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# GENETIC DIVERGENCE ANALYSIS IN GROUNDNUT (*ARACHIS HYPOGAEA* L.) UNDER CALCAREOUS SOIL OF NORTHEN KARNATAKA

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**ABSTRACT**
Groundnut (*Arachis hypogaea* L.) is an important annual oilseed legume crop, valued as a rich source of proteins, minerals and vitamins. It is an unpredictable crop due to its underground pods development. For improvement of yield in groundnut direct selection is often misleading. The knowledge of existing variability is essential for developing high yielding genotypes in groundnut. An experiment was conducted with 43 gronudnut genotypes at college of agriculture, Vijayapura, UAS Dharwad, during *kharif,* 2013-14 to study the genetic diversity for IDC resistance related traits, yield and its component characters. The estimates of GCV and PCV were high for net plot yield (22.722 and 47.915) and low heritability with moderate GA as % mean was observed for net plot yield (22.5 and 22.197). The genotypes were highly diverse for IDC resistance and classified into 18 clusters. The diversity among the genotypes measured by intra-cluster & inter cluster distance in the present investigation was adequate for improvement of groundnut genotypes for IDC resistance by hybridization and selection. Seventeen clusters found to be solitary these can be used as promising parents for hybridization programme for obtaining high heterotic response for IDC resistance and thus better sergeants in groundnut.

## INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop grown worldwide on 25.41 mha with a production of 45.65 million tonnes. In India, groundnut (5.25 mha, 9.47 mt) is the second most important oilseed next to soybean (12.2 mha, 11.95 mt) (Faostat, 2013). Iron plays an important role in photosynthesis, respiration, nitrogen fixation, DNA synthesis, hormone production, chlorophyll formation and is also a component of various redox and iron-sulphur enzymes (Zheng, 2010). Iron deficiency chlorosis (IDC) is common world-wide among crops grown in calcareous, alkaline, coarse textured, eroded and low organic matter containing and cold region soils as iron is less available for uptake in these soils. Iron deficiency is a problem in most calcareous soils and they are widespread with an estimated 800 mha worldwide, mainly concentrated in areas with arid or Mediterranean climates (Land FAO and Plant Nutrition Management, 2000). High pH and bicarbonate ion concentration in calcareous soils leads to IDC by suppressing iron uptake and/or translocation in plants (Li-Xuan *et al.,* 2005).

In India, more than one-third of the soils are calcareous and spread mostly in the low rainfall areas of the western and central parts of the country, where groundnut is a major crop. Hence, IDC is more prevalent in the Saurashtra Region of Gujarat, Marathwada Region of Maharashtra and parts of Rajasthan, Tamil Nadu and Karnataka states in India causing considerable reduction in pod yield (16-32%) (Singh, 2001; Singh *et al.,* 1995). Acute iron deficiency leads to death of plants and complete crop failure. Soil application of 'Fe' as ferrous sulphate has often been recommended to alleviate the problem of iron chlorosis and also concomitant loss in yield (Irmak *et al.,* 2012). However, this is of little benefit to the crop as iron ionizes and gets converted into insoluble ferric ($Fe^{3+}$) compounds which are unavailable to plants. Foliar application of ferrous sulphate has been often suggested (Frenkel *et al.,* 2004), but the major problem is poor translocation of applied 'Fe' within the plant (Hüve *et al.,* 2003). Although foliar spray of chelated form provides 'Fe' in available form, their use is not popular and economically not feasible in the semi-arid tropics where groundnut is mainly grown as a rainfed subsistence crop. IDC response is usually assessed by visual chlorosis rating (VCR) and SPAD values in groundnut (Li and Yan-Xi 2007; Samdur *et al.,* 2000) and also other legumes like soybean, dry bean, etc. SPAD values are an indirect measurement of chlorophyll concentration based on the transmission of red light (at 650 nm) and infrared light (at 940 nm) through a leaf sample. Higher SPAD values indicate a lower incidence of leaf chlorosis. Higher VCR and lower SPAD values indicates susceptibility, while lower VCR and higher SPAD values indicates resistance to IDC.

In the present study, deals with assessment of genetic divergence for IDC resistance related traits, yield and its component characters in groundnut genotypes.

