

GENETIC VARIABILITY CHARACTER ASSOCIATION AND HERITABILITY OF ADVANCED BREEDING LINES OF GROUNDNUT (*Arachis hypogaea* L.)

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ABSTRACT

Groundnut is considered as an important cash crop especially among the poor communities in dry and intermediate zones of Sri Lanka. Crop improvement of groundnut is predominantly done using conventional breeding technologies. Therefore, understanding the genetic variability, heritability and other genetic parameters of existing genetic resources are highly useful in improving the breeding program. The genetic variability, character association and heritability of 18 groundnut genotypes which mostly consisted of advanced breeding lines developed at Grain Legumes and Oil Crops Research and Development Center, Angunakolapelessa (GLORDC) were studied during 2022/23 Maha season. The experiment was layout in RCBD design with 3 replicates and qualitative and quantitative parameters were recorded according to groundnut descriptor. Significant differences were observed in characters other than leaf length and number of pods per plant. PCV and GCV magnitude was moderate for height of main stem (PCV 19.57, GCV 15.49), plant width or spread (PCV 15.22 GCV 11.87), seed length (PCV 18.88 GCV 14.34) and pod length (PCV 13.01 GCV 11.80). High heritability was observed for main stem height (RD62.60 GA25.24), pod length (RD82.21 GA 22.04) and 100 seed weight (RD81.33 GA 35.52) with high Genetic advance. These traits are mainly controlled by additive gene action and are shown to be responsive to further improvement. Yield was observed to have a positive and highly significant correlation with pod weight per plant (0.646**). 100 seed weight was observed to have a positive and highly significant correlation with seed length (0.637**) and seed width (0.729**). These correlation indices can be used as indirect selection criteria in generation advancements. Overall, sufficient variability was observed in the breeding lines observed and selections based on traits of interest need to be carried out in order to advance such promising lines in the pipe line.

Keywords: Correlation analysis, Genetic variability, Groundnut, Heritability

INTRODUCTION

Groundnut (*Arachis hypogaea* L) is one of the most important crops with both economic and nutritional value in the world. It provides a good supply of protein, oil, and other crucial nutrients. On a dry seed basis, groundnut seeds contain 22–32% protein and 46%–58% oil (Zhuang et al., 2019). In Sri Lanka, the dry and intermediate zones are where groundnut crops are primarily grown. The annual cultivation area in 2020 was 15,752 hectares and 27,602 tons of pods were produced (Agstat, 2020). Sri Lanka's groundnut improvement program continues to rely on plant introductions from international research centers. Since Sri Lanka has no wild relatives of groundnut, foreign parent material was used to develop varieties through hybridization and selection (Jeewani et al., 2021). Plant genetic variability plays a critical role in shaping plant traits such as growth, development, disease resistance and adaptation to environmental conditions. This diversity is the basis for improving crop yields, developing new varieties and ensuring the sustainability of agriculture in the face of challenges such as climate change and food security issues. To identify suitable genotypes and create effective

breeding plans in the context of peanut breeding, understanding the scope and nature of genetic variation is essential. Additionally, Correlation is a biometrical approach that brings out the intensity of the association between two pairs of characters and provides information on those components that could serve as criteria for the selection of candidates in a breeding program (Reddy et al, 2023). Understanding the genetic variability and related genetic components of the available genetic materials would be important in plant breeding programs as it can provide valuable information on the variability of traits of interest and how to improve such traits. With this intention present study was carried out in order evaluate the variability of advanced breeding lines developed at Grain Legume and Oil Crop Research and Development Centre in Angunakolapelessa, Sri Lanka. In addition, to pinpoint certain features that could be targeted for further improvement, character association and heritability of advanced breeding lines of groundnut were examined in parallel.

MATERIALS AND METHODS

Experimental Location

The study was carried out during the *Maha* season of 2022/23 at the Grain Legume and Oil Crop Research and Development Centre in Angunakolapelessa, which is located in the Hambantota District of the Southern Province. This area falls under the Low Country Dry Zone (DL1b) and receives an average annual rainfall between 1020 to 1050mm with an average annual temperature ranging from 28-31°C. The soil type of the experimental site was identified as Reddish Brown Earth (RBE).

