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Research Note

Correlation and path coefficient analyses in large seeded peanut (*Arachis hypogaea* L.) for kernel yield

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Abstract

Expression of complex traits like yield is the result of interaction of several yield contributing features. In the current research, association analysis and path analysis were conducted in an experiment involving 65 peanut genotypes to determine association of kernel yield and its component traits. Plant height, number of secondary branches per plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, 100 seed weight and protein content recorded positive significant correlation with kernel yield per plant. The results of PCA and Ward dendrogram pattern jointly inferred that plant height, number of mature pods per plant, number of immature pods per plant, pod yield per plant, 100 seed weight, oleic acid content and oleic linoleic acid ratio were found to be closely associated with kernel yield per plant. Further, results of path analysis suggested that number of mature pods per plant, 100 seed weight, number of secondary branches per plant and sound mature kernel per cent were leading in determining the kernel yield of peanut through direct positive effects and indirect positive effects via different yield attributing traits.

Keywords: Peanut, Correlation, Path Analysis, PCA, Kernel Yield

Peanut (*Arachis hypogaea* L.) is an annual legume crop planted for its superior edible oil and easily digestible protein found in its seeds. In India, Gujarat and Andhra Pradesh are the major groundnut growing states. India ranks second in peanut production (67.27 lakh tonnes) after China (175 lakh tonnes) with an export of 6,41,125

tonnes of confectionery types (FAO, 2019). India is the largest exporter of groundnut to Asian countries with a total worth of Rs.1836.12 crore in 2009-10, Rs.4398.01 crore in 2014-15 and Rs. 2535.06 crore in 2018-19 (Palanis Singh *et al.*, 2020). The fluctuating trend of peanut exports in India is mainly due to instability of yields

attributed to environmental effect, cultivation practices and lack of large seeded genotypes. Large seeded varieties attract higher price in global market for edible nuts. One of the earliest confectionery varieties to be grown in India was Birsa Bold 1 (Rahman *et al.*, 1995). Yield is a complex character that develops from the interactions of several traits that contribute to yield. It is important to understand the links between these traits in order to improve yield. Additionally, a number of components directly or indirectly influence the pod yield through other traits, which creates a complexity for breeder during selection. As a result, path coefficient analysis, which divides the correlation coefficient into the direct and indirect effects of the variables, may present a more logical picture of the association.

The present investigation comprised of 65 peanut genotypes, obtained from ICRISAT (Hyderabad), ARS (Kadiri) and RARS (Tirupati). The experiment was laid out during *Kharif*, 2019 at Agricultural College Farm, Bapatla, Andhra Pradesh. Each genotype was sown in two row plot, each row measuring 4 metres in length, were sown in the experiment in two replications adopting randomized block design, with a spacing of 45 cm between the rows and 15 cm between the plants. The experimental plot was maintained with recommended agronomic practices to raise a healthy crop. Morphological observations were recorded from five randomly selected plants in each of the genotype per replication for yield contributing traits. Days to 50% flowering and days to maturity were recorded on plot basis. Quality traits like oil content, protein content and fatty acids were estimated by using NIRS (model XDS RCA-FOSS Analytical AB, ICRISAT). Total soluble sugar content and free amino acids were estimated by adopting the method suggested by Sadasivam and Manickam (1961). The recorded data were statistically analyzed in INDOSTAT 9.2 Ver. and Meta R programme software. The standard method of Singh and Chaudhary (1977) was used to estimate phenotypic and genotypic correlation coefficients. Direct and indirect effects of component characters on kernel yield were computed using the method suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Principal Component Analysis (PCA) was carried according to procedure given by Banfield (1978).

The results of association analysis among 21 characters studied in 65 peanut genotypes are presented in **Table 1**. A significant positive association was recorded between the kernel yield per plant with plant height, number of secondary branches per plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, sound mature kernel per cent, 100 seed weight and protein content both at genotypic and phenotypic levels. The magnitude of relationship with kernel yield per plant was highest in case of pod yield per plant followed by number of mature pods per plant, 100 seed weight and plant height both at genotypic and

phenotypic levels. Protein content, number of immature pods per plant and number of secondary branches per plant were found to be strongly correlated with the kernel yield per plant at genotypic level while moderately correlated with the kernel yield per plant at phenotypic level. Oleic acid content exhibited significant positive correlation with kernel yield per plant at phenotypic level. These results suggested that peanut kernel yield per plant may be improved successfully by genotype selection based on these traits. Similar results were reported by Trivikramareddy *et al.* (2017) and Kumari and Sasidharan (2020) for pod yield per plant, number of mature pods per plant, 100 seed weight; Godhani *et al.* (2020) for plant height and number of immature pods per plant and Pavankumar *et al.* (2014) for protein content. As opposed to this, character like days to 50% flowering exhibited a substantial negative correlation with kernel yield per plant at the phenotypic level but not at the genotypic level, indicating that environmental factors may have an impact on this association. Bhargavi *et al.* (2017) also recorded significant association between days to 50% flowering and kernel yield per plant.

