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Genetic variation and heritability of kernel physical quality traits and their association with selected agronomic traits in groundnut (*Arachis hypogeae*) genotypes from Uganda

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Breeding for improvement of physical kernel traits has a direct implication on acceptance of groundnut varieties. However, the genetic parameters associated with these traits are not well documented. Ten groundnut lines were evaluated in a Randomized Complete Block Design experiment with three replicates in 2015. Data were collected on yield parameters and pod and kernel physical traits. Mean values were used to determine the characters' phenotypic, genotypic, environmental variances, phenotypic and genotypic coefficients of variation. Broad sense heritability and genetic advance as a percentage of mean were estimated for each trait. Significant variation existed in most traits. The coefficients of variation were low for all traits (<50%), except for hundred seed weight and pod numbers/plot, implying a low environmental influence, and ease of selection. Heritability was greater than 80% for most traits whereas genetic advance as percentage of the mean ranged from low in shelling percentage (15%) to high in hundred seed weight (>80%). Dry pod weight was positively correlated with pod and seed size traits. High broad sense heritability and high genetic advance for kernel physical quality traits showed the role of additive genes in the control of these traits, and thus the possibility for indirect selection for yield traits.

Key words: Correlation, genotype, inheritance, pod size, seed size.

INTRODUCTION

The cultivated groundnut (*Arachis hypogaea* L.) is one of the most important legume cash crops grown for use as food and oil (Birthal et al., 2010). Though a native of South America, the crop is grown in over 100 countries around the world. Covering an area of 23.95 million hectares with a production estimated at 36.45 million

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tonnes and an average productivity of 1520 kg/ha. Around 90% of the total production is concentrated in developing countries located in the semi-arid tropics with India and China contributing close to 50% of global output. In Africa, major produces include Nigeria, Senegal, and Sudan. In Uganda, the crop is the second most important legume after common beans (*Phaseolus vulgaris* L.) (Okello et al., 2013), and is produced mainly in the eastern and northern semi-arid dry regions of Uganda (Ronner and Giller, 2012). It is a non-animal source of protein, and used as cash and food crop. In addition, groundnut is grown by small holder farmers with little or no inputs (Mugisha et al., 2011; Mugisha et al., 2014). In the last decade, there has been a noticeable increase in the acreage devoted to the groundnuts in Uganda; however, the productivity of the crop has almost stagnated in the same period (FAOSTAT, 2012), while demand for the crop as a source of food is on the increase. Genetic improvement of the crop remains the most feasible option given the groundnut production landscape in Uganda.

Genetic improvement of a crop depends on the power of genetic diversity within the crop species. Adequate variability improves the possibility for selections and hybridization. The genotypic and phenotypic coefficient variation is helpful in exploring the nature of variability in the breeding population (Acquaah, 2012). Genotypic correlations have been used as an effective tool to determine the relationships among agronomic traits in genetically diverse population for enhanced progress in crop improvement (Bello et al., 2006). Binodh et al. (2008) confirmed that information on character association in crops is important for effective and rapid selection in crop improvement. In addition, the estimate of heritability provides an indication of transmissibility of characters.

Heritability measures the proportion of phenotypic variance which is heritable (Acquaah, 2012). Estimate of heritability provides power to breeders to allocate resources necessary to effectively select for desired traits and to efficiently achieve maximum genetic gain (Smalley et al., 2004). There are different ways to estimate heritability. It may be estimated as broad-sense or narrow-sense, on single plant, individual plot or the mean of entry (Nyquist, 1991 cited in Ogunniyan and Olakajo, 2014). Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and further suggests reliable crop improvement through selection of such traits. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of these parameters (Shukla et al., 2006; Nwangburuka and Denton, 2012).

Continuous improvement of groundnut is imperative for the increased competitiveness of the crop. This can be achieved through effective selection of suitable parental materials of significant genetic variability. The objective of the present study is to estimate the genetic variation, genetic associations, heritability and expected genetic advance for kernel physical and selected agronomic traits in the commonly grown groundnut varieties in Uganda and to evaluate suitable selection criteria for further yield improvement.

