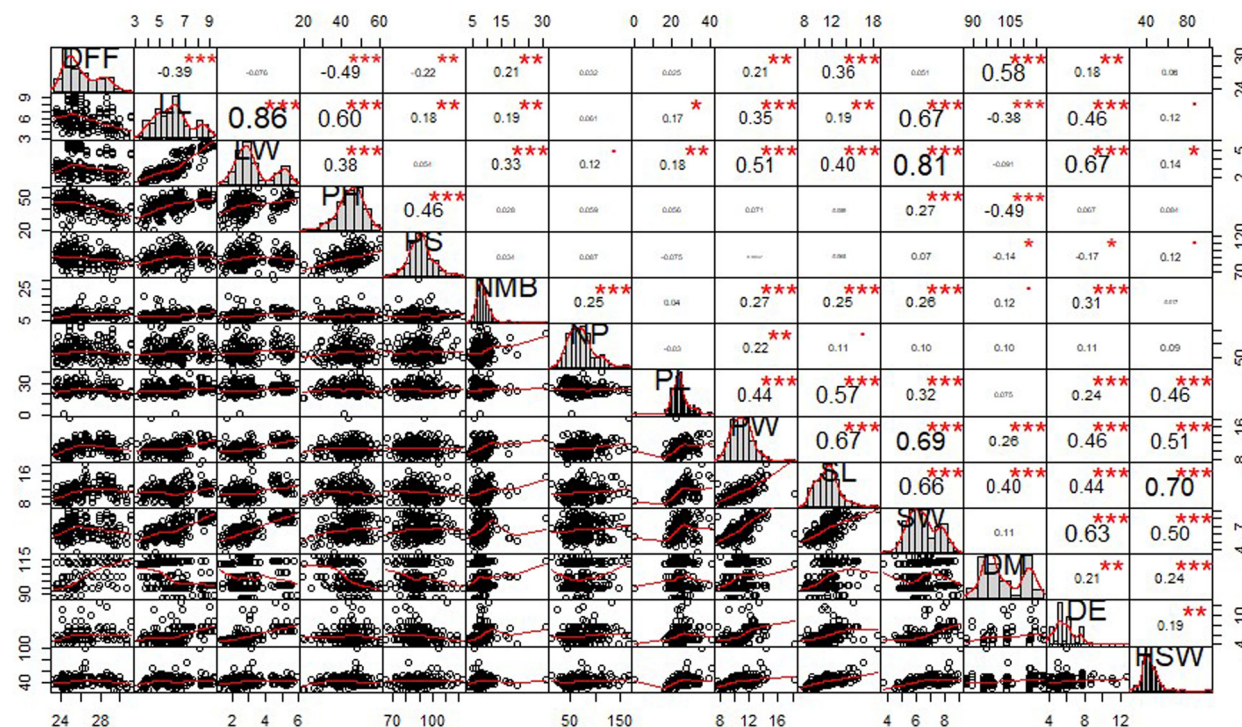


Figure 4. Correlation co-efficient between different morphological traits of 217 groundnut accessions.

et al., 2018; Banla *et al.*, 2020). In particular, the high variability in flowering behaviour (days to first flowering), days to maturity and yield (depicted by number of pods) showed that the studied groundnut accessions are adapted to a wide range of environments supported also by alternative agronomic practices in the different agroecologies from which they were collected. The lack of genetic variation among the accessions for traits such as days to emergence, leaf length and width and seed length and width is consistent with the findings of previous studies (Upadhyaya *et al.*, 2003; Banla *et al.*, 2020).

In this study, the relative contribution of each trait to the observed variation among the groundnut accessions was inferred using PCA. The results showed that with the exception of days to emergence, all the quantitative traits recorded in this study contributed to the phenotypic diversity observed in the groundnut accessions. However, the most discriminating agro-morphological traits were number of pods per plant, plant height, 100 seed weight, plant spread and number of main branches. These results are in agreement with the findings of Mofokeng *et al.* (2021) who found all quantitative traits except yield as highly informative in the phenotypic differentiation of South African groundnut accessions. In the present study, the first four PC's accounted for 67.78% of the observed phenotypic variation, which is comparable to the 68% recorded for accessions from Mediterranean basin (Yol *et al.*, 2018) but slightly higher and lower than the 64% and 80% displayed by South African accessions (Mofokeng *et al.*, 2021), and Togolese and Senegalese accessions, respectively (Banla *et al.*, 2020).

