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Parent-offspring regression, correlation and genetic advance of drought and yield traits at early generation in groundnut (*Arachis hypogaea* L.)

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A study was carried out to estimate the parent-offspring regression and correlation and, to determine genetic advance of yield and drought related traits of groundnut at early segregating populations. All the experiments were conducted in the dry season 2015/2016 at the International Crops Research Institute for the Semi-Arid Tropics ICRISAT Samanko, Mali under full irrigation and drought stress conditions. The data were collected on plot basis on both water-stressed and fully irrigated plots in the F1, F2 and F2:3 generations of two populations. Data collected included chlorophyll concentration (SCMR), Specific Leaf Area (SLA) (cm2/g) and Pod Yield (PY)(kg/ha). Results of the parent offspring regression for the two populations evaluated both water regimes were low and revealed importance of non-genetic effects. Consequently, the genetic advances for the two crosses were mostly low to moderate irrespective of the generation and environment under study. Selection at early generation in groundnut could be slow under drought. Based on the findings, selection for drought tolerance would be inefficient to identify high yield and drought tolerant lines at early generation in groundnut. The highest heritability estimates for F1:F2 were 42% for SCMR 60 DAS and at 80 DAS under well-watered conditions, 20% ± 0.20 for SLA at 60 DAS and at 80 DAS under drought stressed conditions. The highest heritability estimates for F2:F3 progenies were observed from SCMR 60 DAS (22% ± 0.09) under well-watered conditions and SLA 60 DAS (22% ± 0.08) under water-stressed conditions.

Key words: Groundnut, heritability, drought stress, breeding.

INTRODUCTION

In a typical breeding methods such as pedigree, single-seed descent (SSD), bulk population and backcrossing, large number of genotypes are advanced through segregating generations (Ntare, 1999). These processes take a long time before identification of superior cultivars. Early Generation Selection (EGS) in self-pollinated crops involves the evaluation of F_2-or F_3-derived lines from a cross between two homozygous parents (Bernado, 2003). EGS may overcome the inability to identify superior yielding individual plants as early as F_2 and therefore speed up the process of developing new groundnut varieties following hybridization of diverse parents. Success in early generation testing was found with highly heritable traits (Rowe, 2009; Yang, 2009). In

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groundnut, Zongo et al. (2017) found that selection of agronomic traits (days to first flowering, 50% flowering, plant height) and early leaf spot disease at early generation selection was effective due to heritability recorded. Anderson et al. (1991) found that selection based on early generation family means was effective for improvement of both late leaf spot (LLS) and early leaf spot (ELS) disease resistance. In groundnut, Anderson et al. (1991) found that selection based on early generation family means was effective for improvement of both LLS and ELS disease resistance. Genetic advance of a trait is the product of narrow-sense heritability, phenotypic variation and the selection intensity. It is therefore a drawing force in selection, which measures the importance of the genes passed from parent to offspring. Sumathi and Ramanathan (1995) in using the parent-offspring regression method, reported moderate heritability estimates in groundnut for pod yield, while Ntare (1999) reported low to moderate heritability as well as correlation for yield and empirical traits such as crop growth rate, reproductive duration and partitioning. For traits characterized by low heritability such as yield, Songsri et al. (2008) proposed selection based on physiological criteria that are correlated with yield. These include traits such as the SPAD Chlorophyll Meter Reading (SCMR) and the Specific Leaf Area (SLA) sought as ‘’surrogate traits’’ in drought (Nageswara-Rao et al., 2001; Upadhyaya, 2005; Songsri et al., 2008; Upadhyaya et al., 2011). These authors reported that both SPAD and SLA displayed additive effects; thus helping in selection for drought in plant crops. Globally, information on heritability of drought related traits such as SCMR and SLA in the groundnut breeding is lacking in Mali. Heritability estimates of drought-related traits SLA and SCMR and their genetic correlation with pod yield will be useful to formulate effective breeding strategies under drought.

The objective of this study was to estimate the parent-offspring regression, correlation and genetic advance of yield and drought related traits of groundnut evaluated under managed drought stress conditions.

MATERIALS AND METHODS

Experimental site and conditions

All the experiments were conducted at the experimental field of International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Samanko in Mali (12°54’N and 8°4’W, 330 m above the sea) in rain-free period in November 2014 to March 2015. The soils are poor in organic matter content, light and generally brown yellow, of tropical ferruginous wash type with pH of 4.5. The mean annual rainfall is 800 m from June to October.

Irrigation water management and experimental design

The experiment was planted in split plot design using two environments as indicated below:

(i) Well-watered (WW) block - received full irrigation throughout the life cycle of the crop (from sowing to harvesting period). Plants were irrigated one to two times per week with 20 mm of water until end-of-season (pod filling to pod maturity) at seven day interval depending on the prevailing weather conditions.

(ii) Water-stressed (WS) block - full irrigation was provided till 50 days after sowing (DAS). The plants were exposed gradually to end-of-season drought from the pod filling until maturity. This period started from the pegging to pod development and maturation. At 50 DAS, drought stress was imposed for 14 days and irrigation was resumed at the 15^{th} day to bring the soil up to saturation. Then, drought stress was imposed for 10 days, followed by irrigation up to saturation. After that, drought stress was imposed for 7 days followed by irrigation up to harvest. This technique was supposed to mimic the end-of-season drought since water was withheld during the critical stage of the reproductive phase.

The two blocks (WW and WS) were separated by an alley that was 25.0 m wide to restrict lateral movement of water from the fully irrigated block to the drought stress block. Irrigation water was supplied with an overhead sprinkler irrigation system designed to dispense 40 mm of water twice per week. Except for the different irrigation treatments, all field management practices were uniform for both the well-watered and water-stressed experiments.

Basal fertilizer of 100 kg ha^{-1} simple super phosphate was applied before hand-planting with one seed per hill. Standard cultural practices, including hand planting, hand weeding while the first as early as 16-20 days after sowing (DAS) were followed. The average ambient temperature during the trial period (November-March) was 26.07°C, with a standard deviation STDEV= 9.55%. The average relative humidity within the same period was 27.17% with a standard deviation STDEV of 16.56%.

