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# Genetic Variability and G×E Interactions in a Diverse Set of Groundnut Accessions

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## ABSTRACT

**Background:** Knowledge of the genetic diversity for various agronomic traits and their interaction with the environment and subsequent classification of genotypes will be beneficial for identification of divergent and stable sources of agronomic traits.

**Methods:** A set of 96 groundnut germplasm accessions belonging to four botanical groups were evaluated for three years (2017 to 2019) for pod yield and component traits using AMMI analysis and subsequently accessions were classified based Euclidean cluster analysis.

**Result:** Among different botanical groups, Virginia genotypes matured late and possessed high SPAD chlorophyll meter readings (SCMR) and pod yield compared to Spanish types. The component traits of pod maturity like days to flowering (first and 50%) showed low heritability and high genotype x environment interaction (GEI) and significant negatively affected sound mature kernel (SMK) and shelling per centage (SP). The cumulative contribution of environment and GEI component to the total variance was the highest in the expression of SP (67%) followed by days to maturity (54%) and days to 50% flowering (52%). Euclidean distance-based cluster analysis grouped the 96 accessions into five major clusters. Cluster I had accessions with higher pod yield, whereas cluster V contained accessions with low SLA, high SCMR and moderate pod yield. High yielding as well as stable accessions identified based on AMMI stability value (ASV) are NRCG 17332, 10076, 17268, 17197, 17108, 10106, 10089 and 17165. Trait specific as well as stable accessions identified in the present study can be useful donors for groundnut breeding programme.

**Key words:** Euclidean distance, Germplasm, Heritability, Pod yield per plant.

## INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a most important oil seed legume crop, cultivated in arid and semi-arid tropical countries of the world. In India, it is grown in an area of 47 lakh hectares with a production of 67 lakh tonnes and average productivity of 1422 Kg/ha (FAO Stat. 2019). Groundnut is a major rainfed crop and vagarious weather conditions often influence the performance of cultivars, results in different phenotypic expression of genotypes among growing seasons. The performance of genotypes is significantly affected by significant genotype × environment interaction effects. To maximize the yield stability, there is need to develop high yielding and stable genotypes through use of diverse donors. Assessment of the genetic variability and diversity of different agronomic traits and their interaction with the environment and subsequent grouping of genotypes for each trait will be helpful for identifying the divergent and stable sources. Hence, present study was aimed for multiyear evaluation of germplasm accessions for pod yield and its component traits to identify efficient donor accessions for trait combination breeding.

## MATERIALS AND METHODS

### Experimental details

The material for present study consisted of 96 groundnut accessions belonging to four botanical groups (60 Spanish; 7 Valencia; 19 Virginia bunch and 10 Virginia runners) collected from Gene Bank, Genetic Resource Unit, ICAR-Directorate of Groundnut Research, Junagadh. Out of 96 genotypes, sixty five belonged to India, five belonged USA, three belonged to Zimbabwe and once each from Argentina, Australia, Brazil, Burma, Central African Republic, China, Camaroon, Congo, Equator, HVO, Korea, Senegal, Sudan, Tanzania, Taiwan and 6 are of unknown origin. The experiment was carried out in a randomized complete block design in three replications from 2017 to 2019 during *kharif* season at Experimental plots of ICAR-Directorate of Groundnut Research, Junagadh,Gujarat. Each accession was planted in a single row of 3 m length and with a spacing of 60×10 cm. Standard agronomic practices were followed to raise healthy crop.

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### Observations recorded

Data on pod yield and its component traits were recorded from five randomly selected plants from each genotype. Days to flower initiation and days to 50 per cent flowering were recorded when first flower opened and 50% of plants in each genotype were flowered respectively. Number of days to taken from date of sowing to physiological maturity of the plant was recorded as days to maturity. The surrogate traits of water use efficiency, specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) were measured at 60 days after planting. SCMR was recorded at 60 days after sowing by collecting the second to third leaves from the top of the main stem of each plant and transported to a laboratory and fresh weight was recorded. SCMR was measured immediately by a Minolta handheld portable SCMR meter (SPAD- 502 plus Minolta, Tokyo, Japan) using four leaflets per sample by ensuring that the SPAD meter sensor fully covered the leaf lamina while avoiding any interference from veins and midribs. The same samples were further measured for leaf area, using a leaf area meter (LI 3100C Area meter, LI COR Inc., USA).

### Statistical analysis

The combined analysis of variance (ANOVA) was computed using general linear mixed model using Proc GLM function of SAS for assessing the effect of environments, genotypes and their interactions. The genotypic and phenotypic correlation coefficients and PCV and GCV estimates were worked out as per method suggested by Aljibouri *et al*. (1958) and Burton and Devane (1953) respectively. A cluster analysis was done on pooled mean values of three years for 12 traits using Euclidean distance and dendrogram was constructed using R Studio 3.0.3. Genotype stability for pod yield was estimated using the AMMI analysis and AMMI stability value (ASV) was calculated as formula suggested by Purchase (1997) with Agricolae package of R.

