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RESEARCH ARTICLE

Correlations, path coefficient analysis and phenotypic diversity of a West African germplasm of Kersting's groundnut [*Macrotyloma geocarpum* (Harms) Maréchal & Baudet]

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Abstract Providing the growing population with quality diet under the changing climate requires renewed efforts on the breeding of orphan grain legumes that need to be adequately characterized for accelerated cultivar development, particularly in sub-Saharan Africa where food and nutritional insecurity remains a critical challenge. In this study, the phenotypic diversity of a West African germplasm of Kersting's groundnut was determined and the possibility for indirect selection explored. In total, 297 accessions collected across diverse ecological zones in Benin and Togo were assessed using 19 descriptors in two contrasting environments. Correlation and path coefficients analyses were performed to determine association patterns among variables. Hierarchical cluster analysis was carried out to group accessions having similar performance across locations. Based on the results, the diversity panel was categorized into four clusters with clusters 2 and 4 containing the best performing accessions. Significant moderate phenotypic correlation was detected between seed coat colour and days to 50% flowering ($r = -0.63$). Likewise, significant and moderate to strong positive genetic correlations were observed between grain yield with number of seeds per pod ($rg = 0.60$), 100 seed weight ($rg = 0.70$), number of seeds per plant ($rg = 0.96$) and number of pods per plant ($rg = 0.90$). However, significant weak negative correlations were revealed among grain yield, days to 50% flowering ($rg = -0.32$) and days to maturity ($rg = -0.30$). Moreover, high direct effects were detected among grain yield and number of seeds per plant, 100 seed weight and days to 50% flowering. The findings imply that indirect selection for grain yield in Kersting's groundnut, using 100 seed weight, number of seeds per plant and days to 50% flowering could be relevant to increase the efficiency of breeding programmes. Accessions 02_AF169, 02_AF51, 02_AF202, 02_AF222, 02_AF196, 02_AF100, 02_AF255, 02_AF216, 02_AF223 and 02_AF199 could also be used as parental lines for the development of high yielding varieties.

Keywords Accession · Indirect selection · *Macrotyloma geocarpum* · Phenotypic diversity · West africa

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Introduction

Recent climate scenarios are predicted to reduce agricultural productivity, especially for major crops (e.g. cereals) grown on a large scale (Leng and Huang 2017; Challinor et al. 2016; Nelson et al. 2009). Under this situation, feeding the growing population in Africa with nutrient-rich diets under the changing climate requires a major refocusing on locally-adapted crop species, including orphan grain legumes (Considine et al. 2017). The concept of orphan grain legumes refers to many pulse species, such as bambara groundnut [*Vigna subterranean* (L.) Verdc.] and Kersting's groundnut [*Macrotyloma geocarpum* (Harms) Maréchal & Baudet], which have received less attention from researchers and are cultivated on a small scale (Cullis and Kunert 2017; Saka et al. 2004). Orphan grain legumes are reported to possess high nutritional values and resilience to most abiotic stresses, highlighting their potential to address food and nutritional security in sub-Saharan Africa in the context of climate change (Considine et al. 2017; Ayenan and Ezin 2016; Cleasby et al. 2016).

Macrotyloma geocarpum (Fabaceae) is cultivated in most West African countries, especially in Ghana, Togo and Benin. The crop has a high economic value with significant contribution to the income and livelihood of resource-limited-farmers (Dansi et al. 2012; Achigan-Dako and Vodouhè 2006). The crop is used as food and folk medicine for the treatment of several diseases, including diarrhoea, cysts and malaria (Assogba et al. 2016; Ayenan and Ezin 2016; Mergeai 1993). In addition, Kersting's groundnut performs well in drought-prone environments, providing farmers with options to adapt to climate change (Ayenan and Ezin 2016; Achigan-Dako and Vodouhè 2006). Unfortunately, in the recent past, Kersting's groundnut production has been declining (Akohoué et al. 2018; Assogba et al. 2016; Ayenan and Ezin 2016; Oyetayo and Ajayi 2011), and production constraints include low yield, high labour requirements and high disease pressure especially in humid zones (Akohoué et al. 2018; Assogba et al. 2016; Achigan-Dako and Vodouhè 2006).

Addressing these constraints requires intensive research efforts in agronomy and breeding to identify best performing cultivars for improved production. In addition, developing effective phenotyping and breeding approaches is a big challenge and requires a good knowledge of the crop and the available genetic resources (Considine et al. 2017). Unfortunately, the existing genetic diversity of Kersting's groundnut has not been sufficiently explored for exploitation in breeding programmes. Morphological characterization of those genetic resources is the first step in the development of improved cultivars with farmers' and consumers' preferred traits (Bayorbor et al. 2010). Recent agro-morphological characterization on Kersting's groundnut used 32 accessions from southern and central Benin (Assogba et al. 2016), excluding cultivars from the semi-arid and arid zones. The authors recorded three clusters of accessions mainly distinguished by seed coat colours. Using a few accessions from a specific environment may not be sufficient to reveal the extent of genetic variability within the species. Akohoué et al. (2018) investigated the diversity of Kersting's groundnut in farmers' fields and reported from three agro-ecological zones of Benin and Togo five landraces based on seed coat colours. Therefore, there is a need to conduct a proper agro-morphological characterization using germplasm from diverse geographical regions to highlight the existing diversity in Kersting's groundnut. Furthermore, association patterns among morphological markers in Kersting's groundnut were poorly understood. Combining simple correlation coefficients among traits with path analysis is required to detect the nature and the direction of interrelationships between grain yield and other traits (Bhatt 1973) as indirect selection for the yield can be a swift approach to increase genetic gains from selection (Lopes et al. 2017; Mashilo et al. 2016).

The objective of this study is to analyse the genetic diversity of 297 accessions of Kersting's groundnut from different countries and agro-ecological zones, including the semi-arid and arid zones. More specifically we: (1) analyse the variability of morphological traits among a large set of Kersting's groundnut accessions gathered from three phytogeographical regions in Benin and Togo, and tested in two different environments, and (2) explore the possibility for indirect selection in Kersting's groundnut through association patterns between morphological traits. We assume that (1) a larger set of accessions of Kersting's groundnut collected from different environments will reveal higher phenotypic diversity than previously recorded; and (2) there is a significant interrelationship between morphological traits that can guide future selection of genotypes.

Materials and methods

Plant material

A diverse panel of 297 accessions of Kersting's groundnut were included in this study. These accessions were collected from a wide range of climatic zones in Benin and Togo and maintained in the genebank of the laboratory of Genetics, Horticulture and Seed Science (GBioS) of the University of Abomey-Calavi (UAC) in Benin Republic. A total of 66 accessions were collected from the Guinean zone, 182 from the Sudano-Guinean zone and 49 from the Sudanian zone in both Benin and Togo (Akohoué et al. 2018). Accessions were autogamous landraces collected in different farmers' fields. They were separated and considered as homogenous based on farmers' knowledge of the landrace. Each accession was included in this study with at least ten individuals planted for each of the two replicates per testing environment. Data were collected on individual plant and aggregated as average values to describe the landraces.