An important objective of this study was to determine the phenotypic relatedness among the groundnut accessions. The grouping pattern displayed by the phylogenetic tree analysis indicates the presence of wide genetic variation in the groundnut accessions, which will be invaluable for breeding and future cross-

combinations to broaden the genetic base of existing groundnut lines. Oliveira *et al.* (2015) opined that in principle, qualitative traits provide additional information on groups and thus associated with a larger number of groups compared to grouping based on quantitative traits. In this study, the larger number of groups revealed by phylogenetic tree analysis of qualitative traits (five) compared to quantitative traits (three) was therefore not surprising. Nonetheless, the grouping pattern obtained from the joint analysis was largely in congruence with the grouping based on quantitative traits. These results reaffirmed that the accessions of the different groups obtained based on quantitative traits were indeed phenotypically dissimilar. Thus, information from the quantitative traits-based cluster analysis could be invaluable for the selection of contrasting parental lines to maximize heterosis during hybridization. This observation is in conjunction with previous reports (Nelimor *et al.*, 2019; Banla *et al.*, 2020).

Information on the association among traits of crops is crucial to determine secondary traits that can be used for indirect selection for a trait of interest. Genetic variability among genotypes and environmental conditions greatly influence the relationship among traits. In this study, PCA-biplot was used to visualize the association among traits. The biplot portrayed acute angles between majority of the traits (e.g. LL and LW, LW and SW, SL and HSW, etc.), suggesting that the traits were positively associated. Taking a cue from the result of the biplot analysis, correlation analysis was performed and the results confirmed that indeed the majority of the traits were positively correlated. To consolidate this finding, a sequential path analysis was performed to identify secondary traits for indirect selection for grain yield. The path analysis identified NMB and PW as first-order traits accounting for 70% of the variation in NP (yield) suggesting that in this set of groundnut accessions, selection for increased NMB and PW could lead to improved yield. The correlation

analysis also identified NMB and PW as the only traits with significant and positive correlation with NP or yield, which indicates the possibility of simultaneous improvement of these traits. The importance of these traits in the genetic improvement of groundnut has been highlighted in earlier studies (Banla *et al.*, 2020; Jahanzaib *et al.*, 2020).

Identification of promising trait-specific accessions for traits of interest is important to facilitate judicious use of germplasm in breeding programmes. Nigam and Aruna (2008) opined that shortened days to first flowering and reduced plant height are important traits for the development of short-duration groundnut cultivars. In this study, the mean values recorded for days to flowering and plant height were lower when compared to those reported for groundnut accessions from the Mediterranean basin (Yol *et al.*, 2018). In particular, accessions GH 9813, GH 9680, GH 9693, GH 9664, GH 9787, GH 9825, GH 9702, GH 9793, GH 9681 and GH 9676, earliness with desirable pod and seed traits, could be good candidates for breeding for earliness in groundnut. Indeed, these accessions originated from Northern Ghana where rainfall is sporadic and short. Perhaps, farmers in this region may have consciously selected earliness as insurance against crop failure due to intermittent droughts during the growing season. Similar findings have been reported in maize (Nelimor *et al.*, 2019). The five accessions (GH 9833, GH 9829, GH 9830, GH 9835 and GH 9750) out-yielded the best check by ~5–30% and the two accessions with high grain and fodder yields (GH 9672 and GH 9665) could serve as instant genetic resources for utilization in breeding programmes to improve groundnut yield.

Conclusion

This study revealed considerable phenotypic diversity in the groundnut accessions held by CSIR-PGRRRI, Ghana. The genetic relationships revealed by analyses of quantitative traits were largely in agreement with the results from joint analyses of qualitative and quantitative traits. PCA, biplot, correlation and sequential path analyses provided comprehensive insight into the inherent association among measured traits. Yield, which is the primary trait of interest, could be improved through indirect selection for genotypes with desirable NMB and PW. Several accessions with desirable traits were identified, which could be exploited to broaden the genetic base of existing lines and to develop new varieties in West and Central Africa. Accessions GH 9833, GH 9829, GH 9830, GH 9835 and GH 9750 could be exploited for yield improvement, GH 9672 and GH 9665 for both grain fodder and yield. The next step following this study is to evaluate selected promising accessions for tolerance to key abiotic (drought and heat) and/or resistance to biotic stresses, particularly leaf spot.

Supplementary material. The supplementary material for this article can be found at <https://doi.org/10.1017/S1479262123000916>.

Author contributions. Richard Adu Amoah, Charles Nelimor and Lawrence Misa Aboagye conceived and designed the experiment. Collins Yeboah Osei, Richard Boapong, Samuel Awuah, Abednago Opoku Mensah, and Yaw Kwarteng conducted the experiment and collected the data. Richard Adu Amoah, Bright Adu Gyamfi and Charles Nelimor validated and analysed the data. Richard Adu Amoah wrote the first draft with contribution from Charles Nelimor, Abraham Yeboah, Victorial Sackey, and Eric Osafo Ansah. All the authors read and approved the content prior to submission.

Competing interests. None.

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