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Genetic variability and heritability studies in groundnut (*Arachis hypogaea* L.) germplasm

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Abstract

The present study was carried out with 220 groundnut mini-core collections made from ICRISAT, Hyderabad to study Genetic Variability, Genetic Advance and heritability. This study was conducted at AC&RI, Vallanad during the year 2022-23. In this study, the estimates of PCV and GCV was expressed higher for plant height, hundred seed weight, primary branches per plant and secondary branches per plant. The presence of phenotypic and genotypic variance for the above characters indicated that these characters were more variable than the other characters studied. Higher heritability and Genetic Advance as a percent of mean (GAM) were observed for all traits included in this study except kernel width and oil content. Therefore, these estimates are useful in selection of genotypes based on phenotypic performance.

Keywords: Groundnut, heritability, ANOVA, PCV, GCV, genetic advance

Introduction

Groundnut (*Arachis hypogaea* L.) is one of the most dynamic oilseed crop, delivering high protein besides significantly meet country's major oil requirement. It is often called by popular appellations as Earthnuts, Peanuts, Goober nut, Monkey nuts and Pygmy nuts. Groundnut belongs to the Fabaceae family spreading widely in tropics and subtropics. The origin of cultivated groundnut (Allotetraploid ($2n = 4X = 40$) species) was from Bolivia situated at the base of Mount Andes (Krapovickas, 2017) extending into North Argentina (Rao, 1988) [22]. Portuguese trading company had introduced groundnut from Brazil to West Africa and then to South-Western India during the 16th century (Ejiko *et al.*, 2015) [7].

Peanut can also be eaten straight because of its greater food value glorified by the fact that it contains more protein (24.35%), carbohydrate (21.26%) besides contain several minerals, antioxidants, flavonoids and vitamins such as niacin (12.1 mg/100g) and choline (52.5 mg/100g) (Bonku *et al.*, 2020) [4]. Globally, Groundnut is grown on 327 million hectares recording a production potential of 539 million tonnes and a productivity of 1648 kg per hectare (FAOSTAT, 2021) [8]. India ranks second largest producer of Peanut after China, followed by Nigeria and USA. In India, 10.1 million tonnes of groundnut are produced over 5.7 million hectares at productivity of 1777 kg per hectare (INDIASTAT, 2022) [11]. Groundnuts are majorly grown in Gujarat followed by Rajasthan, Tamil Nadu, Andhra Pradesh and Karnataka during Kharif and Rabi seasons.

Genetic diversity in a crop species explained by the heritable variation registered in a mini-core germplasm collections within a population of same species. This tool has presented the crop breeders to evolve the new and improved cultures bearing desirable traits through infusing effective selection for use as donor or as a new variety. Genetic diversity help breeders to develop cultivars for specific traits like quality enhancement besides abiotic and biotic tolerance (Bhandari *et al.*, 2017) [3]. Plant breeders exploit the genetic diversity to choose superior genotypes with the heritability estimation because of good indicator of transmission of traits from parents to progeny (Gangadhara *et al.*, 2023) [8].

Materials and Methods

The field trials were laid at AC&RI, Killikulam during Rabi season of 2022-23 in 'D' block farm. Geographical location of the experimental field is at 8°46' N latitude and 77°42' E longitude and at an altitude of 40 m above MSL. The experimental materials consisted of 220 groundnut mini-core collections made from ICRISAT, Hyderabad besides the check varieties

availed from the parent department Genetics and Plant Breeding, Killikulam, Vallanad during the year 2022-23. During Rabi 2022-23, the field experiment was conducted in augmented block design with 10 blocks each block consisted of 22 test entries and four checks. The groundnut mini-core collections (220 numbers) along with resistant (ICG 6022) and susceptible checks (TMV 2, TMV 7 and TMV 13) were sown in main field by adopting a spacing of 30 cm between rows and 20 cm between plants. The collected data were used for determining the analysis of association and genetic divergence studies. Analysis of Variance was obtained by using TNAU STAT software. Genetic Variability parameters such as PCV and GCV, heritability and GAM were estimated according to Burton *et al.*, (1953) [5], Lush (1940) [15] and Johnson *et al.*, (1955) [12] respectively.

