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Genetic variability studies in large seeded peanut (*Arachis hypogaea* L.)

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Abstract
The present investigation was carried out with 66 genotypes of peanut, pooled from ICRISAT, Patancheru, Hyderabad, ARS, Kadiri and RARS, Tirupati and experiment laid out in a randomized block design with two replications at Agricultural College farm, Bapatla, Guntur, Andhra Pradesh during *kharif* – 2019 to study the genetic variability on 21 characters of peanut. For all of the traits, analysis of variance revealed that the mean sums of squares owing to genotypes were significant.. Results of genetic parameters showed that traits *viz*., number of mature pods per plant, number of immature pods per plant, weight of pods per plant, kernel weight per plant, 100 seed weight, free amino acids, total soluble sugars and oleic linoleic acid ratio showed high genetic variability (GCV and PCV), high heritability (H_{bs}) coupled with high genetic advance as per cent of mean (GAM), indicating the predominance of additive gene action in these traits. Direct selections for higher phenotypic values of these traits will be effective in improvement of these characters among the genotypes.

Keywords: Peanut, GCV, PCV, Heritability, GAM

Introduction
Peanut (*Arachis hypogaea* L.) is popularly referred as the "King of oilseeds" and is a self-pollinated annual herbaceous legume belonging to the family *Leguminoceae*. It is a native to South America (Brazil) and is cultivated all around the world *viz*., tropical, sub-tropical and warm temperate regions. Peanut is amongst the most important protein-rich vegetable oilseed crops. Nutritionally it contains 36% to 54% oil, 16% to 36% protein and 10% to 20% carbohydrates. It supplies about 5.6 calories per kernel when eaten raw and 5.8 calories per kernel when consumed roasted (Sendekie *et al*., 2020) [22]. India ranks second in peanut production (67.27 lakh tonnes) and is after that to China (175 lakh tonnes) with an export of 641125 tonnes of confectionery types, earning foreign exchange of Rs. 5429.22 crores (FAO, 2019) [7]. India used to export nuts with 40 to 60 counts from handpicked selections from existing small seeded varieties due to lack of large seeded genotypes. The efforts made at national level to improve confectionery peanuts, as well as work at the Bhabha Atomic Research Centre (BARC), resulted in the introduction of various large seeded genotypes, including TG1, TKG 19A and Somnath for cultivation in India (Kale *et al*., 2000) [11]. Birsa Bold 1 was one of India's first confectionary types to be grown (Rahman *et al*., 1995) [19]. As peanut is a key oilseed crop and also used for confectionary purpose, there is a need to progress the quality traits of peanut. Genetic variability is a vital prerequisite for crop improvement programme for obtaining high yielding varieties, through the estimation of diverse genetic parameters such as genotypic and phenotypic coefficient of variations, heritability and genetic advance. Therefore, the current experiment was designed to estimate the genetic parameters for yield and quality traits in large seeded peanut.

Materials and Methods
The experimental material comprised of sixty six lines of peanut genotypes, pooled from ICRISAT, Patancheru, Hyderabad, ARS, Kadiri and RARS, Tirupati. The experiment was laid out in a randomized block design with two replications and sown two rows of each genotype of 4 m length with spacing of 45 cm between rows and 15 cm between the plants during *kharif* - 2019 at Agricultural College farm, Bapatla, Guntur, Andhra Pradesh. The recommended package of practices were followed for raising a healthy crop and all necessary plant protection measures were taken to control the insect pests and diseases. The data were recorded from five randomly selected plants in each of the genotype per replication for yield and quality traits.