Genetic Materials

Eighteen groundnut breeding lines have been used for this study, all of which have been developed through hybridization and selection at GLORDC. The pedigrees and other information on the breeding lines are listed in Table 1.

Experimental Design

The experiment was conducted in a randomized complete block design (RCBD) with three replications. The plot size was 3 × 1.8 meters and each plot was spaced 0.5m apart. All cultural practices were carried out according to DOA recommendations. Randomly selected five plants of each plot were used to collect quantitative and qualitative data according to groundnut descriptor published by Plant Genetic Resources Center, Department of Agriculture, 1995. Eleven quantitative traits (Table 2) were considered during morphological characterization.

Statistical analysis

The SAS (statistical analysis software) version 9.4 was used to test the significant differences using the analysis of variance (ANOVA) procedure at the level of LSD ($P \leq 0.05$) and to compare the means of significant traits. Pearson correlation was applied using SPSS statistical package to find out the inter-correlation among the traits.

Analysis of genetic parameters

Following equations were used to estimate the genetic parameters using the values of ANOVA table.

Genotypic Variance (σ_g^2) and Phenotypic Variance (σ_p^2)

$$\sigma_g^2 = \frac{MSG - MSE}{r}$$

$$\sigma_p^2 = \sigma_g^2 + MSE$$

(Singh, 1985)

Where,

σ_g^2 is the Genotypic Variance, σ_p^2 is the Phenotypic variance, MSG is the genotypic mean square, MSE is the error mean square, r is the replication number

Phenotypic and Genotypic Coefficient of Variation (PCV and GCV)

The phenotypic and genotypic coefficient of variation were estimated as per formula given by (Sivasubramanian S & Madhavamenon P, 1973).

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

$$RD = (PCV - GCV / PCV)$$

Where,

PCV is the phenotypic coefficient of variation, GCV is the genotypic coefficient of variation, $\bar{X}$ is the grand average of the traits, σ_p^2 is the phenotypic variance, σ_g^2 is the genotypic variance, RD is the relative difference between PCV and GCV.

The estimated values of PCV and GCV were categorized by (Sivasubramanian & Madhavamenon, 1973; Robinson & Comstock, 1950).

0 – 10%	= Low
10% – 20 %	= Intermediate
More than 20 %	= High

Heritability Estimates

Heritability refers to the proportion of genotypic variance with phenotypic variance multiplied by hundred. The formula was given by (Falconer, 1996) was followed:

$$h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The heritability percentage was categorized by (Johnson et al., 1955) (Assefa et al., 1999).

0 – 30%	= Low
31 – 60%	= Intermediate
Greater than 60%	= High

Estimated and Expected Genetic Advance

Expected genetic gain (GA) was calculated according to Johnson, et al., 1955.

Selection intensity (K) was assumed to be 5%. Genetic advance was categorized (Juangsamoot, et al., 2012).

0–10%	= Low
10–20%	= Intermediate
Greater than 20%	= High

$$GA = K \times \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times h_b^2 \times 100$$

Here K is the intensity constant. Selection according to Adewale et al. (Adewale et al., 2010).

The rate is 2.06 at the point when the K is at 5%.