## RESULTS AND DISCUSSION

Significant differences were observed among the groundnut accessions belonging to four botanical groups studied for pod yield and its component traits (Table 1 and 2). The pooled mean values of 96 germplasm accessions for three years for days to first flowering and days to 50% flowering varied from 23-30 days and 25-33 days respectively. 96 germplasm accessions matured in minimum duration of 93 days and maximum of 109 days. Pod yield per plant ranged from 2 to 13g, SCMR ranged from 23 to 37 and KLWR ranged from 1.5 to 2.1. Wide range of variation was observed for pod and kernel traits *viz.,* HPW, SMK and SP were ranged from 41-111g, 47-67%, 55-65% respectively.

**Table 1:** ANOVA and sum of squares per centage on G, E and G × E derived from AMMI stability model for days to flowering, maturity and water use efficiency traits.

| Source of variation | df | DFI | % Var | DFF | % Var | DMT | % Var | SCMR | % Var | SLA | % Var |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ENV | 2 | 294.74 | 17.98 | 619.55 | 23.03 | 1947.35 | 24.53 | 2228 | 29.52 | 196876 | 27.79 |
| Rep (ENV) | 3 | 1.28 | | 13.17 | | 243.09 | | 6 | | 546 | |
| GEN | 95 | 13.05** | 37.81 | 18.65** | 32.94 | 34.05 | 20.38 | 57** | 36.09 | 2589** | 17.36 |
| GEN × ENV | 190 | 4.86** | 28.19 | 8.24** | 29.1 | 25.81** | 30.89 | 14** | 18.05 | 1425 | 19.1 |
| Residual | 285 | 1.83 | | 2.68 | | 10.93 | | 9 | | 1772 | |
| Total | 575 | 5.70 | | 9.36 | | 27.61 | | 26 | | 2464 | |
| **AMMI Model** | | | | | | | | | | | |
| IPCA1 | 96 | 8.06 | | 14.12 | | 36.4 | | 17.62 | | 2144 | |
| IPCA2 | 94 | 1.61 | | 2.23 | | 15.0 | | 10.98 | | 10.98 | |

DFI-Days to first flower initiation; DFF- Days to 50% flowering DMT- Days to maturity.
SCMR-SPAD chlorophyll meter reading; SLA-Specific leaf area.

**Table 2:** ANOVA and sum of squares per centage on G, E and G × E derived from AMMI stability model for pod yield and attributing traits.

| Source of variation | Df | PYL | % Var | HPW | % Var | SMK | % Var | SP | % Var | KLWR | % Var |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ENV | 2 | 564.0 | 15.69 | 12169.9 | 15.16 | 5178.7 | 18.31 | 20726.6 | 53.87 | 0.07 | 0.51 |
| Rep (ENV) | 3 | 5.9 | | 213.4 | | 331.9 | | 292.1 | | 0.11 | |
| GEN | 95 | 34.6** | 45.78 | 986.6** | 58.36 | 133.7** | 22.46 | 85.6* | 10.57 | 0.13** | 46.51 |
| GEN × ENV | 190 | 7.1** | 18.75 | 99.5 | 11.78 | 86.2** | 28.95 | 58.9 | 14.53 | 0.03* | 24.41 |
| Residual | 285 | 4.9 | | 80.6 | | 56.6 | | 53.7 | | 0.03 | |
| Total | 575 | 12.5 | | 279.3 | | 98.4 | | 133.8 | | 0.05 | |
| **AMMI Model** | | | | | | | | | | | |
| IPCA1 | 96 | 9.56 | | 120.3 | | 108.2 | | 109.88 | | 0.042 | |
| IPCA2 | 94 | 4.57 | | 78.3 | | 63.8 | | 6.75 | | 0.026 | |

PYL-Pod yield per plant (g); HPW- Hundred pod weight; SMK-Sound mature kernel (%); SP-Shelling per centage; KLWR-Kernel length to width ratio.

**Variability among botanical groups**

In Subspecies *fastigiata* accessions (both Spanish and Valencia), the pooled mean values of three years for days to first flowering, days to 50% flowering and days to maturity were varied from 23-28 days, 25-30 days, 95-104 days respectively. SCMR ranged from 23-37, HPW ranged from 41-104g, SMK (%) ranged from 49-67%, SP ranged from 57-76%, KLWR ranged from 1.5 to 2.1 and pod yield per plant ranged from 2-12g (Fig 1 and 2). In Subspecies *hypogaea* accessions (both Virginia bunch and Virginia runners), the pooled mean values of three years of days to first flowering, days to 50% flowering, days to maturity, SCMR, pod yield per plant, HPW, SMK (%), SP and KLWR were ranged from 24-30 days, 26-33 days, 96-106 days,37-32, 3-13g, 53-111g, 49-66%, 55-72% and 1.6-2.1 respectively.

