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Assessment of genetic variability among groundnut accessions under natural rosette disease infestation in Malawi

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ABSTRACT

Groundnut production in East and South African region is low due to several constraints. Success in development of resilient varieties rides on genetic diversity in available germplasm for key traits in question. This study was undertaken to dissect the magnitude of variability among groundnut accessions. The experimental design was an alpha lattice design replicated thrice. Significant differences in yield traits were observed among the accessions. There was high phenotypic (PCV) and genotypic (GCV) coefficient of variation in most of the traits except for the number of primary branches and shelling percentage. A combination of high heritability and genetic advance was recorded for the number of secondary branches, height, seed yield and rosette incidence. This indicates that it is possible to carry out phenotypic selection based on the mean for successful improvement of yield and resistance to rosette disease.

Keywords: Genetic advance, genetic variation, groundnut, heritability, rosette disease

RÉSUMÉ

La production d'arachide dans les régions d'Afrique orientale et australe est faible en raison de plusieurs contraintes. Le succès dans le développement de variétés résilientes repose sur la diversité génétique du matériel génétique disponible pour les caractères clés en question. Cette étude a été entreprise pour comprendre l'ampleur de la variabilité entre les souches d'arachide. Le plan expérimental était un bloc complet aléatoire répété trois fois. Des différences significatives des caractéristiques de rendement ont été observées entre souches. Il y avait un coefficient de variation phénotypique et génotypique élevé dans la plupart des caractères, à l'exception du nombre de branches primaires et du pourcentage de décorticage. Une combinaison d'héritabilité élevée et de progrès génétique a été enregistrée pour le nombre de branches secondaires, la hauteur, le rendement en graines et l'incidence des rosettes. Cela indique qu'il est possible d'effectuer une sélection phénotypique basée sur la moyenne pour une amélioration réussie du rendement et de la résistance à la maladie de la rosette.

Mots-clés: Arachide, variation génétique, héritabilité, progrès génétique, maladie de la rosette

INTRODUCTION

Groundnut is a self-pollinated crop grown worldwide in the tropics mainly for its high-quality oil and for various uses as food (Maiti, 2002; Singh and Nigam, 2016). The kernels

contain 47-53% of edible oil, 24-36% of vegetable protein, 10-15% of carbohydrates, and are a good source of minerals, vitamins and fibre (Nautiyal *et al.*, 2002; Talawar, 2004). Groundnut is an important crop in terms of

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value and quantity in Malawi, predominantly grown by smallholder farmers under low-input production system (Longwe-Ngwira *et al.*, 2012). However, there has been fluctuations in groundnut production and yields stand at an average of 759.77 kg ha⁻¹, compared to yield of 2000-4000 kg ha⁻¹ in major producing countries (Singh and Nigam, 2016).

Several factors constraint groundnut production in Malawi. These includes abiotic and biotic stresses, socioeconomic factors, climatic factors and edaphic factors (Minde *et al.*, 2008; Prasad *et al.*, 2010; Chala *et al.*, 2014; Chikowo *et al.*, 2015). Amongst the most important biotic constraints is groundnut rosette disease (GRD), a viral disease responsible for devastating losses of up to 100% in susceptible cultivars (Minde *et al.*, 2008; Anitha *et al.*, 2014).

Generation of high yielding resilient varieties with market preferred traits is a priority for addressing groundnut yield gap. Genetic variability acts as a basis for development of such improved cultivars upon which selection thrives (Acquaah, 2009; Govindaraj *et al.*, 2015). The knowledge of how variable a population of interest is, enables the construction and planning of an ideal genotype (Singh, 2001; Zaman *et al.*, 2011). The variability of key traits has to be heritable (Holland *et al.*, 2003). Genotypic and phenotypic variation and genetic advance have been reported for several traits in groundnut (Korat *et al.*, 2009; Zaman *et al.*, 2011; Rao *et al.*, 2014; Yusuf *et al.*, 2017). The coefficients of variation provide a basis to compare diversity of quantitative traits while high heritability and genetic advance suggest possibility of effective phenotypic selection (Holland *et al.*, 2003; Acquaah, 2009; You *et al.*, 2016). These parameters indicate the genetic potential of a given germplasm that dictates the success in breeding programmes (Shrestha, 2016). The objective of this study was to assess the level of variability among groundnut accessions for

yield under natural GRD infestation.

MATERIALS AND METHODS

Plant materials. Initial evaluation was done with a total of one hundred and eighty-nine (189) groundnut test material and three (3) local popular checks in year 2008/2009 season (Table 1). Twenty-five (25) groundnut accessions and the same two (2) resistant checks and one susceptible popular check (Table 2) were used in the second season (2017/2018) of evaluation. Cultivars CG7 and JL 24 (susceptible to GRD), and ICGV-SM 99568 and ICGV-SM 90704 (resistant to GRD) that are popular released varieties in Malawi, were used as local checks.

Experimental site. The accessions were evaluated at Chitedze Agricultural Research Station (33° 38' E and 13° 85' S), from December 2008 to May 2009 for the larger set of materials; and from February to June 2018 for the subset. The station is located 16 km west of Lilongwe (Malawi) with an altitude of 1146 meters above sea level (masl). The accessions were evaluated under natural GRD infestation, since the station is a hotspot area with high GRD pressure during the growing season. The temperature ranges between 16° C and 24° C with a mean annual rainfall of 892 mm.

Experimental design and management. The larger set (2008/2009) and sub-set (2018/2019) experiments were laid in a 16 x 12 and 7 x 4 alpha lattice design in a randomized complete block design with three replications each. Spreader rows of genotype JL24 that is highly susceptible to GRD were sown around the trials to enhance GRD inoculum build-up. The plot size was 3 rows of 3 m long, with row and between plants spacing of 0.6 m and 0.15 m, respectively. The field was kept free of weeds by hand weeding which was done thrice. Harvesting and shelling were done manually.

