

Biological Forum – An International Journal

15(11): 520-525(2023)

ISSN No. (Print): 0975-1130 ISSN No. (Online): 2249-3239

Studies on variability for Yield and Yield Attributing Traits in Groundnut [*Arachis hypogaea* (L.)]

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(Received: 12 September 2023; Revised: 14 October 2023; Accepted: 22 October 2023; Published: 15 November 2023)

(Published by Research Trend)

ABSTRACT: Evaluating the presence of variability is crucial when planning a breeding program for efficient genetic improvement and promising variety development. This assessment ensures a diverse genetic pool, providing the raw material needed to select and breed individuals with desirable traits. Forty-two groundnut genotypes were evaluated for the assessment of genetic variability, heritability and genetic advance expressed as *percent* of mean during *Kharif* 2022. Analysis of variance revealed existence of quite substantial differences among the genotypes for all the characters examined. The values of GCV were slightly lower than PCV showing a minor effect of environment over all the characters. Moderate values of GCV and PCV were recorded for characters like, pod yield per plant, number of mature pod per plant, 100-kernel weight, plant height and harvest index. Harvest index, pod yield per plant and number of mature pod per plant showed the high estimates of heritability along with the high genetic advance expressed as *per cent* of mean, indicating the preponderance of additive gene action in governing the inheritance nature of these characters and selection for these traits would be advantageous for genetic improvement.

Keywords: Genetic variability, Groundnut, GCV, PCV, Heritability, Genetic advance.

INTRODUCTION

"Groundnut (Arachis hypogaea L.) plays a pivotal and indispensable role as a leading oilseed crop within the boundaries of India, as well as across tropical and subtropical domains globally. The term 'groundnut' finds its etymology rooted in the ancient Greek word, with 'Arachis' signifying a leguminous plant, and 'hypogaea' elegantly indicating the underground development of pod. This complicated process demonstrates that the pods mature gracefully beneath the terrestrial surface. Groundnut is most unpredictable crop in the world because of the pods develop underground (an unusual feature known as positive geotropism) and by-which we cannot predict the crop yield (Weiss, 2000). Generally, the pods of peanut are 3 to 7 cm long and normally containing one to four seeds, which is major component of yield. The cultivated groundnut exhibits highly selfpollination. It has also a prominent height as a member of the leguminous group, characterized by a chromosomal arrangement denoted as 2n=4x=40 and securely settled within the botanical family known as Fabaceae (Kushman and Beattie 1946). In the context of groundnut production, India trails only China, securing its status as the second-largest contributor to this realm. Notably within the Indian countryside, the state of

Gujarat emerges as a foundation stone in the cultivation of groundnut, enveloping a extensive area of 2.16 million hectares and composing the harvest of an abundant 4.13 million tons, thus giving a productivity of 1912 kg per hectare during the period marked as 2021-22 (Anonymous, 2021-22). The versatility of groundnut finds resonance in its multilayered utility, on both sides of culinary oil extraction and delicious confectionery creations. The kernels of groundnut contain good amount of oil (comprising 48-50%) and protein content (comprising 25-28%). Groundnut oil contains high amount of oleic and linoleic acid. The relative proportion of oleic acid and linoleic acid in groundnut oil determines oil quality and storage life (Wagh et al., 2023). Remarkably, a mere 100g of groundnut kernels gives a caloric endowment of 564 kcal (Jambunathan, 1991). Symbiotic bacteria (*Rhizobium* sp.) are present in the root nodules of groundnut, which is the main component of nitrogen fixation by crop. Peanuts are important in crop rotations because they lower the requirement of fertilizer that contains nitrogen and also increase soil fertility because of their capacity to fix nitrogen. As per the national peanuts board mainly four types of peanuts that is Runner, Virginia, Spanish and Valencia. A systemic breeding program relies on knowledge of the type and degree of variability in population resulting from genetic

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and non-genetic causes. The study of the level of genetic variability present in the existing genotype has become crucial, since genetic variability is necessary for the beginning of an efficient and effective breeding strategy. The study of genetic advance with heritability estimates could further clarify the nature of characters which can be improved through selection. Therefore, the present study was planned to estimate variability, heritability and genetic advance expressed as per cent of mean for yield and its attributing traits.