Based on days to maturity, days to first flowering and days to 50% flowering, the accessions classified in the order: Virginia Runner >Virginia Bunch>Valencia >Spanish bunch accessions. Highest SCMR was observed in Virginia Runner followed by Virginia Bunch and Spanish bunch. Lowest pod yield was found in Valencia whereas highest pod yield was observed in Virginia accessions. Highest hundred pod and kernel weight were observed in Virginia bunch and Spanish bunch accessions. Spanish bunch accessions showed higher shelling percentage whereas, Virginia bunch accessions had higher HPW and pod yield as result of prolonged pod filling period (Clements *et al.* 2002; Gupta *et al.* 2016; Kunta *et al.,* 2021). Sub species differences for pod maturity and morphological traits between *hypogaea* and *fastigiata* were also reported by Onemli (1990), Putnam *et al.* (1991), Nautiyal *et al.* (2002), Singh (2004) and Kunta *et al.* (2021).

**Heritability and correlation between pod yield and its component traits**

Significant G×E interactions were also depicted by considerable differences in genotypic variances across the years. Pod yield per plant, SCMR and kernel characteristics exhibited high heritability estimates (Table 3) suggesting the effectiveness for selection in improvement of these traits. The component traits of days to maturity like days to first and 50% flowering had low heritability estimates and also, they correlated significant negatively with SMK and SP (Table 4) suggesting that considerable reduction of pod yield at the cost SMK and SP in case of short duration accessions. Hence, the shelling percentage (SP) and sound mature kernel (SMK%) are two sensitive traits to assess the pod maturity and pod yield in developing short duration groundnut varieties. Further, the cumulative contribution of environment and GEI component to the total variance was more than 50% in the expression of SP, days to maturity and days to 50% flowering suggesting the more influence of more environment on the expression of these traits. Cox (1979) and Nigam (1994) reported considerable influence of temperature and photoperiod on vegetative as well as reproductive growth of groundnut. Pod yield per plant correlated significant positively with all the traits except SLA. SCMR related closely with chlorophyll content (Akkasaeng *et al.,* 2003) and it indicates the photosynthetic active light transmittance of leaf (Richardson *et al.* 2002), whereas SLA correlated negatively with SCMR and water use efficiency (Upadhyaya *et al*., 2011). SCMR had high heritability and high positive correlation with pod yield, whereas SLA correlated with negatively with pod yield. Hence SCMR is most useful physiological trait than SLA (Kalariya *et al.*, 2017; Gangadhara *et al.,* 2020) in developing water use efficient varieties.

**Genotype × Environment interaction and AMMI analysis of pod yield**

Significant G×E interaction effects were observed for all traits except hundred pod weight and shelling percentage. The combined analysis indicated that the genotype and GEI account for more than 50% of the total variance for all traits except SLA and SP. The cumulative contribution of environment and GEI component to the total variance was highest in the expression of shelling percentage (67%) followed by days to maturity (54%) and days to 50% flowering (52%) suggesting the more influence of more environment on the expression of these traits (Table 1 and 2). The cumulative contribution of genotype component to the total variance was highest in the expression of hundred pod

**Table 3:** Pooled heritability estimates and Variance components for 13 traits.

| Trait | $\sigma^2$ g | $\sigma^2_R$ | $\sigma^2_E$ | $\sigma^2_{G\times E}$ | $h^2_{(BS)}$ | GM | CV | LSD (0.05) |
|---|---|---|---|---|---|---|---|---|
| DFI | 1.36 | 1.82 | 1.51 | 1.52 | 62.7 | 25.24 | 5.36 | 1.54 |
| DFF | 1.74 | 2.68 | 3.13 | 2.78 | 55.8 | 27.38 | 5.98 | 1.86 |
| DMT | 1.37 | 10.93 | 8.8 | 7.44 | 24.2 | 99.19 | 3.33 | 3.76 |
| SCMR | 7.17 | 8.57 | 11.53 | 2.89 | 75.0 | 29.81 | 10.0 | 3.00 |
| SLA | 130.3 | 513 | 842 | 89.5 | 42.9 | 223.0 | 10.1 | 17.1 |
| PYLDP | 4.59 | 4.93 | 2.9 | 1.08 | 79.5 | 6.84 | 32.5 | 2.50 |
| HPW | 147.8 | 80.6 | 62.17 | 9.45 | 89.9 | 68.0 | 13.2 | 10.2 |
| SMK | 7.92 | 56.63 | 25.09 | 14.7 | 35.5 | 57.7 | 13.0 | 8.60 |
| SP | 8.04 | 5.42 | 0.05 | 0.63 | 82.8 | 70.4 | 11.4 | 8.30 |
| KL | 1.24 | 0.72 | 16.69 | 0.25 | 85.9 | 10.8 | 7.84 | 0.97 |
| KW | 0.08 | 0.17 | 5.16 | 0.03 | 68.8 | 6.18 | 6.73 | 0.47 |
| KLWR | 0.02 | 0.03 | 0 | 0.004 | 73.8 | 1.75 | 9.17 | 0.18 |

