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# Genetic Diversity and Root Characters of Yield Components of Some Selected Groundnut (Rachis Hypogeal L.) Genotypes under Irrigated Condition, Gezira State, Sudan.

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***Abstract:*** *Fifty groundnut genotypes and three checks were evaluated in augmented design with five blocks at the Gezira Research Station Farm. It is located at latitude 14$^{O}$, 24$^{'}$ N, longitude 33$^{O}$, 29$^{'}$ E and 407 m above sea level. Agricultural Research Corporation (ARC), Sudan during 2016 to study variability in root characters and genetic diversity under selection pressure. There is a lack of information on root traits for groundnut genotypes and the relationship between rooting traits and groundnut yield under terminal drought. From the result found variability between shoot dry weight, root dry weight, root shoot ratio, shoot length, root length and root volume. Genetic divergences in 50% flowering, plant height, number of branches per plant, number of pods per plant, number of double seeded pods per plant, number of single seeded pods per plant, pods yield per plant, kernels weight per plant, hundred seed weight, shelling percentage, hay weight, total plant weight, harvest index and pods yield per hectare divided the genotypes according to similarity.*

***Keywords:*** *Groundnut, Drought, root traits, Variability, Cluster , Kiriz, , Gezira, Sudan.*

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## I. Introduction

Groundnut or peanut (*Arachis hypogaea* L.) belongs to the family Leguminosae. It is a highly self-pollinated crop and appears to be originated in Brazil. It is one of the most wide–spread and important food legumes in the world. The total annual world production is about 25 million tons of unshelled nuts, 70% of which is contributed by India, China and U.S.A. (Haj Hussein, 2004). Peanut is an important source of plant oil and protein worldwide. The oil content in peanut seeds ranges from 45–60% and protein ranges from 22–35% in different varieties (Nalini and Rajeev, 2014).

Groundnut is an allotetrapoloid (2n=4x=40), which originated through the hybridization of two diploid species with distinct genomes (*A. duranensis* the AA genomes donor and *A. ipaensis* the BB donor) giving rise to a sterile hybrid. A spontaneous duplication of the chromosomes restored fertility which formed the tetraploid species *A. monticola* and gave rise to the cultivated peanut but left the plant reproductively isolated from its wild relations (Anthony, 2014).

The groundnut production is concentrated in Asia and Africa (56% and 40% of the global area and 68% and 25% of the global production, respectively). India, China, and the United States have been the leading producers for over 25 years and grow about 70% of the world crop. Other important producers are Nigeria, Senegal, Sudan and Argentina (Abu Assar *et al*., 2016).

The Sudan average national area in 2014/15 of groundnut was 1.3 million hectare. The rain-fed cropped area of groundnut was 93% compared to 7% for the irrigated sector, while, in 2015/16 the average national area was 2.2 million hectare. The average national production of groundnut in 2014/15 was 0.96 million metric tons and 1.9 million metric tons in 2015/16. The rain fed sector production is 1.1 million metric tons which constitutes about 77 % of the total groundnut production in the Sudan (FAO STAT 2015). The average yield of groundnut in Sudan was 0.77 ton/hectare in 2014/15. The average yield in the irrigated sector was 1.8 ton/hectare which is more than two times the yield of the rain-fed sector while, and in season 2015/16 was 0.86 ton/hectare (FAO STAT 2015).

Groundnut breeding program in the Sudan focus on development of high yielding, early maturing, and spreading bunch types adapted to the irrigated Vertisols, development of early maturing, drought tolerant cultivars for the rain-fed sandy soils of western Sudan, selection of large-seeded Virginia types for production

in northern Sudan, development of genotypes with tolerance to infection by *Aspergillus flavus*, and development and release of genotypes with high oil content and high kernel yield. (Haj Hussein, 2004).

The objective of the study was to evaluate 50 groundnut genotypes for root variability, and genetic diversity to provide information that might be useful for groundnut breeding program.