## MATERIALS AND METHODS

The experimental material for the present investigation

consisted of 43 genotypes of groundnut obtained from the International Crop Research Institute of Sami Arid Tropic, (Patancheru) Hyderabad, Telangana (India), BARC, Mumbai and UAS, Dharwad. The present experiment was conducted in randomized block design in three replication with two rows of each genotype in 40x10 spacing under calcareous soil, confirmed through lab analysis, at college of agriculture, Vijayapura during *kharif*, 2013-14. All the recommended agronomic cultural practices and plant protection measure were followed as and when required.

Observations were recorded on five randomly selected plants from each genotype in each replication for characters, SPAD chlorophyll meter reading at 30, 60 and 90 days after sowing on third fully opened leaf from top of the main stem, plant height (cm.), Number of primary branches per plant, number of pods per plant and post harvest observations like, biomass per plot (g), pod yield per plant (g), net plot yield (g), shelling %(g), 100 seed weight (g). Visual chlorotic rating score (using 1-5 scale, Singh and Chaudhari, 1993) was done on individual plant basis. Replication wise data for each character were subjected for analysis of variance, various genetic parameters were estimated and then multivariate analysis of $D^2$ statistic was done. The genotypes were grouped into different cluster following the tocher's method. The relative contributions of different characters towards genetic divergence were also worked out.

## RESULTS AND DISCUSSION

Large differences were observed between phenotypic coefficient of variation and genotypic coefficient of variations for all the traits under study indicating higher influence of environment on these traits. In the present investigation, the estimates of GCV and PCV were high for net plot yield (22.722 and 47.915) (Table 1). Moderate GCV and high PCV were observed in haulm yield (18.954 and 45.488) and yield per plant (18.495 and 41.738) indicating substantial variability and scope for improvement. Low heritability coupled with high genetic advance as percent of mean was recorded for net plot yield (22.5% and 22.197), indicates the predominance of additive gene action. The current conclusions are supported by Meena *et al.,* 2015, Mukesh *et al.,* 2016 and Vijaykumar *et al.,* 2016.

On the basis of magnitude of $D^2$ value, 43 genetically diverse genotypes were grouped into 18 clusters [Table 2]. The highest numbers of genotypes were presented in cluster I which contained 26 genotypes and rests of the clusters were solitary.

On considering cluster mean in respect of these eighteen clusters (Table 3), highest cluster mean value was recorded in cluster X for the net plot yield (164.50), in cluster VII highest cluster mean for shelling % (106.73), number of pods per plant (92.00), VCR_30 & 60 (3.00), in cluster XII highest cluster mean for yield per plant (8.48) and number of primaries (6.10), in cluster XVII highest cluster mean for SCMR_90 (43.70) and SCMR_30 (36.53)., highest cluster mean value for SCMR_60 (35.45) and plant height (18.40) in cluster IX, highest cluster mean for 100 seed weight (31.33) in cluster XVII.

The intra and inter cluster values are presented in Table 4. The highest intra-cluster distance was observed in case of

**Table 1: Estimates of variability parameters for different characters of Ground nut**

| Genetic Parameters | VCR 30 | VCR 60 | VCR 90 | SCMR 30 | SCMR 60 | SCMR 90 | Plant height (cm) | No. of primaries/ plant | No.pods per plant | Haulm yield/plot (g) | Yield / plant (g) | Net Plot Yield (g) | Shelling % | 100 seed weight (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ó2g | 0.056 | 0.040 | 0.118 | -0.067 | -5.983 | 12.829 | 2.037 | 0.141 | 1.510 | 3.033 | 0.833 | 56.670 | 20.971 | 2.278 |
| GCV | 11.367 | 8.722 | 15.534 | 1.031 | 8.599 | 11.940 | 11.446 | 7.983 | 13.047 | 18.954 | 18.495 | 22.722 | 7.941 | 6.256 |
| ó2p | 0.675 | 0.469 | 0.580 | 51.118 | 79.722 | 87.996 | 18.216 | 0.777 | 10.563 | 17.467 | 4.244 | 95.700 | 92.725 | 16.278 |
| PCV | 39.362 | 29.745 | 34.389 | 28.434 | 31.390 | 31.271 | 34.232 | 18.724 | 34.504 | 45.488 | 41.738 | 47.915 | 16.699 | 16.726 |
| $h^2$ (BS) | 08.300 | 08.600 | 20.400 | -0.100 | -7.500 | 14.600 | 11.200 | 18.200 | 14.300 | 17.400 | 19.600 | 22.500 | 22.600 | 14.000 |
| GA (5%) | 0.141 | 0.121 | 0.320 | -0.019 | -1.380 | 2.817 | 0.983 | 0.330 | 0.957 | 1.495 | 0.833 | 20.876 | 4.486 | 1.163 |
| GAM(5%) | 6.763 | 5.269 | 14.455 | -0.077 | -4.853 | 9.392 | 7.884 | 7.011 | 10.163 | 16.269 | 16.883 | 22.197 | 7.780 | 4.821 |
| GM | 2.087 | 2.302 | 2.215 | 25.145 | 28.445 | 29.998 | 12.468 | 4.708 | 9.419 | 9.188 | 4.935 | 94.048 | 57.666 | 24.122 |