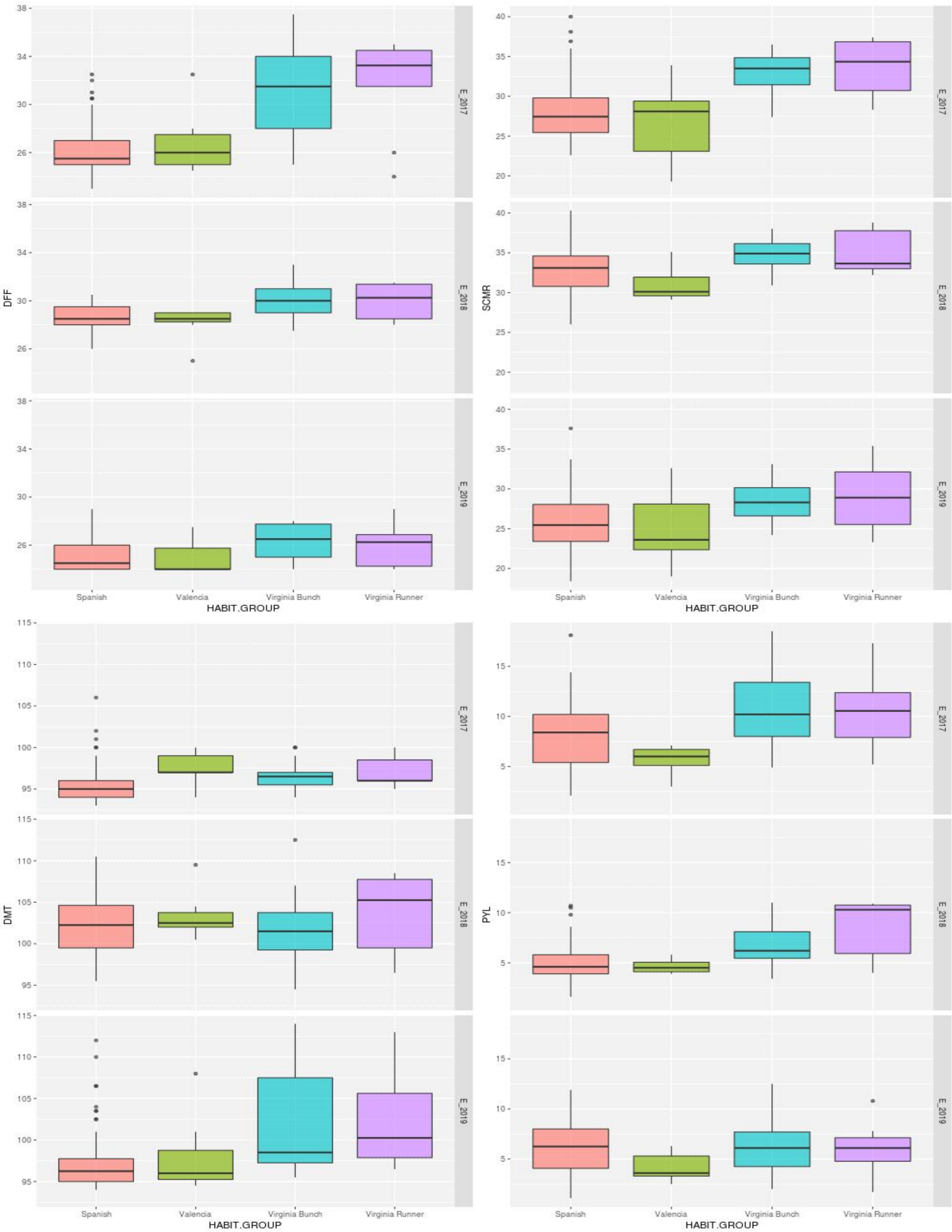


**Fig 1:** Variation for days to flowering, matuirty and pod yield.

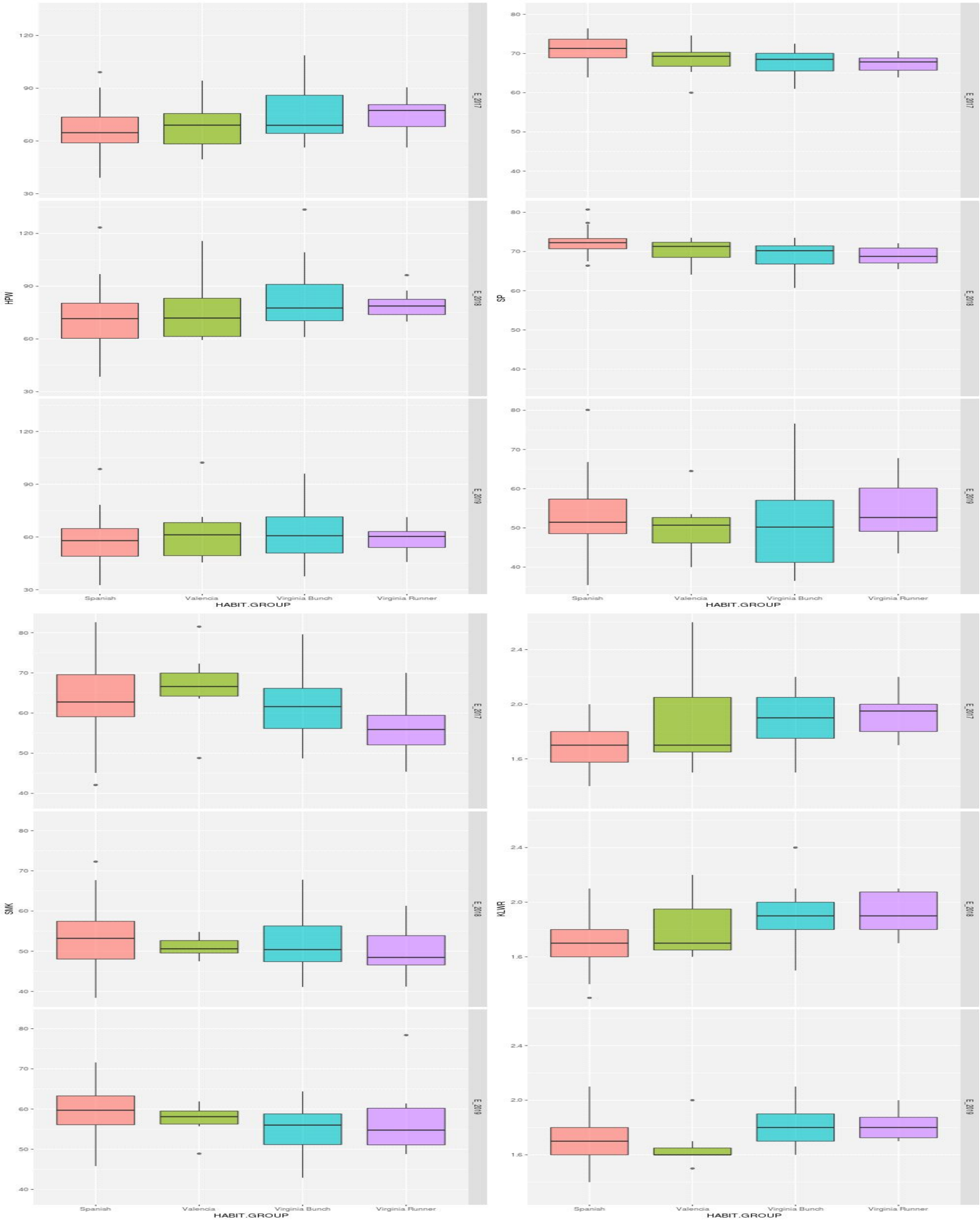


**Fig 2:** Variation for pod and kernel characteristics in 96 groundnut accessions.

weight (58%) followed by kernel length to width ratio (46%) and pod yield per plant (45%).

AMMI analysis for pod yield showed that the first principal component axis accounted for 68% of the total variation and the second accounted for 31% (Fig 3). The environments E_2018 and E_2019 had IPCA1 scores near zero and all accessions performed well in these environments as the favourable conditions were prevailed. Genotypes that were positioned further along the positive direction of a vector tended to show higher grain yield, reflecting better adaptation to that environment (Kempton, 1984). In general accessions exhibit a high degree of yield