Data collection. Data were recorded on GRD

Table 1. List of groundnut genotypes evaluated in the 2008/2009 cropping season

Entry	Genotype	Remark
1	ICG14705	Accession
2	ICG13099	Accession
3	ICG6888	Accession
4	ICG12988	Accession
5	ICG5475	Accession
6	ICG115	Accession
7	ICG4598	Accession
8	ICG8760	Accession
9	ICG2106	Accession
10	ICG10036	Accession
11	ICG5327	Accession
12	ICG6813	Accession
13	ICG297	Accession
14	ICG36	Accession
15	ICG13858	Accession
16	ICG11088	Accession
17	ICG14106	Accession
18	ICG3240	Accession
19	ICG9905	Accession
20	ICG12625	Accession
21	ICG12672	Accession
22	ICG15042	Accession
23	ICG3992	Accession
24	ICG5221	Accession
25	ICG3053	Accession
26	ICG332	Accession
27	ICG3027	Accession
28	ICG14127	Accession
29	ICG3584	Accession
30	ICG6375	Accession
31	ICG11862	Accession
32	ICG6646	Accession
33	ICG14475	Accession
34	ICG15419	Accession
35	ICG9418	Accession
36	ICG4527	Accession
37	ICG9315	Accession
38	ICG397	Accession
39	ICG4750	Accession
40	ICG1711	Accession
41	ICG4998	Accession
42	ICG2772	Accession
43	ICG5286	Accession
44	ICG3681	Accession
45	ICG2381	Accession
46	ICG928	Accession
47	ICGV-SM95741	Accession
48	ICG11322	Accession

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49	ICG8285	Accession
50	ICG7906	Accession
51	ICG721	Accession
52	ICG6201	Accession
53	ICG2019	Accession
54	ICG1142	Accession
55	ICG5609	Accession
56	ICG11651	Accession
57	ICG12000	Accession
58	ICG8567	Accession
59	ICG1668	Accession
60	ICG12370	Accession
61	ICG10092	Accession
62	ICG4670	Accession
63	ICG188	Accession
64	ICG11426	Accession
65	ICG2738	Accession
66	ICG15190	Accession
67	ICG11515	Accession
68	ICG111	Accession
69	ICG6892	Accession
70	ICG7963	Accession
71	ICG12921	Accession
72	ICG12276	Accession
73	ICG6703	Accession
74	ICG13787	Accession
75	ICG163	Accession
76	ICG13941	Accession
77	ICG7190	Accession
78	ICG5662	Accession
79	ICG1415	Accession
80	ICG13856	Accession
81	ICG13942	Accession
82	ICG6263	Accession
83	ICG8517	Accession
84	ICG8490	Accession
85	ICG442	Accession
86	ICG9249	Accession
87	ICG9666	Accession
88	ICG11457	Accession
89	ICG11855	Accession
90	ICG3102	Accession
91	ICG15309	Accession
92	ICG3421	Accession
93	ICG9507	Accession
94	ICG6407	Accession
95	ICG6913	Accession
96	ICG1519	Accession
97	ICG9842	Accession
98	ICG13603	Accession
99	ICG5891	Accession

100	ICG5016	Accession
101	ICG12189	Accession
102	ICG513	Accession
103	ICG3746	Accession
104	ICG7969	Accession
105	ICG2777	Accession
106	ICG7181	Accession
107	ICG532	Accession
108	ICG10566	Accession
109	ICG14482	Accession
110	ICG11249	Accession
111	ICG6654	Accession
112	ICG12879	Accession
113	ICG81	Accession
114	ICG4543	Accession
115	ICG4538	Accession
116	ICG2773	Accession
117	ICG6667	Accession
118	ICG3775	Accession
119	ICG10185	Accession
120	ICG9961	Accession
121	ICG11144	Accession
122	ICG5745	Accession
123	ICG14118	Accession
124	ICG4684	Accession
125	ICG7000	Accession
126	ICG10479	Accession
127	ICG14630	Accession
128	ICG4955	Accession
129	ICG7153	Accession
130	ICG9809	Accession
131	ICG14523	Accession
132	ICG14008	Accession
133	ICG9037	Accession
134	ICG4412	Accession
135	ICG14985	Accession
136	ICG5494	Accession
137	ICG1274	Accession
138	ICG13491	Accession
139	ICG2511	Accession
140	ICG9777	Accession
141	ICG156	Accession
142	ICG10474	Accession
143	ICG4343	Accession
144	ICG434	Accession
145	ICG334	Accession
146	ICG5827	Accession
147	ICG5195	Accession
148	ICG4911	Accession
149	ICG10554	Accession
150	ICG4156	Accession

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151	ICG1137	Accession
152	ICG14710	Accession
153	ICG8106	Accession
154	ICG4729	Accession
155	ICG4389	Accession
156	ICG11687	Accession
157	ICG14466	Accession
158	ICG12682	Accession
159	ICG3673	Accession
160	ICG1973	Accession
161	ICG118	Accession
162	ICG5236	Accession
163	ICG11219	Accession
164	ICG5779	Accession
165	ICG2925	Accession
166	ICG8083	Accession
167	ICG76	Accession
168	ICG13982	Accession
169	ICG7243	Accession
170	ICG1399	Accession
171	ICG6766	Accession
172	ICG862	Accession
173	ICG6057	Accession
174	ICG4746	Accession
175	ICG12697	Accession
176	ICG9157	Accession
177	ICG875	Accession
178	ICG11109	Accession
179	ICG3343	Accession
180	ICG6402	Accession
181	ICG13723	Accession
182	ICG10384	Accession
183	ICG6993	Accession
184	ICG5663	Accession
185	ICG2857	Accession
186	ICG10890	Accession
187	ICG6022	Accession
188	ICG15287	Accession
189	ICG5051	Accession
190	JL 24	Local variety check
191	ICGV-SM 90704	Improved variety check
192	ICG 12991	Local variety check

Table 2. List of groundnut genotypes identified from the 2008/2009 season and evaluated in the 2017/2018 study

