

Biological Forum – An International Journal

15(11): 263-269(2023)

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

Studies on Genetic variability, Correlation and Path coefficient Analysis for Yield Contributing and Quality Traits in Marker Assisted Derived Advanced Backcross Lines of Groundnut (Arachis hypogaea L.)

V. Mani Prasad^{1*}, CH. V. Durga Rani², G. Seshu³ and S.N.C.V.L. Pushpavalli² ¹Department of Genetics and Plant Breeding, College of Agriculture, PJTSAU, Hyderabad (Telangana), India. ²Department of Molecular Biology and Biotechnology, Institute of Biotechnology, PJTSAU, Hyderabad (Telangana), India. ³Assistant Professor, Department of Genetics and Plant Breeding, Agricultural college, PJTSAU, Jagitval (Telangana), India.

(Corresponding author: V. Mani Prasad*)

(Received: 09 September 2023; Revised: 07 October 2023; Accepted: 20 October 2023; Published: 15 November 2023) (Published by Research Trend)

ABSTRACT: In the present study, 30 advanced backcross lines (BC₁F₅ and BC₂F₄) along with their parents were evaluated for 13 quantitative and quality traits in randomized block design with two replications. Yield is a polygenic and complex trait, which is significantly influenced by the environment. Direct selection for yield is less efficient, indirect selection through yield contributing traits can greatly enhance efficiency of plant breeding. The components of genetic variance revealed that phenotypic coefficient of variation (PCV) values was higher than genotypic coefficients of variation (GCV) for all the characters indicating the environment effect on genotypes. High GCV and PCV were recorded for number of pods per plant whereas, high heritability coupled with high GAM was observed in number of pods per plant, plant height, seed yield per plant and pod yield per plant. Pod yield per plant showed a positive and significant association with number of pods per plant, seed yield per plant, shelling outturn, pod length and 100 seed weight at both genotypic and phenotypic level. Path analysis revealed that seed yield per plant showed high positive direct effect whereas, shelling outturn and 100 seed weight contributed significant amount of indirect effects towards pod yield per plant.

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

INTRODUCTION

The cultivated groundnut (Arachis hypogaea L.), is a self-pollinated, allotetraploid (2n = 4x = 40) and major oilseed crop which belongs to the family Fabaceae. Groundnut is a native of South America (Brazil) and is grown in over 100 countries, between 40°N to 40° S latitude in a tropical warm climate. In India, groundnut is used as an oilseed and food crop because of its palatability. Groundnut kernels are valued as a rich source of oil (48- 50%), protein (25-28%), carbohydrates (10-20%) and provide 564 kcal of energy for every 100g of kernels (Arya et al., 2016). The groundnut seed oil contains 80% of fatty acids and majorly occupies oleic acid (36-67%) and linoleic acid (15-43%) a monounsaturated fatty acid (MUFA) and polyunsaturated fatty acid (PUFA), respectively (Janila et al., 2016). As groundnut is a major oilseed crop used in confectionery, there is a need to improve groundnut quality attributes. Value addition through quality enhancement will generate a large amount of foreign exchange. As a result, selection for quality features in groundnut is required in breeding programmes.

Crop improvement requires knowledge regarding the magnitude of variability and the extent to which desirable characteristics are heritable. The variability available in breeding material is crucial for the selection Prasad et al.,

of superior plant types because superior plant selection is not based solely on yield but also on yield contributing traits. The genetic makeup of the plant and the environment mostly govern the phenotypic expression of the plant character. As a result, the observed phenotypic variability must be partitioned into heritable and non-heritable components using appropriate genetic parameters such as phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were useful in the effective selection, heritability and genetic advance as percent of mean (GAM) are plant breeding tools used in determining the magnitude and direction of selection. The efficiency of selection mainly depends on the direction and magnitude of association between yield and its components. Correlation analysis provides an opportunity to study the magnitude and direction of association of yield with its components and also among various components. Correlation between two characters may be due to linkage and / or pleiotropy. If caused by linkage, an undesirable correlation can be disrupted through hybridization followed by selection in segregating generations (Ramakrishnan et al., 2017). Correlation measures the level of dependence among traits, but it is often very difficult to determine the actual mutual effects among traits. Path coefficient

Biological Forum – An International Journal 15(11): 263-269(2023)

analysis is very important technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable (Kumar *et al.*, 2019). Therefore, the present study estimated the genetic parameters, correlation and path coefficient analysis for 13 quantitative and quality traits.