Results and Discussion

Analysis of variance (ANOVA)

The mean sum of squares for treatment was significant positively at 1 percent level for days to fifty percent flowering, plant height, , number of primary branches per plant, kernel length, number of secondary branches per plant, hundred seed weight, oil content, number of pods per plant, shelling percent, number of seeds per pod, number of mature pods per plant and single plant yield while kernel weight alone had registered positive value but non-significant value at both five and one percent level. The expression of significant value for greater number of quantitative traits studied among 220 groundnut germplasm, indicated the presence of divergence in test genotypes. This eventually consents retrieval of some useful donors towards reorientation and selection of elite genotypes for yield and its contributing traits.

Mean Performance

The achievement of breeding programme depends upon the choice of elite genotypes based on the mean performance. Selection of desirable and superior plants can be made possible through the mean performance of the groundnut genotypes for thirteen quantitative traits. The plant height mean value spanned from 9.18 cm to 44.25 cm with a *per se* value of 22.38cm among the 220 groundnut genotypes studied. The mean value recorded as 41.03 days to 50% flowering and the late and early flowering were exhibited between 52 days and 26 days respectively. The maximum and minimum value obtained for number of primary branches per plant was 23.5 and 2.25. The mean value exhibited for number of primary branches per plant as 8.95. For number of secondary branches, the range of value varied between 0 and 55.25 and the average number of secondary branches per plant was recorded as 10.88. The range of value for kernel length was spanned from 0.85 cm to 1.92 cm while mean recorded as 1.3 cm. Kernel width had exhibited the maximum and minimum value as 1.08 cm and 0.49 cm respectively and the mean value for kernel width was reported as 0.78 cm. It was inferred that the maximum and minimum value were reported between 59.60g and 15.25g respectively besides an average 100 seed weight was as 36.31g. The average performance for number of pods per plant was recorded as 44.55 while the maximum and minimum value range between 67.75 and 31. The mean value for number of mature pods per plant was registered as 42.09 while the range of value recorded as 28.25 to 64.25. The mean value had a range of

1.50 and 3.50 for number of seeds per plant besides the overall mean for this trait recorded as 2.01. The lowest and highest mean value recorded for this trait reported to range between 33 percent and 84 percent, respectively and the average mean for this trait was recorded as 67.22 percent. For oil content, the minimum and maximum mean value exhibited between 43.25 percent and 56.96 percent while the average value was recorded as 49.08 percent. The average mean value for pod yield per plant was reported as 16.20 g while the maximum and minimum value exhibited between 28.33 g and 5.7 g, respectively.

Genetic Variability Parameters

The extent of genetic variability and the degree of its heritability accessible in the germplasm determines the effective superior genotype. The heritability value along with genetic gain estimation helps in forecasting the effectiveness of selecting the best individuals among population (Johnson *et al.*, 1955) [12]. The results showed that the PCV value for all thirteen biometrical traits was higher than that of GCV which indicates the role of environment on the phenotype of the crop. Similar outcomes was reported by John *et al.* (2007) [11], Mubai *et al.* (2019) [17], Namrata *et al.* (2016) [18], Sab *et al.* (2018) [24], Aparna *et al.* (2018) [2]. Perusal of genetic variance of thirteen biometrical traits indicated that the PCV value ranged from 3.6% (oil content) to 101.67% (number of secondary branches). Higher PCV value was shown by number of secondary branches (101.67%), number of primary branches (54.88%), pod yield per plant (28.51%), plant height (24.41%), hundred seed weight (22.42%). Kernel length (17.51%), number of mature pods per plant (16.99%), number of pods per plant (16.93%), number of seeds per pod (15.24%), shelling percentage (13.95%), kernel width (12.79%) and days to 50% flowering (10.36%) had exhibited moderate PCV while the lower PCV was reported for oil content (3.6%).

Genotypic coefficient of variation (GCV) was ranged from -1.07% (oil content) to 100.07% (number of secondary branches). The greater GCV value was reported by number of secondary branches (100.07%), number of primary branches (53.66%), pod yield per plant (27.46%), plant height (22.61%), hundred seed weight (21.82%). Moderate GCV value was shown by number of mature pods per plant (16.05%), number of pods per plant (15.86%), Kernel length (15%), shelling percentage (13.59%), number of seeds per pod (12.22%), days to 50% flowering (10.27%). Further, kernel width and oil content had recorded lower GCV values of 8.23% and -1.07% respectively. Hampannavar *et al.* (2018) [9], John *et al.* (2007) [11], Kumari *et al.* (2020) [14], Manoharan *et al.* (1990) [16] have reported the same for plant height. Patil *et al.* (2014) [21], Rao *et al.* (2014) [23], Shukla *et al.* (2014) [25], Zaman *et al.* (2011) [26] have high GCV and PCV reported for hundred seed weight. Further Dandu *et al.* (2012) [6] reported high GCV and PCV for primary and secondary branches per plant.