MATERIALS AND METHODS

The experimental material had 42 groundnut genotypes belonging to different botanical types viz; Spanish bunch and Virginia bunch evaluated at Cotton Research Station, Sardarkrushinagar Dantiwada Agricultural University, Talod during *kharif* 2022. Sowing took place on the 5th of July, 2022. The entire arrangement followed a Randomized Block Design, encompassing four replications. Each individual entry was sown within a single row spanning 4 meters in length, maintaining a spacing configuration of $45 \text{ cm} \times 10 \text{ cm}$. The temperature ranges from 25°C to 35°C and the average humidity was 91.5 % along with 675.5 mm total rainfall received during entire crop period. The experimental material was evaluated for ten characters viz., days to 50 % flowering, days to maturity, plant height (cm), number of primary branch per plant, number of mature pod per plant, pod yield per plant (g), 100-kernel weight (g), shelling percentage (%), harvest index (%) and oil content (%). Observations were recorded for five randomly selected plants from each genotype in each replication at appropriate crop growth stage except with time taken for half blossoming and days taken for full ripeness. Oil content was estimated with the help of Nuclear Magnetic Resonance (NMR) machine.

Statistical analysis. The data collected for all traits underwent for analysis of variance using the methodology proposed by Panse and Sukhatme (1978). Various variability parameters were calculated from the different formula given by respected scientists.

Coefficients of Variation: The amount of inherent variability present within the population of crop can be estimated in large scale by observing the genotypic and phenotypic coefficients of variation. The genotypic coefficient of variation measures the innate genetic differences between population and reveals the relative genetic diversity among them. On other hand, phenotypic coefficient of variation consists of all type of variability, including genetic and environmental types. These coefficients are crucial tools for biological study because they provide a quantifiable view of the degree of diversity present within a population and direct selection methods for better results. Using the formula proposed by Burton (1952), the genotypic and phenotypic coefficients of variation are estimated for several traits. Phenotypic coefficient of variation (PCV%):

$$PCV\% = \frac{\sqrt{\sigma_p^2}}{\sqrt{\tau}} \times 100$$

• Genotypic coefficient of variation (GCV%):

$$\text{GCV\%} = \frac{\sqrt{\sigma_{\text{g}}^2}}{\bar{x}} \times 100$$

Where, σ_p^2 = Phenotypic variance, σ_g^2 = Genotypic variance and x = Population mean

Heritability (broad sense) h²_(b): In mostly plant breeding experiment, the broad sense heritability $[h^{2}_{(b)}]$ is calculated rather than narrow sense heritability, because narrow sense heritability is the ratio additive genotypic variance to total or phenotypic variance. Genotypic variance contains both additive and non-additive genetic variance. For narrow sense heritability, we must need to obtain additive genetic variance from the total genetic variance, but it is very difficult to separate both from each other and makes calculation very complex and tedious. While, broad sense heritability is the ratio of genetic variance to total phenotypic variance. There is no need to separate in case of broad sense heritability. Heritability (broad sense) $h^{2}_{(b)}$ is good component that delineates the fraction of overall phenotypic variability in a population that comes from the total genetic divergence. It was calculated using the formula suggested by Allard (1960):

$$h_{(b)}^2 \% = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

Expected genetic advance (GA) (Genetic gain):

It measures how much selected plants' mean genotypic values have improved relative to their ancestral population. It might be determined using Allard's (1960) approach with a selection intensity of 5% and a constant of 2.06 for "k".

G.A. = $h^{2}_{(b)} \times K \times \sigma_{p}$

Where,

Κ

= Genetic advance

G.A. Heritability (broad-sense) $h^{2}(b)$ _

Selection intensity at 5 percent (2.06) Phenotypic standard deviation =

σ_p Genetic advance expressed as *percent* of mean:

The formula proposed by Johnson et al. (1955) was used to compute the genetic advance express as a percentage of the mean.

Genetic gain
$$\% = \frac{\text{Expected genetic advance (GA)}}{100} \times 100$$

x Table 2 showed the categorization of genetic estimations. Sivasubramanian and Madhavamenon (1973)categorized GCV and PCV. Robinson et al. (1949) categorized heritability and Johnson et al. (1955) categorized GAM.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters studied (Table 3). These gives the evidence of sufficient amount of variability present among the genotypes and we can use them as parent for future breeding programme for further genetic improvement by utilizing suitable breeding method. Here, replication was significant in oil content, which was may be due to polygenic nature of these trait and it was affected by factors like soil heterogeneity and environment determinants. The values of various parameters like, GCV, PCV, heritability and GAM was displayed in Table 4.