MATERIALS AND METHODS

Study areas and their characteristics

This study was conducted in the first season of 2015 in four purposefully selected districts of Uganda, representing the major groundnut growing regions of Uganda. These districts include: Hoima, Masindi, Lira, and Kumi. These districts also represent different ethnic communities and agro-ecological zones (AEZ). In the western zone, trials were hosted in Masindi District (Pakanyi sub county, Labong village) and Hoima District (Bugambe sub county, Mairirwe village). This area is predominantly inhabited by the Bantu speaking Banyoro ethnic group. This area receives two rainfall peaks (1200 to 2000 mm), April/May and August/September, respectively. The average annual temperature for this area is 22.9°C. The major economic activity in this area is agriculture with much prominence given to food crops. Lira District is part of the Lango sub region in Northern Uganda. In this district, the trials were hosted in Adek'Okwok sub county, Barr-opuu village. The majority of the population are ethnic Langi and the predominant language is Luo. This region has got a diversified and vibrant economy. The region receives between 1000 to 1400 mm of rainfall annually in a bimodal rainfall pattern - from March to May and again from August to October. The average annual temperature range for this area is 23.6°C. Kumi District is part of the Teso sub-region. It is home to Iteso and Kumam ethnicities. This region receives annual rainfall of about 1100 to 1200 mm, distributed between two seasons of March to May and September to November. Late February/early March is usually the long dry season period while Mid-June to late July is the short one with an annual average temperature of 24°C. In this district, trials were hosted in Atutur sub-county, Kellim village. All the trial sites in each district were selected with the help of local agricultural extension staff.

Genotypes, experimental design and crop management

A total of ten popular (landraces and improved) groundnut varieties were used in this study (Table 1). These were planted out on farmers' fields in each of the four districts. In each district, one central location was identified to host the trial. The trial was set up as randomized complete block design (RCBD) with 3 replications. In each location, blocking was done with respect to direction of variation in the field. In case of a slope, blocks and plots were set perpendicular to the slope direction. In other cases, where there were no obvious slopes, blocking was generally carried out to minimise the within and between plot variation in the field. In each location, treatments were assigned to plots randomly and independently for each block. Single groundnut seeds were planted in 4 row, 2 m– long plots with 45 cm inter row, and at 15 cm between planting stations, respectively. All trials were managed by farmers. No fertilisers or other agrochemicals were applied.

Data collection

Yield data were collected on plot basis. Data were recorded from

Table 1. Cultivar name, source, and attributes of the popular groundnut variety lines in Uganda.

Cultivar name	Source	Attribute
Oluk-oluk-arema	Farmers	Medium, red seed colour
Etesot	Farmers	Medium, Tan seed colour
Gambia	Farmers	Medium, white seed colour
Igola	SGV	Large, Tan seed colour
Red beauty	Farmers	Small-medium, red seed colour
Two- seeded type	Farmers	Small, red seed colour
Serenut 11T	SGV	Released, drought tolerant, GRVD and leaf spot resistance; giant pods and seeds
Serenut 2 T	SGV	Released, highly drought tolerant, GRVD and leaf spot resistance, large seed, and Tan coloured
Serenut 6 T	SGV	Released, GRVD resistant; giant pods and seeds, Tan seed colour
Serenut 8 R	SGV	Released drought tolerant, GRVD and leaf spot resistant, Medium seed size, red seed colour

SGV, GRVD means Serere groundnut variety, and Ground rosette virus disease, respectively.

the middle rows excluding plants at the end of rows for each variety to record data on the following traits: pod yield per plant (g). Pods were sundried for two weeks and weighed to determine the dried pod yield (g/plot). Other parameters such as 100-kernel weight (g), and shelling percentage (%) were also determined. In order to measure 100-kernel weight, a random sample of 100 of well-filled seeds (avoiding shrivelled and broken ones) was drawn and its weight was recorded in grams. To quantify shelling percentage (%), pod weight was recorded from each plant in grams. Then, the weight of kernels after shelling the pods of same plant was recorded in grams, and expressed as:

Shelling percentage (%) = (Kernel weight(g))/(Pod weight (g)) × 100

Pod and seed size traits (pod diameter, pod length, Pod length – diameter ratio, seed length, seed width, ratio of seed length to seed diameter) were measured according to the method of Lal et al. (2014).

Data analysis

Data were analysed for ANOVA using Genstat version 14 (Payne et al., 2011). Means were separated using Fisher's protected $LSD_{0.05}$. Genetic parameters were computed using Excel software. Genotypic and phenotypic variances, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance and genetic gain were computed using standard formulas.