Entry number	Accession	Origin
1	CG 7 (local check)	Malawi
2	ICG 10384	Nigeria
3	ICG 11249	Tanzania
4	ICG 11426	India
5	ICG 11651	China
6	ICG 12509	Unknown
7	ICG 12672	Bolivia
8	ICG 12697	India
9	ICG 12921	Zimbabwe
10	ICG 12988	India
11	ICG 13942	Unknown
12	ICG 13982	USA
13	ICG 14985	Unknown
14	ICG 15405	Unknown
15	ICG 2106	India
16	ICG 334	China
17	ICG 3584	India
18	ICG 3681	USA
19	ICG 405	Unknown
20	ICG 4955	India
21	ICG 5745	Puerto Rico
22	ICG 6022	Unknown
23	ICG 6057	USA
24	ICG 6813	Senegal
25	ICG 9507	Philippines
26	ICG 9809	Mozambique
27	ICGV-SM 90704 (control)	Malawi
28	ICGV-SM 99568 (control)	Malawi

disease incidence (%) and grain yield in the two seasons of evaluation, 2008/2009 and 2017/2018. Visual observations on growth characteristics were further applied in selection of genotypes to include in the 2017/2018 evaluation. Additional data that were recorded for the sub-set experiment conducted in 2017/2019 included number of branches, height, days to flowering and maturity, plant height, number of pods, pod width, pod length, 100 seed weight and shelling percentage. Disease data scoring were based on the method by Waliyar *et al.* (2007), while yield and agronomic traits were recorded as described by IBPGR and ICRISAT (1992). Groundnut rosette disease (GRD) development

was recorded visually at 60, 80 and 100 days after sowing, and the average after analysis was presented in the results. The number of plants showing GRD symptoms in each plot was determined by counting and disease incidence was expressed as a percentage of the infected to the total number of plants (Waliyar *et al.*, 2007). Severity was recorded using a 1 to 5 rating scale, where: 1 = no symptoms, 2 = symptoms on 1 to 20% foliage but no stunting, 3 = symptoms on 21 to 50% foliage and stunting, 4 = severe symptoms on 51 to 70% foliage and stunting, and 5 = severe symptoms on 71 to 100% foliage, stunting and dead plants (Waliyar *et al.*, 2007). Severity scores were transformed by $\ln(x+1)$

before analysis in order to have residual terms following normal distribution (Gomez and Gomez, 1984).

Time to flowering and maturity were determined as the number of days between sowing date and when 50% of plants in a plot flowered and matured, respectively. Plant height (PH), and number of primary (NPB) and secondary branches (NSB) were recorded at 85 days after planting. Plant height was taken using a ruler at harvest.

Yield and yield components. Pods per plant (NPP) were recorded at harvest by counting the mature pods on five plants and a mean determined for each plot. Pod length (PL) and pod width (PW) were measured on 10 pods randomly chosen, at the lengthiest and widest points, respectively. The pods were sun dried to 8-10% moisture content and weighed to determine pod yield per plot. A pod sample of 100 g was randomly drawn from each plot was shelled and seed weight was expressed as a percentage of the pod weight before shelling to get shelling percentage (SP). Hundred seeds were counted and weighed to get hundred seed weight (HSW) in grams.

Data analysis. Analysis of variance (ANOVA) was done using Genstat 18th Edition (Payne, 2014), following the tests of Shapiro-Wilk and Bartlett for residual normality and variance homogeneity, respectively.

Variance components. Genotypic, environmental and phenotypic variances were estimated, using the mean square values, which were equated to their respective expectations (Singh *et al.*, 1993). The estimates of the variance components of each trait were computed as follows:

$$\sigma_e^2 = MS_E$$

Where: σ_e^2 is the environmental variance and MSE is the residual mean square

$$\sigma_g^2 = \frac{MSG - MS_E}{r}$$

Where: σ_g^2 is the genotypic variance, MSG=genotypic mean square, and MSE =residual mean square and r= number of replications.

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where: σ_p^2 is the phenotypic variance, σ_g^2 genotypic variance; σ_e^2 =environmental variances.

Genotypic, phenotypic and environmental coefficients of variation. These were determined based on Johnson *et al.* (1955) as indicated below:

$$GCV (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} * 100$$

Where: GCV=genotypic coefficient of variation, σ_g^2 =genotypic variance and \bar{X} = overall mean.

$$PCV (\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} * 100$$

Where: PCV=phenotypic coefficient of variation, σ_p^2 =phenotypic variance and \bar{X} = overall mean.

$$ECV (\%) = \frac{\sqrt{\sigma_e^2}}{\bar{X}} * 100$$

Where: ECV=environmental coefficient of variation, σ_e^2 =environmental variance and \bar{X} =overall mean.

These different coefficients of variation were classified according to Sivasubramanian and Menon (1973) as: low (0-10%), moderate (11-20%), and high (21% and above).

Heritability and genetic advance. Broad-sense heritability was determined following the method by Falconer and Mackay (1996):

$$H^2 (\%) = \frac{\sigma_g^2}{\sigma_p^2} * 100$$

Where: H^2 is the broad-sense heritability, σ_g^2 and σ_p^2 are genetic and phenotypic variances, respectively.

The heritability values were classified as indicated by Singh (2001), to be low (<40%), moderate (41-60%), moderately high (61-79%) and very high (80% and above). Genetic advance was determined according to Acquaah (2009) using the formula:

$$GA = k * H^2 * \sigma_p$$

Where: GA is the genetic advance, $k = 1.4$

corresponding to 20% of selection pressure, H^2 = broad sense heritability and σ_p =square root of phenotypic variance. The genetic advance as percentage of the mean, was derived as indicated below

$$GAM (\%) = \frac{GA}{\bar{X}} * 100$$

Where: GA=genetic advance; \bar{X} =overall mean. GAM was classified as being low (<10%), moderate (11-20%) and high (>20%) (Johnson *et al.*, 1955).