Genetic resources and hybridization techniques

The material tested was part of an ongoing breeding program for tolerance to drought. The F1, F_2 and $F_{2:3}$ generations from the two populations ICGV 91317/ICGV 87378 and ICIAR 19BT/ICGS 44 were used.

Experiment 1

Sixty five groundnut genotypes comprising 20 F_1 and 45 F_2 for population five (ICGX-IS 13005 = ICGV 91317/ICGV 87378) on one hand, and 15 F_1 plus 45 for population twelve (ICGX-IS 13012 = ICIAR 19 BT /ICGS 44) on the other, were evaluated under managed drought stress conditions. The population 5 and the population 12 were named cross I and cross II, respectively in this study (Table 1). The experimental design was the split plot with two replicates (Table 2). An experimental plot consisted of two rows of 15 m long, with bulk plants within a row spaced 0.5 m. One groundnut seed was planted per hill.

Experiment 2

Ninety six groundnut genotypes comprising 45 $F_{2:3}$ progenies for population 5 (ICGX-IS 13005 = ICGV 91317/ICGV 87378) and population 12 (ICIAR 19 BT/ICGS 44) were evaluated in a 9 x 11 alpha lattice with two replications. An experimental plot consisted of a 4 m single row with 0.6 m space. Two checks Fleur11 and 47-10 were used but excluded during the analyses because the evaluation of heritability parent-offspring regression and correlation were based on segregating materials.

Data collection

Data collected included Chlorophyll concentration (SCMR) at 60

Table 1. Number of F_1 and F_2 plants from the two populations used in the study.

Population	Entry	Pedigree	Generation	Number of plants
1	ICGX-IS 13005F1-B1	ICGV 91317/ICGV 87378	F_1	40
2	ICGX-IS 13012F1-B1	ICIAR 19 BT / ICGS 44	F_1	40
1	ICGX-IS 13005F2-B1	ICGV 91317/ICGV 87378	F_2	90
2	ICGX-IS 13012F2-B1	ICIAR 19 BT / ICGS 44	F_2	90

and 80 DAS, Specific Leaf Area (SLA) (cm^2/g) at 60 and 80 DAS and Pod Yield (PY) (kg/ha). Individual plants were harvested and their pods stripped from the plant for adequate sun drying. Individual pod weights were recorded for each F_1 and F_2 individual plant. For $F_{2:3}$ populations, data from progenies mean were used.

Data analysis

Separate analyses of variance (ANOVA) were done for each cross or population, generation and water regime using SAS (SAS Institute, 2009). Generations and individual families (genotypes) were considered to be random. Adjusted means from the lattice designs (Patterson et al., 1978) were used in the combined ANOVA across water regimes for each population. Parent-offspring regression (*b*) coefficients were obtained by regressing F_2 bulks on F_1 bulks and F_3 families or progenies mean on F_2 bulks using PROC REG in SAS. To quantify additive genetic variation (narrow-sense heritabilities) in intergeneration segregating, separate parent-offspring regressions for the population I and population II were performed for F_2/F_1 and F_3/F_2 progenies as described by Smith and Kinman (1965): $h^2=b/r_{op}$. Where, *b* is the regression coefficient or slope and, r_{op} is the relationship of parent-offspring. Heritability estimates were grouped as high (>50%), moderate, (20 to 50%), and low (<20%) as suggested by Stansfield (1986). Linear regression coefficients (*b*) was calculated by regression of F_2 progeny means (Yi) on F_1 plants means (Xi) and likewise, F_3 progenies means (Yi) were regressed on F_2 plants means (Xi). Standard error (SE) for the slope of the regression was calculated according to the method of Ibrahim and Quick (2001). Since the bulked F_2 and their bulked F_1 parents were grown in the same experiment, they were expected to be environmentally correlated (Holland et al., 2003).

Estimate of genetic advance (GA)

The genetic advance was estimated as followed: GA = i*h^2*Vp (Falconer and Mackay, 1996); Where, i= selection intensity (1.76 for the top 10%), Vp = phenotypic variance and, h^2 = the narrow sense heritability. Negative estimates were considered equal to zero (Robinson et al., 1955; cited in Gusmini and Wehner, 2007) and were reported as suggested Dudley and Moll (1969). Derivations from negative estimates from another negative value were also considered to be zero and omitted (Gusmini and Wehner, 2007).

RESULTS

Mean squares of traits measured for the three generations

Results of analyses of variance (ANOVA) for the F_1, F_2 and F_3 generations for cross I and cross II evaluated under both water regimes were as presented in Table 3.

In cross I, variations among F_1 progenies mean squares were significant (P<0.05) for SCMR at 60 DAS trait under water-stressed conditions. Under well-watered conditions, F_3 genotypes mean squares were significant for SCMR at 60 and 80 DAS, pod yield, SLA at 60 DAS and PY under well-watered conditions whereas F_3 genotypes were not significant for any studied traits evaluated under water-stressed conditions (Table 3). None of the three generations (F_1, F_2 and F_3) was consistently alike when evaluated under well-watered and water-stressed conditions.

In cross II, the progenies showed high variation regarding generations and water regimes for some traits (Table 3). The mean squares for F_1 genotypes were not significant for any trait except for SLA at 60 DAS where very highly significant (P<0.001) differences were found under both well-watered and water-stressed conditions. Under water-stressed conditions, no significant differences were detected among F_2 genotypes while significant (P<0.05) differences were observed among genotypes for SLA at 60 DAS. Also, highly significant (P<0.01) differences among F_2 genotypes were observed for the SLA at 60 DAS and pod yield traits (Table 3). F_3 genotypes showed significant (P<0.05) differences for SLA at 60 DAS and very highly significant (P<0.001) differences for pod yield under well-watered conditions. Mean squares for F_3 genotypes evaluated under water-stressed conditions showed highly significant (P<0.01, P<0.001) differences for SCMR at 60 DAS and pod yield, respectively.