Description of experimental sites

Field experiments were carried out under rain-fed conditions from August to December 2017 at Sékou in southern Benin and Savè in central Benin. Sékou and Savè belong to the Guinean and the Sudano-Guinean phytogeographical regions respectively. The Guinean region is a humid area with a bimodal rainfall pattern with an average of 1200–1500 mm/year (Adomou 2005). The total rainfall amount recorded during the period of the experiments at Sékou was 360.67 mm. The relative humidity ranged from 76.80 to 87.90% with an average of 82.46%. The temperature varied between 24.66 and 30.24 °C with an average of 27.20 °C. This phytogeographical region is characterised by Guinean savannas, mosaic of semi-deciduous rainforest and clear forests. The soil is predominantly ferriferous. The cropping systems in this region include cereal crops (*Zea mays* L., *Sorghum bicolor* (L.) Moench) and legumes (*Vigna unguiculata* (L.) Walp., *Arachis hypogea* L. and *M. geocarpum*). The Sudano-Guinean phytogeographical region is characterized by a unimodal rainfall with an average of 1100–1300 mm/year (Adomou 2005). The total rainfall recorded during the time of the experiments at Savè was 160.76 mm while the relative humidity ranged from 49.80 to 84.30% with an average of 69.00%. In addition, the temperature varied between 22.85 and 34.38 °C with an average of 27.23 °C. The vegetation in the Sudano-Guinean region is composed of mosaic of semi-deciduous rainforest and savannas while the cropping systems are based on cereals (*Z. mays* L., *S. bicolor* (L.) Moench), legumes (*V. unguiculata* (L.) Walp., *A. hypogea* L. and *M. geocarpum*), roots and tubers (*Dioscorea* spp.and *Manihot esculenta* Crantz) (Akoègninou et al. 2006). This region is characterized by a ferruginous soil type.

Experimental design and management

At each location, the experiments were conducted using an incomplete block design (alpha design) with two replicates. The field plan was generated using the package "Agricolae" in R software (De Mendiburu 2017) with an efficiency factor of 0.89. Each replicate was composed of 20 incomplete blocks with 15 experimental units as the block size. Per replicate, each experimental unit was a ridge of 3.00 m long containing 10 plants with 0.30 m inter-row and intra-row spacing (Bampuori 2007). Weeding was done systematically every two weeks in each location. Compound fertilizer NPK 15:15:15 was applied to plants four weeks after sowing at a rate of 100 kg/ha (Kouelo et al. 2012). The Conti-Zeb 5_80% WP (mancozeb) fungicide was sprayed every two weeks with 500 g/ha to control fungal infestations.

Data collection

Fifteen (15) quantitative and four qualitative morphological descriptors (Table 1) were recorded using the descriptors list developed by the World Vegetable Centre for *Macrotyloma* species (AVRDC 2015). Quantitative variables included the diameter of the plant, plant height, leaflet length, leaflet width, petiole length, days to 50% flowering, days to maturity, number of seeds per plant, number of seeds per pod, number of pods per plant, seed length, seed width, seed thickness, 100 seed weight and grain yield. The qualitative variables recorded were seed coat

Table 1 Morphological descriptors and data collection for agro-morphological characterization of Kersting's groundnut

Descriptor	Code	Unit	Data collection
Seed coat colour	SCC	–	Recorded on mature seeds using colour chart
Flower colour	FLC	–	Flower petals colour recorded on open flowers using colour chart
Petiole colour	PTC	–	Petiole colour recorded using colour chart
Pod colour	POC	–	Recorded on fresh mature pods
Diameter of plant	DIP	cm	Horizontal distance between two opposite points
Plant height	PLH	cm	Measured on ten plants form cotyledon scar to tip of plant
Leaflet length	LEL	cm	Distance between the leaflet tip and the pulvinus measured on the third fully opened leaf from the tip
Leaflet width	LEW	cm	Width of the broadest portion of the third fully opened leaf from tip measured
Petiole length	PEL	cm	Measured on 10 plants from the base of petiole to beginning of limber
Date to 50% flowering	DFF	days	Determined by noting the number of days (d) from sowing that 50% of plants had at least one flower
Days to maturity	DTM	days	Determined by noting the number of days from sowing that 90% of plant have mature pods
Number of seeds per pod	NSPod	seeds/pod	Counted number of seeds developed per pod
Number of pods per plant	NPP	pods/plant	Counted number of pods developed per plant
Number of seeds per plant	NSP	Seeds/plant	Counted number of seeds developed per plant
Seed length	SIL	mm	Recorded on 5 seeds per plot
Seed width	SWi	mm	Recorded on 5 seeds per plot
Seed thickness	STh	mm	Recorded on 5 seeds per plot
100 seed weight	100SW	g	Estimated using the average value of ten samples of 10 seeds. Estimated value is validated when the coefficient of variation is below 5%
Grain yield	GRY	kg/ha	Product of average grain yield per plant at 10.5–11.5% moisture content and plant population

colour, petiole colour, and flower and pod colours. The grain yield was determined at 10.50–11.5% moisture content. According to Bampuori (2007), Kersting's groundnut grain yield varies with plant population per hectare. Therefore, the grain yield was estimated as follows:

$$GRY(\text{kg/ha}) = \textit{average grain yield per plant}\,(\text{kg/plant}) * \textit{plant population}\,(\text{plant/ha}).$$

The plant population per hectare was estimated using the following formula (Adebooye et al. 2006):

Pp = [10,000 m^2 × *number of plants per stand*]/[*product of spacing*], with Pp = plant population per hectare.

Therefore, the plant population in this study was estimated at 111,111.11 plants/ha.

Data analysis

Quantitative data were explored to identify eventual outliers using the R package "outliers" (Komsta and Komsta 2011). Descriptive statistics were used to depict qualitative traits variation in Kersting's groundnut. Analysis of variance was performed on quantitative variables to check whether there were significant differences among accessions and locations. The Spearman's rank correlation analysis was performed to determine correlations among qualitative traits, and among qualitative traits and grain yield, yield components, days to 50% flowering and days to maturity. The Pearson correlation analysis was carried out to reveal association patterns among quantitative variables. Furthermore, genetic correlations analysis and broad sense heritability estimates were performed across locations on quantitative traits using the META-R programme (Crossa 2014). Path coefficient analysis was conducted using the R package "Agricolae" to decompose genetic correlations into direct and indirect effects (De Mendiburu 2017). Grain yield (GRY) was considered as the response variable while days to 50% flowering (DFF), days to maturity (DTM), 100 seed weight (100SW), number of seeds per plant (NSP), number of pods per plant (NPP) and number of seeds per pod (NSPod) were included in the analysis as independent variables.

Moreover, the factor analysis of mixed data (FAMD) and the hierarchical cluster analysis (HCA) were conducted on both qualitative and quantitative variables, using the R package "FactoMineR", to group accessions into different categories (Lê et al. 2008). Analysis of Similarities (ANOSIM) was performed to test the degree of separation between clusters. A dendrogram was generated using the function "daisy" of the R package "vegan" and the average agglomeration method based on the 19 variables (Grum and Atieno 2007). An analysis of variance was then conducted to identify discriminant quantitative variables between clusters. All analyses were performed using the R software version 3.2.0 (R Core Team 2017).