Table 3. Means of yield and GRD incidence of 189 groundnut genotypes evaluated under artificial GRD inoculation in 2008/2009 growing season

Genotype	Grain yield (kg/ha)	GRD incidence (%)	Response classification
ICG10036	89.80	41.05	RE
ICG10092	71.60	65.45	MRE
ICG10185	123.70	87.04	SS
ICG10384	152.70	97.37	SS
ICG10474	138.70	81.48	SS
ICG10479	10.90	90.28	SS
ICG10554	102.90	94.23	SS
ICG10566	322.10	71.38	MRE
ICG10890	62.50	100.00	SS
ICG11088	282.20	50.00	RE
ICG111	118.40	69.57	MRE
ICG11109	191.10	98.15	SS
ICG11144	111.40	85.42	SS
ICG11219	91.60	93.05	SS
ICG11249	286.90	71.93	MRE
ICG11322	293.10	57.08	RE
ICG1137	106.00	88.86	SS
ICG1142	100.40	69.16	MRE
ICG11426	243.60	66.05	MRE
ICG11457	102.70	76.79	MRE
ICG115	235.60	26.12	RE
ICG11515	188.80	57.97	RE
ICG11651	403.40	50.08	RE
ICG11687	128.50	91.67	SS
ICG118	268.50	94.23	SS
ICG11855	179.80	76.80	MRE
ICG11862	105.20	56.74	RE
ICG12000	22.20	67.58	MRE
ICG12189	228.00	75.00	MRE
ICG12276	113.20	77.43	MRE

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ICG12370	97.40	75.00	MRE
ICG12625	229.50	51.71	RE
ICG12672	152.80	50.55	RE
ICG12682	70.40	95.45	SS
ICG12697	272.60	92.00	SS
ICG1274	111.70	91.67	SS
ICG12879	193.80	85.12	SS
ICG12921	236.40	76.79	MRE
ICG12988	593.00	10.32	RE
ICG13099	358.60	0.00	RE
ICG13491	106.00	91.67	SS
ICG13603	228.20	83.00	SS
ICG13723	161.10	100.00	SS
ICG13787	226.30	41.05	RE
ICG13856	209.20	79.33	MRE
ICG13858	321.30	53.54	RE
ICG13941	270.30	63.46	MRE
ICG13942	136.60	77.78	MRE
ICG13982	148.90	98.55	SS
ICG1399	153.00	82.88	SS
ICG14008	239.70	74.17	MRE
ICG14106	330.10	54.00	RE
ICG14118	115.50	75.83	MRE
ICG14127	215.10	47.72	RE
ICG1415	112.10	81.21	SS
ICG14466	101.00	85.00	SS
ICG14475	48.40	64.00	MRE
ICG14482	59.20	81.04	SS
ICG14523	240.60	81.48	SS
ICG14630	89.30	76.43	MRE
ICG14705	382.30	0.00	RE
ICG14710	111.40	89.29	SS
ICG14985	163.10	98.45	SS
ICG15042	207.20	54.46	RE
ICG1519	236.40	76.34	MR
ICG15190	128.90	60.11	MRE
ICG15287	10.80	100.00	SS
ICG15309	85.90	77.98	MRE
ICG15419	114.20	64.57	MRE
ICG156	176.50	90.00	SS
ICG163	175.50	80.52	SS
ICG1668	138.40	60.42	MR
ICG1711	204.90	66.73	MRE
ICG188	147.40	73.81	MRE
ICG1973	194.30	65.00	MRE
ICG2019	244.70	73.43	MRE
ICG2106	370.70	32.81	RE
ICG2381	174.50	67.56	MR
ICG2511	92.60	91.67	SS
ICG2738	65.30	65.27	MRE
ICG2772	102.60	55.08	RE

ICG2773	135.40	86.23	SS
ICG2777	223.80	86.08	SS
ICG2857	81.30	100.00	SS
ICG2925	238.40	89.29	SS
ICG297 2	74.80	46.26	RE
ICG3027	83.80	54.09	RE
ICG3053	56.50	55.49	RE
ICG3102	152.20	80.96	SS
ICG3240	318.80	54.13	RE
ICG332	203.50	56.70	RE
ICG334	136.70	86.36	SS
ICG3343	147.40	90.74	SS
ICG3421	268.60	81.49	SS
ICG3584	366.60	63.19	MRE
ICG36	219.00	45.50	RE
ICG3673	127.30	95.65	SS
ICG3681	256.70	63.46	MRE
ICG3746	85.90	82.14	SS
ICG3775	137.80	88.74	SS
ICG397	250.70	64.44	MRE
ICG3992	190.50	26.79	RE
ICG4156	197.30	92.38	SS
ICG434	189.50	93.08	SS
ICG4343	180.20	92.86	SS
ICG4389	56.80	94.83	SS
ICG4412	193.80	73.75	MRE
ICG442	85.20	82.37	SS
ICG4527	108.80	57.53	RE
ICG4538	110.20	66.15	MRE
ICG4543	186.30	77.38	MRE
ICG4598	69.00	29.29	RE
ICG4670	124.60	70.05	MRE
ICG4684	75.30	87.82	SS
ICG4729	166.00	94.83	SS
ICG4746	20.50	90.09	SS
ICG4750	144.20	63.89	MRE
ICG4911	198.90	92.31	SS
ICG4955	222.30	85.71	SS
ICG4998	150.80	59.08	RE
ICG5016	137.20	75.08	MRE
ICG5051	0.00	100.00	SS
ICG513	98.60	80.95	SS
ICG5195	88.60	93.75	SS
ICG5221	107.60	54.14	RE
ICG5236	192.60	96.15	SS
ICG5286	139.50	57.68	RE
ICG532	124.60	80.30	SS
ICG5327	129.50	38.26	RE
ICG5475	548.70	15.62	RE
ICG5494	220.30	91.49	SS
ICG5609	253.90	63.24	MRE