Mean performance of the populations under the two water regimes

In cross I, the highest pod mean was found in F_3 progenies under well-watered conditions followed by the F_2 progenies whereas F_2 progenies exhibited the highest pod mean under water-stress conditions followed by F_3 progenies. There was a tendency for better pod yield harvesting in well-water than water-stressed, except for F_2 progenies as shown for the mean and the mean range (Table 4). The mean performance for the F_1, F_2 and F_3 progenies were similar for the trait SCMR at 60 DAS. The F_1 progenies showed the highest mean for SCMR at 60‘ DAS under both well-watered and water-stressed

Table 2. List of the two populations comprising each 45 $F_{2:3}$ progenies used.

S/N	Population 1 or cross I		S/N	Population II or cross II	
	Genotype	Pedigree		Genotype	Pedigree
1	ICGX-IS 13005F2-B1-106	ICGV 91317/ICGV 87378	1	ICGX-IS 13012F2-B1-105	ICIAR 19 BT / ICGS 44
2	ICGX-IS 13005F2-B1-11	ICGV 91317/ICGV 87378	2	ICGX-IS 13012F2-B1-114	ICIAR 19 BT / ICGS 44
3	ICGX-IS 13048F2-B1-12	ICGV 91317/ICGV 87378	3	ICGX-IS 13012F2-B1-115	ICIAR 19 BT / ICGS 44
4	ICGX-IS 13005F2-B1-132	ICGV 91317/ICGV 87378	4	ICGX-IS 13012F2-B1-130	ICIAR 19 BT / ICGS 44
5	ICGX-IS 13005F2-B1-14	ICGV 91317/ICGV 87378	5	ICGX-IS 13012F2-B1-140	ICIAR 19 BT / ICGS 44
6	ICGX-IS 13005F2-B1-167	ICGV 91317/ICGV 87378	6	ICGX-IS 13012F2-B1-15	ICIAR 19 BT / ICGS 44
7	ICGX-IS 13005F2-B1-171	ICGV 91317/ICGV 87378	7	ICGX-IS 13012F2-B1-156	ICIAR 19 BT / ICGS 44
8	ICGX-IS 13005F2-B1-182	ICGV 91317/ICGV 87378	8	ICGX-IS 13012F2-B1-20	ICIAR 19 BT / ICGS 44
9	ICGX-IS 13005F2-B1-185	ICGV 91317/ICGV 87378	9	ICGX-IS 13012F2-B1-207	ICIAR 19 BT / ICGS 44
10	ICGX-IS 13005F2-B1-187	ICGV 91317/ICGV 87378	10	ICGX-IS 13012F2-B1-24	ICIAR 19 BT / ICGS 44
11	ICGX-IS 13005F2-B1-189	ICGV 91317/ICGV 87378	11	ICGX-IS 13012F2-B1-268	ICIAR 19 BT / ICGS 44
12	ICGX-IS 13005F2-B1-19	ICGV 91317/ICGV 87378	12	ICGX-IS 13012F2-B1-276	ICIAR 19 BT / ICGS 44
13	ICGX-IS 13005F2-B1-198	ICGV 91317/ICGV 87378	13	ICGX-IS 13012F2-B1-281	ICIAR 19 BT / ICGS 44
14	ICGX-IS 13005F2-B1-205	ICGV 91317/ICGV 87378	14	ICGX-IS 13012F2-B1-29	ICIAR 19 BT / ICGS 44
15	ICGX-IS 13005F2-B1-222	ICGV 91317/ICGV 87378	15	ICGX-IS 13012F2-B1-297	ICIAR 19 BT / ICGS 44
16	ICGX-IS 13005F2-B1-252	ICGV 91317/ICGV 87378	16	ICGX-IS 13012F2-B1-312	ICIAR 19 BT / ICGS 44
17	ICGX-IS 13005F2-B1-262	ICGV 91317/ICGV 87378	17	ICGX-IS 13012F2-B1-319	ICIAR 19 BT / ICGS 44
18	ICGX-IS 13005F2-B1-287	ICGV 91317/ICGV 87378	18	ICGX-IS 13012F2-B1-381	ICIAR 19 BT / ICGS 44
19	ICGX-IS 13005F2-B1-301	ICGV 91317/ICGV 87378	19	ICGX-IS 13012F2-B1-40	ICIAR 19 BT / ICGS 44
20	ICGX-IS 13005F2-B1-359	ICGV 91317/ICGV 87378	20	ICGX-IS 13012F2-B1-431	ICIAR 19 BT / ICGS 44
21	ICGX-IS 13005F2-B1-37	ICGV 91317/ICGV 87378	21	ICGX-IS 13012F2-B1-475	ICIAR 19 BT / ICGS 44
22	ICGX-IS 13005F2-B1-381	ICGV 91317/ICGV 87378	22	ICGX-IS 13012F2-B1-491	ICIAR 19 BT / ICGS 44
23	ICGX-IS 13005F2-B1-388	ICGV 91317/ICGV 87378	23	ICGX-IS 13012F2-B1-50	ICIAR 19 BT / ICGS 44
24	ICGX-IS 13005F2-B1-40	ICGV 91317/ICGV 87378	24	ICGX-IS 13012F2-B1-518	ICIAR 19 BT / ICGS 44
25	ICGX-IS 13005F2-B1-404	ICGV 91317/ICGV 87378	25	ICGX-IS 13012F2-B1-520	ICIAR 19 BT / ICGS 44
26	ICGX-IS 13005F2-B1-411	ICGV 91317/ICGV 87378	26	ICGX-IS 13012F2-B1-525	ICIAR 19 BT / ICGS 44
27	ICGX-IS 13005F2-B1-425	ICGV 91317/ICGV 87378	27	ICGX-IS 13012F2-B1-528	ICIAR 19 BT / ICGS 44
28	ICGX-IS 13005F2-B1-450	ICGV 91317/ICGV 87378	28	ICGX-IS 13012F2-B1-534	ICIAR 19 BT / ICGS 44
29	ICGX-IS 13005F2-B1-46	ICGV 91317/ICGV 87378	29	ICGX-IS 13012F2-B1-537	ICIAR 19 BT / ICGS 44
30	ICGX-IS 13005F2-B1-470	ICGV 91317/ICGV 87378	30	ICGX-IS 13012F2-B1-554	ICIAR 19 BT / ICGS 44
31	ICGX-IS 13005F2-B1-481	ICGV 91317/ICGV 87378	31	ICGX-IS 13012F2-B1-561	ICIAR 19 BT / ICGS 44
32	ICGX-IS 13005F2-B1-488	ICGV 91317/ICGV 87378	32	ICGX-IS 13012F2-B1-562	ICIAR 19 BT / ICGS 44
33	ICGX-IS 13005F2-B1-49	ICGV 91317/ICGV 87378	33	ICGX-IS 13012F2-B1-563	ICIAR 19 BT / ICGS 44
34	ICGX-IS 13005F2-B1-494	ICGV 91317/ICGV 87378	34	ICGX-IS 13012F2-B1-566	ICIAR 19 BT / ICGS 44
35	ICGX-IS 13005F2-B1-498	ICGV 91317/ICGV 87378	35	ICGX-IS 13012F2-B1-571	ICIAR 19 BT / ICGS 44
36	ICGX-IS 13005F2-B1-5	ICGV 91317/ICGV 87378	36	ICGX-IS 13012F2-B1-576	ICIAR 19 BT / ICGS 44
37	ICGX-IS 13005F2-B1-50	ICGV 91317/ICGV 87378	37	ICGX-IS 13012F2-B1-586	ICIAR 19 BT / ICGS 44
38	ICGX-IS 13005F2-B1-559	ICGV 91317/ICGV 87378	38	ICGX-IS 13012F2-B1-600	ICIAR 19 BT / ICGS 44
39	ICGX-IS 13005F2-B1-586	ICGV 91317/ICGV 87378	39	ICGX-IS 13012F2-B1-62	ICIAR 19 BT / ICGS 44
40	ICGX-IS 13048F2-B1-591	ICGV 91317/ICGV 87378	40	ICGX-IS 13012F2-B1-69	ICIAR 19 BT / ICGS 44
41	ICGX-IS 13005F2-B1-65	ICGV 91317/ICGV 87378	41	ICGX-IS 13012F2-B1-75	ICIAR 19 BT / ICGS 44
42	ICGX-IS 13005F2-B1-85	ICGV 91317/ICGV 87378	42	ICGX-IS 13012F2-B1-78	ICIAR 19 BT / ICGS 44
43	ICGX-IS 13005F2-B1-90	ICGV 91317/ICGV 87378	43	ICGX-IS 13012F2-B1-84	ICIAR 19 BT / ICGS 44
44	ICGX-IS 13005F2-B1-91	ICGV 91317/ICGV 87378	44	ICGX-IS 13012F2-B1-93	ICIAR 19 BT / ICGS 44
45	ICGX-IS 13005F2-B1-93	ICGV 91317/ICGV 87378	45	ICGX-IS 13012F2-B1-98	ICIAR 19 BT / ICGS 44