Results

Characterization of Kersting's groundnut accessions using variation in qualitative traits

The variation of petiole, flower and pod colours is shown in Fig. 1. Two types of petioles were observed, including the purple and green petioles. Flower types included flowers with white, pink and purple petals (Fig. 1). Two types of pods were observed, namely the purple and white pods (Fig. 1). Moreover, the four qualitative traits (petiole, flower, pod and seed colours) presented different distributions among Kersting's groundnut accessions (Fig. 2). The analysis of seed coat colours showed that about 79.87% of accessions had white seed coat (WC), 5.37% had red seed coat (RC), 13.42% had black seed coat (BC) and 1.34% were characterized by white seed with black eye (WBE) (Fig. 2a). For flower colour, about 79.87% of accessions were characterized by white petals (WF), 13.42% had pink petals (PiF), 1.34% had purple petals (PuF) and 5.37% presented both pink and purple petals (PiF + PuF) observed on different flowers (Fig. 2b). About 86.58% of accessions showed green petioles (GP) while 13.42% of them were characterized by green and purple petioles observed on the same plant (Fig. 2c). Likewise, 86.58% of accessions had white pods while 13.42% had purple pods (Fig. 2d).

Highly significant ($p < 0.001$) correlation coefficients were observed among the four qualitative traits (Table 2). Strong phenotypic correlations were observed between seed coat colour with flower colour ($r = 0.96$), petiole colour ($r = 0.82$), pod colour ($r = 0.82$) and between petiole colour and pod colour ($r = 0.98$). Moderate phenotypic correlations were observed between flower colour with petiole colour ($r = 0.77$) and pod colour ($r = 0.77$). These association patterns were relevant to group Kersting's groundnut accessions into four different categories with seed coat colour being the most discriminating qualitative trait among them (Fig. 3). The first category was composed of 100% white seeded accessions (Fig. 3c). These accessions were characterized by white flowers, white pods and green petioles. The second category contained 100% red seeded accessions (Fig. 3b). In this category, all accessions presented a mixture of pink and purple flowers, white pods and green petiole. The third category was composed of all black seeded accessions (Fig. 3a), which were characterized by pink flowers, purple pods and pink petioles. The fourth category contained all white seed coat with black eye accessions (Fig. 3d). Accessions of this category were characterized by purple flowers, white pods and green petioles.

Variation of quantitative traits among Kersting's groundnut accessions across locations

Analysis of variance (ANOVA) across locations revealed significance for location, accessions and accessions × location interaction mean squares for most traits (Table 3). The model of ANOVA used in this study explained a high proportion (R^2-values ranges from 62.13 to 93.13%) of the variability in the 15 quantitative traits (Table 3). The effect of location was significant ($p < 0.05$) for all traits apart from the number of seeds per plant and number of pods per plant (Table 3). In addition, accession × location interaction was highly significant for traits such as the diameter of the plant, plant height, leaflet length,

Purple petioles

Green petioles

White flowers

White pods

Pink flowers

Purple flowers

Purple pods

Fig. 1 Petiole, flower and pod types based on colour patterns in Kersting's groundnut

Fig. 2 Distribution of qualitative traits in Kersting's groundnut. WC = white seed coat, RC = red seed coat, BC = black seed coat, WBE = white seed coat with black eye, WF = white flower, PiF = pink flower, PuF = purple flower, GP = green petiole, PuP = purple petiole, WPod = white pod, PuPod = purple pod

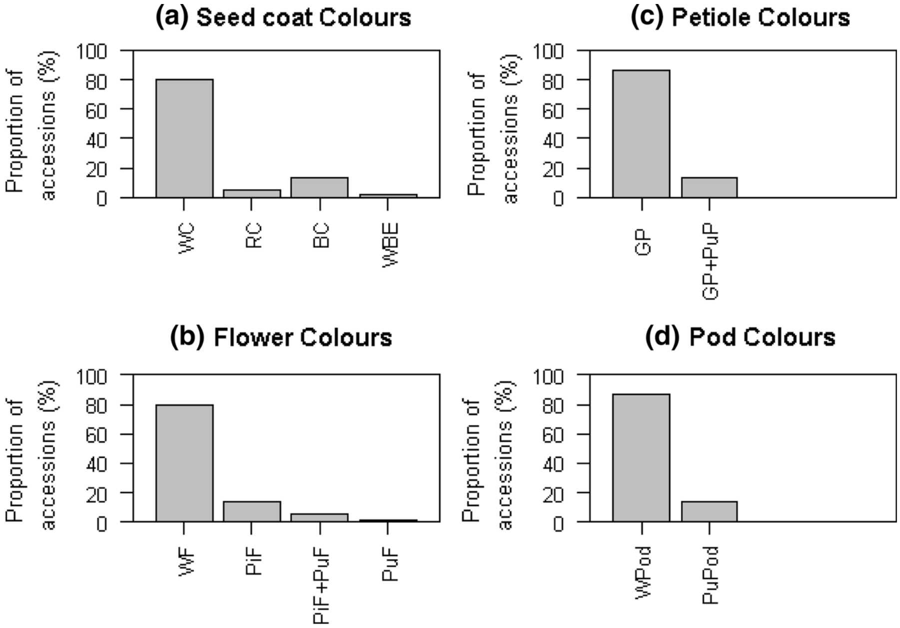

Table 2 Spearman's rank correlations matrix among qualitative variables in Kersting's groundnut

Variables	Seed coat colour	Flower colour	Petiole colour	Pod colour
Seed coat colour	1.00			
Flower colour	0.96***	1.00		
Petiole colour	0.82***	0.77***	1.00	
Pod colour	0.82***	0.77***	0.98***	1.00

***$p < 0.001$

Fig. 3 Groups of Kersting's groundnut accessions based seed coat colour patterns. **a** Black seeded accessions, **b** red seeded accessions, **c** white seed coat with black eye accessions, **d** white seeded accessions

petiole length, 100 seed weight, grain yield, number of seeds per plant, and number of pods per plant (Table 3). The effect of accession × location interaction could be attributed to the difference in environmental conditions from one location to another. The effect of accession was highly significant ($p < 0.05$) for all traits except seed width and seed thickness (Table 3).

Furthermore, the coefficient of variation (CV) ranged from 4.39 to 42.37%. Highest values of CV were obtained for grain yield (42.37%), number of seeds per plant (36.18%) and the number of pods per plant (34.80%) (Table 4). Broad-sense heritability estimates were high for most quantitative traits, including the diameter of the plant (DIP), plant height (PLH), leaflet length (LEL), one hundred seeds weight (100SW), seed length (SIL), days to 50% flowering (DFF), days to maturity (DTM), petiole length (PEL), grain yield (GRY), number of seeds per plant (NSP) and number of pods per plant (NPP). This highlights the relatively high genetic variability among accessions.