$\sqrt{\sigma_p^2}$ is the standard deviation of phenotype, h_b^2 is the broad sense heritability, $\bar{X}$ is the grand mean values of traits

Table 1. Advanced breeding lines and varieties used in the study

Line No.	Pedigree	Remarks
GLS – 2022 – 01	Lanka jumbo × ICGV 3777	Advance breeding line
GLS – 2022 – 02	06233 × 2018 -1	Advance breeding line
GLS – 2022 – 03	06233 × 2018 -2	Advance breeding line
GLS – 2022 – 04	2742 × Indi	Advance breeding line
GLS – 2022 – 05	2742 × Indi	Advance breeding line
GLS – 2022 – 06	2018 × Lanka Jumbo	Advance breeding line
GLS – 2022 – 07	Lanka jumbo × 2018	Advance breeding line
GLS – 2022 – 08	06233 × ICGV 3777	Advance breeding line
GLS – 2022 - 09	2018 × 06233	Advance breeding line
Lanka Jumbo	ICGV05200	Recommended variety
GMS – 2022 – 01	Lanka Jumbo × ICGV 3777	Advance breeding line
GMS - 2022 – 02	ICGV 2742 × ICGV 3487	Advance breeding line
GMS – 2022 – 03	2742 × ANK 2014	Advance breeding line
GMS – 2022 – 04	2742 × ICGV 3777-1	Advance breeding line
GMS – 2022 – 05	2742 × ICGV 3777-2	Advance breeding line
GMS – 2022 – 06	ICGV04195× ICGV0073	Advance breeding line
Tissa	Irradiated mutant of a Vietnam variety	Recommended variety
ANKG 1	Tissa × Red spanish	Recommended variety

Table 2. Summary of uantitative data collected during the study

No	Trait	Description and measurement type
1	Height of main stem (cm)	Data were taken from five plants after 60-85 days and measured from the cotyledonary axil up to terminal bud.
2	Plant width or spread (cm)	Data were taken from five plants after 45-60 days and measured at the widest point, from the branch tip to branch tip.
3	Leaf Length (mm)	Data was taken after at the third leaf of the main stem, the apical leaf, when fully expanded, randomly average from 10 plants.
4	Leaf width (mm)	Data was taken after at the third leaf of the main stem, the apical leaf, when fully expanded, randomly average from 10 plants .
5	Pod Width	Data was taken, randomly average with from 10 pods. A digital Vernier calliper was used to measure width.
6	Pod Length	Data was taken same pods, A digital Vernier calliper was used to measure length.
7	Seed Width	Data was taken, randomly average with from 10 seeds. A digital Vernier calliper was used to measure width.
8	Seed Length	Data was taken same seed. A digital Vernier calliper was used to measure length.
9	100 Seed Weight	Data measured of 100 dried seeds using a standard measuring scale.
10	No of Pods per Plant	Data counted after the harvesting, randomly average values from five plants.
11	Pod weight per plant	Data weighted of dried pods per plant, randomly average values from five plants.
12	Oil content	5g of dry seeds were taken and all 18 varieties were tested separately
13	Shelling %	100g of dry pods were taken and all 18 varieties were tested separately
14	Maturity index	15 dry pods were taken and all 18 varieties were tested separately
15	Number of seeds per pod	Randomly average values from five plants.

RESULTS AND DISCUSSION

Variability in quantitative traits among the groundnut genotypes

Generally the groundnut oil accounts 44–56% of the dry seed weight (Chen et al, 2010). Oil content, shelling %, maturity index and No. of seeds/pod of tested genotypes were given in Table 4. The observed oil content values ranged from 29.30% (GMS-2022-6) to 55.14% (GLS-

2022-8). It was in the ranges of previous findings and generally in the range of 40-50 % (Tiwari et al, 2021). The observed shelling % values ranged from 60% (GLS-2022-4, GLS-2022-6 and GLS-2002-9) to 75% (GMS-2022-4). The observed maturity index values ranged from 1.72 (Lanka jumbo) to 2.71 (Tissa). It was noticed that large seed size lines showed lower maturity index.