## II. Materials and Methods

The experimental material consisted of 50 introduced and locally developed genotypes and three checks (Kiriz, Tozi and Alahmadi). The experiment was conducted for one season in the summer of 2015 at Gezira Research Station Farm (GRSF) and Greenhouse 2016 Wad Medani, Sudan. The experiment was laid in an augmented design consisting of five block, the three checks were replicated in each block in the plot size was one row of 7 m long. The greenhouse experiment was arranged in randomized complete block design with three replications. Observations on seven characters were recorded on randomly selected five plants from each genotype. The data were subjected to different statistical analysis *viz.*, analysis of variance, magnitude of genetic variability and genetic diversity were performed following the standard procedures.

## III. Results and Discussion

The analysis of variance results of 14 characters of fifty groundnut genotypes and three checks are presented in it. There are significant differences among genotypes in number of pods/plant, number of double seeded pods/plant, pods yield/plant hay weight/plant, total plant weight and pod yield/ha while days to 50% flowering, plant height, number of branches/plant, number of single seeded pods/plant, kernel weight/plant, 100-seed weight, shelling out-turn % and harvest index had shown no significant differences.

The mean squares for shoot dry weight, root dry weight, root shoot ratio, shoot length, root length and root volume showed highly significant differences among the genotypes. Root systems are important plant parts for taking up water and nutrients from the soil and to communicate with shoots to maintain integrated overall plant growth and health. Jogloy, *et al*., (2010) reported significant differences for shoot dry weight, root dry weight, root-to-shoot ratio, root length and root volume of 12 peanut genotypes. Also Jogloy, *et al*., (2014) studied drought conditions and found significant differences for root dry weight, root length and root volume under two water regimes of 11 genotypes. Similar results were reported by Thakur *et al*., (2015) for twenty five groundnut genotypes. The best genotypes for shoot dry weight ICGV 93104 (4.9g), Root dry weight C109A-7-4-B-4-3-B-B-B (1.5g), Root shoot ratio C109A-80-2-12-1-B (39.6%), root length ICGV88373 (41.3cm) and root volume ICGV-92167 (3.8ml).

Morphological clustering refers to grouping of the genotypes according to their similarities in the morphological traits. In the dendrograms the genotypes were grouped into six main groups based on 75% similarity in 50% flowering, plant height, number of branches per plant, number of pods per plant, number of double seeded pods per plant, number of single seeded pods per plant, pods yield per plant, kernels weight per plant, hundred seed weight, shelling percentage, hay weight, total plant weight, harvest index and pods yield per hectare (A, B, C, D, E and F). Most of the genotypes were in group B (22) followed by 10 genotypes in A, 9 genotypes in C, 5 genotypes in F, 4 genotypes in D and 3 genotypes in E. The distribution of the genotypes in the subgroups divided to nine groups based on 90% similarity the genotypes were aggregated in nine subgroups with 10 genotypes in group C, 9 genotypes in subgroup F, 7 in D, 6 genotypes in A, 5 genotypes in (E,I) , 4 genotypes in (B,G) and 3 genotypes in sub group H.

Armghan, *et al*., (2014) Based on morpho-physiological parameters groundnut genotypes were divided into eight groups. Babiker (2012) study the similarity in 200 accessions in pearl millet depends on morphological traits and found four groups. Zaman, *et al*.,(2010) study of the multivariate analysis of divergence, genotypes were grouped into five clusters in 34 genotypes. Sardar *et al*., (2017) also study genetic divergence in 36 genotypes and classified into 10 clusters.

The phenotype based dendrogram reflected extremely wide variations among the groundnut genotypes. For instance, at 100% similarity levels each genotype stood exclusively by itself reflecting that none of the genotypes had mutual phenotypic trait with any other. Genotypes within each group shared some phenotypic traits.