Table 3 Mean square values of the analysis of variance of quantitative variables in Kersting's groundnut across Sékou and Savè

Variables	Locations (ddl = 1)	Accessions (ddl = 296)	Rep (ddl = 1)	Acc * Loc (ddl = 296)	Residual (ddl = 563)	R^2
DIP	911.20***	13.00***	9.70ns	10.80***	5.13	84.64
PLH	2532.60**	7.30***	18.40*	5.30***	2.80	91.50
LEL	639.10***	0.90***	2.20*	0.70***	0.45	93.13
LEW	223.64***	0.45*	7.42***	0.37ns	0.37	81.56
PEL	627.20***	5.30***	7.90*	4.10***	2.30	79.74
100SW	2393.20***	10.30***	0.40ns	5.00***	3.00	90.43
SIL	149.29***	0.75***	1.48ns	0.08ns	0.45	79.74
SWi	167.93*	26.50ns	25.89ns	27.16ns	0.16	62.13
STh	24.94***	1.33ns	0.95ns	1.37ns	0.08	62.47
DFF	4304.00*	43.00***	0.86ns	0.53ns	3.00	91.48
DTM	58,794.00**	89.00***	7.00ns	46.00ns	47.00	88.99
GRY	64,880.00*	177,321.00***	821,381.00**	1923.00*	108,847.00	75.79
NSP	308.00ns	792.00***	4349.00**	865.00***	501.00	74.17
NPP	1011.20ns	466.20***	2721.10**	507.50***	288.30	74.86
NSPod	2.55***	0.02***	0.00ns	0.01ns	0.01	73.40

ns non-significant

DIP = diameter of plant (cm), PLH = plant height (cm), LEL = leaflet length (cm), LEW = leaflet width (cm), PEL = petiole length (cm), 100SW = 100 seed weight (g), SIL = seed length (mm), SWi = seed width (mm), STh = seed thickness (mm), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod, Rep = replication, Acc = accession, Loc = location, ddl = degree of freedom

***$p < 0.001$; **$p < 0.\ 01$; *$p < 0.05$;

In addition, mean values of quantitative traits of individual accession across locations revealed relatively high ranges that are important for consideration (Table 4). The diameter of the plants varied from 11.00 to 30.47 cm while plant height ranged from 7.50 to 23.44 cm, the leaflet length ranged from 4.50 to 9.82 cm and the leaflet width varied from 2.50 to 6.21 cm (Table 4). Petiole length ranged from 2.50 to 7.75 cm. The highest values of the diameter of the plant, plant height, leaflet length, leaflet width and petiole length were observed in accessions 02_AF282, 02_AF300 and 02_AF258. Moreover, 100 seed weight ranged from 7.1 to 16.28 g. The highest 100 seed weight was recorded in accessions 02_AF202 and 02_AF222. Seed length varied from 6.90 to 9.30 mm with an average of 7.83 mm (Table 4). High values of seed length were revealed by accessions 02_AF216, 02_AF287, 02_AF239, 02_AF234, 02_AF204 and 02_AF197. Furthermore, days to 50% flowering ranged from 37 to 54 days while days to maturity ranged from 97 to 120 days. The highest days to 50% flowering and days to maturity were recorded in accession 02_AF287 while the lowest value was observed in accession 02_AF210. Considering yield traits, the grain yield ranged from 126.89 to 1444.29 kg/ha (Table 4). The highest value was observed in accession 02_AF169 while the lowest value was recorded in accession 02_AF288. Moreover, the highest number of seeds per plant and the number of pods per plant were observed in accessions 02_AF169, 02_AF51 and 02_AF100. In contrary, the highest number of seeds per pod was recorded in accession 02_AF290.

Phenotypic correlations among morphological traits in Kersting's groundnut

The Spearman's rank correlation analysis between qualitative and important quantitative variables showed significant ($p < 0.05$) relationships for 100SW, DFF, and DTM (Table 5). Weak positive and significant correlations were detected among 100SW with SCC (r = 0.36), FLC (r = 0.36), PTC (r = 0.33) and POC (r = 0.33). In contrast to 100SW,

Table 4 Description of quantitative variables in Kersting's groundnut across Sékou and Savè

Variables	Unit	Min	Max	Mean	SD	CV (%)	H^2
DIP	cm	11.00	30.47	20.01	2.87	14.34	0.45
PLH	cm	7.50	23.44	14.60	2.26	15.48	0.47
LEL	cm	4.50	9.82	6.85	0.79	11.53	0.44
LEW	cm	2.50	6.21	4.26	0.53	12.44	0.29
100SW	g	7.10	16.28	10.98	1.64	14.94	0.71
SIL	mm	6.90	9.30	7.83	0.44	5.62	0.33
SWi	mm	4.73	8.80	5.41	0.39	7.20	0.38
STh	mm	3.50	6.23	4.10	0.29	7.07	0.07
DFF	days	37.00	54.00	47.73	3.37	7.06	0.86
DTM	days	97.00	120.00	111.16	4.88	4.39	0.87
GRY	kg/ha	126.89	1444.29	499.70	211.74	42.37	0.43
PEL	cm	2.50	13.77	7.75	1.68	21.68	0.52
NSP	Seeds/plant	12.50	95.03	39.08	14.14	36.18	0.45
NPP	Pods/plant	10.41	74.50	31.18	10.85	34.80	0.47
NSPod	Seeds/pod	1.08	1.50	1.24	0.07	5.65	0.37

DIP = diameter of plant (cm), PLH = plant height (cm), LEL = leaflet length (cm), LEW = leaflet width (cm), PEL = petiole length (cm), 100SW = 100 seed weight (g), SIL = seed length (mm), SWi = seed width (mm), STh = seed thickness (mm), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod, Min = minimum; Max = maximum; SD = standard deviation, CV = coefficient of variation, H^2 = broad sense heritability

Table 5 Spearman's rank correlations matrix between qualitative and quantitative variables in Kersting's groundnut

Variables	SCC	FLC	PTC	POC
100SW	0.36*	0.36*	0.33*	0.33*
DFF	− 0.63**	− 0.63**	− 0.49**	− 0.49**
DTM	− 0.37*	− 0.36*	− 0.31*	− 0.31*
GRY	0.12	0.12	0.10	0.10
NSP	− 0.01	0.00	− 0.02	− 0.02
NPP	− 0.03	− 0.03	− 0.05	− 0.05
NSPod	0.18	0.18	0.18	0.18

SCC = seed coat colour, FLC = flower colour, PTC = petiole colour, POC = pod colour, 100SW = 100 seed weight (g), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod

**$p < 0.01$; *$p < 0.05$

moderate negative correlations were observed between DFF and the following variables: SCC (r = − 0.63), FC (r = − 0.63), PTC (r = − 0.49) and POC (r = 0.49). Weak negative correlations were observed between DTM with SCC (r = − 0.36), FLC (r = − 0.37), PC (r = − 0.31) and POC (r = − 0.31). However, no significant correlations were detected between qualitative variables and GRY, NSP, NPP and NSPod.