MATERIAL AND METHODS

The present experiment was conducted during rabi at Regional Agricultural Research Station, Palem, Telangana State. The site of experimentation falls under a semi-arid climate and comes under Southern Telangana Zone on 16°351 latitudes, 78°1' longitude and altitude of 642 m above mean sea level. The 30 advanced backcross progenies (18 BC1F5 and 12 BC₂F₄) along with parents(K6, ICGV 13193 and ICGV 15033)were raised in a randomized block design with two replications. Each progeny was sown in two rows of 2.5 m length with a spacing of 30 cm between rows and 10 cm between plants with no gaps between rows. Observations were recorded in 5 randomly selected plants for 13 quantitative characters viz., plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod yield per plant, seed yield per plant, shelling out turn, pod length, pod width, 100 seed weight, oil and protein content, while the days to 50% flowering was recorded on whole line/ progeny basis.

Statistical analysis. The data were subjected to statistical analysis using Indostat software. The analysis of variance and their significance for all the traits were worked out as suggested by Panse and Sukhatme (1985). The genotypic and phenotypic coefficient of variation (PCV) were calculated by the formula given by Burton (1953). Heritability in broad sense (h^2) and genetic advance as percent of mean were estimated as per Allard (1960); Johnson *et al.* (1955). The correlation coefficients and path analysis were carried out by the following methods of Al-Jibouri *et al.* (1958); Dewey and Lu (1959) respectively.

RESULTS AND DISCUSSIONS

The analysis of variance showed significant differences for 13 quantitative and quality traits. It indicates presence of substantial amount of variation in experimental material under investigation. Estimates of PCV values are greater than GCV values across all traits, showing that variation was induced not only by genotypes but also by environmental effects (Table 1). The genotypic coefficient of variation (GCV) ranged from 2.48 to 21.37 and the phenotypic coefficient of variation (PCV) ranged between 3.62 to 22.6 (Fig. 1). High estimates of GCV (21.37) and PCV (22.66) were recorded in number of pods per plant indicating the presence of wide range of variation and can be further improved by simple selection process. Similar results were found in Aruna et al. (2019); Kumari and Sasidharan (2020); Shinde et al. (2019); Mandal et al. (2017). Heritability in a broad sense (h^2 bs) was ranged from 35.8 to 94.6 and genetic advance as percent of mean (GAM) was varied from 3.06 to 40.79 for all the characters (Fig. 2).

High heritability in a broad sense does not always imply better response to selection, because it includes non-additive genetic action. As a result, estimation of genetic advance further narrows down the response of selection. Heritability coupled with genetic advance as per cent of mean provides a very effective measure for nature of inheritance and effectiveness of selection for a particular character (Johnson et al. 1955) and furnished below (Table 2). High heritability accompanied with high GAM were recorded for number of pods per plant, plant height, seed yield per plant and pod yield per plant indicates these traits have been less influenced by the environment and controlled by additive gene effects and have high selection value, which can be exploited using simple selection strategies. These findings are in conformity with reports of Kumari and Sasidharan (2020); Aruna et al. (2019); Mandal et al. (2017). High heritability coupled with moderate genetic advance per mean was observed in pod length and pod width which indicates these traits were governed by both additive and non-additive gene effects and selection is less effective whereas, improvement among these traits can be achieved by breeding methods such as diallel selective mating. Similar findings were reported by Muibai et al. (2020); Jonah et al. (2012). Moderate heritability accompanied with moderate GAM were observed in protein content and number of primary branches per plant which suggest that additive gene action was involved, and there is still scope for improvement of these traits through selection. These findings are in agreement with the reports of Shukla and Rai (2014); John et al. (2011). Moderate heritability combines with low GAM were recorded for oil content, 100 seed weight, days to 50% flowering and shelling out turn. As a result, these characters are improved further through selection or single plant selection or inter-mating among selected individuals. These results were supported by Kumari and Sasidharan (2020); Pappammal et al. (2020); Aruna et al. (2019): Byadagi et al. (2018): Pattidar et al. (2017). High GCV (21.37) coupled with high heritability (94.6) and GAM (40.79) were observed in number of pods per plant suggested that environment had a lesser influence on the expression of these trait, and this character is governed by an additive gene action hence, selection for this trait was effective.