The values of genotypic coefficient of variation were slightly lower than phenotypic coefficient of variation showing a minor effect of environment over all the characters (Table 4). This effect reduced by following

various methods carefully like, proper site selection, crop rotation, improved irrigation management, Integrated Pest Management (IPM), varietal selection, crop protection. microclimate manipulating, proper optimizing the fertilizer application etc. Moderate values of GCV and PCV were recorded for characters like, harvested output per individual, number of mature pod per plant, mass of a hundred seeds, length of mature plant at time of harvesting and harvest index, indicates moderate variability present in population. This happens because of there may be greater role of environment factors (climate, soil, pests and diseases) on the expression of these traits and also due to the performance of genotype is differed in changing environment. Similar results for various traits obtained by different peoples viz., Gupta et al. (2015); Ashutosh et al. (2017); Veer et al. (2021) for pod yield per plant, Ashutosh et al. (2017) and Bhargavi et al. (2016) for quantity of fully grown pods per individual, Gupta et al. (2015); Bhargavi et al. (2016); Yadav et al. (2023) for 100-kernel weight, Zaman et al. (2011); Gupta et al. (2015); Chavadhari et al. (2017); Raza et al. (2018) for plant height and Ashutosh et al. (2017); Roy et al. (2018); Raza et al. (2018); Kumar et al. (2019) for harvest index. There was low GCV and moderate PCV observed for shelling percentage. Veer et al. (2021); Shendekar et al. (2023) observed similar result for low GCV and Gupta et al. (2015); Aparna et al. (2018); Raza et al. (2018) observed similar result for moderate PCV for shelling percentage.

While, low GCV and PCV were observed for oil content followed by time taken for full growth, days to 50 per

cent flowering and primary branches per plant. This shows that there doesn't seem a lot of diversity in the qualities that have been detected in the groundnut population, which can limit the possibilities for development through breeding and simple selection for improvement of these traits. Similar results obtained by Kumar *et al.* (2019); Wagh *et al.* (2023) for oil content, Shendekar *et al.* (2023) for days to maturity and days to 50% flowering and Veer *et al.* (2021) for primary branches per plant.

Heritability was estimated to predict the inheritance capacity of genotypes to transfer characters (Genes) from one generation to another. Heritability is a fundamental parameter in quantitative genetics, which deals with the inheritance of complex and quantitative traits which is influenced by polygenes. Characters which displayed high heritability are more likely to respond to selection as they have a stronger genetic component. High heritability estimates were observed for various characters like, harvest index followed by pod yield per plant, quantity of fully grown pods per individual, plant height and primary branches per plant, indicated that all these characters were governed by additive gene action and presence of least environmental influence.

Genetic advance expressed as *percent* of mean was high for pod yield per plant, mature pods per plant and ratio of edible yield to total biomass, indicating the predominance of additive gene action and straight selection could be effective for improvement of these characters. While, other characters show moderate to low values.

Sr. No.	Genotype		Sr. No.	Genotype	Genotype		Genotype	
1.	JSSP- 68		16.	JB- 1487		31.	JVB- 2571	
2.	JSSP- 69		17.	J- 114		32.	JVB- 2577	
3.	JSSP- 70		18.	JB- 1488		33.	KDG- 128	
4.	JSSP- 71		19.	JB- 1505		34.	IVK I 2021-1	VB
5.	JSSP-72		20.	TG- 88		35.	IVK I 2021-4	VD
6.	JSSP- 73	VB	21.	ICGV- 16697	SB	36.	IVK I 2021-5	
7.	NRCGCS- 623	VВ	22.	ICGV- 16668		37.	IVK I 2021-6	
8.	JVB- 2523		23.	GJG- 9		38.	IVK I 2021-9	
9.	JVB- 2525		24.	GJG- 32		39.	ISK I 2021-1	
10.	Kaushal		25.	TG- 37A		40.	ISK I 2021-3	CD
11.	GG- 20		26.	JL- 501		41.	ISK I 2021-6	SB
12.	GJG- 22		27.	JVB- 2551		42.	ISK I 2021-7	
13.	J- 108		28.	JVB- 2552	VD			
14.	J- 109	SB	29.	JVB- 2564	VB			
15.	J- 110		30.	JVB- 2565				

* VB= Virginia bunch type, SB= Spanish bunch type; Source: Cotton Research Station, S.D.A.U, Talod

Table 2:	Categorization	of genetic	estimates.
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Estimates	GCV&PCV (%)	Heritability (h ² _b) (%)	GAM (%)
Low	0 to 10	0 to 30	0 to 10
Moderate	10 to 20	30 to 60	10 to 20
High	More than 20	More than 60	More than 20