To better understand the relationships among 21 traits of peanut PCA based on the correlation matrix (**Fig. 1A**) and dendrogram generated by Ward method were used (**Fig. 1A**). The first two PCAs (PC1 – 29.39%, PC2 – 27.94%) collectively explained 57.33% of variation and this low proportion of variation was previously reported by Ajay *et al.* (2012). The relationships among the different yield and quality traits are graphically displayed by plotting the first two PCs scores (**Fig. 1A**). In the PCA, biplot separates the traits that are overlaying on a plot as vectors, with the length of the vectors describing the relative degree of variability in each trait recognized on biplot. The traits like, 100 seed weight, plant height, oleic acid content, oleic linoleic acid ratio, number of primary branches per plant, day to 50% flowering, linoleic acid content, palmitic acid content and number of mature pods per plant all had relatively long vectors based on PC1 and PC2 axes. Thus, indicating that they showed considerable variation among the 65 peanut genotypes studied. The PC1 and PC2 axes were used to classify 21 traits into four diverse groups. The first group included sound mature kernel percent, 100 seed weight, plant height, protein content, pod yield per plant and kernel yield per plant. The number of mature pods per plant, the number of immature pods per plant, oleic acid content and oleic linoleic acid ratio were all grouped together in second. Third group contained traits like linoleic acid content, palmitic acid content, free amino acids, stearic acid content and oil content. The fourth group had characters *viz.*, number of secondary branches per plant, number of primary branches per plant, days to 50% flowering, days to maturity, shelling percentage and total soluble sugars. All the traits showed positive correlation with other traits present in their own group.

Table 1. Genotypic and phenotypic correlation coefficients between kernel yield and kernel yield component traits in peanut

S.No.Character	r	DF	DM	PH	NPP	NSPP	NMPP	NIMPP	PYP	KYP	SMKP	SHP	HSW	OC	PC	FAA	TSS	PAC	SAC	OAC	LAC	OLR
1	DF	r _g	1.000																			
2	DM	r _p	1.000																			
3	PH	r _g	0.093	1.000																		
4	NPP	r _g	0.043	1.000	1.000																	
5	NSPP	r _g	-0.588**	-0.311*	1.000	1.000																
6	NMPP	r _g	-0.380**	-0.218*	1.000	1.000	1.000															
7	NIMPP	r _g	0.889**	0.034	-0.561**	1.000	1.000	1.000														
8	PYP	r _g	0.434**	0.080	-0.277**	1.000	1.000	1.000	1.000													
9	KYP	r _g	0.428**	-0.023	-0.129	0.944**	1.000	1.000	1.000	1.000												
10	SMKP	r _g	0.302**	0.093	-0.098	0.526**	1.000	1.000	1.000	1.000	1.000											
11	SHP	r _g	-0.003	0.014	0.196	0.315*	0.221	1.000	1.000	1.000	1.000	1.000										
12	HSW	r _g	0.019	0.008	0.228**	0.203*	0.217*	1.000	1.000	1.000	1.000	1.000	1.000									
13	OP	r _g	0.047	0.080	-0.017	0.292*	0.231	0.501**	1.000	1.000	1.000	1.000	1.000	1.000								
14	PP	r _g	0.034	0.124	-0.031	0.173*	0.192*	0.452**	1.000	1.000	1.000	1.000	1.000	1.000	1.000							
15	FAA	r _g	-0.268*	-0.081	0.547**	0.102	0.456**	0.736**	0.353**	1.000	1.000	1.000	1.000	1.000	1.000	1.000						
16	TSSP	r _g	-0.184*	-0.062	0.316**	0.050	0.263**	0.487**	0.292**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000					
17	PAC	r _g	-0.176	-0.153	0.431**	0.203	0.331*	0.640**	0.387**	0.997**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000				
18	SAC	r _g	-0.184*	-0.099	0.322**	0.081	0.234**	0.512**	0.285**	0.732**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000			
19	OAC	r _g	-0.066	-0.233	0.221	-0.146	0.211	-0.006	0.209	0.254*	0.407**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		
20	LAC	r _g	-0.039	-0.201*	0.137	-0.044	0.166	-0.014	0.137	0.205*	0.334**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
21	OLR	r _g	0.337**	0.072	-0.253*	0.754**	0.197	0.083	0.167	-0.153	0.172	0.246*	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	0.270**	0.009	-0.130	0.274**	0.164	0.061	0.068	-0.133	0.122	0.202*	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	-0.285*	-0.311*	0.637**	-0.125	0.051	0.091	-0.093	0.478**	0.464**	0.223	-0.103	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	-0.251**	-0.278**	0.477**	-0.078	0.039	0.095	-0.082	0.398**	0.417**	0.213*	-0.078	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	-0.090	-0.110	0.079	0.005	0.054	0.084	-0.229	0.024	-0.061	-0.106	-0.164	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	-0.057	-0.085	0.064	0.050	0.061	0.061	-0.181*	-0.010	0.044	-0.064	-0.116	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	-0.196	0.211	0.079	-0.213	-0.024	0.271*	0.313**	0.378**	0.327**	0.297*	-0.037	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	-0.177*	0.187*	0.007	-0.083	-0.002	0.129	0.223*	0.270**	0.259**	0.223**	-0.038	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	0.159	-0.014	0.041	0.119	0.066	-0.108	-0.066	-0.002	-0.045	0.169	0.015	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	0.136	-0.018	0.032	0.065	0.043	-0.110	-0.068	0.006	-0.034	0.164	0.021	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	0.187	0.314**	-0.431**	0.138	-0.041	-0.150	-0.217	-0.284*	-0.191	-0.060	0.275*	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	0.173	0.262**	-0.325**	0.068	-0.053	-0.144	-0.180*	-0.229*	-0.174	-0.064	0.208*	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	0.044	0.012	-0.028	-0.197	0.076	-0.496**	-0.300*	-0.074	-0.004	0.260*	0.064	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	0.034	0.010	-0.040	0.068	-0.398**	-0.265**	-0.050	-0.009	0.247**	0.042	0.034	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	0.093	-0.124	-0.050	0.228	0.404**	0.106	-0.011	0.161	0.123	-0.124	0.074	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	0.092	-0.102	-0.051	0.084	0.268**	0.104	0.014	0.098	0.087	-0.103	0.056	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	-0.114	0.053	0.074	0.244	-0.046	0.632**	0.372**	0.179	0.219	-0.160	0.016	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	-0.104	0.037	0.055	0.130	-0.033	0.569**	0.312**	0.140	0.173*	-0.130	0.044	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	-0.012	-0.140	-0.019	-0.219	0.036	-0.553**	-0.436**	-0.090	-0.197	0.099	-0.167	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	-0.015	-0.124	-0.007	-0.114	0.026	-0.506**	-0.394**	-0.079	-0.167	0.095	-0.140	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _g	0.061	0.171	-0.096	0.356**	-0.010	0.601**	0.520**	0.088	0.171	-0.145	0.053	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		r _p	0.055	0.149	-0.076	0.187*	0.008	0.546**	0.462**	0.075	0.151	-0.133	0.053	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