Correlation analysis. Yield is a complex attribute that results from the interaction of various yield components. Understanding the relationships between yield and other characters are essential in any plant breeding programme in order to make the best use of these relationships in selection of desirable characters. The effectiveness of selection is primarily determined by the direction and magnitude of the association between yield and its components when selection pressure is applied to improve any trait that is strongly correlated with yield, it also influences several other correlated characters at the same time. As a result, correlation coefficient studies allow us to understand the nature and extent of the association of yield with its components, as well as among other components. The results were discussed in present study are furnished in Table 3. Pod yield per plant showed a positive and

Prasad et al.,

significant association with number of pods per plant (rg=0.5148**, rp=0.4232**), seed yield per plant (rg=0.9689**, rp=0.8460**), outturn shelling (rg=0.7594**, rp=0.3806**), pod length (rg=0.4328**, rp=0.3110**) and 100 seed weight (rg=0.2693*, rp=0.2943*) at both genotypic and phenotypic level but number of secondary branches per plant (rp=0.2946*) shows positive significant relation at phenotypic only and protein content (rg=0.2650*) showed positive significant association at genotypic only. The variation in the relation of secondary branches per plant and protein content with pod yield per plant at phenotypic and genotypic level indicates impact of the environment on these traits. The significant correlation indicates that there is strong association between various traits and positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneous improvement of both characters. These results emphasized the effectiveness of these characters in terms of their contribution towards pod yield per plant. Similar results were reported by Kumari and Sasidharan (2020); Shinde et al. (2019); Shendekar et al. (2023); Tulsi et al. (2017) for 100 seed weight; Chandrashekhara et al. (2020); Killada et al. (2023); Trivikrama et al. (2017) for number of pods per plant; Mohapatra and Khan (2020); Shinde et al. (2019) for shelling outturn; Mandal et al. (2017) for seed yield per plant; Jonah et al. (2012) for pod length and John et al. (2008) for number of secondary branches per plant; Chandrashekhara et al. (2020) for plant height; Kumar et al. (2020) for number of primary branches per plant; Shinde et al. (2019); Bhakal and Lal (2017) for days to 50% flowering; Mohapatra and Khan (2020); Gupta et al. (2015) for oil content; Krishnamurthy et al. (2015) for protein content and Jonah et al. (2012) for pod width.

Path Coefficient analysis. Path coefficient analysis is a cause-and-effect relationship and distinct from correlation coefficient by measuring the relative magnitude of direct and indirect effects of characters on

complex dependent characters such as yield. It aids breeders in determining the best and most important component traits during selection to improve yield. The present results of genotypic and phenotypic path coefficient results are furnished in Table 4 and diagrammatically represented in Fig. 3. Among various traits seed yield per plant, number of pods per plant and 100 seed weight exhibited positive direct effect and also significantly positive associated with pod yield per plant at both genotypic and phenotypic level but oil content exhibited a positive direct effect (G=0.1791, P=0.0478) on pod yield per plant and exerted a positive significant and non-significant association at genotypic and phenotypic level respectively (rg=0.5357**, rp=0.1353). On the contrary, shelling percentage exhibited negative direct effect but significantly positive correlation with pod yield per plant at both genotypic and phenotypic level. The strong association might be due to the positive indirect effects through plant height and pod width both at phenotypic and genotypic level. Similar results were reported by Patel et al. (2021) for seed yield per plant; Alam (2014) for number of secondary branches per plant; Mandal et al. (2017) for number of pods per plant, shelling outturn, pod length; Mohapatra and Khan (2020) for 100 seed weight and oil content. It revealed that maximum direct effect and significant indirect contribution exhibited by seed yield per plant, as well as appreciable indirect effects exhibited by shelling outturn and100seed weight towards pod yield per plant. Moreover, these characters have high positive and significant association with pod yield per plant and hence, they may be regarded as the most essential yield contributing characters and appropriate importance might give to these characters while selecting for high yield in groundnut.

The high values of phenotypic residual values (0.4283) compared to genotypic residual (0.2501) might be due to the influence of other dependent variables which are not included in the study.