**Table 4:** Estimated phenotypic ($r_p$) and genotypic ($r_g$) correlation coefficients combined across environments.

| Traits | R | DFI | DFF | DMT | SCMR | SLA | PYLDP | HPW | SMK | SP |
|---|---|---|---|---|---|---|---|---|---|---|
| DFF | $r_p$ | 0.930** | 1 | | | | | | | |
| | $r_g$ | 0.999** | 1 | | | | | | | |
| DMT | $r_p$ | 0.397** | 0.441** | 1 | | | | | | |
| | $r_g$ | 0.999** | 0.999** | 1 | | | | | | |
| SCMR | $r_p$ | 0.386** | 0.440** | 0.213 | 1 | | | | | |
| | $r_g$ | 0.453** | 0.529** | 0.369** | 1 | | | | | |
| SLA | $r_p$ | -0.215 | -0.271** | -0.204 | -0.624** | 1 | | | | |
| | $r_g$ | -0.265* | -0.360** | -0.449** | -0.927** | 1 | | | | |
| PYL | $r_p$ | 0.235* | 0.242* | -0.010 | 0.553** | -0.307** | 1 | | | |
| | $r_g$ | 0.187 | 0.225* | 0.062 | 0.644** | -0.490** | 1 | | | |
| HPW | $r_p$ | -0.019 | 0.027 | 0.060 | 0.353** | -0.168 | 0.574** | 1 | | |
| | $r_g$ | -0.048 | 0.014 | 0.227 | 0.418** | -0.267** | 0.634** | 1 | | |
| SMK | $r_p$ | -0.416** | -0.418** | -0.242* | -0.132 | 0.174 | 0.085 | 0.297** | 1 | |
| | $r_g$ | -0.903** | -0.868** | -0.748** | -0.220 | 0.489** | 0.157 | 0.379** | 1 | |
| SP | $r_p$ | -0.319** | -0.344** | -0.267** | -0.037 | 0.148 | 0.008 | -0.056 | 0.447** | 1 |
| | $r_g$ | -0.627** | -0.741** | -0.975** | -0.075 | 0.291** | 0.005 | -0.125 | 0.999** | 1 |
| KLWR | $r_p$ | 0.370** | 0.439** | 0.295** | 0.419** | -0.237 | 0.390** | 0.476** | -0.353** | -0.396** |
| | $r_g$ | 0.504** | 0.660** | 0.617** | 0.578** | -0.366** | 0.483** | 0.575** | -0.764** | -0.626** |