**Table 1. Mean, range, genetic and phenotypic variaces for 14 characters in 53 of groundnut genotypes.**

| | Character | Overall Mean | SE± | Prop. level | Range | Variance | |
|---|---|---|---|---|---|---|---|
| | | | | | | genotypic | phenotypic |
| 1 | Days to 50% flowering | 32.3 | 2.12 | ns | 29-36.6 | 4.067 | 15.3 |
| 2 | Plant height (cm) | 30.8 | 2.0 | ns | 21.8-40.8 | 1.266 | 11.28 |
| 3 | Number of branches/plant | 7.98 | 0.69 | ns | 5.1-10.4 | 0.642 | 1.84 |
| 4 | Number of pod/plant | 18.51 | 2.32 | * | 10.7-34.4 | 74.46 | 88.01 |
| 5 | Number of double pods/plant | 15.17 | 2.4 | * | 8.9-24.3 | 91.46 | 105.93 |
| 6 | Number of single seedpod/plant | 2.83 | 0.33 | ns | 1.6-4.4 | 0.867 | 1.15 |
| 7 | Pod yield/plant | 23.7 | 2.3 | * | 16.1-43.5 | 66.61 | 80.81 |
| 8 | Kernels weight /plant (g) | 12.91 | 1.3 | ns | 8.2-18.4 | 12.01 | 16.89 |
| 9 | 100-seed weight | 54.27 | 6.8 | ns | 32.7-84.7 | 31.26 | 148.44 |
| 10 | Shelling out-turn % | 55.71 | 6.2 | ns | 33.7-83.9 | 159.7 | 257.07 |
| 11 | Hay weight/plant (g) | 38.53 | 4.8 | * | 14.5-63.8 | 139.0 | 198.5 |
| 12 | Total plant weight (g) | 62.23 | 6.5 | * | 32.6-107.4 | 375.9 | 484.29 |
| 13 | Harvest index | 38.54 | 2.1 | ns | 23.6-50.4 | 16.0 | 27.16 |
| 14 | Pod yield/ha | 2991 | 315.7 | * | 1933-4257 | 306332 | 555567 |

**Table 2. Means and range for 6 root characters in 53 of groundnut genotypes.**

| | Character | Overall Mean | SE± | Prop. level | Range |
|---|---|---|---|---|---|
| 1 | Shoot length(cm) | 17.7 | 1.108 | ** | 14.3-21.8 |
| 2 | Root length(cm) | 27.22 | 3.245 | * | 2.0.0-41.3 |
| 3 | Shoot dry weight(g) | 3.9 | 0.40 | ** | 2.1-6.4 |
| 4 | Root dry weight(g) | 1.02 | 0.12 | ** | 0.7-1.5 |
| 5 | Root shoot ratio | 27.2 | 3.47 | ** | 19.3-39.6 |
| 6 | Root volume (ml) | 2.1 | 0.29 | ** | 1.3-3.8 |

**Table 3. Distribution in cluster one of 53 genotypes of groundnut grown at Gezira Research station in season 2015.**

| Cluster no. | No. of Genotypes | No. of Genotypes | Genotypes |
|---|---|---|---|
| A | 1,40,27,30,37,38,3,12,19,34 | 10) | C91-26 -2 -2, ICGV88222, C 153 A-SSD-46-1-1-1-B, ICGV-94204, ICGV-94222, C 153 A-SSD-1-1-1-B, C92-26 -2 -1,C109 A 61-1-1 -B-1-1-1-B-B-B, ICGV-92151, C 244-11-2-B |
| B | 2,42,35,36,47,51,28,41,46,52,5,23,39 ,53,7,49,24,14,17,45,29,44 | (22) | C92-26 -2 -1, ICGV88438, C 169-13-1-1-1-13, ICGV892018-F2-B-B-B-B-B, Seni-1,kiriz, ICGV-94216, ICGV88421, C 109 A-7-4-B-B,Tozi, ICGV-895039-F2-SSD-S-S-D, ICGV-93041, C 91-2-3-6-1-2-B,Ahmadi, C95 A – 1- 1- 2, Seni-2, ICGV-93057, C50-231-B-B-9-13, C109 A-7-4-B-4-3-B-B-B, C 109 A-80-2-12-1-B, ICGV-94217,C 228-B-B-B |
| C | 6,22,21,43,16,20,25,8,15 | (9) | ICGV-86229,ICGV-92930, ICGV-92173, ICGV88492, C109 A-63-2-B, ICGV-92167, ICGV-93104, ICGV- 86869,C153 A-SS-28-1-3-B |
| D | 9,10,11,13 | (4) | ICGV- 86347, C97B – 38 – 2 -1, C153 A – S – SD -50-1-1-13, C186-15-1-1-1-B |
| E | 4,50,18 | (3) | ICGV-88398, ICGV86229,ICGV88373 |
| F | 26,48,32,31,33 | (5) | ICGV-94198,ICGV-88424, ICGV89242-F2B2-B1-B1-B-B, C109 A-87-B-B,C 244-11-1-B |