			Ra	nge			h^2 (bs)	
Sr. No.	Traits	Mean	Minimum	Maximum	GCV (%)	PCV (%)	(%)	GAM (%)
1.	Days to 50% flowering	39.45	36.00	41.5	2.48	4.15	35.8	3.06
2.	Plant height (cm)	14.65	10.82	21.72	17.43	18.38	89.9	34.03
3.	No. of Primary branches per plant	7.22	6.00	8.80	8.40	13.88	36.6	10.46
4.	No. of Secondary branches per plant	37.97	32.90	43.20	4.97	6.09	66.7	8.36
5.	No. of Pods per Plant	12.94	8.20	18.40	21.37	22.66	94.6	40.79
6.	Pod Yield per plant (g)	9.49	6.31	11.09	13.15	15.21	74.8	23.44
7.	Seed Yield per Plant (g)	6.59	3.81	8.04	14.68	16.69	77.4	26.62
8.	Shelling out turn (%)	66.52	60.41	74.22	4.30	7.30	34.7	5.22
9.	Pod Length (mm)	24.99	21.80	27.40	5.88	6.67	77.8	10.69
10.	Pod Width (mm)	11.80	9.50	13.50	8.60	10.17	71.5	14.99
11.	100 Seed weight	40.03	35.57	42.60	2.92	4.80	37.1	3.67
12.	Oil content (%)	53.73	50.40	59.15	2.45	3.62	45.9	3.42
13.	Protein content (%)	23.26	19.35	28.25	9.14	12.38	54.5	13.90

Table 1: Estimation of genetic parameters for 13 quantitative traits in 30 backcross lines along with parents.

Table 2: Different types of estimates of genetic parameters in quantitative and quality characters of advanced backcross lines of groundnut.

Sr. No.	Character	Genetic Parameter	Gene effects	Influence of environment	
1.	Plant height Number of pods per plant Pod yield per plant Seed yield per plant	High heritability with high GAM	Additive	Low	
2.	Pod length Pod width	High heritability with moderate GAM	Additive	Low	
3.	Number of primary branches per plant Protein content	Moderate heritability with moderate GAM	Additive and non- additive	Medium	
4.	100 seed weight Oil content Shelling outturn Days to 50% flowering	Moderate heritability with low GAM	Non-additive	High	

Table 3: Genotypic (G) and Phenotypic (P) correlation coefficients of yield contributing and quality traits.

Character		DFF	РН	NPB/P	NSB/P	NPP	SY/P	SH%	PL	PW	100 SW	Oil content	Protein Content	Pod yield per plant
DFF	$\mathbf{r}_{\mathbf{g}}$	1.0000	0.2795*	0.4187**	-0.2928*	0.3953**	-0.0343	0.0390	0.5218**	- 0.3399**	- 0.3949**	-0.1790	-0.0849	-0.0062
	rp	1.000	-0.2276	0.2611**	-0.0530	0.224	-0.0187	-0.1105	-0.2629 *	-0.0475	-0.0420	-0.0985	0.0257	0.0882
DU	rg		1.0000	-0.2644*	- 0.4502**	- 0.3852**	0.4915**	- 0.4680**	-0.1784	0.2922*	0.0405	- 0.3156**	0.2713**	0.5284**
	rp		1.000	0.3244**	0.3521**	0.3842**	0.3560**	-0.1480	-0.1556	0.2547 *	-0.0152	-0.1897	0.1945	0.4010**
NPB/P	rg			1.0000	0.5934**	0.0378	-0.0676	0.1689	-0.2353	-0.2115	- 0.5505**	-0.0205	- 0.6152**	-0.2359
	rp			1.000	0.2630*	0.1663	-0.2288	-0.0916	-0.0942	-0.1764	-0.1654	-0.0563	-0.2335	-0.2355
NSB/P	rg				1.0000	0.3186**	0.3091*	0.5829**	0.3097*	-0.3112*	-0.0518	0.1151	-0.0885	0.2056
	rp				1.000	0.2527 *	0.2895 *	0.2205	0.2803 *	-0.0949	0.0834	-0.0307	-0.0991	0.2946*
NPP	rg					1.0000	0.5363**	0.6501**	0.1953	0.0492	0.1195	0.1585	0.4455**	0.5148**
	rp					1.000	0.4364**	0.3670**	0.1715	0.0243	0.0827	0.0849	0.3210*	0.4232**
SY/P	rg						1.0000	0.8334**	0.3155**	-0.1160	0.2788*	0.4584**	0.2405*	0.9689**
	rp						1.000	0.6453**	0.2487 *	-0.0671	0.2102	0.1689	0.0605	0.8460**
	rg							1.0000	-0.0244	-0.3076*	0.0657	0.6984**	0.0623	0.7594**
SH%	rp							1.000	0.0171	-0.2999 *	-0.0645	0.2695 *	-0.0304	0.3806**
рī	rg								1.0000	0.3163**	0.7066**	0.0045	0.2161	0.4328**
IL	rp								1.000	0.2735 *	0.3311**	0.0065	0.1392	0.3110**
PW	rg									1.0000	0.5865**	-0.1967	0.1636	0.0840
1.00	rp									1.000	0.2666*	-0.1178	0.1094	0.1427
100 SW	rg										1.0000	-0.1861	0.4188**	0.2639*
	rp										1.000	-0.1994	0.2313	0.2943*
Oil	rg											1.0000	0.0453	0.5357**
content	rp											1.000	0.0853	0.1353
Protein	rg												1.0000	0.2650*
content	rp												1.000	0.0863