Estimation of variability parameters

Genetic variance

It is the variance contributed by genetic causes or the genetic occurrence of difference among the individuals due to their genetic makeup. It was calculated by using the formula given by Baye (2002),

Genotypic variance ($\delta^2 g$) = MSP- (MSe/r)

Where, $\delta^2 g$ = Genotypic variance, MSP = Mean square for phenotypes (varieties), MSe = Error mean square and r = Number of replication.

Phenotypic variance

It is the sum of variance contributed by genetic causes and environmental factors and was computed as formula given by Al-Jibouri (1958).

$$\delta^2 p = \delta^2 g + \delta^2 e$$

Where, $\delta^2 p$ = Phenotypic variance, $\delta^2 g$ = Genotypic variance and, $\delta^2 e$ = Error variance.

Genotypic coefficient of variation (GCV)

The magnitude of genetic variation existing in a character was estimated by the formula given by Burton (1952),

$$GCV = \frac{\sqrt{V_g}}{\bar{x}} X100$$

Where, Vg = Genotypic variance and $\bar{X}$ = General mean of the character under study

Phenotypic coefficient of variation (PCV)

The magnitude of phenotypic variation existing in a character was estimated by the formula given by Burton (1952),

$$PCV = \frac{\sqrt{V_p}}{\bar{x}} X100$$

Where, V_p = Phenotypic variance and $\bar{X}$ = General mean of the character under study

Heritability

Heritability in the broad sense was calculated by the formula given by Falconer and Mackay (1996),

$$H^2 = (Vg/Vp) \times 100$$

Table 2. Mean values, coefficients of variation, ranges and mean squares of some selected agronomic characters of 10 groundnut lines in selected groundnut growing regions of Uganda.

Character	Mean	CV (%)	Range	Mean square	Between	Error	P-value
			Min	Max	Lines df = 9	df = 98	
Dry pod weight/plot (g)	126.5	9.2	91.15	157.58	7437.5	136.1	<.001
Hundred seed weight (g)	48.51	9.6	34.32	69.83	2534.25	21.54	<.001
Sound mature Kernels (%	74.4	20.6	60	81.3	725.9	234.2	0.003
Shelling out turn (%)	68.06	4.3	64.91	70.37	44.17	8.72	<.001
Pod length (cm)	2.74	14	2.46	3.14	0.99	0.15	<.001
Pod diameter (cm)	1.27	14	1.12	1.35	0.077	0.032	0.016
Seed length (cm)	1.3	15	1.14	1.52	0.33	0.04	<.001
Seed diameter (cm)	0.78	13.9	0.7	0.85	0.05	0.01	<.001
PL/PD (cm)	2.13	12.1	1.86	2.38	0.66	0.07	<.001
SL/SD (cm)	1.65	14.2	1.57	1.82	0.12	0.06	0.04
Pod number	875	25.9	650	1044	296295	51245	<.001

PL/PD (cm), Df, CV, and SL/SD (cm) means Pod length to diameter ratio, Degrees of freedom, Coefficient of variation, and Seed length to diameter ratio.

Where, H^2 = Heritability (broad sense), Vg = Genotypic variance and Vp = Phenotypic variance

Expected genetic advance

It was measured by the formula proposed by Lush (1949).

$$GA = \frac{V_g}{V_p} = \sqrt{V_p} \times K = \frac{V_g}{\sqrt{V_p}} \times K$$

Where, GA = Genetic advance, Vg = Genotypic variance, Vp = Phenotypic variance, K = Selection differential (constant) i.e. 2.06 at 5% selection intensity.

Genetic gain

It was calculated by using the following formula suggested by Johnson et al. (1955),

$$\text{Genetic gain} = \frac{GA}{x} \times 100$$

Where, GA = Genetic advance and $\bar{X}$ = General mean of the character under study.

RESULTS

Variation for physical kernel traits and agronomic traits of groundnut in selected growing regions of Uganda

The results of analysis of variance are presented in Table 2. The analysis of variance revealed that mean squares due to genotypes were found to be significant for all the characters under investigation (P ≤ 0.05 to P≤ 0.01). The dry pod weight/plot (ranged from 91.15 to 157.58 g), hundred seed weight (ranged from 34.32 to 69.83 g), sound mature kernels (ranged from 60 to 81.3%), shelling out turn (ranged from 64.91 to 70.37 %), Pod length (ranged from 2.46 to 3.14 cm), pod diameter (ranged from 1.12 to 1.35 cm), pod length to diameter ratio (ranged from 1.86 to 2.38), seed length (ranged from 1.14 to 1.52 cm), seed diameter (ranged from 0.70 to 0.85 cm), seed length to diameter ratio (ranged from 1.57 to 1.82), number of pods per plot (ranged from 650 to 1044) had 126.5, 48.51g; 74.4, 68.06%; 2.74, 1.27, 1.30, 0.78 , 2.13 cm, 1.65, and 875 as average trait scores, respectively.

