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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 (330 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 |

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|---|---|---|
| 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: $\sigma_e^2$ is the environmental variance and MSE is the residual mean square

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

Where: $\sigma_g^2$ 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: $\sigma_p^2$ is the phenotypic variance, $\sigma_g^2$ genotypic variance; $\sigma_e^2$ =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, $\sigma_g^2$ =genotypic variance and $\bar{\mathbf{X}}$= overall mean.

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

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

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

Where: ECV=environmental coefficient of variation, $\sigma_e^2$ =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, $\sigma_g^2$ and $\sigma_p^2$ 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 $\sigma_p$ =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 (2>1%) (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 |

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|---|---|---|---|
| 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 |

| | | | |
|---|---|---|---|
| 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 | | |
|---|---|---|---|---|---|---|
| | $\sigma_g^2$ | $\sigma_e^2$ | $\sigma_p^2$ | 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 |

$\sigma_g^2$ -genotypic variances, $\sigma_e^2$ environmental variance, and $\sigma_p^2$ - 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 ICVG-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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