Heritability and Genetic Advance Studies

Based on phenotypic performance, the estimation of heritability helps in selection of genotypes. The maximum and minimum heritability value was reported as 98.44% for days to 50% flowering and - 8.89% for oil content respectively. The morphometric traits *viz.*, days to 50 percent flowering (98.44%), number of secondary branches (96.88%),

number of primary branches (95.58%), shelling percentage (95%), hundred seed weight (94.76%), pod yield per plant (92.77%), number of mature pods per plant (89.18%), number of pods per plant (87.67%), plant height (85.78%), kernel length (73.35%) and number of seeds per pod (64.36%) were registered higher heritability value. Moderate heritability value recorded for kernel width (41.39%) while the lower heritability value was exhibited by oil content to an extent of -8.89%. Genetic Advance as percent of Mean (GAM) value observed for thirteen biometrical traits ranged from -0.6% (oil content) to 202.92% (number of secondary branches). The GAM value was recorded as higher for number of secondary branches (202.92%) followed by number of primary branches

(108.07%), pod yield per plant (54.49%), hundred seed weight (43.77%), plant height (43.14%), number of mature pods per plant (31.22%), number of pods per plant (30.59%), shelling percentage (27%), kernel length (26.47%), days to 50% flowering (21.01%) and number of seeds per pod (20.21%). Moderate GAM value was reported for kernel width (10.91%) and low GAM value was exhibited by oil content (-0.6%). Higher heritability and GAM were observed for all traits included in this study except kernel width and oil content and the results are in accordance with Dandu *et al.* (2012) [6], John *et al.* (2013) [10], Kumari *et al.* (2020) [14], Narasimhulu *et al.* (2013) [19], Nath *et al.* (2002) [20], Patil *et al.* (2014) [21], Sab *et al.* (2018) [24], Zaman *et al.* (2011) [26].

Table 1: Analysis of Variance for observed biometrical traits

| Source of variation | df | Mean Sum of Squares (MSS) | | | | | | | | | | | | |
|---------------------|-----|---------------------------|----------|----------|----------|--------|---------|---------|-----------|-----------|--------|---------|--------|----------|
| | | PH | DFL | PB | SB | KL | KW | HSW | NP | NMP | SN | SH | OC | SPY |
| Block | 9 | 326.93** | 410.35** | 0.89** | 187.86** | 0.07** | 0.035** | 17.12** | 375.75** | 455.55** | 0.34** | 0.35 | 0.50 | 86.70** |
| Treatment | 223 | 28.56** | 22.30** | 24.78** | 118.25** | 0.04** | 0.007 | 64.88** | 70.98** | 68.07** | 0.12** | 93.44** | 3.14** | 23.82** |
| Checks | 3 | 34.33** | 385.62** | 100.57** | 72.70** | 0.26** | 0.002 | 15.60** | 1611.67** | 1770.85** | 3.90** | 58.33** | 2.95** | 275.90** |
| Test entry | 219 | 26.88** | 15.04** | 23.84** | 118.44** | 0.04** | 0.007** | 65.77** | 47.83** | 42.15** | 0.07** | 94.34** | 3.15** | 19.95** |
| Check vs Test | 1 | 378.66** | 522.02** | 1.90** | 213.67** | 0.10** | 0.018** | 16.73** | 519.65** | 637.04** | 0.23** | 0.85** | 0.46 | 113.60** |
| Error | 27 | 0.61 | 0.07 | 0.01 | 0.12 | 0.007 | 0.007 | 0.13 | 1.52 | 1.56 | 0.02 | 0.46 | 0.63 | 0.35 |

*Significant at 5% level; **Significant at 1% level

Where,

PH – Plant height (cm), DFL – Days to 50% flowering, PB – Number of Primary branches per plant, SB - Number of Secondary branches per plant, KL – Kernel Length (cm), KW – Kernel Width (cm), HSW – Hundred seed weight (g), NP – Number of pods per plant, NMP – Number of Mature pods per plant, SN – Number of seeds per pod, SH – Shelling percentage, OC – Oil content (%), SPY – Pod yield per plant (g)