DFF: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm); PW: Pod Width(mm)



Fig. 1. Estimates of GCV (%) and PCV (%) in backcross lines along with parents.



Fig. 2. Estimates of heritability and GAM in backcross lines along with parents.

				-	_	_		-	- 0					
Character		DFF	РН	NPB/P	NSB/P	NPP	SY/P	SH%	PL	PW	100 SW	Oil content	Protein Content	Correlation with podyield / plant
DFF	G	- 0.4800	0.1342	- 0.2010	0.1405	- 0.1897	0.0164	- 0.0187	0.2505	0.1632	0.1896	0.0859	0.0407	-0.0062
	Р	0.1007	- 0.0229	0.0263	- 0.0053	0.0224	- 0.0019	- 0.0111	- 0.0265	- 0.0048	- 0.0042	-0.0099	0.0027	0.0882
РН	G	0.0717	- 0.2564	0.0678	0.1154	0.0988	0.1260	0.1200	0.0457	- 0.0749	- 0.0104	0.0809	-0.0696	-0.5284**
	Р	0.0288	- 0.1267	0.0411	0.0446	0.0487	0.0451	0.0188	0.0197	0.0323	0.0019	0.0240	-0.0244	-0.4010**
	G	0.1241	- 0.0783	0.2963	0.1758	0.0112	- 0.0200	0.0500	- 0.0697	- 0.0627	- 0.1631	-0.0061	-0.1823	-0.2359
NPB/P	Р	- 0.0309	0.0384	- 0.1184	- 0.0311	- 0.0197	0.0271	0.0108	0.0112	0.0209	0.0196	0.0067	0.0276	-0.2355
NOT	G	0.1322	0.2033	- 0.2680	- 0.4517	- 0.1439	- 0.1396	- 0.2633	- 0.1399	0.1406	0.0234	-0.0520	0.0400	0.2056
NSD/F	Р	0.0042	- 0.0280	0.0209	0.0794	0.0201	0.0230	0.0175	0.0223	- 0.0075	0.0066	-0.0024	-0.0079	0.2946*
NPP	G	0.1766	- 0.1721	0.0169	0.1423	0.4467	0.2396	0.2904	0.0872	0.0220	0.0534	0.0708	0.1990	0.5148**
	Р	0.0090	- 0.0155	0.0067	0.0102	0.0403	0.0176	0.0148	0.0069	0.0010	0.0033	0.0034	0.0129	0.4232**
SY/P	G	- 0.0348	- 0.4985	- 0.0685	0.3135	0.5440	1.0143	0.8453	0.3201	- 0.1176	0.2828	0.4649	0.2439	0.9689**
	Р	0.0157	- 0.2980	- 0.1915	0.2423	0.3653	0.8371	0.5402	0.2082	- 0.0562	0.1759	0.1414	0.0506	0.846**
CITO/	G	0.0165	0.1984	- 0.0716	0.2471	- 0.2757	0.3533	- 0.4240	0.0104	0.1304	- 0.0279	-0.2961	-0.0264	0.7594**
51170	Р	0.0191	0.0256	0.0158	0.0381	- 0.0634	- 0.1115	- 0.1728	0.0030	0.0518	0.0112	-0.0466	0.0053	0.3806**
ÐĨ	G	0.0453	0.0155	0.0204	0.0269	0.0170	0.0274	0.0021	- 0.0869	0.0275	- 0.0614	-0.0004	-0.0188	0.4328**
TL	Р	- 0.0040	0.0023	- 0.0014	0.0042	0.0026	0.0037	0.0003	0.0150	0.0041	0.0050	0.0001	0.0021	0.3110*
PW	G	0.0304	0.0262	0.0189	0.0279	- 0.0044	0.0104	0.0276	0.0283	- 0.0896	0.0525	0.0176	-0.0147	0.0840
1 W	Р	0.0076	0.0410	0.0284	0.0153	0.0039	0.0108	0.0483	0.0440	0.1609	0.0429	-0.0190	0.0176	0.1427
100 SW	G	0.0213	0.0022	- 0.0297	0.0028	0.0065	0.0151	0.0035	0.0381	0.0317	0.0540	-0.0100	0.0226	0.2639*
100 5 W	Р	- 0.0019	- 0.0007	- 0.0074	0.0038	0.0037	0.0095	- 0.0029	0.0149	0.0120	0.0450	-0.0090	0.0104	0.2943*
Oil content	G	0.0321	- 0.0565	0.0037	0.0206	0.0284	0.0821	0.1251	0.0008	0.0352	0.0333	0.1791	0.0081	0.5357**
On content	Р	0.0047	0.0091	0.0027	0.0015	0.0041	0.0081	0.0129	0.0003	0.0056	0.0095	0.0478	0.0041	0.1353
Protein	G	0.0019	0.0061	0.0138	0.0020	0.0100	0.0054	0.0014	0.0048	0.0037	0.0094	0.0010	0.0224	0.2650*
Protein content	Р	0.0004	0.0028	0.0034	0.0015	- 0.0047	0.0009	0.0004	0.0021	- 0.0016	- 0.0034	-0.0013	-0.0147	0.0863 0.0863
	0.0004 0.0028 0.0047 0.0009 0.0021 0.0016 0.0034 0.0 Genotypic Residual Effect = 0.2501 Phenotypic Residual Effect = 0.4283 Direct effects are shown in bold font 0.0												nt	