Table 4. Variability in Oil content, shelling %, Maturity index and No. of seed/pod

Treatment	Oil content %	Shell ing %	Maturity index	No of seeds/pod
GLS-2022-1	45.49	70	2.16	1,2
GLS-2022-2	43.63	65	2.02	1,2
GLS-2022-3	41.86	65	2.21	1,2
GLS-2022-4	46.09	60	2.00	1,2
GLS-2022-5	53.54	65	2.16	1,2
GLS-2022-6	49.17	60	1.99	1,2,3
GLS-2022-7	31.21	65	2.06	1,2
GLS-2022-8	55.14	65	2.15	1,2
GLS-2022-9	40.53	60	2.06	1,2
Lanka Jumbo	35.48	70	1.72	1,2
GMS-2022-1	43.674	65	2.49	1,2,3,4
GMS-2022-2	48.15	70	4.22	1,2
GMS-2022-3	41.66	70	2.27	1,2,3
GMS-2022-4	44.05	75	2.04	1,2,3,4
GMS-2022-5	43.52	70	1.74	1,2
GMS-2022-6	29.30	65	2.13	1,2,3
Tissa	45.59	70	2.71	1,2
ANKG1	40.72	70	2.22	1,2

Analysis of variance in growth and yield parameters

All characters showed significant variation except for leaflet length and number of pods per plant (Table 5). Further, Pod weight per plant was found to be significantly different among the lines at p value of 0.05 level. 100 seed weight of the lines ranged from 23.5-63.3g indicating high variation among the tested lines. However, Co-efficient of variation in yield contributing traits such as Number of Pods/plant and Pod weight/plant showed high values indicating influence of environmental factors.

Genetic Parameter Analysis

The estimated GCV and PCV values were found less than 10% for the traits such as leaf length (GCV 2.77% and PCV 9.57%), leaf width (GCV 3.85% and PCV 8.07%), seed width (GCV 7.64% and PCV 10.24%) and pod width (GCV 8.22% and PCV 9.35%). Other traits showed moderate GCV and PCV values, such as height of main stem (GCV 15.49%, PCV 19.57%), plant width (GCV 11.87%, PCV 15.22%), pod length (11.80%, PCV 13.01%), and seed length (GCV 14.34%, PCV 18.88%). 100 seed weight (PCV 21.20%), no of pods per plant (PCV 29.16%), pods weight per plant (PCV 32.31%) and yield (PCV 22.43%) were showed more than 20% phenotypic coefficient of variance values (Table 6).

Broad sense heritability was varied and classified accordingly. Height of main stem (62.60%), plant width or spread (60.82%), pod length (82.21%), pods width (77.28%), 100 seed weight (81.33%) had high

heritability values (more than 60%). Generally, moderate (30%-60%) heritability values were marked for the traits like seed length (57.66%), seeds width (55.73%) and yield (38.61%). Leaf length (8.44%), leaf width (22.72%), no of pods per plant (12.43%) and pods weight per plant (29.59%) had low heritability values (Less than 30%). Genetic advance was ranged between the lowest (1.66%) for leaf length and 100 seed weight (35.52%). Height of main stem (25.24%), seed length (22.43%), pod length (22.04%), 100 seed weigh (35.52%) had high genetic advance value (more than 20%).

Further, intermediate (10%-20%) genetic advance values were marked for the traits like plant width or spread (19.08%), seed width (11.76%), pods width (14.89%), pods weight per plant (19.69%) and yield (17.84%). No. of pods per plant (7.47%) and leaf length (1.66%) and leaf width (3.78%) had low genetic advance values (Less than 10%). Similar results were reported by Gupta et al, 2015, Vinithashri et al, 2019 where high heritability values coupled with high GA values were observed for 100 seed weight and yield per plant, indicating these traits were mainly governed by additive gene action. In the present study, yield contributing traits such as number of pods per plant and pod weight per plant showed low heritability values. However, 100 seed weight showed high value for heritability estimates. In our genetic materials studied, high variation was observed for the seed size, which can be clearly identified visually. Jonson et al. 1955 suggested that heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone. Accordingly, in the present study seed related traits have given high values for both heritability and genetic advance, suggesting phenotypic selection would be productive.