Results on Pearson's correlation analysis showing relationships among quantitative variables are presented in Table 6. Highly significant ($p < 0.001$) and strong positive correlations were observed between PLH and PEL (r = 0.95), DFF and DTM (r = 0.88), NSP and GY (r = 0.96), NPP and GRY (r = 0.93), NSP and NPP (r = 0.98). In addition, highly significant ($p < 0.001$) and moderate positive correlations were observed among DIP and PLH (r = 0.53), PLH and LEL (r = 0.59), DIP and LEL (r = 0.76), 100SW and GRY (r = 0.78). Significant ($p < 0.05$) and weak positive correlations were detected between DIP and LEW (r = 0.30), DIP and PEL (r = 0.33), LEL and PEL (r = 0.31), LEL and LEW (r = 0.37), 100SW and NSP (r = 0.39), 100SW and NPP (r = 0.35), 100SW and NSPod (r = 0.36), NSP and NSPod (r = 0.37). Moderate positive correlations were observed between SL and STh (r = 0.45), GRY and NSPod (r = 0.41). In addition, significant ($p < 0.05$) and moderate negative

Table 6 Pearson correlations matrix among quantitative variables in Kersting's groundnut

Variables	DIP	PLH	LEL	LEW	100SW	SIL	SWi	STh	DFF	DTM	GRY	PEL	NSP	NPP	NSPod
DIP	1.00														
PLH	0.53**	1.00													
LEL	0.76***	0.59**	1.00												
LEW	0.30*	0.23	0.37*	1.00											
100SW	0.03	0.05	0.04	− 0.01	1.00										
SIL	0.04	− 0.02	0.03	− 0.06	0.18	1.00									
SWi	− 0.09	− 0.04	0.01	− 0.11	0.03	0.03	1.00								
STh	0.02	0.03	0.00	0.04	0.05	0.45**	0.00	1.00							
DFF	− 0.08	− 0.10	− 0.08	0.19	− 0.47**	− 0.14	0.01	− 0.04	1.00						
DTM	− 0.07	− 0.06	− 0.08	0.13	− 0.49**	− 0.17	− 0.02	− 0.03	0.88***	1.00					
GRY	0.01	0.01	− 0.02	0.05	0.78***	0.10	− 0.03	− 0.01	− 0.35*	− 0.29*	1.00				
PEL	0.33*	0.95***	0.31*	0.12	0.04	− 0.03	− 0.05	0.04	− 0.09	− 0.04	0.02	1.00			
NSP	0.02	0.01	− 0.02	0.06	0.39*	0.07	− 0.03	− 0.01	− 0.10	− 0.10	0.96***	0.02	1.00		
NPP	0.00	0.00	− 0.02	0.06	0.35*	0.04	− 0.03	0.00	− 0.06	− 0.07	0.93***	0.01	0.98***	1.00	
NSPod	0.08	0.06	0.02	− 0.01	0.36*	0.14	− 0.03	0.01	− 0.22	− 0.21	0.41*	0.07	0.37*	0.23	1.00

DIP = diameter of plant (cm), PLH = plant height (cm), LEL = leaflet length (cm), LEW = leaflet width (cm), PEL = petiole length (cm), 100SW = 100 seed weight (g), SIL = seed length (mm), SWi = seed width (mm), STh = seed thickness (mm), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod

***$p < 0.001$; ** $p < 0.01$; * $p < 0.05$

correlations were detected between 100SW and DFF (r = − 0.47), 100SW and DTM (r = − 0.49). Significant ($p < 0.05$) and weak negative correlations were detected between DFF and GRY (r = − 0.35), DTM and GRY (r = − 0.29) (Table 6). Non-significant phenotypic correlations were observed between GRY and growth traits (DIP, PLH, LEL, LEW and PEL) and seed size traits (SIL, SWi and STh).

Genetic correlations and path coefficient analysis among quantitative traits

At genetic level, results from Table 7 revealed significant associations between many quantitative variables. Highly significant ($p < 0.001$) and strong positive genetic correlations were detected between PLH and PEL (rg = 0.96), DTM and DFF (rg = 0.97), GRY and NSP (rg = 0.96), GRY and NPP (rg = 0.90), and NSP and NPP (rg = 0.98). Moderate positive genetic correlations were observed between DIP and PLH (rg = 0.50), PLH and LEL (rg = 0.57), 100SW and NSP (rg = 0.50), 100SW and NSPod (rg = 0.62), GRY and NSPod (rg = 0.60), NSP and NSPod (rg = 0.53), DIP and LEL (rg = 0.78) and 100SW and GRY (rg = 0.70). In addition, relatively weak positive genetic correlations were detected between DIP and PEL (rg = 0.31) LEL and PEL (rg = 0.32), and 100SW and NPP (rg = 0.38). On the other hand, highly significant ($p < 0.001$) and moderate negative genetic correlations were revealed between DFF (rg = − 0.66), and DTM (rg = − 0.70) with 100SW. Also, weak negative genetic correlations were observed between DFF (rg = − 0.32) and DTM (rg = − 0.30) with GRY. However, no significant genetic correlations were detected between SIL and STh, although a relatively high phenotypic correlation was observed between them.

Results on path coefficient analysis between grain yield (GY) as the response variable, and 100SW, DFF, DTM, NSP, NPP and NSPod as the independent variables, are summarized in Table 8. Direct path values were lower than 1, revealing that inflation due to multicollinearity among independent variables was low. High direct path coefficients were detected between NSP (0.62), followed by 100SW (0.42) and DFF (− 0.38) with GRY. The direct effect DTM with GRY was positive (0.16) while the genetic correlation was negative (rg = − 0.30). Moreover, high indirect path coefficients were detected between GRY and NPP (0.61) via NSP, DTM (− 0.33) via 100SW, NSPod (0.33) via NSP, NSPod (0.26) via 100SW with GRY.

Principal component and hierarchical cluster analyses in Kersting's groundnut

The FAMD analysis performed on the 19 variables across the two locations revealed that the three first principal components (PCs) with eigenvalues > 1, accounted for 70.51% of the morphological variability. PC1, PC2 and PC3 explained respectively 29.05%, 23.85% and 17.61% of the total variation. The first principal component (PC1) was highly correlated with 100 seed weight, seed length, the number of seeds per pod, days to maturity, days to 50% flowering, seed coat, flower, and pod colour (Table 9). The second principal component (PC2) was highly correlated with growth parameters such as leaflet length, plant height, the diameter of the plant, leaflet width and petiole length. The third principal component (PC3) was correlated with grain yield, the number of seeds per plant and the number of pods per plant (Table 9). Since the grain yield was highly correlated with PC3, the hierarchical cluster analysis was performed using the three principal components.

The HCA analysis revealed four different clusters of Kersting's groundnut accessions (Fig. 4). These four clusters were significantly distinct (ANOSIM R-value = 0.82, $p < 0.001$) from each other. The HCA results were supported by the dendrogram constructed using the average agglomeration method for the 19 morphological variables (Fig. 5). In fact, the dendrogram grouped all accessions into four distinct clusters (I, II, III and IV) at a Gower's dissimilarity of 0.25. Furthermore, the pairwise comparisons showed highly significant differentiation among all pairs of clusters (Table 10). Discriminant variables included growth parameters (DIP, PLH, LEL, LEW and PEL), flowering and maturity time (DFF and DTM), seed parameters (100SW, SIL and STh) and yield and yield components (GRY, NSP, NPP and NSPod).

Cluster 1 (60.27% of accessions) and cluster 3 (5.05% of accessions) were composed of late flowering accessions (DFF = 51.21 days for cluster 1 and DFF = 49.02 days for cluster 3) that were late maturing (DTM = 112.18 days for cluster 1 and DTM = 113.98 for cluster 3) (Table 11). These clusters were predominantly composed of white seeded accessions.