Table 2: Genetic variability parameters for biometrical quantitative traits

| Traits | Range | Mean | PCV (%) | GCV (%) | h ² (%) | GAM (%) |
|--------|---------------|-------|---------|---------|--------------------|---------|
| PH | 9.18 – 44.25 | 22.53 | 24.41 | 22.61 | 85.78 | 43.14 |
| DFL | 26 – 52 | 40.83 | 10.36 | 10.27 | 98.44 | 21.01 |
| PB | 2.25 – 23.5 | 8.94 | 54.88 | 53.66 | 95.58 | 108.07 |
| SB | 0 – 55.25 | 10.74 | 101.67 | 100.07 | 96.88 | 202.92 |
| KL | 0.85 – 1.93 | 1.3 | 17.51 | 15 | 73.35 | 26.47 |
| KW | 0.49 – 1.08 | 0.78 | 12.79 | 8.23 | 41.39 | 10.91 |
| HSW | 15.25 – 59.6 | 36.35 | 22.42 | 21.82 | 94.76 | 43.77 |
| NP | 31 – 67.75 | 44.66 | 16.93 | 15.86 | 87.67 | 30.59 |
| NMP | 28.25 – 64.25 | 42.23 | 16.99 | 16.05 | 89.18 | 31.22 |
| SN | 1.5 – 3.5 | 2.01 | 15.24 | 12.22 | 64.36 | 20.21 |
| SH | 33 – 84 | 67.26 | 13.95 | 13.59 | 95 | 27 |
| OC | 43.25 – 56.22 | 49.09 | 3.6 | -1.07 | -8.89 | -0.6 |
| SPY | 5.7 – 28.33 | 16.26 | 28.51 | 27.46 | 92.77 | 54.49 |

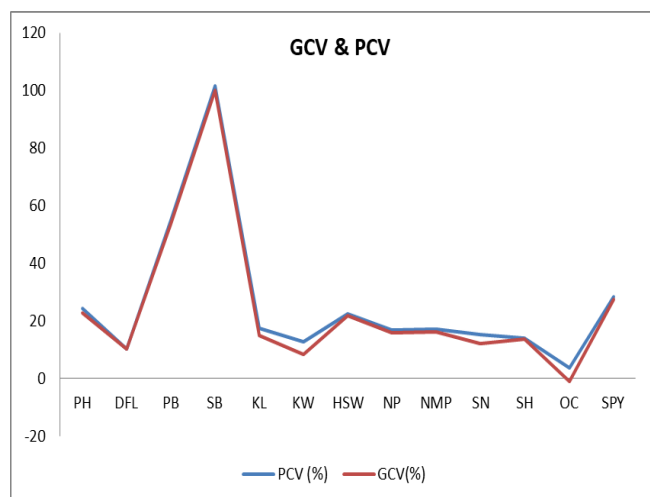


Fig 1: Graphical representation of genotypic and phenotypic covariance obtained for various traits

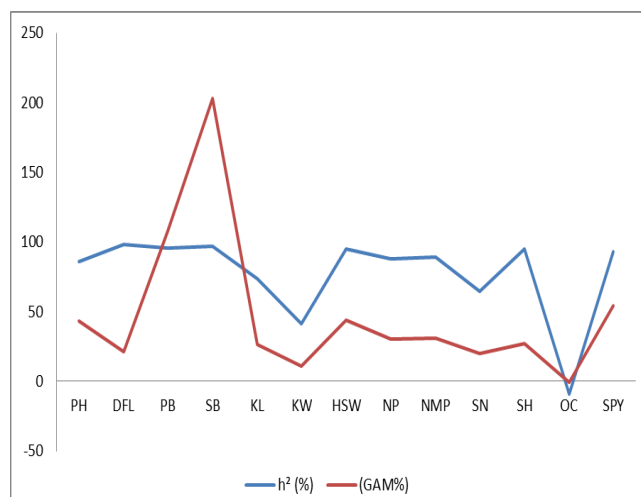


Fig 2: Graphical representation of heritability and GAM obtained for various traits

Conclusion

In this study, the estimates of PCV and GCV was expressed higher for plant height, primary branches per plant, secondary branches per plant and hundred seed weight. Higher heritability and genetic advance as a percent of mean was observed for all traits included in this study except kernel width and oil content which indicates that the presence of additive genes in these traits and further suggest for crop improvement through selection of such traits.

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