Sr.		Mean sum of square							
No.	Characters	Replications	Genotypes	Error					
	Degree of freedom (d.f)	3	41	123					
1.	Days to 50% flowering	6.441	11.926**	2.472					
2.	Days to maturity	8.334	14.356**	3.593					
3.	Plant height	32.002	170.063**	17.258					
4.	Number of primary branch per plant	0.101	0.616**	0.065					
5.	Number of mature pod per plant	1.536	32.529**	1.389					
6.	Pod yield per plant	1.594	66.221**	1.999					
7.	100-kernel weight	63.881	128.827**	25.262					
8.	Shelling percentage	10.926	129.627**	20.674					
9.	Harvest index	3.419	100.094**	1.375					
10.	Oil content	21.361**	0.539**	0.184					

Table 3: Analysis of variance (ANOVA) for different characters of groundnut genotypes.

*, ** Significant at 0.05 and 0.01 level of significance, respectively

Table 4: Range of variation, mean, variability parameters, heritability and genetic advance for ten characters in groundnut.

Sr. No.	Characters	Mean	Range	σ^2_{g}	$\sigma^2{}_p$	σ^2_e	GCV (%)	PCV (%)	h ² b (%)	GA	GAM (%)
1	Days to 50% flowering	29.40	26.25-35.0	2.36	4.83	2.47	5.22	7.47	48.87	2.21	7.53
2	Days to maturity	119.62	115.50-124.50	2.69	6.28	3.59	1.37	2.09	42.82	2.21	1.84
3	Plant height (cm)	53.49	40.40-65.80	38.20	55.45	17.25	11.55	13.92	68.88	10.56	19.75
4	Number of primary branch per plant	6.05	5.25-7.05	0.14	0.20	0.06	6.13	7.45	67.80	0.63	10.40
5	Number of mature pod per plant	18.92	13.85-24.40	7.78	9.16	1.38	14.74	16.00	84.85	5.29	27.98
6	Pod yield per plant (g)	25.03	17.50-32.30	16.05	18.04	1.99	16.01	16.97	88.92	7.78	31.10
7	100 kernel weight (g)	42.78	32.97-55.85	25.89	51.15	25.26	11.89	16.71	50.62	7.45	17.43
8	Shelling percentage (%)	56.63	45.18-72.00	27.23	47.90	20.67	9.21	12.22	56.85	8.10	14.31
9	Harvest index (%)	49.17	38.89-63.48	24.68	26.05	1.37	10.10	10.38	94.72	9.96	20.25
10	Oil content (%)	48.80	48.13-49.49	0.08	0.26	0.18	0.610	1.06	32.55	0.35	0.71

Where,

 σ_{g}^{2} , σ_{p}^{2} , GCV (%), PCV (%), h_{b}^{2} (%), GA and GAM (%) are genotypic variance, phenotypic variance, genotypic coefficient of variance, phenotypic coefficient of variance, broad sense heritability, genetic advance and genetic advance expressed as *percent* of mean, respectively.

Table 5: Mean values of genotypes for different characters in groundnut.