Table 7 Genetic correlations matrix among quantitative variables in Kersting's groundnut

Variables	DIP	PLH	LEL	LEW	100SW	SIL	SWi	STh	DFF	DTM	GRY	PEL	NSP	NPP	NSPod
DIP	1														
PLH	0.50**	1													
LEL	0.78***	0.57**	1												
LEW	0.00	0.00	0.00	1											
100SW	0.11	0.16	0.13	0.00	1										
SIL	0.00	0.00	0.00	0.00	0.00	1									
SWi	0.00	0.00	0.00	0.00	0.00	0.00	1								
STh	0.12	0.18	0.04	0.00	0.23	0.00	0.00	1							
DFF	− 0.13	− 0.17	− 0.16	0.00	− 0.66**	0.00	0.00	− 0.08	1						
DTM	− 0.13	− 0.09	− 0.16	0.00	− 0.70**	0.00	0.00	− 0.10	0.97***	1					
GRY	0.03	− 0.03	− 0.05	0.00	0.70**	0.00	0.00	0.02	− 0.32*	− 0.30*	1				
PEL	0.31*	0.96***	0.32*	0.00	0.14	0.00	0.00	0.19	− 0.15	− 0.06	− 0.01	1			
NSP	0.04	− 0.05	− 0.06	0.00	0.50**	0.00	0.00	0.03	− 0.17	− 0.14	0.96***	− 0.03	1		
NPP	0.01	− 0.06	− 0.06	0.00	0.38*	0.00	0.00	0.03	− 0.11	− 0.09	0.90***	− 0.05	0.98***	1	
NSPod	0.14	0.12	0.04	0.00	0.62**	0.00	0.00	0.17	− 0.09	− 0.05	0.60**	0.12	0.53**	0.04	1

DIP = diameter of plant (cm), PLH = plant height (cm), LEL = leaflet length (cm), LEW = leaflet width (cm), PEL = petiole length (cm), 100SW = 100 seed weight (g), SIL = seed length (mm), SWi = seed width (mm), STh = seed thickness (mm), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod

***$p < 0.001$; **$p < 0.01$; *$p < 0.05$

Table 8 Results of direct (boldfaced diagonal) and indirect effects path coefficients analysis between grain yield and related traits in Kersting's groundnut

Variables	100SW	DFF	DTM	NSP	NPP	NSPod	GRY
100SW	**0.42**	0.25	− 0.33	0.31	0.05	0.00	0.70**
DFF	− 0.27	− **0.38**	0.03	− 0.11	− 0.01	0.00	− 0.32*
DTM	− 0.29	− 0.37	**0.16**	− 0.09	− 0.01	0.00	− 0.30*
NSP	0.21	0.07	− 0.07	**0.62**	0.13	0.00	0.96***
NPP	0.16	0.04	− 0.04	0.61	**0.13**	0.00	0.90***
NSPod	0.26	0.03	− 0.02	0.33	0.00	**0.00**	0.60**

100SW = 100 seed weight (g), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod

***$p < 0.001$, **$p < 0.01$, *$p < 0.05$

Table 9 Correlation between variables and the three first principal components

Variables	Principal component		
	1	2	3
100 Seeds weight	**0.79**	0.00	0.22
Seed length	**0.63**	0.00	0.00
Seed width	0.00	0.00	0.00
Seed thickness	0.00	0.00	0.00
Number of seed per pod	**0.47**	0.00	0.21
Grain yield	**0.38**	0.00	**0.90**
Leaflet length	0.16	**0.89**	− 0.15
Plant height	0.14	**0.94**	0.00
Number of seeds per plant	0.14	0.00	**0.97**
Diameter of plant	0.13	**0.87**	− 0.13
Leaflet width	0.12	**0.83**	0.00
Petiole length	0.11	**0.85**	0.00
Days to maturity	− **0.64**	0.21	0.17
Days to 50% flowering	− **0.83**	0.19	0.20
Number of pods per plant	0.00	0.12	**0.96**
Seed coat colour	**0.87**	0.05	0.04
Flower colour	**0.81**	0.05	0.03
Petiole colour	**0.76**	0.02	0.03
Pod colour	**0.76**	0.02	0.03

Significant correlation coefficients are shown in bold

In cluster 1, 92.74% of accessions were white seeded, 5.03% red seeded and 2.23% were white with black eye accessions. Similarly, 80.00% of accessions in cluster 3 were white seeded while 20% were red seeded. Furthermore, accessions of clusters 1 and 3 produced the lowest grain yield (394.46 kg/ha for cluster 1 and 450.82 kg/ha for cluster 3), 100 seed weight (10.23 g for cluster 1 and 11.05 g for cluster 2), number of seeds per plant (33.33 seeds/plant for cluster 1 and 36.06 seeds/plant for cluster 2), number of pods per plant (27.16 pods/plant for cluster 1 and 29.02 pods/plant for cluster 3) and number of seeds per pod (1.22 seeds/pod for cluster 1 and 1.24 seeds/pod for cluster 3) (Table 11). Despite these resemblances, clusters 1 and 3 showed some differences with regard to growth parameters. In contrast to cluster 1, accessions of cluster 3 were characterized by the highest diameter of the plant, plant height, leaflet length, leaflet width and petiole length.

Cluster 2 (19.53% of accessions) was composed of intermediate flowering (DFF = 47.05 days) and maturing (DTM = 109.54 days) accessions characterized by the highest grain yield (775.9 kg/ha), number of seeds per plant (59.94 seeds/plant), number of pods per plant (46.99 pods/plant), number of seeds per pod (1.26 seeds/pod) and a high 100 seed weight (11.29 g). In addition, 89.66% of accessions of cluster 2 were white seeded, 3.44% red seeded, 5.17% black seeded and 1.72% white with black eye.

Furthermore, cluster 4 (15.15% of accessions) was composed of early flowering (DFF = 41.52 days) and maturing (DTM = 104.86 days) accessions which were characterized by relatively high grain yield (582.53 kg/ha) and number of seeds per plant (37.6 seeds/plant). In addition, accessions of this cluster produced the highest number of seeds per pod (1.29 seeds/pod) and were characterized by the highest seed length (8.3 mm), seed thickness