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Days to 50% flowering and days to maturity were recorded on plot basis. The mean values were used for analysis for variance. The statistical analysis for variance was worked out according to Panse and Sukhatme (1985) [17]. The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton (1952) [5]. The estimates of PCV and GCV were classified as low (< 10%), moderate (10 - 20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973) [23].

$$PCV = \sqrt{\sigma_p^2} \times 100 \div \overline{X} \qquad (1)$$

Where; PCV = Phenotypic coefficient of variation
$\overline{X}$ = Mean value of the trait

$$GCV = \sqrt{\sigma_g^2} \times 100 \div \overline{X} \qquad (2)$$

Where; GCV = Genotypic coefficient of variation
$\overline{X}$ = Mean value of the trait

Heritability in broad sense was estimated by using the formula given by Allard (1960) [1] and was expressed in percentage. The estimates of heritability were classified as low (< 50%), moderate (50 - 70%) and high (> 70%) according to Robinson (1966) [20].

$$\text{Heritability } (h^2) \text{broad sense} = \left(\frac{\sigma_g^2}{\sigma_p^2}\right) \times 100 \qquad (3)$$

Where, σ_g^2 = Genotypic variance
σ_p^2 = Phenotypic variance

Genetic advance and genetic advance as per cent of mean were computed and categorized as low (< 10%), moderate (10 - 20%) and high (> 20%) according to the method suggested by Johnson et al. (1955) [10].

$$\text{Genetic advance (GA)} = I\sigma_p h^2 \qquad (4)$$

Where, I = Selection differential (2.06) at five per cent intensity
σ_p = Phenotypic standard deviation, h^2 (bs) = Heritability in broad sense

$$\text{Genetic Advance as per cent of Mean} = \frac{GA}{\overline{X}} \times 100 \qquad (5)$$

Where, GA = Genetic advance
$\overline{X}$ = General mean

Genetic parameters were calculated on 21 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of mature pods per plant, number of immature pods per plant, weight of pods per plant (g), kernel weight per plant (g), sound mature kernel per cent (%), shelling percentage (%), 100- seed weight (g), oil content (%), protein content (%), free amino acids (μg g^{-1}), total soluble sugars (%), palmitic acid (%), stearic acid (%), oleic acid (%), linoleic acid (%) and oleic linoleic acid ratio by using standard statistical procedures.

Results and Discussion

Analysis of variance indicated that the mean sums of squares due to genotypes were found to be significant for all the traits. This indicates the presence of phenotypic variability among peanut genotypes for kernel yield and its contributing traits, non-significant mean squares for replications for each character indicative of homogeneity of experimental plot (Table 1).

The GCV and PCV values indicated that lot of variability exists among the different traits of genotypes at genotypic and phenotypic level and better chances of improvement is possible by selection. The PCV was slightly higher than GCV for all the traits, indicating influence by environment on the expression of the traits. The sufficient amount of variability present in the nature would provide the scope to the breeder for further improvement. High values of GCV and PCV were recorded for secondary branches per plant, number of mature pods per plant, number of immature pods per plant, weight of pods per plant, kernel weight per plant, 100 seed weight, free amino acids, total soluble sugars and oleic linoleic acid ratio which indicates that the variation for these characters substantially contributes to the total variability (Table 2) and these outcome overlap with in advance reports presented by Arunakumari et al. (2019) [3] for secondary branches per plant and number of mature pods per plant; Nistha Mohapathra and Hasan Khan (2020) [15] for number of immature pods per plant, weight of pods per plant and kernel weight per plant; Vinithashri et al. (2019) [24] for 100 seed weight; Arunakumari et al. (2019) [3] for free amino acids and total soluble sugars and Patidar and Nadaf (2017) [18] for oleic linoleic acid ratio.

In the present study moderate values of PCV and GCV were noticed for days to 50% flowering, palmitic acid, stearic acid and linoleic acid (Table 2). It indicated that these characters exhibited less variation and these results coincide with earlier reports made by Aparna et al. (2018) [2] for days to 50% flowering; Nistha Mohapathra and Hasan Khan (2020) [15] for palmitic acid and Saini and Sharma (2018) [21] for stearic acid and linoleic acid. In the present study low values of PCV and GCV were noticed for days to maturity, sound mature kernel per cent, shelling percentage, oil content, protein content and oleic acid (Table 2) and it indicates that these characters exhibited very less variation to total variability and similar results were obtained by Kumari and Sasidharan (2020) [12] for days to maturity; Nistha Mohapathra and Hasan Khan (2020) [15] for sound mature kernel per cent; Boodi et al. (2017) [4] and Gonyanayak et al. (2018) [8] for shelling percentage and Patidar and Nadaf (2017) [18] for oil content, protein content and oleic acid.