Sr. No.	Genotype	Days to flowering	Days to maturity	Plant height (cm)	Number of primary branch per plant	Number of mature pod per plant	Pod yield per plant (g)	100- Kernel weight (g)	Shelling percentage (%)	Harvest index (%)	Oil content (%)
1.	JSSP- 68	27.50	115.50	65.80	5.80	17.40	21.75	49.21	62.10	46.01	48.30
2.	JSSP- 69	28.50	118.00	57.05	6.45	23.65	30.25	36.30	54.33	50.82	48.13
3.	JSSP-70	28.00	116.75	51.80	5.80	15.40	20.25	44.63	48.16	57.69	48.24
4.	JSSP-71	30.25	120.00	58.05	5.75	16.70	20.20	33.97	52.90	51.32	48.54
5.	JSSP-72	30.00	118.25	63.60	6.10	18.58	25.20	47.07	52.43	53.37	48.73
6.	JSSP-73	29.00	119.00	60.65	5.65	13.85	20.20	50.02	66.38	45.81	48.57
7.	NRCGCS- 623	27.50	117.75	60.00	6.20	16.85	21.55	46.00	61.75	43.67	48.63
8.	JVB- 2523	29.50	120.50	57.85	6.15	18.40	25.85	37.57	51.43	41.93	48.47
9.	JVB- 2525	29.50	120.75	52.25	6.30	19.36	24.25	46.77	54.63	48.87	48.35
10.	Kaushal	31.00	120.50	47.00	6.30	15.35	21.40	36.69	50.45	48.34	48.49
11.	GG- 20	28.25	117.75	60.45	6.20	16.05	23.70	48.03	58.16	47.35	48.76
12.	GJG- 22	29.25	120.25	61.10	5.65	14.65	20.40	48.23	59.50	47.69	48.83
13.	J- 108	29.25	120.00	57.35	6.00	20.55	30.00	44.48	54.30	49.66	48.29
14.	J- 109	28.25	121.00	46.10	6.10	14.55	17.50	38.34	72.00	55.09	48.42
15.	J- 110	29.25	119.75	52.65	5.40	17.63	22.00	44.60	57.30	51.39	49.14
16.	JB- 1487	27.00	118.00	45.95	5.90	21.95	29.30	43.17	59.38	59.68	49.20
17.	J- 114	28.00	118.50	48.65	5.45	19.45	25.03	42.14	51.09	48.93	49.32
18.	JB- 1488	30.00	123.25	48.30	6.40	22.85	30.40	38.19	53.08	54.01	48.44
19.	JB- 1505	30.00	122.50	50.35	6.20	22.05	27.95	40.77	56.01	56.42	48.81
20.	TG- 88	27.50	117.75	43.70	5.35	17.21	18.85	43.38	63.14	52.38	48.78
21.	ICGV- 16697	28.25	119.00	49.65	5.85	22.86	32.30	44.76	56.07	50.43	49.20
22.	ICGV- 16668	31.25	121.50	54.40	6.10	20.95	27.60	38.05	53.19	49.35	48.90
23.	GJG-9	35.00	124.50	64.35	5.25	16.60	19.55	41.88	62.08	45.50	48.61
24.	GJG- 32	30.50	120.50	50.80	6.20	23.18	28.60	42.86	59.90	51.01	49.00
25	TG- 37A	29.75	119.50	56.70	6.05	24.40	30.40	38.29	49.20	53.36	48.67
26	JL- 501	29.75	120.25	60.15	5.35	17.05	20.70	33.95	47.64	63.48	49.04
27	JVB- 2551	29.75	120.25	59.45	6.20	18.85	26.15	55.85	58.71	42.59	49.11
28	JVB- 2552		117.00	58.15	6.45	17.05	27.05	51.54	66.31	38.89	48.93
29	JVB- 2564	31.00	120.25	40.40	5.80	17.60	21.80	34.91	53.49	46.65	49.01
30	JVB- 2565	32.00	122.00	43.30	6.10	16.55	26.10	48.54	51.32	47.11	49.49
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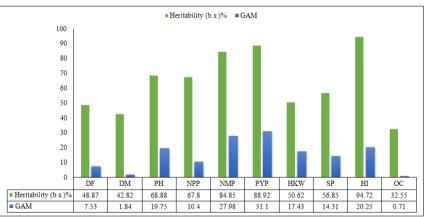
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31	JVB- 2571	31.25	120.50	45.80	6.25	20.05	24.90	40.35	55.40	47.01	48.95
32	JVB- 2577	29.00	118.25	45.75	6.65	21.35	30.73	49.78	56.18	43.74	48.71
33	KDG- 128	28.50	118.25	48.70	6.20	22.15	26.80	41.07	54.18	51.57	48.67
34	IVK I 2021-1	26.25	116.75	61.10	6.00	16.05	21.95	47.79	63.51	47.97	49.20
35	IVK I 2021-4	29.75	119.75	55.05	6.30	18.35	22.05	41.62	49.98	43.32	49.40
36	IVK I 2021-5	29.50	120.25	46.50	6.15	17.99	25.20	37.61	59.67	43.93	48.36
37	IVK I 2021-6	31.00	120.75	49.45	7.05	23.87	30.75	37.23	45.18	49.87	49.33
38	IVK I 2021-9	29.25	119.00	58.45	6.20	18.85	26.50	54.14	60.34	42.87	49.41
39	ISK I 2021-1	32.75	122.75	50.65	6.35	22.15	28.90	41.23	59.91	49.74	48.77
40	ISK I 2021-3	26.50	117.00	58.60	6.35	19.90	28.40	46.13	64.66	45.15	48.36
41	ISK I 2021-6	28.75	119.25	54.35	5.35	16.05	19.10	32.97	56.79	53.56	49.35
42	ISK I 2021-7	31.00	121.00	46.25	6.65	20.30	29.50	36.74	56.36	47.83	48.90
Gene	eral mean	29.40	119.62	53.49	6.05	18.92	25.03	42.78	56.63	49.17	48.80
Range	Minimum	26.25	115.50	40.40	5.25	13.85	17.50	32.97	45.18	38.89	48.13
Kalige	Maximum	35.00	124.50	65.80	7.05	24.40	32.30	55.85	72.00	63.48	49.49
S.E.m. ±		0.79	0.95	2.08	0.13	0.59	0.71	2.51	2.27	0.59	0.21
C.I). at 5%	2.20	2.65	5.81	0.36	1.65	1.98	7.03	6.36	1.64	0.60
	C.V.%	5.35	1.58	7.77	4.23	6.23	5.65	11.75	8.03	2.38	0.88