conditions while the F_2 progenies exhibited the highest mean for SCMR at 80 DAS under water-stressed and well-watered conditions. The mean range for the three generations F_1, F_2 and F_3 lines for SLA at 60 DAS and for

Table 3. Mean squares from ANOVA of measured traits for F_1, F_2 and F_3 progenies from two populations evaluated under both well-watered and water-stress.

Trait	Gen¥	Population I		Population II	
		Well-watered	Water-stress	Well-watered	Water-stress
SCMRf	F_1	8.09	12.85*	6.59	4.78
	F_2	10.84	10.59	8.28	9.99
	F_3	6.28*	4.01	6.41	10.40**
SCMRz	F_1	5.56	5.67	14.44	7.75
	F_2	143.35	19.97	9.72	6.12
	F_3	12.88**	18.45	16.66	13.56
SLAf	F_1	3685.40	3122.1	2192.7	3499.50
	F_2	3016.03	3088.50	4335.7*	2372.10
	F_3	2910.4***	1874.40	2330.7*	2199.40
SLAz	F_1	2523.90	3372.50	5736.8**	3676.7**
	F_2	2574.90	2919.40	3334.4**	2286.10
	F_3	2914.70	2522.80	2220.7	2638.40
PY	F_1	53.78	19.90	29.99	30.90
	F_2	63.49	44.43	53.4***	50.40
	F_3	34.2**	14.00	50.5***	19.4***

¥Gen= Generation. *, **, ***P<0.05, P<0.01 and P<0.001, respectively. PY= pod yield (kg/ha), SCMRf=SPAD meter reading at 60 DAS, SCMRz=SPAD meter reading at 80 DAS, SLAf= Specific leaf area (cm^2/g) at 60 DAS, SLAz=Specific leaf area (cm^2/g) at 80 DAS.

SLA at 80 DAS were close and similar across generations (Table 4). The mean of two generations F_1 and F_2 lines were similar for the trait SLA at 60 DAS and for SLA at 80 DAS under both well-watered and water-stressed conditions whereas the mean for the SLA at 60 DAS and for SLA at 80 DAS for F_3 lines were the highest under both well-watered and water-stressed conditions.

The coefficient of variation (CV %) and R square (R^2) for the pod yield for the F_1, F_2, F_3 generations ranged from 20.95 to 38.50% under well-watered and water-stressed conditions, respectively. The traits SCMR at 60 DAS and SCMR at 80 DAS showed low coefficient of variation across generations and water-regimes. The lowest CV (%) for the trial was 4.31% with R^2= 0.63 while the highest was 38.50% with R^2 = 0.84. Across water regimes, the highest CV% for SLA at 60 DAS and SLA at 80 DAS were respectively 29.57% with R^2=0.54 and 35.31% with R^2=*0.48* (Table 4).