Correlation of traits

Pearson's Correlation Coefficient of Analysis among 12 quantitative Traits of groundnut lines were listed in the table 7. Among the growth parameters leaf width and length along with Plant spread and height at main stem were highly correlated. Seed traits such as seed length, width and 100 seed weight were highly correlated. Additionally, pod weight per plant were significantly correlated with seed and pod related traits. Yield was positively correlated with characters such as pod weight per plant and seed width. These results supported the findings of Wang et al, 2023 and Reddy et al, 2023. Since, improvement of yield is a key objective in groundnut breeding program, selection for seed related traits and yield components such as number of pods per plant would be important criteria.

Table 5. Summary of the 12 traits studied -variation revealed by Analysis of variance

Traits	DF(17) (treatment)	MEAN± SEM	max	min	St dev	CV%
LL	12.79 NA	34.68±0.48	40.96	24.04	3.57	9.13
LW	4.44 *	21.64±0.25	25.92	15.8	1.87	7.09
HMS	92.57**	32.75±0.86	48.8	21	6.29	11.97
PLWD	129.78**	50.26±1.03	66.2	29	7.54	9.53
PL	46.19**	14.77±0.18	17.3	12.14	1.36	5.49
PWD	4.86**	64.54±1.46	80	25	10.76	4.46
SL	18.03**	15.33±0.39	27.81	10.19	2.85	12.28
SWD	1.34**	7.77±0.11	9.86	6.08	0.79	6.81
NPPP	30.66 NA	16.99±0.66	32.4	10.2	4.88	27.29
PWPP	54.55*	18.12±0.78	32.65	8.69	5.75	27.11
HSW	260.21**	46.94±1.34	62.35	23.58	9.86	9.16
Yield	0.24**	1.64±0.05	2.5	0.79	0.38	17.57

Note: ** Significant at $P < 0.001$ level, * Significant at $P < 0.05$ level.

Legend: df: degree of freedom; ns: no significant; SEM: standard error of the mean; St Dev: standard deviation; Max: maximum; MN: minimum; CV: coefficient of variance; LL : leaf length; LW : leaf width; HMS : height of main stem; PLWD : plant width; PL: pod length; PWD : pod width; SL : seed length; SWD : seed width; NPPPOP : No of pods per plant; NWPOP : Pods weight per plant; HSW : 100 seed weight

Table 6. Estimation of Variance Components, Relative Difference, Heritability of groundnut

	MSG	MSE	σ_g^2	σ_p^2	PCV	GCV	RD	h_b^2	GA
Leaflet length (mm)	12.79	10.02	0.92	10.94	9.54	2.77	70.95	8.44	1.66
Leaflet width mm	4.43	2.36	0.69	3.05	8.07	3.85	52.33	22.72	3.78
Height of main stem (Cm)	92.57	15.37	25.73	41.10	19.57	15.49	20.88	62.60	25.24
Plant width or spread (Cm)	129.78	22.94	35.61	58.55	15.22	11.87	22.01	60.82	19.08
Seed length (mm)	18.03	3.54	4.83	8.37	18.88	14.34	24.06	57.66	22.43
Seeds width (mm)	1.34	0.28	0.35	0.63	10.24	7.64	25.35	55.73	11.76
Pod length (mm)	46.18	3.11	14.36	17.47	13.01	11.80	9.33	82.21	22.04
Pods width (mm)	4.86	0.43	1.48	1.91	9.35	8.22	12.09	77.28	14.89
100 seed weight (g)	260.21	18.49	80.57	99.07	21.20	19.12	9.82	81.33	35.52
No of pods/plant	30.66	21.51	3.05	24.56	29.16	10.28	64.74	12.43	7.47
Pod weight/ plant	54.55	24.13	10.14	34.27	32.31	17.57	45.59	29.59	19.69
Yield	0.24	0.08	0.05	0.13	22.43	13.94	37.86	38.61	17.84

Table 7. Pearson's Correlation Coefficient of Analysis among 12 quantitative Traits of Groundnut lines