Where, DF= Days to flowering, DM = Days to maturity, PH= Plant height (cm), NPP= Number of primary branch per plant, NMP= Number of mature pod per plant, HKW= 100-kernel weight (g), SP= Shelling percentage (%), HI= Harvest index (%), OC= Oil content (%).

Fig. 1. Graphical comparison of Genotypic and Phenotypic coefficient of variation.



Where, DF= Days to flowering, DM= Days to maturity, PH= Plant height (cm), NPP= Number of primary branch per plant, NMP= Number of mature pod per plant, HKW= 100-kernel weight (g), SP= Shelling percentage (%), HI= Harvest index (%), OC= Oil content (%),

Fig. 2. Graphical comparison of Heritability and Genetic Advance as *percent* of mean.

High estimates of heritability along with high genetic advance expressed as *percent* mean was observed for harvest index followed by pod yield per plant and mature pods per plant, indicating the preponderance of additive gene action in governing the inheritance nature of these characters. So, selection for these traits would be beneficial for genetic improvement. However, careful consideration of environmental factors, genetic diversity and potential trade-offs is necessary to ensure that the selected traits result in balanced, resilient and sustainable crop varieties. Similar results recorded by Roy *et al.* (2018); Raza *et al.* (2018) for harvest index Suthar *et al.*, Biological Forum – An International Journal 15(11): 520-525(2023)

and Vinothini et al. (2023) for pod yield per plant and number of mature pod per plant. High heritability coupled with moderate GAM was observed for plant height and number of primary branch per plant, indicating that these characters were controlled by both additive and non-additive genes. Which indicates the pace of progress might not be rapid and careful selection, innovative techniques and genetic diversification can collectively contribute to enhancing genetic gains in groundnut traits. Similar results of high heritability were obtained by Gupta et al. (2015); Veer et al. (2021) for plant height and number of primary 524

branch per plant, while, moderate GAM were observed by Raza *et al.* (2018) for plant height and Ashutosh *et al.* (2017); Aditya *et al.* (2021) for primary branches per plant. Whereas, moderate heritability coupled with low GAM were observed for days taken for half blossoming, days taken for full ripeness and oil content, revealed the presence of non-additive gene effect and there was high influence of environment in the expression of these characters and therefore, selection would be not effective. Similar findings obtained by Roy *et al.* (2018); Kumar *et al.* (2019); for oil content, while, Raza *et al.* (2018); Veer *et al.* (2021) observed similar result for low GAM for days to maturity.

CONCLUSIONS

From present investigation, the results of analysis of variance showed sufficient variability present among the genotypes of groundnut. High estimates of heritability coupled with high GAM was observed for harvest index followed by pod yield per plant and mature pods per plant, indicating selection for these traits would be beneficial for genetic improvement in future breeding programs. The higher mean values of the genotypes for pod yield per plant were observed for ICGV-16697 followed by IVK I 2021-6, JVB-2577 and TG-37A (Table 5) highlights the best genotypes for genetic improvement and we can used as parents in further breeding programme.

Acknowledgements. The authors are thankful to Dr. D.G. Patel, Assistant Research scientist, Cotton Research Station, S. D. Agricultural University, Talod, Gujarat for providing the facilities, genotypes and support for conducting of my experiment.

Conflict of Interest. None.

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How to cite this article: D.M. Suthar, D.G. Patel, P.R. Patel and N.V. Soni (2023). Studies on variability for Yield and Yield Attributing Traits in Groundnut [*Arachis hypogaea* (L.)]. *Biological Forum – An International Journal*, *15*(11): 520-525.