Association between pairs of some characters of 10 groundnut lines popularly grown in Uganda

Correlation coefficients among traits recorded in this study are presented in Table 3. Most of the traits had positive significant phenotypic association with each other. Dry pod weight (g/plot) was significant and positively correlated with pod diameter (r = 0.3, P ≤ 0.01), pod length (r = 0.2, P ≤ 0.05), seed diameter (r = 0.3, P ≤ 0.01), seed length (r = 0.3, P ≤ 0.01), and HSW (r = 0.7, P ≤ 0.01). Pod diameter was significantly and highly positively correlated with seed diameter (r = 0.8, P ≤ 0.01), seed length (r =0.8, P ≤ 0.01), and seed length to seed diameter ratio (r = 0.8, P ≤ 0.01).

Variances, coefficients of variation, heritability and genetic advance for traits in the groundnut lines popularly grown in Uganda

Phenotypic, genotypic and environmental variances as well as their coefficients of variation are presented in

Table 3. Pearson's correlation analysis for physical traits and selected agronomic traits of 10 groundnut lines popularly grown in Uganda.

PD_pod	-																			
PL_pod	0.8	**	-																	
Pod_No	0.0		-0.1		-															
SD_seed	0.8	**	0.5	**	0.1		-													
SL_SD	0.8	**	0.7	**	0.1		0.6	**	-											
SL_seed	0.8	**	0.5	**	0.0		0.9	**	0.8	**	-									
SMS_%	0.4	**	0.3	**	-0.1		0.5	**	0.3	**	0.4	**								
HSW	0.2	*	-0.1		-0.2	*	0.4	**	0.0		0.5	**	0.1		-					
DPW	0.3	**	0.2	*	-0.4	**	0.3	**	0.0		0.3	**	0.1		0.7	**	-			
Shelling_%	-0.1		-0.1		0.1		0.1		-0.2		0.0		0.2	*	0.3	**	0.2	**	-	
	PD_pod		PL_pod		Pod_No		SD_seed		SL_SD		SL_seed		SMS_%		HSW		DPW		shelling_%	

PD_Pod = Pod diameter; PL_pod = Pod length; SD_Seed = Seed diameter; SL_SD = ratio of seed length to seed diameter; SL_seed = Seed length; SMS = Percentage of sound mature kernels; HSW = Hundred seed weight; DPY = Dry pod yield; Shelling_% = Shelling percentage.

Table 4. Variability, heritability and expected genetic advance of some relevant agronomic characters of groundnut cultivars popularly grown in Uganda.

Traits	Phenotypic variance (δ^2_P)	Genotypic variance (δ^2_g)	Environmental variance (δ^2_E)	PCV (%)	GCV (%)	Heritability (%)	Genetic advance (%) mean
PD_pod	0.045	0.035	0.01	16.7	14.7	0.77	21.9
PL_pod	0.844	0.795	0.049	33.5	32.5	0.94	61.5
Pod_No	245050	227968.333	17081.67	56.6	54.6	0.93	101.4
SD_seed	0.036	0.032	0.004	24.3	22.9	0.89	40.2
SL_SD	0.061	0.043	0.018	15	12.5	0.7	17
SL_seed	0.296	0.283	0.013	41.7	40.8	0.96	78.8
SMS_%	491.7	413.633	78.067	29.8	27.3	0.84	44.9
HSW	2512.71	2505.53	7.18	103.3	103.2	1	211.2
DPW	7301.4	7256.033	45.367	67.5	67.3	0.99	137.2
shelling_%	35.45	32.543	2.907	8.7	8.4	0.92	15.3

PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; H^2- bs = Broad sense heritability; GAM = Genetic gain as percentage of the mean; PD_Pod = Pod diameter; PL_pod = Pod length; SD_Seed = Seed diameter; SL_SD = ratio of seed length to seed diameter; SL_seed = Seed length; SMS = Percentage of sound mature kernels; HSW = Hundred seed weight; DPY = Dry pod yield; Shelling_% = Shelling percentage.