In the cross II, the highest pod yield was found in F_3 progenies under across the two water regimes. Pod mean under well-water conditions was greater pod mean under water-stressed across the three generations. The mean performance for F_1, F_2 and F_3 progenies were mostly similar for SCMR at 60 DAS and SCMR at 80 DAS. For the trait SCMR at 60 DAS, it ranged from 39.03 to 44.19 whereas for the trait SCMR at 80 DAS, it varied between 35.84 and 42.85 (Table 4). The highest mean for SCMR at 60 DAS under both well-watered and water-stressed conditions was recorded on F_2 progenies. Likewise, the highest mean for SCMR at 80 DAS was recorded on the F_2 progenies under both water-stressed and well-watered conditions. The mean range for the three generations F_1, F_2 and F_3 lines for SLA at 60 DAS and for SLA at 80 DAS were close and similar. The lowest mean for SLA at 60 DAS was observed on F_2 progenies with 146.39 cm^2/g and the lowest mean for SLA at 80 DAS was recorded on 161.60 cm^2/g on F_1 progenies under both stress and non-stress conditions. The mean of two generations $F_1$and F_2 lines were similar and close for the traits SLA at 60 DAS and SLA 80 DAS under both well-watered and water-stressed conditions. The F_3 lines mean for SLA at 60 DAS and for SLA at 80 DAS were the higher than those observed for the same traits with the F_1 and F_2 lines irrespective of the water regimes (Table 4). The lowest coefficient of variation (CV%) for the trial was 5.28 with R^2= 0.66 and the highest observed was 41.09% with R^2=0.51. The CV for the pod yield for the F_1, F_2, and F_3 generations ranged from 14.08% to 32.28% under well-watered and water-stressed conditions. The traits SCMR at 60 DAS and SCMR at 80 DAS showed low coefficient of variation across generations and water-regimes. Across water regimes, the highest CV% for SLA at 60 DAS and SLA at 80 DAS were respectively 41.09% with R^2=0.51 and

Table 4. Variability of traits of F_1, F_2 and $F_{2:3}$ progenies of 2 groundnut populations evaluated under well-watered and water stress conditions.

	Trait	Population I				Population II		
		Water regime	Mean ± SE	R^2	CV (%)	Mean ± SE	R^2	CV (%)
Generation F1	SCMR60DAS	WW	44.41±0.46	0.62	5.03	39.93±0.46	0.66	5.28
		WS	43.96±0.46	0.74	5.21	41.78±0.46	0.52	7.10
	SCMR80DAS	WW	37.66±0.46	0.44	7.31	39.08±0.46	0.67	8.30
		WS	40.83±0.46	0.38	7.68	40.92±0.46	0.44	9.65
	SLA60DAS	WW	212.28±10.43	0.74	19.72	166.59±10.43	0.37	36.9
		WS	158.50±10.43	0.63	29.33	175.38±10.43	0.65	25.16
	SLA80DAS	WW	166.82±9.22	0.48	31.41	161.60±9.22	0.83	22.04
		WS	167.26±9.22	0.76	23.72	161.81±9.22	0.79	19.37
	PY	WW	10.27±1.24	0.61	29.16	11.93±1.24	0.37	14.08
		WS	9.67±1.24	0.84	38.50	10.83±1.24	0.58	12.41
Generation F2	SCMR60DAS	WS	43.05±2.35	0.49	8.29	44.19±1.93	0.60	6.08
		WW	43.38±2.35	0.60	7.01	43.84±1.93	0.62	6.29
	SCMR80DAS	WS	43.94±6.25	0.57	26.07	42.13±2.73	0.59	8.43
		WW	41.51±6.25	0.58	10.18	42.85±2.73	0.50	7.74
	SLA60DAS	WS	188.82±37.44	0.62	26.23	183.47±42.11	0.72	26.56
		WW	184.91±37.44	0.54	29.57	146.39±42.41	0.51	41.09
	SLA80DAS	WS	162.47±38.01	0.48	35.31	171.60±29.72	0.78	19.95
		WW	178.93±38.01	0.58	29.23	164.29±29.72	0.62	26.8
	PY	WW	16.79±6.95	0.70	31.13	13.71±5.97	0.85	32.28
		WS	16.64±6.95	0.59	32.95	11.83±5.97	0.60	26.86
Generation F2:3	SCMR60DAS	WW	42.27±1.23	0.68	4.41	42.33±1.62	0.57	5.73
		WS	38.43±1.23	0.63	4.31	39.03±1.62	0.69	5.75
	SCMR80DAS	WW	41.20±2.20	0.70	5.97	40.87±2.58	0.63	8.17
		WS	35.59±2.20	0.63	10.05	35.84±2.58	0.58	10.64
	SLA60DAS	WW	217.73±27.99	0.76	14.93	237.15±29.40	0.72	14.92
		WS	224.06±27.99	0.53	20.26	207.46±29.40	0.68	19.51
	SLA80DAS	WW	204.09±37.63	0.52	28.98	195.81±32.75	0.57	23.22
		WS	200.25±37.63	0.64	22.24	212.67±32.75	0.57	22.5
	PY	WW	19.15±2.72	0.71	20.95	18.72±2.38	0.77	20.97
		WS	11.94±2.72	0.61	30.61	11.82±2.38	0.81	20.37

WW= well-watered, WS=Well-water-stress. PY (kg/ha), SCMR and SLA (cm2/g) = pod yield, SPAD Chlorophyll meter reading and specific leaf area, respectively.

26.80% with R^2=0.62 (Table 4).