**Table 4. Distribution in cluster two of 53 genotypes of groundnut grown at Gezira Research station in season 2015.**

| Cluster no. | Genotypes | No. of Genotypes | Genotypes |
|---|---|---|---|
| a | 1,40,27,30,37,38 | (6) | C91-26 -2 -2, ICGV88222, C 153 A-SSD-46-1-1-1-B, ICGV-94204, ICGV-94222, C 153 A-SSD-1-1-1-B |
| b | 3,12,19,34 | (4) | C31-4 -9 – 9 -2, C109 A 61-1-1 -B-1-1-1-B-B-B, ICGV-92151, C 244-11-2-B |
| c | 2,42,35,36,47,51,28,41,46,52 | (10) | C92-26 -2 -1,ICGV88438,C 169-13-1-1-1-13,ICGV892018-F2-B-B-B-B-B,Seni-1,Kiriz,ICGV-94216,ICGV88421,C 109 A-7-4-B-B,Tozi |
| d | 5,23,39,53,7,49,24 | (7) | ICGV-895039-F2-SSD-S-S-D,ICGV-93041, C 91-2-3-6-1-2-B,Ahmadi, C95 A – 1- 1- 2, Seni-2, ICGV-93057 |
| e | 14,17,45,29,44 | (5) | C50-231-B-B-9-13, C109 A-7-4-B-4-3-B-B-B, C 109 A-80-2-12-1-B, ICGV-94217, C 228-B-B-B |
| f | 6,22,21,43,16,20,25,8,15 | (9) | ICGV-86229, ICGV-92930, ICGV-92173, ICGV88492, C109 A-63-2-B, ICGV-92167, ICGV-93104, ICGV- 86869, C153 A-SS-28-1-3-B |
| g | 9,10,11,13 | (4) | ICGV- 86347, C97B – 38 – 2 -1, C153 A – S – SD -50-1-1-13, C186-15-1-1-1-B |
| h | 4,50,18 | (3) | ICGV-88398, ICGV86229,ICGV88373 |
| i | 26,48,32,31,33 | (5) | ICGV-94198,ICGV-88424,ICGV89242-F2B2-B1-B1-B-B, C109 A-87-B-B,C 244-11-1-B |