	Leaf length	Height of main stem	Leaf width	Plant width	No. of pods / plant	Pods weight / plant	Pod length	Pod width	Seed length	Seed width	100 seed weight	Yield	Oil content	Shelling %	Maturity index
Leaf length	1	0.226	.898**	.535*	-0.448	-0.207	0.098	-0.021	-0.005	-0.089	-0.103	-.50*	.069	-.004	-.111
Height of main stem		1	0.247	.650**	0.175	-0.408	-.665**	-.713**	-.531*	-.479*	-.508*	-.220	-.050	.373	.272
Leaf width			1	.540*	-0.26	-0.048	-0.148	0.042	-0.214	0.032	-0.123	-.253	.093	-.074	-.124
Plant width				1	0.059	-0.001	-0.406	-0.168	-0.253	-0.026	0.017	-.096	.110	.137	-.048
No. Of pods per plant					1	.561*	-0.458	-0.14	-0.289	-0.116	-0.239	.435	.005	-.354	-.172
Pods weight per plant						1	0.188	.647**	0.392	.535*	.540*	.646**	.262	-.723**	-.383
Pod length							1	.529*	.897**	0.275	.545*	-.165	.048	-.420	-.146
Pod width								1	.534*	.778**	.847**	.372	-.014	-.548*	-.299
Seed length									1	0.383	.637**	.045	.185	-.495*	-.181
Seed width										1	.729**	.583*	-.060	-.211	-.284
100 seed weight											1	.449	.178	-.323	-.130
Yield												1	.281	-.089	-.286
Oil content													1	-.070	.238
Shelling %														1	.210
Maturity index															1

CONCLUSIONS

Conventional breeding is practiced in order to create variability and to select superior lines for further testing. In the present study several advanced breeding lines were evaluated for their growth and yield traits. The results indicate sufficient amount of variability was observed among the materials except for traits such as leaf length and number of pods per plant. However, results indicates that it is difficult to find superior lines in terms of yield and other physical quality traits in comparison to existing varieties. The estimates such as phenotypic and genotypic variance exhibited that phenotypic values were marginally higher than genotypic values for all traits because this character's expression is influenced by the environment. This was consistent with the findings of Mahalaxmi et al.,(2005), Aruna Kumari et al., (2019) and Kakeeto et al.,(2019). The greater divergence between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values is the indication of high effects of the environment to a certain degree, specially yield related traits. The estimated result of relative difference (RD) was very high for traits like yield, No .of pods per plant and pod weight per plant indicating direct selection would be difficult for such traits. High heritability values along with high genetic advance (GA) values were shown in traits like 100 seed weight and number of pods per plant suggesting greater additive effect of genes which provide effective selection for traits improvement directly (Hasan Khan et al, 2020). According to Pearson's correlation of traits for yield, selection would be beneficial by considering traits such as pod weight per plant and other seed size characters. It was evident that improvement of physical traits such as seed size can be achieved simply through direct selection. However, it is unclear how to improve the yield parameters to come up with superior varieties, which need further studies.