Table 4: Genotypic (G) and Phenotypic (P) path coefficients of yield contributing and quality traits.

DFF: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm); PW: Pod Width(mm)



Fig. 3. Phenotypic and Genotypic path diagram for pod yield per plant.

CONCLUSIONS

From the above discussions, on variability and genetic parameters, it is evident that number of pods per plant, plant height, pod yield per plant and seed yield per plant showed high heritability coupled with high GAM which, depicts these traits are less influenced by environment and governed by additive gene effects hence, simple direct selection may be effective to improve these traits. Correlation coefficient analysis revealed that seed yield per plant showed highly positive and significant association with pod yield per plant followed by number of pods per plant, shelling out turn, pod length, number of secondary branches per plant, 100 seed weight, pod width, oil and protein content are the most essential characters, which might contribute significantly towards higher pod yield per plant. Path analysis revealed that seed yield per plant showed high positive direct effect whereas, shelling outturn and 100 seed weight contributes significant amount of indirect effects towards pod yield per plant. Hence, they may be regarded as important traits for selecting high yield in groundnut.

FUTURE SCOPE

Identifying seed yield per plant as significantly positive and direct effect on yielding in groundnut suggesting breeders to select it as the most essential yield contributing character and importance is to be given while, yield improvement in groundnut.

Conflict of Interest. None.

REFERENCES

- Alam, M. K. (2014). Genetic correlation and path coefficient analysis in groundnut (*Arachis hypogaea L.*). SAARC Journal of Agriculture, 12(1), 96-105.
- Al-Jibouri, H., Miller, P. A. and Robinson, H. F. (1958). Genotypic and environmental variances and covariance's in an upland cotton cross of interspecific origin. *Agronomy Journal*, *50*, 633-637.
- Allard, R. W. (1960). Principles of Plant Breeding, John Wiley and Sons Inc., New York, USA. 485.
- Aruna Kumari, E. K., John, D., Mohan Reddy 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, 8(7), 393-400.