Abbreviations: ó²g = Genotypic variation; GCV = Genotypic coefficient of variation; ó²p = Phenotypic variation; PCV = Phenotypic coefficient of variation; $h^2$ b.s = Heritability in broad sense; G.A = Genetic advance; GAM=Genetic Advance as % Mean; GM; General Mean; VCR 30= Visual Chlorotic Rating at 30 Days After Sowing; VCR 60= Visual Chlorotic Rating at 60 Days After Sowing; VCR 90= Visual Chlorotic at 90 Days After Sowing ; SCMR= SPAD chlorophyll Meter Reading at 30 Days after sowing; SCMR=SPAD chlorophyll Meter Reading at 60 Days after sowing and SCMR 90=SPAD chlorophyll Meter Reading at 90 Days after sowing.

**Table 2: Distribution of 43 Ground nut genotypes into different clusters**

| Cluster | No. of genotypes | Genotype |
|---|---|---|
| I | 26 | GPBD-4, GPBD-5, G-2-52, Dh-40, Dh-3-30, DGS-1, S-230, Dh-8, Dh-216, Dh-10, ICGV-06099, ICGV-06420, ICGV-05155, ICGV-06146, ICGV-87846, ICGV-93468, ICGV-86031, TG-37A, TG-51, TG-67, TG-68, TG-69, TG-72, JG (Thin shell), MG-8 (Dwarf) and R-9227 |
| II | 1 | A30b |
| III | 1 | ICGV-00350 |
| IV | 1 | ICGV-91114 |
| V | 1 | R-8808 |
| VI | 1 | TGLPS-3 |
| VII | 1 | TMV-2 |
| VIII | 1 | Dh-86 |
| IX | 1 | JSP-39 |
| X | 1 | JL-24 |
| XI | 1 | ICGV-02266 |
| XII | 1 | GBFDS-272 |
| XIII | 1 | ICGV-06040 |
| XIV | 1 | Mutant -III |
| XV | 1 | TAG-24 |
| XVI | 1 | TG-26 |
| XVII | 1 | Dh-2000-1 |
| XVIII | 1 | TG-38 |