Table 4. Similarly, heritability and expected genetic advance are presented in the table. Both the variances of phenotype and genotype of all traits studied were low except, those of number of pods per plot, HSW, and Dry pod weight/plot had low. Correspondingly, both coefficients of variation

for the phenotype and genotype were generally low, except for number of pods per plot, seed length, hundred seed weight, and dry pod weight. Heritability ranged from 70 to 100% whereas expected genetic advance ranged from low 15.3% in shelling percentage to 137% in hundred seed weight.

DISCUSSION

Coefficients of variation and ranges of the 10 seed and agronomic characters of groundnut explained that significant variation existed in all the characters. Similar results were also reported by Patidar et al. (2014), Maurya et al. (2014), Shukla and Rai (2014), Rai et al. (2014), Rao et al. (2014) and Nalluri et al. (2017). Ranges were very high for all the characters. The wide range in values of the traits was adequate to distinguish the groundnut lines using these traits. The low CVs in the values of the traits may be expected because the lines comprise landraces and popular released groundnut varieties which over several generations have resulted in fixation of genes at different loci.

The phenotypic variances were higher than the genotypic variances for all traits implying that environment influences the inheritance of these characters, and effect varied with trait under consideration. This agrees with findings of Maurya et al. (2014) and Zekeria et al. (2017). Low coefficients of variation for the phenotype and genotype were observed, except for number of pods per plot, seed length, hundred seed weight, and dry pod weight, encourages the use of yield parameters in the selection of suitable parents for crosses or line improvement. This agrees with finding of Shukla and Rai (2014), and Nalluri et al. (2017). Pod and seed traits such as pod length, percentage of mature kernels, and seed diameter may also be considered in case there is need to support the yield parameters because their coefficients of variation were comparatively large. Similar findings were reported by Patidar et al. (2014), and Maurya et al. (2014).

Dry pod weight (g/plot) was positively correlated with pod diameter, pod length, seed diameter, seed length, and HSW. Roy et al. (2003), Gopal (2008), and Kakeeto (2017) reported a similar result. Pod diameter was significantly and highly positively correlated with seed diameter, seed length, and seed length to seed diameter ratio. This observation implies that instead of tediously measuring seed sizes, an easier measurement can be done using pod diameter.

Heritability is the percentage of phenotypic variance that is attributed to genetic variance. In the present study, heritability was high (>80%) for most traits studied. High heritability indicates that the environmental influence is minimal on the characters. This implies that, any of the characters studied here can therefore be used for selection. Nalluri et al. (2017), John et al. (2008), and Narasimhulu et al. (2012) have also reported high heritability for different yield contributing traits in groundnuts. High value of heritability in broad sense indicates that the character is least influenced by environmental effects. Similar observations were made by Shukla and Rai (2014).

Heritability estimates along with genetic advance as per cent of mean are more helpful in predicting the gain under selection than heritability estimates alone. The expected advance that was low for pod diameter, seed diameter, seed length to width ratio, and shelling percentage may be compensated for by their high heritability. High heritability coupled with high genetic advance as percent of mean was recorded in pod length, pod number per plot, seed length, and hundred seed weight indicating the preponderance of additive gene action in controlling the inheritance of this character and offers high feasibility for improvement through simple selection procedures. Similar results were reported by John et al. (2008), Thakur et al. (2011), and Bhargavi et al. (2017).

Moderate heritability accompanied with low genetic advance as per cent of mean was observed in pod diameter, seed diameter, seed length-width ratio, shelling per cent indicating the preponderance of non-additive gene action as well as influence of environment. The improvement of this trait might be possible through heterosis breeding. Similar result was reported by Korat et al. (2009) and Zaman et al. (2011) and Bhargavi et al. (2017).

Conclusion

High heritability coupled with high genetic advance as per cent of mean was recorded in pod length, pod number per plot, seed length, and hundred seed weight indicating the preponderance of additive gene action in governing the inheritance of these characters and offers scope for improvement through simple selection procedures. Moreover, this study also found pod diameter to be highly positive and significantly correlated with seed length, seed diameter, seed length to width ratio, and pod length; it implies instead of using pod yield, pod number and pod diameter could be considered for evaluating large populations of groundnut lines for further improvement. The results from the present study were outcomes of a one-season evaluation. It is generally believed that evaluation carried out across the year (at least two seasons) would derive reliable conclusions on the range of characters in this study. Therefore, our results provide some useful information for genetic improvement of the cultivated groundnut.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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