- Arya, S. S., Salve, A. R. and Chauhan, S. (2016). Peanuts as functional food: a review. *Journal of Food Science* and Technology, 53(1), 31-41.
- Bhakal, M. and Lal, G. M. (2017). Estimation of genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.) Germplasm. *Chemical Science Review and Letters*, 6(22), 1107-1112.
- Burton, G. W. (1953). Quantitative inheritance in grasses. Proceeding on 6th International Grassland Congress Journal, 1, 277-283.
- Byadagi, U. R., Venkataravana, P. and Priyadarshini, S. K. (2018). Genetic variability studies in F ₂ and F ₃ populations of three crosses of groundnut (*Arachis hypogaea* L.). Journal of Pharmacognosy and Phytochemistry, 7(5), 3139-3143.
- Chandrashekhara, G., Nadaf, H., & Babu, B. N. (2020). Estimates of Genetic Variability in Selected Advanced Breeding Lines of Groundnut for Morphological, Yield and Its Contributing Traits under Imposed Endof-Season Drought Stress. *Current Journal of Applied Science and Technology*, 39(14), 108-118.
- Dewey, D. R. and Lu, K. H. (1959). A Correlation and path analysis of crested wheat grass seed production. *Agronomy Journal*, 51, 5-16.
- Gupta, R. P., Vachhani, J. H., Kachhadia, V. H., Vaddoria, M. A. and Barad, H. R. (2015). Correlation and path analysis in virginia groundnut (*Arachis hypogaea L.*). *Electronic Journal of Plant Breeding*, 6(1), 248-252.
- Janila, P., Pandey, M. K., Shasidhar, Y., Variath, M. T., Sriswathi, M., Khera, P., Manohar, S. S., Patne, N., Vishwakarma, M. K., Mishra, G. P., Radhakrishnan, T., Manivannan, N., Dobariya, K. L., Vasanthi, R. P. and Varshney, R. K. (2016). Molecular breeding for introgression of fatty acid desaturase mutant alleles (ahFAD2A and ahFAD2B) enhances oil quality in high and low oil containing peanut genotypes. *Plant Science*, 242, 203-213.
- John, K., Reddy, P. R. and Reddy, P. H. (2011). Genetic variability for morphological, physiological, yield and yield traits in F₂ populations of groundnut (*Arachis* hypogaea L). International Journal of Applied Biology and Pharmaceutical Technology, 2(4), 463-469.
- John, K., Vasanthi, R. P., Venkateswarlu, O., Murali Krishna, T. and Harinath Naidu, P. (2008). Genetic analysis of pod yield and resistance to biotic stresses in groundnut (*Arachis hypogaea* L.). *Legume Research*, 31(3), 227-229.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. Agronomy Journal, 47(7), 314-318.
- Jonah, P. M., Aliyu, B., Kadams, A. M. and Wamannda, D. T. (2012). Variation in Pod Yield Characters and Heritability Estimates in Some Cultivars of Bambara

Prasad et al.,

Biological Forum – An International Journal 1

15(11): 263-269(2023)

Groundnut (Vigna subterranea (L.) Verdc. Academic Journal of Plant Sciences, 5(2), 50-55.