**Table 3: Mean values of genotypes present in different clusters for different characters**

| Char. Cluster | VCR 30 | VCR 60 | VCR 90 | SCM R30 | SCM R60 | SCM R90 | Plant height (cm) | No. of primaries /plant | No. pods per plant | Haulm yield/ plot(g) | Yield / plant (g) | Net Plot Yield (g) | Shelling % | 100 seed weight (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 2.15 | 2.33 | 2.28 | 24.10 | 28.77 | 28.95 | 11.92 | 4.70 | 8.99 | 8.51 | 4.42 | 86.30 | 56.67 | 23.50 |
| II | 2.25 | 2.50 | 2.75 | 21.10 | 23.90 | 21.50 | 12.58 | 5.10 | 6.75 | 10.40 | 3.83 | 54.70 | 52.10 | 27.33 |
| III | 2.25 | 2.50 | 2.25 | 27.93 | 25.85 | 29.78 | 13.75 | 5.45 | 9.75 | 10.15 | 6.10 | 89.03 | 58.83 | 27.83 |
| IV | 1.75 | 2.25 | 1.75 | 28.78 | 26.55 | 32.80 | 12.48 | 4.55 | 7.65 | 13.13 | 5.00 | 92.08 | 43.18 | 23.90 |
| V | 2.75 | 3.00 | 3.25 | 21.63 | 20.50 | 18.43 | 12.90 | 4.80 | 8.95 | 8.00 | 4.28 | 94.33 | 47.95 | 23.53 |
| VI | 1.75 | 2.00 | 2.00 | 26.13 | 34.35 | 33.45 | 17.50 | 4.75 | 13.40 | 13.10 | 6.83 | 141.40 | 63.25 | 23.85 |
| VII | 3.00 | 3.00 | 3.00 | 21.70 | 20.40 | 19.50 | 14.40 | 4.10 | 92.00 | 9.23 | 4.70 | 96.30 | 106.73 | 25.09 |
| VIII | 2.00 | 2.50 | 1.75 | 26.18 | 29.43 | 35.88 | 14.08 | 4.50 | 11.15 | 12.83 | 7.03 | 133.08 | 64.53 | 20.23 |
| IX | 2.00 | 1.50 | 2.00 | 30.58 | 35.45 | 32.53 | 18.40 | 4.05 | 9.25 | 10.08 | 6.03 | 147.13 | 61.88 | 23.60 |
| X | 1.75 | 2.00 | 1.75 | 24.58 | 30.20 | 33.20 | 14.60 | 5.10 | 11.65 | 12.88 | 8.28 | 164.50 | 63.88 | 25.88 |
| XI | 2.25 | 2.50 | 2.25 | 25.65 | 25.45 | 32.63 | 9.45 | 5.30 | 8.92 | 13.68 | 3.55 | 40.03 | 47.88 | 22.60 |
| XII | 2.25 | 2.00 | 1.50 | 25.90 | 29.68 | 37.05 | 13.13 | 6.10 | 15.25 | 12.03 | 8.48 | 159.73 | 61.85 | 23.28 |
| XIII | 2.25 | 2.75 | 3.25 | 27.70 | 26.60 | 21.65 | 9.33 | 4.25 | 8.85 | 5.05 | 4.68 | 95.70 | 61.00 | 28.83 |
| XIV | 1.25 | 2.50 | 1.75 | 22.60 | 29.88 | 34.03 | 16.05 | 5.35 | 12.20 | 11.28 | 6.75 | 113.53 | 57.00 | 25.05 |
| XV | 1.25 | 2.25 | 2.00 | 30.03 | 27.65 | 35.00 | 12.83 | 4.10 | 11.05 | 4.53 | 5.60 | 127.78 | 69.93 | 25.90 |
| XVI | 2.25 | 1.75 | 1.75 | 30.05 | 30.73 | 35.05 | 10.68 | 3.95 | 10.95 | 6.70 | 6.00 | 112.58 | 64.43 | 25.83 |
| XVII | 1.75 | 2.00 | 2.00 | 27.73 | 27.95 | 41.00 | 9.20 | 4.40 | 7.45 | 6.23 | 5.00 | 52.00 | 53.20 | 31.33 |
| XVIII | 1.00 | 1.50 | 1.00 | 36.53 | 30.55 | 43.70 | 14.88 | 4.45 | 8.15 | 14.68 | 5.18 | 86.45 | 68.60 | 22.38 |
| %Contr. | 3.77 | 2.99 | 3.21 | 6.09 | 4.76 | 0.78 | 7.97 | 11.07 | 8.64 | 5.98 | 6.76 | 8.08 | 15.50 | 14.40 |

Abbreviations: VCR 30 = Visual Chlorotic Rating at 30 Days After Sowing; VCR 60 = Visual Chlorotic Rating at 60 Days After Sowing; VCR 90 = Visual Chlorotic at 90 Days After Sowing ; SCMR = SPAD chlorophyll Meter Reading at 30 Days after sowing; SCMR = SPAD chlorophyll Meter Reading at 60 Days after sowing and SCMR 90 = SPAD chlorophyll Meter Reading at 90 Days after sowing.