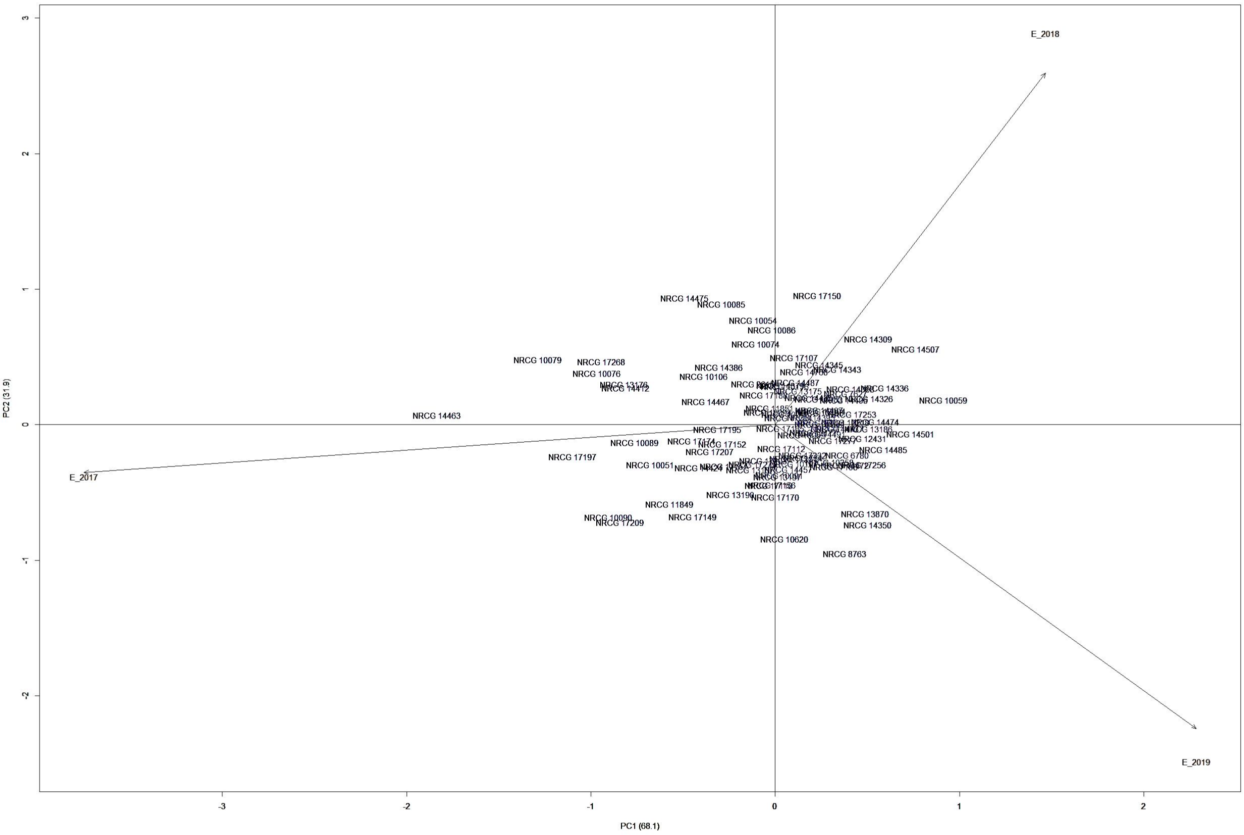


**Fig 3:** AMMI biplot of 96 germplasm accessions for pod yield and three environments.

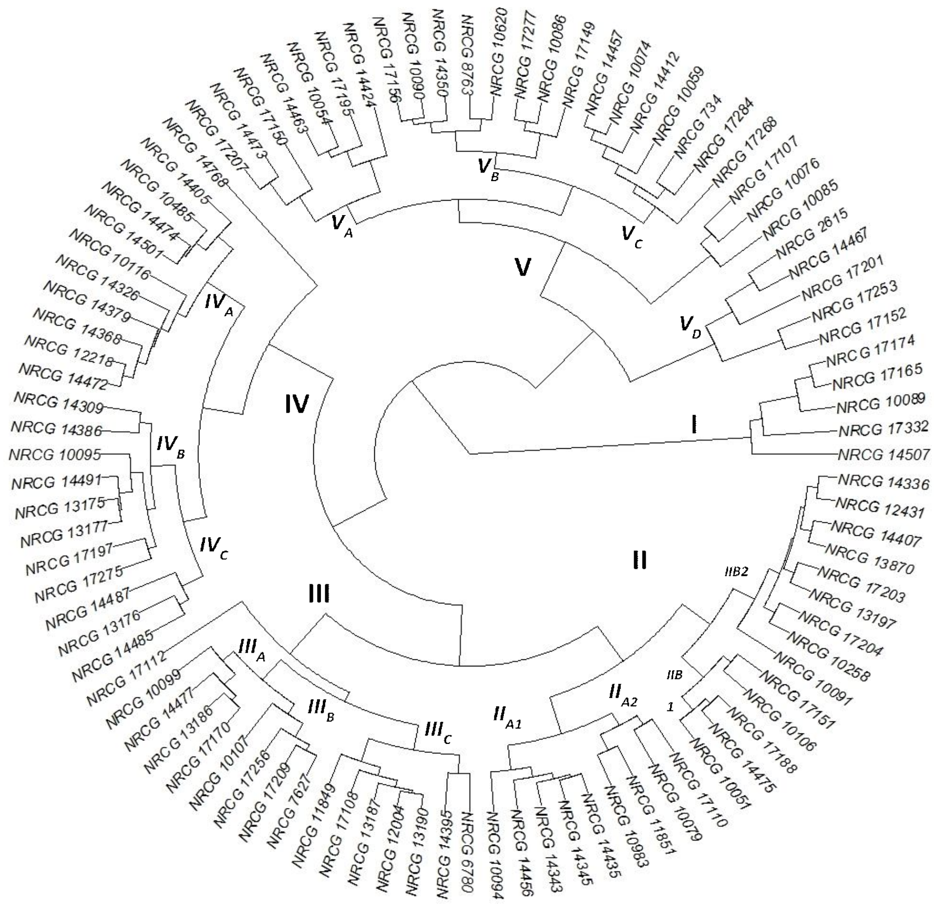


**Fig 4:** Dendrogram showing 5 major clusters of groundnut accessions based on Euclidean distance.

variability reflected by the high degree of dispersion in the biplot. AMMI stability value (ASV) is the distance from zero in a two-dimensional scatter gram of IPCA1 scores against IPCA2 scores. It is estimated based on the relative contributions of the principal component axis scores (IPCA1 and IPCA2) to the interaction sum of squares for each genotype. Smaller the ASV indicates more stable genotypes. Incorporating the mean yield and ASV for selection of genotypes is useful rather than single criteria. High yielding as well as stable accessions identified are NRCG 17332, 10076, 17268, 17197, 17108, 10106, 10089, 17165, 17174, 10059, 10074, 17151,10085,10086,17149 and 17275 (Table 5).