The heritability estimates in 'broad sense' comprises both additive and non-additive gene effects (Hanson et al., 1956) [9] and in narrow sense includes only additive components (Lush, 1949 in animals and Johnson et al., 1955 in plants) [13, 10]. Knowledge of heritability of traits is an essential tool, which can be employed by the breeder in improving the trait underspecified situation.

In the current investigation, all the characters showed low to high estimates of broad sense heritability ranging from 27.53% (number of primary branches per plant) to 99.64% (linoleic acid). The characters viz., days to 50% flowering, days to maturity, number of mature pods per plant, number of immature pods per plant, weight of pods per plant, kernel weight per plant, sound mature kernel per cent, 100 seed

weight, oil content, protein content, free amino acids, total soluble sugars, palmitic acid, stearic acid, oleic acid, linoleic acid and oleic and linoleic acid ratio showed very high estimates of broad sense heritability (Table 2). These results indicate that the selection based on these traits would be effective as they are likely to be controlled by additive genes (Panse, 1942) [16]. A character having higher heritability estimate in self-pollinated crop is more likely to be controlled by additive genetic variation, thus selection could be more suitable through phenotypic means (Falconer, 1960) [6].

In the present study, high heritability coupled with high genetic advance as per cent of mean was obtained for the characters *viz.*, days to 50% flowering, number of mature pods per plant, number of immature pods per plant, weight of pods per plant, kernel weight per plant, 100 seed weight, free amino acids, total soluble sugars, stearic acid, linoleic acid and oleic linoleic acid ratio (Table 2) and similar results previously registered by Aparna *et al*. (2018) [2] for days to 50% flowering and number of mature and immature pods per plant; Kumari and Sasidharan (2020) [12] and Nistha Mohapathra and Hasan Khan (2020) [15] for weight of pods per plant, kernel weight for plant and 100 seed weight; Arunakumari *et al*. (2019) [3] and Meghaldevi *et al*. (2019) [14]

for free amino acids; Arunakumari *et al*. (2019) [3] for total soluble sugars; Nistha Mohapathra and Hasan Khan (2020) [15] for stearic acid and linoleic acid and Patidar and Nadaf (2017) [18] for oleic linoleic acid ratio. Selection made through these characters would be effective as they are more likely to be controlled by additive gene action.

Results showed that moderate heritability coupled with moderate genetic advance as percent of mean for shelling percentage (Table 2). Thus these traits are not suitable for effective selection of desirable plants as these traits are predominantly under non additive genetic control. Such findings are also reported made by Boodi *et al*. (2017) [4] and Gonyanayak *et al*. (2018) [8]. High heritability coupled with moderate genetic advance as per cent of mean was observed for sound mature kernel per cent, protein content, palmitic acid and oleic acid and it's implying the prevalence of both additive and non additive gene action in the inheritance of these traits (Table 2) and these results were in agreement with findings noticed by Arunakumari *et al*. (2019) [3] and Nistha Mohapathra and Hasan Khan (2020) [15] for sound mature kernel per cent; Nistha Mohapathra and Hasan Khan (2020) [15] and Saini and Sharma (2018) [21] for palmitic acid and Patidar and Nadaf (2017) [18] for oleic acid.

Table 1: Analysis of variance for kernel yield and its contributing traits in peanut