**Table 4: Average intra and inter-cluster distance based on corresponding $D^2$ values**

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII | XIII | XIV | XV | XVI | XVII | XVIII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 2.06 | 2.44 | 2.49 | 2.83 | 2.57 | 2.52 | 2.93 | 3.43 | 3.72 | 2.88 | 2.62 | 4.40 | 3.37 | 3.59 | 3.33 | 3.10 | 3.78 | 3.97 |
| II | | 0.00 | 2.13 | 1.84 | 2.21 | 4.23 | 3.88 | 6.01 | 5.19 | 3.36 | 2.03 | 6.00 | 4.10 | 3.82 | 5.68 | 4.97 | 3.08 | 4.87 |
| III | | | 0.00 | 2.62 | 2.63 | 2.12 | 2.72 | 3.10 | 3.52 | 1.80 | 3.00 | 2.68 | 3.12 | 2.55 | 3.71 | 2.72 | 2.84 | 3.79 |
| IV | | | | 0.00 | 2.36 | 3.49 | 4.89 | 4.24 | 4.47 | 2.76 | 1.86 | 4.76 | 5.55 | 3.46 | 6.38 | 4.88 | 4.50 | 4.40 |
| V | | | | | 0.00 | 3.20 | 2.13 | 4.54 | 4.14 | 3.26 | 2.84 | 4.54 | 2.49 | 4.83 | 4.78 | 4.46 | 5.51 | 7.33 |
| VI | | | | | | 0.00 | 2.11 | 1.56 | 2.03 | 1.37 | 3.80 | 2.61 | 3.36 | 2.61 | 2.10 | 2.53 | 5.27 | 2.93 |
| VII | | | | | | | 0.00 | 3.08 | 3.71 | 2.77 | 4.41 | 4.09 | 1.93 | 5.38 | 2.92 | 2.15 | 5.77 | 5.73 |
| VIII | | | | | | | | 0.00 | 4.74 | 1.82 | 4.24 | 2.42 | 5.75 | 2.61 | 3.89 | 3.71 | 7.04 | 3.88 |
| IX | | | | | | | | | 0.00 | 3.47 | 6.39 | 5.92 | 3.33 | 6.60 | 2.81 | 2.69 | 5.27 | 3.37 |
| X | | | | | | | | | | 0.00 | 4.11 | 1.48 | 4.61 | 2.23 | 3.28 | 2.92 | 5.12 | 3.61 |
| XI | | | | | | | | | | | 0.00 | 4.60 | 5.28 | 4.44 | 6.68 | 5.09 | 4.74 | 4.12 |
| XII | | | | | | | | | | | | 0.00 | 6.75 | 3.77 | 5.30 | 3.67 | 7.60 | 5.63 |
| XIII | | | | | | | | | | | | | 0.00 | 7.07 | 2.44 | 2.72 | 4.17 | 6.72 |
| XIV | | | | | | | | | | | | | | 0.00 | 4.58 | 5.96 | 5.04 | 5.15 |
| XV | | | | | | | | | | | | | | | 0.00 | 1.94 | 3.60 | 4.19 |
| XVI | | | | | | | | | | | | | | | | 0.00 | 3.45 | 3.58 |
| XVII | | | | | | | | | | | | | | | | | 0.00 | 4.46 |
| XVIII | | | | | | | | | | | | | | | | | | 0.00 |

cluster I (2.06). The maximum inter cluster distance was found between cluster XII and XVII (7.60), followed by cluster XVII and cluster VIII (7.04) and cluster XIII and XVIII (6.72). The corroborative findings were reported by Kumar and Joshi, 2013, Meena *et al.,* 2015, Mukesh *et al.,* 2016 and Vijaykumar *et al.,* 2016. Thus, crossing between the genotypes belonging to cluster pair separated by very high inter-cluster distances, as mentioned above, mat through desirable transgressive segregates which indicated that the genotype belonging to these cluster pairs, with very high inter-cluster distances, may produce desirable transgressive segregates and an opportunity for selection better genotypes in succeeding generations. The results revealed that different genotypes from different source and state were included in different clusters, indicating that genetic diversity and geographic diversity are not related. Emphasis may be given for improving the characters like, haulm yield, pod yield per plant, net plot yield and number pods per plant.

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