### Cluster analysis and identification of trait specific germplasm

Following the procedure of Euclidean distance, 96 groundnut accessions were grouped into five major clusters (Fig 4) based on pooled mean values (2017-2019). Cluster V was the largest with 30 accessions followed by cluster II, IV and III had 23, 22 and 16 accessions respectively. Remaining 5 accessions were found in cluster I. Cluster I had accessions with higher pod yield and early flowering and higher SCMR. Sub cluster VD contains accessions with low SLA and high

**Table 5:** Identification of stable groundnut accessions based on AMMI Stability value (ASV) and Yield Stability index (Ysi).

| Accession | ASV | rASV | YSI | rYSI | Mean |
|---|---|---|---|---|---|
| NRCG 17332 | 0.313 | 16 | 17 | 1 | 12.5 |
| NRCG 10076 | 1.462 | 92 | 94 | 2 | 12.1 |
| NRCG 17268 | 1.456 | 91 | 94 | 3 | 12.0 |
| NRCG 17197 | 1.621 | 94 | 98 | 4 | 11.9 |
| NRCG 17108 | 0.560 | 47 | 52 | 5 | 11.3 |
| NRCG 10106 | 0.667 | 61 | 67 | 6 | 11.1 |
| NRCG 10089 | 1.121 | 84 | 91 | 7 | 11.0 |
| NRCG 17165 | 0.049 | 1 | 9 | 8 | 10.9 |
| NRCG 17174 | 0.671 | 62 | 71 | 9 | 10.0 |
| NRCG 10059 | 1.346 | 89 | 99 | 10 | 10.0 |
| NRCG 10074 | 0.613 | 54 | 65.5 | 11.5 | 9.9 |
| NRCG 17151 | 0.507 | 41 | 52.5 | 11.5 | 9.9 |
| NRCG 10085 | 0.987 | 77 | 90 | 13 | 9.7 |
| NRCG 14463 | 2.684 | 96 | 110 | 14 | 9.7 |
| NRCG 14475 | 1.179 | 85 | 100 | 15 | 9.7 |
| NRCG 10086 | 0.701 | 64 | 80 | 16 | 9.2 |
| NRCG 17149 | 0.941 | 74 | 91 | 17 | 9.1 |
| NRCG 17275 | 0.343 | 20 | 38 | 18 | 9.1 |

SCMR and moderate pod yield. Sub cluster IVA had late maturing and moderate SLA with lower pod yield. Cluster I and V had accession with higher pod yield, whereas low yielding accessions were found in cluster IV.

Progress in crop improvement mainly depends on use of diverse and new sources for pod yield and component traits. Use of promising donors as parental sources in breeding programme will generate diverse population and development of improved groundnut verities. The evaluation of 96 germplasm accessions for three years resulted in identification of trait specific germplasm accessions that recorded desirable traits/trait combination. Early maturity constitutes important drought escaping mechanism and short duration groundnut varieties has an advantage of fitting in paddy and potato fallow cropping systems. Early maturing (96 days) accessions were found in SB group are NRCG 10107, NRCG 10116, NRCG 17275, NRCG 10983, NRCG 14456, NRCG 17156, NRCG 17170, NRCG 17151 and NRCG 17204. SCMR is more pertinent trait for drought tolerance associated with leaf nitrogen and drought tolerance (Kalariya *et al*., 2017; Gangadhara *et al*., 2020). Germplasm accessions showing higher SCMR (35-37) are NRCG 17150, NRCG 17107, NRCG 17201 and NRCG 17275 in SB group and NRCG 10059, NRCG 14467, NRCG 10085 in VR group. Low SLA germplasm are preferred for breeding drought tolerant groundnut, accessions NRCG 17201, NRCG 17107, NRCG 17253, NRCG 14485, NRCG 17152 had low SLA (189-208cm$^2$ g$^{-1}$).

Accessions (NRCG 14456, NRCG 17201, NRCG 10094, NRCG 14405) belonging to SB group were showed high SP (70-76%). Seed size had highly positive correlation with seed weight (Chiow and wynne, 1983). Kernel shape and size is important visible feature for consumer's preference as well as for processing purpose. Groundnut accessions NRCG 14463, NRCG 17195, NRCG 17165, NRCG 17332, NRCG 17188, NRCG 14412, NRCG 10079, NRCG 10089, NRCG 13176, NRCG 14487 showed large kernel size. High yielding accessions are NRCG 17197, NRCG 17108, NRCG 10106,NRCG 17174, NRCG 17151, NRCG 17149, NRCG 17275, NRCG 17150, NRCG 10051 in Spanish bunch (SB) group (9-12 g); NRCG 17332, NRCG 10076, NRCG 10089, NRCG 17165, NRCG 14463 in Virginia bunch (VB) group (10-12 g) and NRCG 17268, NRCG 10059, NRCG 10074, NRCG 10085, NRCG 14475, NRCG 10086 in VR group (9-12 g).

## CONCLUSION

A wide range of variation was observed among germplasm accessions belonging to four botanical groups. Two traits, shelling percentage (SP) and sound mature kernel (% SMK) are two sensitive/critical traits to assess pod maturity. Trait specific accessions in each botanical group as well as stable accessions for pod yield, identified in the present study can be useful donors for short duration varieties development programme.

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