REFERENCES

- Adewale, B. D., Kehinde, O. B., Aremu, C. O., Popoola, J. O., & Dumet, D. J. (2010). Seed metrics for genetic and shape determinations in African yam bean [*Fabaceae*] (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich.) harms. *African Journal of Plant Science*. 4(4), 107-115.
- Agstat, 2020. Agricultural statistics. Volume xvii, Socio Economic and Planning Centre, Department of Agriculture, Peradeniya, Sri Lanka. Pg. 23.
- Aruna Kumari E., John K., Mohan Reddy D and Latha P. (2019). Studies on Genetic Variability for Yield, Yield Attributing Traits, Physiological and Quality Traits in Groundnut [*Arachis hypogaea* L.]. *International Journal of Current Microbiology and Applied Sciences*. Vol. 8 No.07.
- Assefa, K., Ketema, S., Tefera, H., Nguyen, H. T., Blum, A., Ayele, M., & Kefyalew, T. (1999). Diversity among germplasm lines of the Ethiopian cereal tef [*Eragrostis tef* (Zucc.) Trotter]. *Euphytica*, 106, 87-97.
- Chen, Z., Wang, M. L., Barkley, N. A., and Pittman, R. N. (2010). A simple allele-specific PCR assay for detecting FAD2 alleles in both A and B genomes of the cultivated peanut for high-oleate trait selection. *Plant Mol. Biol. Rep.* 28, 542–548.
- Falconer, D. S., & Mackay, T. F. C. (1996). Introduction to quantitative genetics, Longman. Essex, England, 254-256.
- Gupta R.P., Vachchani J.H., Kachhadia V.H., Vaddoria M.A and Reddy P. (2015). Genetic variability and heritability studies in Virginia groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, 6(1): 253-256.
- Hasan Khan M., Rafii M.Y., Ramlee S.I., Jusoh M and Mamum A. (2020). Genetic Variability, Heritability, and Clustering Pattern Exploration of Bambara Groundnut (*Vigna subterranea* L. Verdc) Accessions for the Perfection of Yield and Yield-Related Traits. BioMed Research International.
- Jeewani, D. G.C., Amarasinghe, Y. P., Wijesinghe, G., & Pushpa Kumara, R. W. (2021). Screening exotic groundnut (*Arachis hypogaea* L.) lines for introducing as a small-seeded variety (ANKGN4/Tiny) in Sri Lanka. *Tropical Agricultural Research and Extension*, 24(4), 330.
- Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Estimation of genetic and environmental variability in soybeans. *Agron. J.*, 47: 314-318.
- Kakeeto, R., Baguma, S.D., Subire, R., Kaheru, J., Karungi, E and Biruma, M. 2019. Genetic variation and heritability of kernel physical quality traits and their association with selected agronomic traits in groundnut (*Arachis hypogaea* L.) genotypes from Uganda. *African Journal of Agricultural Research*. 14(10): 597-603.
- Mahalakshmi, P., Manivannan, N. and Muralidharan, V. (2005). Variability and correlation studies in groundnut (*Arachis hypogaea* L.). *Legume Research*, 28(3): 194-197.
- Reddy P., Sabara P., Shital M., Kulkarni G.U., Sapara G.K and Tomer S.R. (2023). Correlation and path analysis among groundnut (*Arachis hypogaea* L.). *Annals of Arid Zone*. 62 (3): 227-234 .
- Robinson, H. F., & Comstock, R. E. (1950). Genotypic and phenotypic correlations in corn and their implications in selection. North Carolina State University. Dept. of Statistics.

- Singh, R. K. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Pub. Ludhiana. New Delhi, Revised Ed., 318.
- Sivasubramanian, S., & Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agric. J*, 60(9-13), 1093-1096.
- Tinee Adlak, Sushma Tiwari, Neha Gupta, M. K. Tripathi, R. S. Sikarwar, Ritu Sastya and Versha Gupta. (2021). Assessment for Yield and Nutritional Profiling of Groundnut with the Help of Allele Specific Markers for Desirable Fatty Acids. *Int.J.Curr.Microbiol. App.Sci.*, 10(02): 1625-1637.
- Vinithashri G., Manivannan N., Viswanathan P L. and Selvakumar T.(2019). Genetic variability, heritability and genetic advance of yield and related traits in F3 generation of groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, 10 (3): 1292 – 1297.
- Wang Z., Zhang Y., Yan L., Chen Y., Kang Y., Hua D., Wang X., Liu K., Jiang H., Lei Y and Liao B. (2023). Correlation and variability analysis of yield and quality related traits in different peanut varieties across various ecological zones of China. *Oil Crop Science*, 8(4). P.236-242.
- Zhuang, W., Chen, H., Yang, M., Wang, J., Pandey, M. K., Zhang, C., Chang, W. C., Zhang, L., Zhang, X., Tang, R., Garg, V., Wang, X., Tang, H., Chow, C. N., Wang, J., Deng, Y., Wang, D., Khan, A. W., Yang, Q., Varshney, R. K. (2019). The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. *Nature Genetics*, 51(5), 865–876.