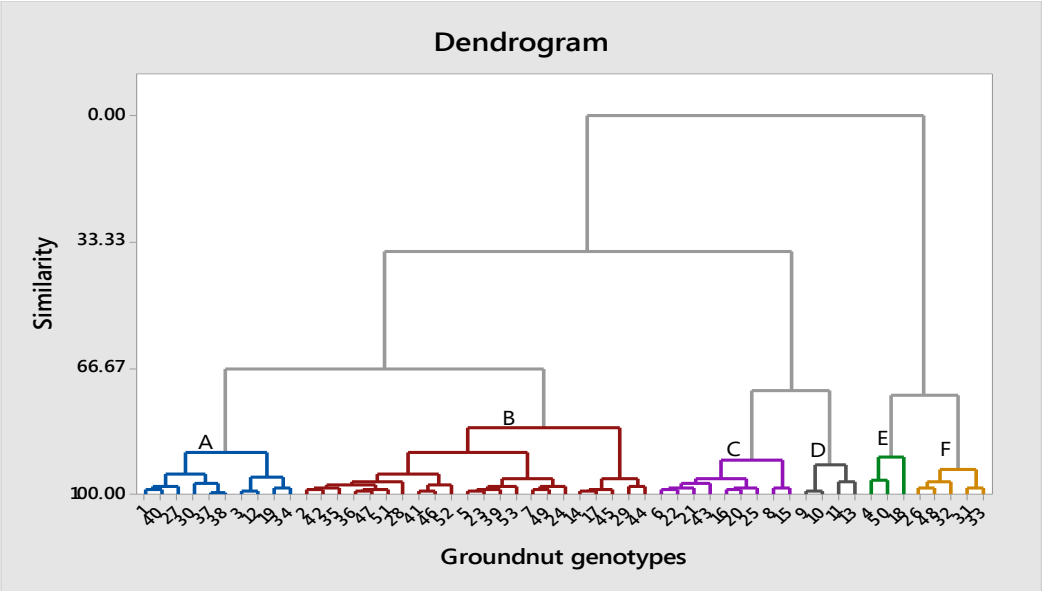


**Fig.(4.1) Dendrogram of phenotypic relationship among 53 genotypes of groundnut using 14 morphological traits in season 2015**

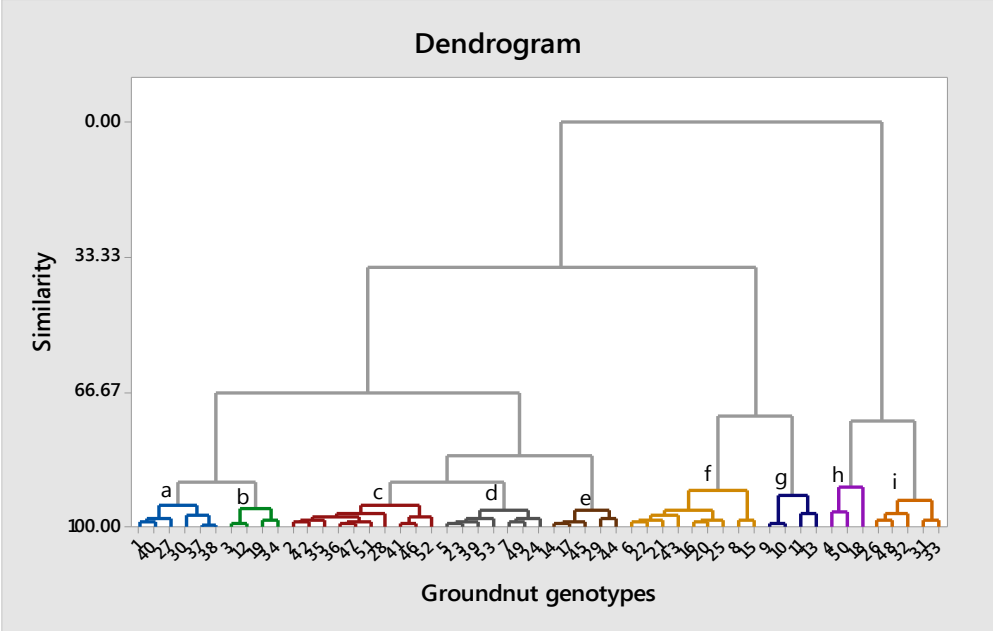


**Fig. (4.2) Dendrogram of phenotypic relationship among 53 genotypes of groundnut using 14 morphological traits in season 2015**

## Conclusions and recommendations

1- The results revealed high estimates of variance among the mean value of genotypes for all root characters studied.

2. genetic diversity throuth cluster group can help in increase diversity by cross between groups.

3. More inter–crossing between distanced parents are needed to create more genetic diversity for high pod yield and quality parameters.

4. Genotypes having large root system could maintain peanut yield under drought condition. Roots are one of the components among all other components which influence overall performance of peanut under terminal drought condition.

## IV. Recommendations

1. The genotypes ICGV-94216, ICGV-94204 and ICGV-88398 proved to be the best for pods yield per plant and number of double seeded pod per plant, these genotypes could be used in different breeding program and will be helpful to develop mapping populations for genetic study.
2. Further research is needed in this area to generate more useful information.

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