Genetic advance, parent-offspring regression and correlation of F_1/F_2 and F_2/F_3 progenies

In cross I, the parent-offspring regression for F_1:F_2 and F_3 progenies ranged from 0% for pod yield to 18% ± 0.15 for SCMR 60 DAS under water-stressed conditions while under well-watered conditions, F_1:F_2 regression varied from 6 ± 0.18% for SLA 80 DAS to 36% for SCMR 80 DAS. Regression of F_2 vs F_3 values ranged from 0.00 for SLA 80 DAS to 18 ± 0.06% for pod yield. No significant relationship was detected between F_2:F_3 progenies and

Table 5. Genetic advance, parent-offspring regression (with their standard errors) and correlation of F_2 on F_1, and $F_{2:3}$ on bulked F_2 mean from Cross I evaluated under well-watered and water-stress conditions.

Trait	ENV	Genetic advance (GA%)		Parent-offspring regression *(b)*		Parent-offspring correlation *(r)*	
		F_2	F_3	F_1:F_2	F_2:F_3	F_1:F_2	F_2:F_3
SCMRf	WW	0.00	1.58	0.14 ± 0.23	-0.02 ± 0.69	0.05	-0.02
	WS	0.63	0.66	0.18 ± 0.12	-0.10 ± 0.06	0.08	-0.08
SCMRz	WW	5.59	4.10	0.36 ± 0.26	0.06 ± 0.02	0.12	0.12
	WS	0.99	2.94	0.16 ± 0.16	-0.24 ± 0.09	0.05	-0.14
SLAf	WW	8.31	6.59	0.28 ± 0.15	-0.28 ± 0.08	0.16	-0.16
	WS	0.00	0.00	0.16 ± 0.11	0.02 ± 0.08	0.08	0.02
SLAz	WW	0.00	0.00	0.06 ± 0.18	-0.22 ± 0.11	0.02	-0.10
	WS	3.75	5.52	-0.16 ± 0.10	0.00 ± 0.09	-0.08	0.00
PY	WW	7.94	10.86	0.12 ± 0.20	0.18 ± 0.06	0.05	0.15
	WS	0.00	0.31	-0.20 ± 0.12	-0.16 ± 0.04	-0.09	-0.18

§ ENV = environments (Well-watered WW and water-stress WS). SCMRf, SCMRz, SLAf, SLAz and PY = SPAD chlorophyll meter reading at 60 DAS at 80DAS, specific leaf area (cm^2/g) at 60 DAS and at 80 DAS and pod yield (kg/ha). GA (%), *b*, and *r* are genetic advance, regression coefficient and correlation coefficient, respectively.

almost all the regression coefficients were negative in cross I (Table 5). Similar trends of negative heritability values via regression of F_1 vs F_2 and that of F_2:F_3 were observed under both drought stress and well-watered conditions in cross II (Table 5). The highest heritability estimates for F_1:F_2 were 42% for SCMR 60 DAS and at 80 DAS under well-watered conditions, 20 ± 0.20% for SLA at 60 DAS and at 80 DAS under drought stressed conditions. The highest heritability estimates for F_2:F_3 progenies were observed from SCMR 60 DAS (22% ± 0.09) under well-watered conditions and SLA 60 DAS (22 ± 0.08%) under water-stressed conditions. Standard error values were often higher than regression coefficients. Inter-generation regression coefficients were lower and not significant for SCMR and SLA for F_1vs F_2 while negative and non-significant correlations were mostly detected for F_2 vs F_3 for most of the traits in cross I (Table 5). For cross II, F_2:F_3 correlations were nonsignificantly negative for all traits studied under drought stress and well-watered conditions as well. Similar trends were detected for pod yield, SCMR 60 DAS and SLA 60 DAS under water-stressed conditions. A positive and significant correlation was found for F_1 vs F_2 with the trait SCMR 80 DAS under well-watered conditions (Table 6).

DISCUSSION

Performance of traits

The ability to maintain dense chlorophyll under water deficit conditions is a drought resistance mechanism (van der Mescht et al., 1999; This et al., 2000; Arunyanark et al., 2008). Genotypic differences were found among lines and the chlorophyll content in the plants decreased as they reached their physiological maturity under water-stressed conditions. SCMR values at 60 DAS were 38.77 under water stress and 42.37 under well-watered conditions. Unlike SCMR at 60 DAS, the SCMR at 80 DAS of plants under stress and non–stress conditions were 35.87 and 41.10, respectively. Thus, genotypes tend to reduce their SLA from 60 DAS to 80 DAS and under drought conditions. SLA was decreased by drought stress and differed between genotypes. These findings were in agreement with the results of Liu and Stützel (2004) working on vegetable amaranth, Songsri et al. (2008) on groundnut, Zhang et al. (2015) on maize. Songsri et al. (2008) reported that groundnut genotypes having an ability to maintain higher SCMR and lower SLA under drought stress should be more tolerant to drought. This indicates that reduction in specific leaf area is a good indication of tolerance to drought and it is a water-saving mechanism where plants tend to reduce their transpiration by closing their stomata.

Parent-offspring regression, correlation and genetic advance

In the cross I, almost all the heritabilities values were low and were negative. Similar trends of negative heritability values via regression of F_1 vs F_2 and that of F_2 vs F_3 were

Table 6. Genetic advance, parent-offspring regression (with standard errors) and correlation of F_2 on F_1, and $F_{2:3}$ on bulked F_2 mean from Cross II evaluated under well-watered and water-stress conditions.