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ICG5662	130.70	77.39	MRE
ICG5663	88.80	100.00	SS
ICG5745	73.80	89.63	SS
ICG5779	174.70	86.28	SS
ICG5827	111.20	78.06	MRE
ICG5891	93.00	63.46	MRE
ICG6022	25.80	100.00	SS
ICG6057	44.70	81.25	SS
ICG6201	224.80	67.89	MRE
ICG6263	294.80	79.83	MRE
ICG6375	24.20	63.75	MRE
ICG6402	141.70	98.86	SS
ICG6407	221.10	73.93	MRE
ICG6646	67.20	58.36	RE
ICG6654	239.30	76.32	MRE
ICG6667	0.00	71.15	MRE
ICG6703	100.90	78.00	MRE
ICG6766	10.90	95.00	SS
ICG6813	272.90	0.00	RE
ICG6813	124.90	44.84	RE
ICG6892	115.40	74.11	MRE
ICG6913	8.20	66.93	MRE
ICG6993	92.10	100.00	SS
ICG7000	172.50	88.21	SS
ICG7153	118.90	80.67	SS
ICG7181	207.50	75.00	MRE
ICG7190	192.20	78.03	MRE
ICG721	279.30	70.69	MRE
ICG7243	33.70	89.66	SS
ICG76	79.80	94.64	SS
ICG7906	82.20	75.00	MRE
ICG7963	99.30	63.54	MRE
ICG7969	187.00	77.34	MRE
ICG8083	90.70	94.64	SS
ICG81	113.80	93.75	SS
ICG8106	60.90	94.64	SS
ICG8285	140.00	71.41	MRE
ICG8490	155.90	70.15	MRE
ICG8517	321.40	66.72	MRE
ICG8567	160.20	75.00	MRE
ICG862	60.00	97.92	SS
ICG875	124.50	80.77	SS
ICG8760	169.20	38.89	RE
ICG9037	56.60	81.82	SS
ICG9157	86.10	98.00	SS
ICG9249	222.30	74.62	MRE
ICG928	205.50	68.33	MRE
ICG9315	59.80	68.43	MRE
ICG9418	206.70	53.13	RE
ICG9507	405.20	69.64	MRE
ICG9666	60.20	82.50	SS
ICG9777	43.50	92.00	SS

ICG9809	112.40	80.98	SS
ICG9842	93.20	76.52	MRE
ICG9905	125.50	50.77	RE
ICG9961	161.40	85.28	SS
ICGV-SM95741	75.70	65.83	RE
Controls			
JL 24	241.80	88.53	SS
ICGV-SM 90704	503.70	0.00	RE
ICG 12991	262.80	0.00	RE
Grand mean	162.3	73.1	
P.Value	<.001	<.001	
SED	68.94	15.78	
L.S.D	192.31	44.02	

*LSD-least significant difference, SED-standard error of differences, GRD-groundnut rosette disease, RE-resistant (0-60%), MRE-moderately resistant (61-80%), SS-susceptible (>80%).

RESULTS

Disease incidence. The results from the 2008/2009 experiment showed that there were significant ($P < 0.05$) differences in rosette disease incidence and yield among the genotypes (Table 3). These were key traits linked to progress, that were used in further selection of genotypes for the validation experiment conducted in 2017/2018. Out of the 189 genotypes evaluated, 40 were resistant, 67 were moderately resistant and 82 were susceptible (Table 3). The mean values of disease incidence (PDI) ranged from 0% to 100% with an average of 72.8%. The most resistant were ICG13099, ICG14705, ICG6813 was in ICG 12988 and the two resistant checks (ICGV-SM 90704 and ICG 12991). The susceptible check JL24 had a PDI of 88.5%.

Significant ($P < 0.001$) differences were observed among the accessions for all traits in the 2017/2018 evaluation of the selected genotypes, except for primary branches and shelling percentage (Table 4). Symptoms for GRD appeared early in the susceptible genotypes, which developed progressively from leaf chlorosis to severe stunting and bushy appearance due to shortened internodes. Disease development in resistant and moderately resistant genotypes was slow. Out of the 28 genotypes evaluated, two were highly resistant and three were susceptible (Table 3).

The mean values of final disease incidence (PDI) ranged from 4.09% to 69.18% with an average of 31.64%. The lowest PDI value was in ICG 12988, followed by the resistant check- ICGV-SM 99568 (7.84%) and ICG 11249 (10.20%) which was resistant. The highest PDI value was recorded for accession ICG 12509. The susceptible check CG7 had a PDI of 40.17%.

Agronomic traits. There was significant ($P < 0.01$) variation in agronomic traits among the assessed genotypes (Table 5). Accessions ICG 12697, ICG 12988, ICG 9507, ICG 2106 and ICG 4955, flowered early (30 days on average), while ICG 13982, ICG 11426 and ICG 6057 had late flowering (42 days on average (Table 6).

The mean days to maturity was 127 with the earliest maturing accessions being ICG 12697 and ICG 10384 which took 116 days, while the late maturing were ICG 6057 and ICG 6813 at 138 DAS. The three high yielding accessions matured between 118 and 125 days. In terms of plant height, ICG 6813 (46.8 mm) and ICG 3681 (137.6 mm) were the shortest accessions while ICG 12988 (316.7 mm) and ICGV-SM 99568 (344.7 mm), which recorded the highest seed yield, were the tallest genotypes. The number of branches varied with mean values of 4 and 7 branches per plant, respectively. ICG 12509, ICG 3584 and ICG 14985 produced the

lowest number of primary branches (three), while the controls CG7 and ICGV-SM 90704, and accession ICG 6813 produced the highest number (five). The number of secondary branches was as low as two (ICG 15045 and ICG 3681) and as high as 15 (ICGV-SM 90704).