- Krishnamurthy, D., Goudar, P. K., Keerthi, C. M. and Babu, H. P. (2015). Groundnut under organic farming: Genetic variability and association studies for yield, quality and disease resistance in recombinant inbred lines. *Legume Research: An International Journal*, 38(5), 627-632.
- Killada, G. K., Akkareddy, S., Muga, S. D., Pinagari, A., Gundrathi, S. V. and Pesaleddula, J. P. (2023). Character Association studies on Foliar Disease Resistance with Yield and Yield Attributing Traits in Groundnut (Arachis hypogaea L.). Biological Forum – An International Journal, 15(9), 640-643.
- Kumar, N., Ajay, B., Al Rathanakumar, T. R., Jadon, K. and Chikani, B. (2019). Genetic variability analyses for yield and physiological traits in groundnut genotypes. *Journal of Oilseeds Research*, 36(1), 1-7.
- Kumar, N., Ajay, B. C., Rathanakumar, A. L., Radhakrishnan, T., Mahatma, M. K. and Kona, P. (2020). Assessment of genetic variability for yield and quality traits in groundnut genotypes. Electronic Journal of Plant *Breeding*, 10(1), 196-206.
- Kumari, K. and Sasidharan, N. (2020). Studies on Genetic Variability, Correlation and Path Coefficient Analysis for Morphological and Yield Traits in Different Arachis spp. International Journal of Current Microbiology and Applied Sciences, 9(11), 1030-1039.
- Mandal, G. S., Das, A., Dutta, D., Mondal, B. and Senapati,
 B. K. (2017). Genetic variability and character association studies in groundnut (*Arachis hypogaea* L). Scholars Journal of Agriculture and Veterinary Sciences, 4(10), 424-433.
- Mohapatra, N. and Khan, H. (2020). Character association and path analysis in F₃ segregating generations for yield and its component traits in groundnut (*Arachis* hypogaea L.). Journal of Pharmacognosy and Phytochemistry, 9(4), 794-799.
- Muibai, N., Mwololo, J. K., Sibiya, J., Musvosvi, C. and Okori, P. (2020). Assessment of genetic variability among groundnut accessions under natural rosette disease infestation in Malawi. African Journal of Rural Development, 4(2), 283-304.
- Panse, V. G. and Sukhatme, P. V. (1985). Statistical methods for agricultural worker, ICAR, New Delhi, 235-246.
- Pappammal, N.A., Rajanbabu, V., Subramanian, A., Nithila, S. and Mothilal, A. (2020). Assessment of genetic variability for yield and component traits in groundnut

(Arachis hypogaea L.) germplasms in sodic and normal soil condition. *Electronic Journal of Plant Breeding*, 11(3), 925-932.

- Patel, C. K., Vachhani, J. H., Kachadiya, V. H., Nayak, J. J. and Jalu, R. K. (2021). Studies on correlation and path analysis for important traits in F₂ generations of groundnut (*Arachis hypogaea* L.). International Journal of Plant Pathology and Microbiology, 1(1), 01-06
- Pattidar, O. P. and Nadaf, H. L. (2017). An assessment of genetic variability and traits association among high oleic advanced breeding lines for yield and quality traits in groundnut (*Arachis hypogaea L.*). *Electronic Journal of Plant Breeding*, 8(1), 201-205.
- Ramakrishnan, P., Manivannan, N., Mothilal, A. and Mahalingam, L. (2017). Correlation studies in back cross derived population for foliar disease resistance in groundnut (*Arachis hypgaea L.*). International Journal of Current Microbiology and Applied Sciences, 6(5), 266-272.
- Shendekar, S. A., Nagesh Kumar, M. V., Meshram, M. R., Gadpayale, D. P., Venu Yadav, T. and Sudini, H. K., (2023). Genetic Parameters, Correlation and Path Analysis for Yield and Yield Contributing Traits in Post Rainy Groundnut (*Arachis hypogaea* L.). *Biological Forum – An International Journal*, 15(4), 400-404.
- Shinde, H. N., Amolic, V. L., Shinde, G. C., More, S. R., Pawar, S. V. and Nimbalkar, C. A. (2019). Genetic variability and association study for different traits in F5 progenies of groundnut. *Journal of Pharmacognosy and Phytochemistry*, 8(5), 1497-1500.
- Shukla, A. K. and Rai, P. K. (2014). Evaluation of groundnut genotypes for yield and quality traits. *Annals of Plant* and Soil Research, 16(1), 41-44.
- Trivikrama Reddy, A., Reddi Sekhar, M., Vijayabharathi, A., Lakshmi Pathy, T., Lakshmikantha Reddy, G. and Jayalakshmi, V. (2017). Correlation and path analysis of kernel yield and its components in Groundnut (Arachis hypogaea L.). International Journal of Current Microbiology and Applied Sciences, 6(12), 10-16.
- Tulsi, R. D., Hemlata, S., Ramesh, K. and Ram, K. (2017). Correlation and path analysis for yield and its contributing traits in groundnut (*Arachis hypogaea* L.). *International Journal of Agricultural Sciences*, 9(10), 3997-3999.

How to cite this article: V. Mani Prasad, CH. V. Durga Rani, G. Seshu and S.N.C.V.L. Pushpavalli (2023). Studies on Genetic variability, Correlation and Path coefficient Analysis for Yield Contributing and Quality Traits in Marker Assisted Derived Advanced Backcross Lines of Groundnut (*Arachis hypogaea* L.). *Biological Forum – An International Journal*, *15*(11): 263-269.