Trait	ENV[§]	Genetic advance (GA%)		Parent-offspring regression (*b*)		Parent-offspring correlation (*r*)	
		F_2	F_3	F_1:F_2	F_2:F_3	F_1:F_2	F_2:F_3
SCMRf	WW	0.50	0.24	0.08 ± 0.21	0.22 ± 0.09	0.04	0.13
	WS	1.19	3.18	-0.12 ± 0.17	-0.10 ± 0.06	-0.06	-0.08
SCMRz	WW	0.00	2.90	0.42 ± 0.11	-0.16 ± 0.10	0.58	-0.09
	WS	0.00	0.00	-0.08 ± 0.16	-0.24 ± 0.09	-0.05	-0.13
SLAf	WW	5.63	7.15	0.10 ± 0.21	0.14 ± 0.07	0.04	0.09
	WS	0.00	2.97	0.20 ± 0.20	0.22 ± 0.08	-0.09	-0.13
SLAz	WW	8.44	9.77	-0.40 ± 0.15	-0.20 ± 0.10	0.03	-0.11
	WS	5.16	3.69	0.22 ± 0.21	0.00 ± 0.11	0.10	0.00
PY	WW	21.75	23.64	0.14 ± 0.12	-0.12 ± 0.07	0.11	-0.09
	WS	0.00	9.21	-0.24 ± 0.21	-0.12 ± 0.04	-0.20	-0.14

[§] ENV = environments (Well-watered WW and water-stress WS). SCMRf, SCMRz, SLAf, SLAz and PY = SPAD chlorophyll meter reading at 60 DAS at 80DAS, specific leaf area (cm^2/g) at 60 DAS and at 80 DAS and pod yield (kg/ha). GA (%), *b*, and *r* are genetic advance, regression coefficient and correlation coefficient, respectively.

observed under both drought stress and well-watered conditions in cross II. This result was in agreement with the findings of Ntare (1999) who reported non-significant F_2:F_3 regression for pod yield and physiological components such as dry matter, crop growth rate and the length of the reproductive period in groundnut. However, among the two crosses or populations, several valuable regression coefficients were detected with highest heritability estimates in F_1:F_2 were 42% for SCMR 60 DAS and at 80 DAS under well-watered conditions, 20% for SLA at 60 DAS and at 80 DAS under drought stressed conditions. The highest heritability estimates in F_2: F_3 progenies were observed for SCMR 60 DAS (22%) under well-watered conditions and SLA 60 DAS (22%) under water-stressed conditions. These results probably involved additive genes for the SLA and SCMR traits. For both crosses, higher standard error values were obtained from parent-offspring heritability estimates, often higher than the regression coefficients. Some (2012) have had similar high value of standard errors of heritability in a study of F_1 orange-flesh sweet potatoes and he concluded that this revealed unexplained factors which were important and prevented a better understanding of the inheritance. Intergeneration coefficients were not significant and they were lower for SCMR and SLA for F_1 vs F_2 while negative and non-significant correlations were mostly detected in F_2 vs F_3 for almost all the traits in cross I. For cross II, F_2:F_3 correlations were negative and non-significant for all traits studied under drought stress and well-watered conditions as well. Similar trends were detected for pod yield, SCMR 60 DAS and SLA 60 DAS under water-stressed conditions. A positive and significant correlation was found for F_1 vs F_2 with the trait SCMR 80 DAS under well-watered conditions. These results were in agreement with conclusions reached by other researchers (Halward et al., 1990; Ntare, 1999) who reported low and non-significant correlations between yields of F_2: F_3 and F_3 and F_4 bulk populations in groundnut. They concluded that selection of pod yields in early generation could be delayed to later generations. Genetic Advance (GA) is a more reliable index for understanding the effectiveness of selection in improving the traits because the estimates are obtained from the product of heritability, phenotypic standard deviation and intensity of selection (Patil et al., 2015). It is therefore a drawing force in selection, which measures the importance of the genes that passed from parent to offspring. The observation of negative values from the variances biases the results of the estimates of heritabilities and genetic advance. This makes it difficult for the prediction. Except for the high genetic advance for SLA 80 DAS (83.75%) under both well-watered and water-stressed conditions, genetic advance for the two crosses were low to moderate irrespective of the generation and environment under study. The GA was low for SLA 80 DAS under water-stressed conditions (8.75%) in F_1. This result is in accordance with results of Vishnuvardhan et al. (2012) who reported GA of 2.58% in genetic variability studies for yield attributes and resistance to foliar diseases in groundnut. Shukla and Rai (2014) reported low GA for pod yield (7.18%) and pod yield per plant (5.18%) in evaluating groundnut genotypes for yield and quality traits. Nath and Alam (2002) reported GA of 16.37% in groundnut.

In the two experiments, twenty individual populations were used at F_1 while forty five individual populations were used in F_2 and F_3. Conclusions were then drawn based on one year evaluation with a small number of segregating populations in two replications. Walker (2012) stated that variance, heritability, and genetic correlations are often estimated in a single study and then considered representative of a population, and this is valid, to the extent that the population represented remains the one of interest. He concluded that if any of these parameters are estimated in a study of one set of genetic material, their application to another genetic material may be questionable depending upon the differences between them. Moreover, Conner and Hartl (2004) reported that twenty families should be considered an absolute minimum, and fifty or more is necessary for reasonable statistical power in quantitative genetic experiments of any design. These authors stated that the number of families that reflect the variance is of prime importance to the power of the analysis. They concluded that a finding of no significant additive variance with less than 50 families should be interpreted with caution, because the lack of significance could easily be due to a lack of statistical power rather than a real lack of variance. For low narrow-sense heritability, Resende et al. (2013) proposed an application of combined selection method such as selection indices. In plant breeding, flexible models or methods are available to help the breeder for selecting promising genotypes. Likewise, Cooper et al. (2013) suggested that because of the low estimates of heritability in yield trait in wheat, indirect selection could be more effective.

Conclusion

Parent-offspring regression for the two populations evaluated under well-watered and water-stress conditions were low to moderate and revealed importance of non-genetic effects. Parent-offspring correlations were also low and mostly showed negative and non-significant coefficients for traits studied under drought stress and well-watered conditions as well as for each of the studied populations. Consequently, the genetic advances for the two crosses were mostly low to moderate irrespective of the generation and environment under study.

Based on the reference populations, progress in selection at early generation in groundnut could be slow for a complex trait like drought. We suggested indirect selection with indices based on pod yield and drought related traits under contrasting drought conditions to identify promising lines since the heritability estimates were low.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Anderson WF, Holbrook CC, Wynne JC (1991). Heritability and Early Generation Selection for Resistance to early and late leafspot in Peanut. Crop Science 31:588-593.