Yield and its components. There were significant ($P < 0.01$) differences in yield and related traits among the evaluated accessions (Table 3; Table 6). The grain yield in 2008/2009

ranged between 10.9 kg/ha (ICG 10479) and 593 kg/ha (ICG 12988) with a mean yield of 162.3 kg/ha (Table 3); whereas in 2017/2018, it ranged from 53.60 kg/ha (ICG 12509) and 1046.40 kg/ha (ICG 12988) with a mean of 303.11 kg/ha (Table 7). The high yielding accession (ICG 12988) out yielded all the checks and was the best performer in the two seasons, while ICG 4955 and ICG 33 out yielded CG7 only in the 2017/2018 evaluation. The other checks namely ICGV-SM 99568 and

Table 4. Means of agronomic traits and GRD incidence of 28 groundnut genotypes evaluated

Genotype	Days to flowering	Days to maturity	Number of primary branches	Number of secondary branches	Plant height(mm)	GRD Incidence (%)	Response classification
ICG 10384	32	116	4	4	216.2	45.88	MRE
ICG 11249	33	117	4	3	250.7	10.20	RE
ICG 11426	42	137	4	8	184.7	36.92	MRE
ICG 11651	32	121	4	4	199.1	55.58	SS
ICG 12509	40	137	3	9	143.6	69.18	SS
ICG 12672	41	135	4	9	193.6	29.30	RE
ICG 12697	30	116	4	3	207.9	18.30	RE
ICG 12921	33	122	4	6	250.0	16.87	RE
ICG 12988	30	119	4	3	316.7	4.09	HRE
ICG 13942	40	136	4	13	160.5	37.11	MRE
ICG 13982	43	130	4	6	177.5	68.18	SS
ICG 14985	37	120	3	6	179.6	38.66	MRE
ICG 15405	33	126	4	2	206.4	23.46	RE
ICG 2106	31	118	4	5	188.9	25.37	RE
ICG 334	33	125	4	4	273.3	23.08	RE
ICG 3584	33	122	3	4	195.3	46.93	MRE
ICG 3681	33	119	4	2	137.6	35.15	MRE
ICG 405	38	126	4	10	250.3	36.99	MRE
ICG 4955	31	118	4	5	255.0	18.96	RE
ICG 5745	37	136	4	10	165.0	37.64	MR
ICG 6022	36	130	4	6	238.4	26.69	RE
ICG 6057	42	138	5	14	197.6	20.99	RE
ICG 6813	40	138	5	14	46.8	35.88	MRE
ICG 9507	30	124	4	4	216.1	32.06	MRE
ICG 9809	33	120	4	3	204.8	23.58	RE
Standard checks							
CG7	38	137	5	13	176.9	40.17	MRE
ICGV-SM 90704	41	137	5	15	182.7	20.81	RE
ICGV-SM 99568	37	122	4	4	344.7	7.84	HRE
Mean	36	127	4	7	205.7	31.64	
LSD (5%)	2.25	4.97	0.86	2.21	53.99	8.31	
SED	1.12	2.47	0.43	1.10	26.81	4.13	
CV (%)	3.84	2.39	13.09	19.89	15.96	15.98	
R-Square (%)	94.45	93.01	73.00	94.35	84.90	94.82	

*LSD-least significant difference, SED-standard error of differences, CV-coefficient of variation; GRD-groundnut rosette disease, HRE-highly resistant, RE-resistant, MRE-moderately resistant, SS-susceptible

ICGV-SM 90704 were among the top five high yielding genotypes. ICG 12509, ICG 10479, ICG 368 and ICG 3584 were among the lowest yielding accessions. The number of pods per plant varied from 3 to 24. Accessions ICG 3681 and ICG 12509 produced the lowest number of pods while ICG 12988 and the check, ICGV-SM 99568 recorded the highest number. The check-CG7 produced an average of 9 pods per plant while ICGV-SM 90704 produced 15. The mean value for hundred seed weight was 35.58 g with genotypes varying from 23.78 (ICG 3584) to 48.90 g (ICG 5745). Pod length had a mean value of 27.26 mm, with accessions ICG 12697 (20.00 mm) and ICG 6022 (48.25 mm) producing the shortest and longest pods, respectively. A mean value of 12.07 mm was observed for pod width, with genotypes varying from 9.08 mm (ICG 9809) to 15.83 mm (ICG 13942). ICG 9809 and ICG 12697 were among the accessions with the smallest pods while ICG 13942 and ICG 6022 were among the accessions

with the largest pods. Genotypes varied from 57.87% (ICG 12509) to 75.70% (ICG 4955) for shelling percentage and a mean of 67.00% was observed.

Variance components derived from the analysis. Summary of components of variance and coefficients of variation is presented in Table 6. All the traits had higher genotypic and phenotypic variances than environmental variance estimates. There was high phenotypic coefficient of variation (PCV) compared to the genotypic (GCV) and environmental coefficients of variation (ECV) (Table 6). The GCV ranged from 5.19% for shelling percentage to 70.70% for seed yield, while PCV varied from 6.17% for maturity period to 73.58% for yield. The ECV for time to maturity span through 2.39% to 20.50% for grain yield. Days to maturity and shelling percentage recorded low values of GCV and PCV ranging between 5.19% and 9.41%, while number of primary branches had

Table 5. Mean squares for agronomic traits of 28 groundnut genotypes evaluated under natural GRD infestation

Source of Variation	DF	DTF	DTM	NPB	NSB	PH
Rep	2	0.16ns	75.87***	0.05ns	0.96ns	3960.31*
Bloc	9	12.83***	97.63***	1.58***	16.97***	2645.20**
Gen	27	49.25***	164.78***	0.70**	44.55***	8924.50***
Residual	45	1.87	9.15	0.27	1.81	1078.00

Significant levels: ns, *, **, ***-non-significant differences, significant differences at 5%, 1% and 0.1%, respectively; Rep-replication, Bloc-block, Gen-Genotype, DF- degree of freedom; DTF-days to flowering, DTM-days to maturity, NPB-number of primary branches, NSB-number of secondary branches, PH-plant height

Table 6. Mean squares for yield traits of 28 groundnut genotypes evaluated under natural GRD infestation

Source of Variation	DF	NPP	PW	PL	SYD	SYDP	SP	HSW	PDI
Rep	2	23.46*	1.85ns	12.65ns	9415.41ns	2.89**	2.44ns	11.89ns	25.33ns
Bloc	9	12.95*	7.88***	56.36***	3546.94***	1.58**	75.78*	56.48***	129.50***
Gen	27	86.86***	7.70***	89.39***	141575.23***	11.29***	63.92**	158.94***	734.50***
Residual	45	5.00	0.78	4.88	3823.00	0.53	27.70	11.38	25.55

Significant levels: ns, *, **, ***-non-significant differences, significant differences at 5%, 1% and 0.1%, respectively; Rep-replication, Bloc-block, Gen-Genotype, DF- degree of freedom, NPP-number of pods per plant, PW-pod width, PL-pod length, SYD-seed yield, SYDP-seed yield per plant, SP-shelling percentage, HSW-hundred seed weight, PDI-final rosette incidence

low GCV (9.45%) and moderate PCV (16.14%). Duration to 50 flowering and pod width had moderate GCV and PCV of 11.16% and 14.55% respectively. High GCV and PCV ranging between 24.86% and 73.58% were recorded for height, disease incidence, secondary branches, pods per plant and grain seed yield.