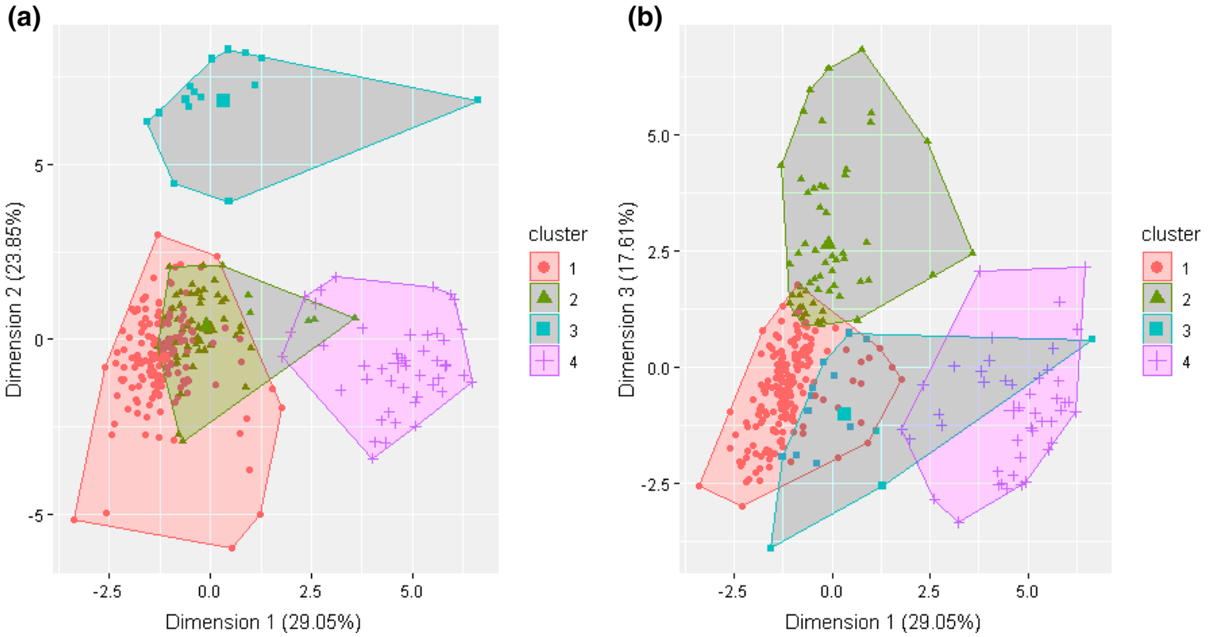

Fig. 4 Cluster plots showing the number of clusters of Kersting's groundnut accessions revealed by the hierarchical cluster analysis (HCA). **a** Dimension 1 versus dimension 2, **b** dimension 1 versus dimension 3. Both **a** and **b** grouped accessions into four clusters

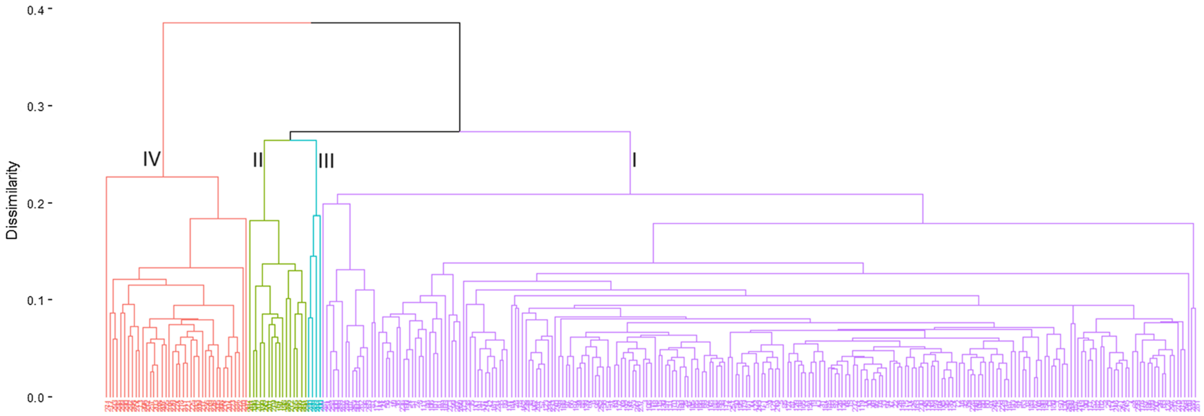

Fig. 5 Dendrogram showing the grouping of accessions using the average agglomeration method based on the Gower's dissimilarity coefficient. Four clusters recorded at the cutting point of 0.25: I = Cluster 1, II = Cluster 2, III = Cluster 3 and IV = Cluster 4

(4.37 mm) and 100 seed weight (13.39 g) (Table 11). Moreover, 80% of accessions of cluster 4 were black seeded, 15.56% were red seeded, and 4.44% of them were white with black eye.

Discussion

Morphological markers variation in Kersting's groundnut

Qualitative traits variation in Kersting's groundnut revealed four groups of accessions contrary to the two groups recorded by Assogba et al. (2016). Previous morphological characterizations have reported only three seed coat colours including white, red and the

Table 10 Results from analysis of similarities (ANOSIM) between clusters of accessions

Clusters	1	2	3	4
Global test				
Global R^{a} = 0.82***				
1	0.00			
2	0.80***	0.00		
3	0.95***	0.93***	0.00	
4	0.98***	0.95***	0.99***	0.00

***$p < 0.001$

^{a}Test statistic comparatively measuring the degree of separation of the clusters

black and not the white with black eye seeded accessions (Assogba et al. 2016; Adu-Gyamfi et al. 2012; Bayorbor et al. 2010). The white with black eye accessions exhibited a new flower colour (purple flowers), suggesting the existence of new genetic diversity in Kersting's groundnut with regard to qualitative traits.

Most quantitative traits revealed high variability among Kersting's groundnut accessions. Broad-sense heritability estimates were high for all traits, except for seed thickness. Despite its limitations in plant breeding, high broad sense heritability estimates indicate that traits are affected by genetic effects and their direct selection could yield positive gains (Visscher et al. 2008). Moreover, the average performances of accessions were higher at Sékou compared with Savè, except for the number of seeds per plant and the number of pods per plant, which were not statistically different across locations. This could be explained by differences in soil types across locations and the low amount of rainfall recorded in Savè during the experiment. According to Assogba et al. (2016) and Kouelo et al. (2012), soil type and fertility level are major factors that affect Kersting's groundnut yield. Although Kersting's groundnut is said to grow in drought-prone environments (Ayenan and Ezin 2016;

Table 11 Description of clusters of Kersting's groundnut accessions

Variables	Cluster 1 (n = 179)	Cluster 2 (n = 58)	Cluster 3 (n = 15)	Cluster 4 (n = 45)	F-value
DIP	19.28 ± 2.11^{a}	19.94 ± 1.80^{a}	**28.84 ± 1.39^{b}**	20.1 ± 1.99^{a}	104.70***
PLH	13.94 ± 1.47^{a}	14.66 ± 1.31^{b}	**22.05 ± 1.43^{c}**	14.65 ± 1.48^{b}	146.30***
LEL	6.65 ± 0.55^{a}	6.77 ± 0.47^{ac}	**9.37 ± 0.32^{b}**	6.93 ± 0.58^{c}	122.90***
LEW	4.13 ± 0.38^{a}	4.28 ± 0.42^{a}	**5.72 ± 0.42^{b}**	4.26 ± 0.44^{a}	72.38***
PEL	7.3 ± 1.220^{a}	7.89 ± 1.11^{b}	**12.68 ± 1.16^{c}**	7.71 ± 1.29^{b}	101.20***
100SW	10.23 ± 1.08^{a}	**12.38 ± 0.94^{b}**	11.05 ± 2.23^{a}	**13.41 ± 1.33^{c}**	92.17***
SIL	7.69 ± 0.35^{a}	7.83 ± 0.41^{a}	7.94 ± 0.61^{a}	**8.3 ± 0.40^{b}**	32.33***
SWi	5.56 ± 3.30	5.45 ± 0.51	5.46 ± 0.41	5.78 ± 0.23	0.15ns
STh	4.09 ± 0.17^{a}	4.13 ± 0.16^{ab}	4.14 ± 0.31^{ab}	**4.37 ± 1.37^{b}**	2.97*
DFF	**51.21 ± 0.84^{a}**	47.05 ± 1.90^{b}	**49.02 ± 3.24^{a}**	41.52 ± 2.27^{c}	416.80***
DTM	**112.18 ± 2.57^{a}**	109.54 ± 2.19^{b}	**113.98 ± 4.43^{a}**	104.86 ± 8.03^{c}	47.66***
GRY	394.46 ± 106.44^{a}	**775.9 ± 206.90^{b}**	450.82 ± 186.11^{a}	**582.53 ± 203.33^{c}**	94.17***
NSP	33.33 ± 7.60^{a}	**59.94 ± 13.42b**	36.06 ± 12.09^{a}	37.6 ± 12.19^{ac}	101.20***
NPP	27.16 ± 6.17^{a}	**46.99 ± 10.36^{b}**	29.02 ± 10.03^{a}	28.72 ± 9.07^{a}	93.05***
NSPod	1.22 ± 0.06^{a}	**1.26 ± 0.06^{b}**	1.24 ± 0.10^{ab}	**1.29 ± 0.08^{bc}**	16.42***