Arunyanark A, Jogloy S, Akkasaeng C, Vorasoot N, Kesmala T, Nageswara Rao RC, Wright GC, Patanothai A (2008). Chlorophyll stability is an indicator of drought tolerance in peanut. Journal of Agricultural and Crop Research 194(2):113-125.

Bernado R (2003). On the effectiveness of early generation selection in self-pollinated crops. Notes. Crop Science 43:1558-1559.

Conner JK, Hartl DL (2004). Quantitative Genetics - Genetic Variation. In: A Primer of Ecological Genetics. (6th Eds. Sunderland Mass Sinauer Associates) 240 p.

Cooper JK, Ibrahim AMH, Rudd J, Hays D, Malla S, Baker J (2013). Increasing Hard Winter Wheat Yield Potential via Synthetic Hexaploid Wheat II. Heritability and combining ability of yield and its components. Crop Science 53:67-73.

Dudley JW, Moll RH (1969). Interpretation and use of estimates of heritability and genetic variances in plant breeding. Crop Science 9:257-261.

Falconer DS, Mackay TF (1996). Introduction to Quantitative Genetics. 4th Ed Benjamin Cummings UK.

Gusmini G, Wehner TC (2007). Heritability and Genetic Variance Estimates for Fruit Weight in Watermelon. HortScience 42(6):1332-1336.

Halward TM, Wynne JC, Monteverde-Penso EJ (1990). The effectiveness of early generation testing as applied to a recurrent selection program in peanut. Peanut Science 17:44-47.

Holland JB, Nyquist WE, Cervantes-Martinez CT (2003). Estimating and Interpreting Heritability for Plant Breeding: An update. Plant breeding Reviews Wiley and Sons 22:9-20.

Ibrahim AMH, Quick JS (2001). Genetic control of high temperature tolerance in wheat as measured by membrane thermal stability. Crop Science 44:1405-1407.

Liu F, Stützel H (2004). Biomass partitioning specific leaf area and water use efficiency of vegetable amaranth (*Amaranthus* spp.) in response to drought stress. Scientia Horticulturae 102(1):15-27.

Nageswara Rao RC, Talwar HS, Wright GC (2001). Rapid assessment of specific leaf area and leaf N in peanut (*Arachis hypogaea* L.) using chlorophyll meter. Journal of Agronomy and Crop Science 189:175-182.

Nath UK, Alam MS (2002). Genetic variability heritability and genetic advance of yield and related traits of groudnut. Journal of Biological Sciences 2(11):762-764.

Ntare BR (1999). Early generation testing for yield and physiological components in groundnut (*Arachis hypogaea* L.). Euphytica 107(2):141-147.

Patil S, Shivanna S, Irappa B, Shweta M (2015). Genetic Variability and Character Association Studies for Yield and Yield Attributing Components in Groundnut (*Arachis Hypogaea* L.). International Journal of Recent Scientific Research 6(6):4568-4570.

Patterson HD, Williams ER, Hunter EA (1978). Block designs for variety trials. The Journal of Agricultural Science 90:395-400.

Resende RMS, Casler MD, Vilela de Resende MD (2013). Selection Methods in Forage Breeding- A Quantitative Appraisal. Crop Science 53:1925-1936.

SAS Institute (2009). SAS Proprietary Software Release 9.3. SAS Institute Inc. Cary NC.

Shukla AK, Rai PK (2014). Evaluation of groundnut genotypes for yield and quality traits. Annals of Plant and Soil Research 16(1):41-44.

Smith JD, Kinman ML (1965). The use of parent-offspring regression as an estimator of heritability. Crop Science 5:595-596.

Some K (2012). Genetic improvement of sweetpotato (*Ipomoea batatas* [L.] lam) for beta-carotene and yield in Burkina Faso. PhD thesis University of Ghana Accra.

Songsri P, Jogloy S, Kesmala T, Vorasoot N, Akkasaeng C, Patanothai A, Holbrook CC (2008). Heritability of Drought Resistance Traits and Correlation of Drought Resistance and Agronomic Traits in Peanut. Crop Science 48:2245-2253.

Stansfield WD (1986). Theory and Problems of Genetics. McGraw- Hill New York.

Sumathi R, Ramanathan MVC (1995). Genetic variability in intraspecific cross of *Arachis hypogaea* L. Karnataka Journal of Agricultural Sciences 8:50-55.

This DC, Borries C, Souyris I, Teulat B (2000). QTL study of chlorophyll content as a genetic parameter of drought tolerance in barley. Barley Genetics Newsletter 30:2023.

Upadhyaya HD (2005). Variability for Drought Resistance Related Traits in the Mini Core Collection of Peanut. Crop Science 45:1432-1440.

Upadhyaya HD, Sharma S, Singh S, Singh M (2011). Inheritance of drought resistance related traits in two crosses of groundnut (*Arachis hypogaea* L.). Euphytica 177:55-66.

Van Der Mescht A, De Ronde JA, Rossouw FT (1999). Chlorophyll fluorescence and chlorophyll content as a measure of drought tolerance in potato. South African Journal of Science 95:407-412.

Vishnuvardhan KM, Vasanthi R, Prasad Reddy KH, Bhaskar Reddy BV (2012). Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut *(Arachis hypogaea* L.). International Journal of Applied Biology and Pharmaceutical Technology 3(1):390-394.

Walker CA (2012). Statistical Applications in Plant Breeding and Genetics. PhD thesis Washington State University Washington DC. USA.

Zhang C, Zhang J, Zhang H (2015). Mechanisms for the relationships between water-use efficiency and carbon isotope composition and specific leaf area of maize (*Zea mays* L.) under water stress. Plant Growth Regulation 77(2):233-243.

Zongo A, Nana AT, Sawadogo M, Konate AK, Sankara P, Ntare BR, Desmae H (2017). Variability and Correlations among Groundnut Populations for Early Leaf Spot, Pod Yield, and Agronomic Traits. Agronomy 7:52.