Heritability and genetic advance. The broad sense heritability and genetic advance ranged from 30.36 to 92.31% and 4.00 to 95.09%, respectively. The shelling percentage and primary branches had low heritability of 30.36%

and 34.26% respectively, while that of pod width (74.72%) and height (70.80%) were moderate. Days to maturity and flowering, hundred seed weight, pods per plant, pod length, percentage of disease incidence and yield had highest broad-sense heritability estimates, ranging between 81.21% and 92.31%. Genetic advance ranged from 0.31 for number of primary branches to 288.24 for seed yield. The genetic advance as percentage of the mean (GAM) was lowest for shelling percentage (4%) and highest for yield (95.09%).

Table 7. Means of yield and traits of 28 groundnut genotypes evaluated under natural GRD infestation

Genotype	Number of pods	Pod width (mm)	Pod length (mm)	Grain yield (kg ha ⁻¹)	Shelling percentage (%)	100 seed weight (g)
ICG 10384	10	11.42	22.75	196.00	70.04	30.33
ICG 11249	19	10.28	23.25	338.60	60.63	28.13
ICG 11426	7	13.33	28.92	166.40	67.47	40.03
ICG 11651	8	11.67	24.17	208.60	67.17	33.25
ICG 12509	3	13.00	24.08	53.60	57.87	35.40
ICG 12672	8	13.92	30.92	234.80	58.62	40.17
ICG 12697	16	9.75	20.00	339.70	71.90	31.61
ICG 12921	8	11.12	22.83	274.10	68.39	38.10
ICG 12988	24	9.83	21.75	1046.40	72.11	30.78
ICG 13942	9	15.83	33.33	230.60	70.72	48.27
ICG 13982	6	11.08	26.25	136.50	74.28	29.70
ICG 14985	9	13.25	27.58	196.80	60.59	36.25
ICG 15405	7	13.53	34.25	176.50	71.78	31.37
ICG 2106	16	10.25	22.17	339.40	67.01	28.25
ICG 334	12	10.67	24.83	403.70	68.66	32.65
ICG 3584	9	10.08	20.42	100.10	65.98	23.78
ICG 3681	3	10.85	30.42	58.10	62.80	27.08
ICG 405	8	12.20	31.25	164.40	59.17	32.75
ICG 4955	16	11.17	21.83	419.80	75.70	31.22
ICG 5745	10	13.08	31.08	310.00	71.30	48.90
ICG 6022	5	15.17	48.25	171.40	61.70	46.33
ICG 6057	9	14.67	31.92	271.30	62.78	45.06
ICG 6813	15	10.75	24.33	272.10	68.09	26.65
ICG 9507	12	12.00	24.25	369.00	72.02	37.18
ICG 9809	12	9.08	22.00	252.40	68.09	28.26
Controls						
CG7	9	14.58	31.33	351.30	71.02	48.26
ICGV-SM 90704	15	12.67	31.75	429.40	63.40	38.20
ICGV-SM 99568	24	12.75	27.50	976.00	66.62	48.33
Mean	11	12.07	27.26	303.11	67.00	35.58
LSD (5%)	3.68	1.45	3.63	101.70	8.66	5.55
SED	1.83	0.72	1.80	50.49	4.30	2.75
CV (%)	20.25	7.32	8.10	20.40	7.86	9.48
R-Square (%)	91.18	88.95	93.06	96.01	65.94	90.40

Table 8. Variance components and coefficients of variation for quantitative traits under study

Trait	Variance components estimates			Coefficients of variation		
	σ_g^2	σ_e^2	σ_p^2	GCV (%)	ECV (%)	PCV (%)
Days to flowering	15.79	1.87	17.66	11.16	3.84	11.80
Days to maturity	51.88	9.15	61.02	5.69	2.39	6.17
Number of primary branches	0.14	0.27	0.42	9.45	13.09	16.14
Number of secondary branches	14.25	1.81	16.06	55.87	19.89	59.31
Plant height	2615.23	1078.81	3694.04	24.86	15.97	29.55
Number of pods/plant	27.29	5.00	32.28	47.32	20.25	51.47
Pod width	2.31	0.78	3.09	12.58	7.32	14.55
Pod length	28.17	4.88	33.05	19.47	8.10	21.09
Grain yield	45917.41	3823.00	49740.41	70.70	20.40	73.58
Shelling percentage	12.07	27.70	39.77	5.19	7.86	9.41
100 seed weight	49.19	11.38	60.57	19.71	9.48	21.87
GRD incidence	236.32	25.55	261.87	48.59	15.98	51.15

σ_g^2 -genotypic variances, σ_e^2 environmental variance, and σ_p^2 - phenotypic variances, respectively; GCV, ECV and PCV are the genotypic, environmental and phenotypic coefficients of variation ;GRD- groundnut rosette disease

Table 9. Genetic components for the yield and traits for the genotypes evaluated

Trait	Broad sense heritability (H ²)	Genetic (%) advance (GA)	Genetic advance as percentage of mean (GAM) (%)
Days to flowering	89.40	5.26	14.77
Days to maturity	85.01	9.30	7.35
Number of primary branches	34.26	0.31	7.74
Number of secondary branches	88.75	4.98	73.69
Plant height	70.80	60.24	29.28
Number of pods per plant	84.53	6.72	60.91
Pod width	74.72	1.84	15.22
Pod length	85.23	6.86	25.16
Seed yield	92.31	288.24	95.09
Seed yield per plant	87.09	2.47	76.40
Shelling percentage	30.36	2.68	4.00
Hundred seed weight	81.21	8.85	24.87
Percentage of disease incidence	90.24	20.44	64.62