High performances are indicated in bold for discriminant variables

DIP = diameter of plant (cm), PLH = plant height (cm), LEL = leaflet length (cm), LEW = leaflet width (cm), PEL = petiole length (cm), 100SW = 100 seed weight (g), SIL = seed length (mm), SWi = seed width (mm), STh = seed thickness (mm), DFF = days to 50% flowering (days), DTM = days to maturity (days), GRY = grain yield (kg/ha), NSP = number of seeds per plant, NPP = number of pods per plant, NSPod = number of seeds per pod

$^{***}p < 0.001$, $^{*}p < 0.05$

^{a,b,c}Used to separate means of clusters, values followed by the same superscript letter are statistically identical

Achigan-Dako and Vodouhè 2006; Mergeai 1993), high humidity and severe water-limited conditions at sensitive growth and developmental stages could affect most morphological traits, such as growth parameters, yield and yield components, as recorded in other grain legumes, including cowpea [*V. unguiculata* (L.) Walp.], groundnut (*A. hypogea* L.), common bean (*Phaseolus vulgaris* L.) (Daryanto et al. 2017) and bambara groundnut (Mwale et al. 2007). The findings suggest that in-depth multi-environment studies, using the Additive Main effects and Multiplicative Interaction models (AMMI) and Genotype plus Genotype × Environment (GGE) biplot (Neisse et al. 2018; Hongyu et al. 2014), should be conducted to shed light on the importance of genotype × environment interaction (GEI) in performance of Kersting's groundnut. In addition, investigating resistance to biotic and abiotic stresses could be relevant for the improvement of Kersting's groundnut.

Possibility for indirect selection for increased breeding efficiency in Kersting's groundnut

Significant moderate relationship was detected between seed coat colour and days to 50% flowering. This implies that selection for earliness in Kersting's groundnut could be done using seed coat colour. However, variation in qualitative traits was not associated with grain yield. This could be explained by the great phenotypic variability within accessions having the same seed coat colour, especially the white seeded accessions. Similar results were reported by previous studies on Kersting's groundnut (Assogba et al. 2016; Adu-Gyamfi et al. 2012; Bayorbor et al. 2010) and bambara groundnut (Gbaguidi et al. 2018; Ntundu et al. 2006).

Additionally, strong positive phenotypic and genetic relationships were detected among grain yield with the number of seeds per plant, the number of pods per plant and 100 seed weight. Likewise, weak to moderate negative phenotypic and genetic correlations were observed between grain yield and dates to flowering and dates to maturity. Association patterns determined only through simple correlation analysis may limit the prediction of selection response (Mashilo et al. 2016). Significant correlation values should be partitioned into direct and indirect cause-and-effect relationships (Mashilo et al. 2016; Bhatt 1973). Results of path analysis in this study showed strong direct effects among grain yield and number of seeds per plant, 100 seed weight and days to 50% flowering. Indirect selection using 100 seed weight could indirectly improve days to maturity and number of seeds per plant. These findings suggest that indirect selection for grain yield through 100 seed weight, number of seeds per plant and days to 50% flowering could be utilized in Kersting's groundnut breeding programmes (Olivoto et al. 2017; Bhatt 1973). Indirect selection significantly improves the efficiency of breeding programmes as reported for other grain legumes including cowpea (Lopes et al. 2017; Bhardu and Navale 2011) and bambara groundnut (Alake et al. 2015). Based on the path results, accessions 02_AF169, 02_AF51, 02_AF202, 02_AF222, 02_AF196, 02_AF100, 02_AF255, 02_AF216, 02_AF223 and 02_AF199 were selected as the top ten high yielding accessions.

Agro-morphological diversity of the West African germplasm of Kersting's groundnut

The hierarchical cluster analysis revealed four clusters of accessions in contrast to Assogba et al. (2016) and Bayorbor et al. (2010) who reported three clusters in Benin and two major clusters in Ghana, respectively. These results showed that phenotypic diversity in Kersting's groundnut genetic resources is much wider than reported in previous studies. In fact, the present study included a broader germplasm collection of Kersting's groundnut from different countries and agro-ecological zones.

From this study, clusters 2 and 4 were composed of the high yielding accessions with the highest 100 seed weight and grain yield. Cluster 2 was composed of intermediate flowering accessions while cluster 4 included early flowering and maturing accessions. Accessions of these clusters representing 34.68% of the germplasm could, thus, be selected as the best genotypes to be included in breeding programmes. These clusters also included accessions selected based on correlation and path coefficient analyses. Contrary to clusters 2 and 4, clusters 1 and 2 were composed of late flowering and maturing accessions with low 100 seed weight, and grain yield and yield components. Therefore, the cluster analysis was relevant in revealing the existing phenotypic diversity in Kersting's groundnut and the selection of best genotypes for breeding programmes. However, understanding the genetic diversity in Kersting's groundnut requires a proper molecular characterization of the whole germplasm to help breeders to make accurate decisions regarding genotypes' performances (Assogba et al. 2016). Moreover, investigating the association between molecular markers and phenotypes would contribute to the understanding of the genetic basis of agronomic traits of Kersting's groundnut, and increase the efficiency of breeding programmes.

Conclusion

This study assessed the phenotypic diversity of Kersting's groundnut and explored possibilities for indirect selection through association patterns among morphological traits. Highly significant correlations were observed among qualitative traits, and among qualitative traits and days to 50% flowering, days to maturity and 100 seed weight. Non-significant correlations were detected between grain yield and qualitative traits. Moderate to strong positive phenotypic and genetic correlations were detected among grain yield, 100 seed weight and yield components. In addition, weak to moderate negative phenotypic and genetic correlations were observed between 100 seed weight and days to 50% flowering, 100 seed weight and days to maturity, and between days to 50% flowering and days to maturity with grain yield. High direct path coefficients were detected among number of seeds per plant, 100 seed weight and days to 50% flowering with grain yield. High indirect path coefficients were observed between grain yield and days to 50% flowering via 100 seed weight. Moreover, four clusters of accessions were recorded with clusters 2 and 4 containing promising accessions. Accessions 02_AF169, 02_AF51, 02_AF202, 02_AF222, 02_AF196, 02_AF100, 02_AF255, 02_AF216, 02_AF223 and 02_AF199 were the top ten high yielding accessions that could be included in breeding programmes for the development of improved cultivars of Kersting's groundnut.

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Compliance with ethical standards

Conflict of interest The authors declared that they have no conflict of interest.

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