S. No.	Traits	Mean Sum of Square		
		Treatment (df = 65)	Replication (df = 1)	Error (df = 65)
1	Days to 50% flowering	27.454**	7.280	2.634
2	Days to maturity	25.090**	3.667	3.190
3	Plant height (cm)	36.069**	3.418	9.664
4	Number of primary branches per plant	0.764*	0.453	0.434
5	Number of secondary branches per plant	3.368**	1.858	0.631
6	Number of mature pods per plant	22.117**	2.417	2.004
7	Number of immature pods per plant	8.625**	0.856	0.985
8	Weight of pods per plant (g)	55.173**	27.235	8.451
9	Kernel weight per plant (g)	26.912**	0.257	3.143
10	Sound mature kernel per cent (%)	75.406**	11.940	3.939
11	Shelling percentage (%)	48.929**	21.211	9.182
12	100 seed weight (g)	1115.669**	28.440	13.968
13	Oil content (%)	11.510**	1.929	1.766
14	Protein content (%)	9.792**	0.644	1.605
15	Free amino acids ($\mu g\ g^{-1}$)	0.405**	0.006	0.002
16	Total soluble sugars (%)	19.706**	0.287	0.309
17	Palmitic acid (%)	1.827**	0.081	0.186
18	Stearic acid (%)	0.320**	0.010	0.032
19	Oleic acid (%)	58.597**	0.273	1.339
20	Linoleic acid (%)	59.937**	0.024	0.110
21	Oleic linoleic acid ratio	31.159**	0.015	0.059

*, ** - Significantly different at 5% and 1% probability levels respectively   df - Degrees of Freedom

Table 2: Genetic parameters for yield and quality traits of peanut

S. No.	Characters	Mean	Range	PCV	GCV	H (bs) %	GAM
1	Days to 50% flowering	32.33	24.00-40.00	12.00	10.90	82.49	20.39
2	Days to maturity	121.30	110.00-127.50	3.10	2.73	77.44	4.95
3	Plant height (cm)	23.02	13.29-31.06	20.77	15.78	57.74	24.70
4	Number of primary branches per plant	5.35	4.02-6.47	14.45	7.58	27.53	8.19
5	Number of secondary branches per plant	4.42	1.59-8.41	31.92	26.41	68.50	45.01
6	Number of mature pods per plant	14.69	9.69-26.03	23.69	21.63	83.38	40.69
7	Number of immature pods per plant	5.76	2.67-13.28	38.08	33.96	79.51	62.38
8	Weight of pods per plant (g)	20.15	8.66-34.23	27.99	23.99	73.43	42.35
9	Kernel weight per plant (g)	12.62	5.73-25.91	30.71	27.31	79.10	50.03
10	Sound mature kernel per cent (%)	82.44	66.80-94.31	7.64	7.25	90.07	14.18
11	Shelling percentage (%)	65.45	52.89-74.81	8.24	6.81	68.40	11.60
12	100 seed weight (g)	85.13	31.77-121.46	27.92	27.57	97.53	56.09
13	Oil content (%)	46.21	41.87-50.89	5.57	4.77	73.40	8.42
14	Protein content (%)	28.22	24.06-33.50	8.46	7.17	71.84	12.52

15	Free amino acids (µg g^{-1})	0.77	0.36-3.48	58.62	58.30	98.91	119.45
16	Total soluble sugars (%)	7.62	3.02-16.12	41.51	40.86	96.91	82.87
17	Palmitic acid (%)	8.83	5.33-11.55	11.36	10.26	81.49	19.07
18	Stearic acid (%)	3.00	2.14-3.97	13.97	12.62	81.63	23.49
19	Oleic acid (%)	54.84	43.77-78.96	9.98	9.76	95.53	19.64
20	Linoleic acid (%)	27.87	2.86-36.62	19.66	19.63	99.64	40.35
21	Oleic linoleic acid ratio	2.61	1.20-27.52	151.48	151.19	99.62	310.86

GCV = Genotypic Coefficient of Variation   PCV = Phenotypic Coefficient of Variation
$H_{(bs)}$ % = Heritability (broad sense) in percentage   GAM = Genetic Advance as per cent of Mean

Conclusion
Significant mean sums of squares due to genotypes were observed for all the traits through analysis of variance. It was revealed that genetic variability analysis will be able to distinguish traits among genotypes. The genotypic variance was slightly smaller than phenotypic variance for majority of traits studied; it showed that environment did exert masking influence on the expression of genetic variability. The traits number of mature pods per plant, number of immature pods per plant, weight of pods per plant, kernel weight per plant, 100 seed weight, free amino acids, total soluble sugars and oleic linoleic acid ratio showed high GCV and PCV, high heritability coupled with high genetic advance as per cent of mean indicating that these characters controlled by additive gene effect thus selection in these traits would be quite effective.

Acknowledgments

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