DISCUSSION

Performance of the groundnut accessions evaluated. The groundnut rosette disease (GRD) was pronounced thus providing a genetic discrimination among the groundnut accessions. The disease incidence was relatively high in the 2008/2009 season with wide variation compared to the 2017/2018 season. This can be attributed to the prevailing weather conditions that were conducive for the vector and disease development during this particular season. The long dry spell which occurred after planting coupled with border rows of the susceptible genotype in both seasons allowed optimal development of the disease. This is in agreement with reports indicating that weather conditions, particularly rainfall, influence GRD development and dry spell favour aphid population growth, leading to high disease incidences (Naidu *et al.*, 1999; Dwivedi *et al.*, 2003; Waliyar *et al.*, 2007). The susceptible accessions manifested the disease symptoms rapidly from chlorosis in some branches to stunting and bushy appearance. Similar results were reported for susceptible genotypes in previous studies (Subrahmanyam *et al.*, 1991; Subrahmanyam *et al.*, 1997; Bua and Opio, 2014). Disease development was slow or none in resistant accessions with mild symptoms in only few or parts of branches.

Ideal genotypes should combine good levels of disease resistance, desired agronomic traits and high yielding capacity to qualify as being adapted or elite. Accordingly, this led to knocking out some of the genotypes after the 2008/2009 cropping season, to conform to the breeding principles of narrowing down to elite parents that would translate to higher genetic gain and progress in breeding. An example of such desirable and ideal genotypes was accession ICG 12988 which out yielded all the controls and recorded the lowest disease incidence, followed by ICG 4955 and ICG 334, which yielded relatively low but demonstrated good levels of resistance. The control ICGV-SM 99568, which

combines GRD resistance, drought tolerance and high yielding ability was also an example of such superior genotypes. Most of the susceptible accessions produced few grains, indicating that the disease affected the yield. The effect of GRD on grain yield could be explained by the reported negative correlations between GRD incidence and pod yield (Van der Merwe *et al.*, 2001; Muitia, 2011; Chintu, 2013). Additionally, this is in line with Thresh (2003) and Panguluri and Kumar (2016) who indicated that GRD affects the yield significantly in susceptible genotypes. Such yield reduction is due to reduction of leaf size and internodes, fewer pod number of which most of them do not produce kernels, and reduced grain weight. Accession ICG 12988 proved to be resistant and high yielding under both natural and artificial infestation in previous studies, agreeing with the current study (Van der Merwe and Subrahmanyam, 1997; Kapewa and Chiyembekeza, 2002; Chintu, 2013). The controls ICGV-SM 99568 and ICGV-SM 90704 had also been reported to be GRD resistant (Waliyar *et al.*, 2007; Monyo *et al.*, 2007; Chattopadhyay *et al.*, 2015). This indicates that this accession and the two controls have stable GRD resistance and can be used to develop resistant varieties.

Genetic components for yield and traits for the genotypes evaluated. The environmental influence on traits is depicted by the phenotypic coefficient of variation that was high in most of the traits as opposed to the genotypic coefficient of variation. Zaman *et al.* (2011) and Yusuf *et al.* (2017) reported smaller differences between PCV and GCV, and this corroborates to the findings of this study. Pod and grain yield, height and GRD incidence had high GCV and PCV values, an indication of high degree of genetic and phenotypic variability from which selection can be applied. Such high variation for these traits have also been reported earlier (Korat *et al.*, 2009; Zaman *et al.*, 2011; Rao *et al.*, 2014; Yusuf *et al.*, 2017). This was as opposed to

shelling percentage and duration to maturity that had low GCV and PCV, an indication of narrow variability and a restricted scope of selection. Similar findings were reported by Maurya *et al.* (2014), and Balaraju and Kenchanagoudar (2016) for shelling percentage, and John *et al.* (2012) and Patil *et al.* (2015) for maturity period. The highest environmental influence on the phenotype was observed for pod and grain yields. This phenomenon may be due to the polygenic nature of these traits as supported by Behera (2007) and Acquaah (2009), who also reported high environmental influence for yield traits.

Heritability is a measure of the proportion of phenotypic variance associated with gene effects and its estimates would be more meaningful and useful in trait prediction selection (Acquaah, 2009). Pod yield, grain yield, height and GRD incidence had high broad-sense heritability and genetic advance. Such combinations indicate existence of additive gene action and the possibility of effective selection for these traits. High heritability alone indicates high correlation between genotype and phenotype, and low environmental contribution to the phenotype (Holland *et al.*, 2003; Acquaah, 2009; You *et al.*, 2016). These combinations have been reported in similar studies by Yusuf *et al.* (2017) for height, Rao *et al.* (2014) and Rathod and Toprope (2018) for number of pods, Zaman *et al.* (2011) and Narasimhulu *et al.* (2012) for hundred seed weight, Khan *et al.* (2000) and Yusuf *et al.* (2017) for grain yield, and Alhassan (2013) for GRD incidence. Contrary to this study, low heritability estimates were reported for grain yield (John *et al.*, 2012; Rathod and Toprope, 2018). Differences in heritability values among the studies could be due to use of different genotypes and/or environment.

High heritability and moderate genetic advance was evident for days to flowering and pod width. Similar findings were reported by John

et al. (2012) and Patil *et al.* (2014). The latter were low for number of primary branches and shelling percentage, an indication of the low genetic potential. These results corroborate with those of Korat *et al.* (2009), Parameshwarappa *et al.* (2010) and Rao *et al.* (2014).

CONCLUSIONS

The results from this study revealed the presence of wide genetic variability among the evaluated accessions which can be exploited in groundnut breeding. High genetic variance components were observed for yield related traits and GRD incidence, indicating the possibility for effective selection of these traits. The low genetic potential for primary branches and shelling percentage indicate that selection for the two traits is limited.

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STATEMENT OF NO CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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