* ** - Significantly different at 5% and 1% probability levels, respectively. r_g - Genotypic correlation, r_p - Phenotypic correlation
 DFF- Days to 50 % flowering, PYP- Pod yield per plant (g), FAA- Free amino acids (µg g⁻¹), DM- Days to maturity, KYP- kernel yield per plant (g), TSS- Total soluble sugars (%), PH- Plant height, SMKP- Sound mature kernel per cent, PAC- Palmitic acid content (%), NPP- Number of primary branches per plant, SHP- Shelling percentage, SAC- Stearic acid content (%), NSPP- Number of secondary branches per plant, HSW- 100 seed weight (g), OAC- Oleic acid content (%), NIMPP- Number of mature pods per plant, OC- Oil content (%), LAC- Linoleic acid content (%), NIMPP- Number of immature pods per plant, PC- Protein content (%), OLR- Oleic linoleic acid ratio

Strong positive relationship of kernel yield per plant with pod yield per plant, number of mature pods per plant, number of immature pods per plant, protein content, 100 seed weight, plant height, sound mature kernel per cent, oleic acid content and oleic linoleic acid ratio is indicated by acute angle between vectors (**Fig. 1A**) less than 90° . The traits like pod yield per plant, protein content, 100 seed weight, plant height and sound mature kernel per cent were negatively correlated with total soluble sugars, days to 50% flowering, shelling percentage and number of primary branches per plant as indicated by obtuse angle ($> 90^\circ$) between them. Number of mature pods per plant, number of immature pods per plant, oleic acid content and oleic linoleic acid ratio were negatively associated with palmitic acid content and linoleic acid content as indicated by obtuse angle ($> 90^\circ$) between them. Biplot showed negative correlation of oleic acid content and oleic linoleic acid ratio with linoleic acid content and stearic acid content and these results were in accordance with the results of Ajay *et al.* (2012). It is conceivable to have genotypes with low oil and high oleic linoleic acid ratio, as shown by the negative correlation between the vectors of oleic acid content and oleic linoleic acid ratio and that of oil content. Since frequent assessment of genotypes for oil quality traits is expensive, breeding for oil quality traits can be done through selection based on yield and morphological traits. Results of biplot vectors showed that oil quality traits like protein content, oleic acid content and oleic linoleic acid ratio were positively correlated pod yield per plant, kernel yield per plant, number of mature pods per plant and number of immature pods per plant indicated that oil quality might be improved through selection based on above agro-morphological traits. The above relationship among different yield and quality traits indicated an opportunity of selecting genotypes with parallel traits for breeding high yielding lines of confectionary type.

The clustering of traits was done based on Ward's method for correlation of kernel yield attributing traits and quality traits by using Meta R programme (**Fig. 1B**). Dendrogram pattern showed that all 21 traits were distributed into 3 major clusters. In the first cluster oleic acid content, oleic linoleic acid ratio and kernel yield per plant were grouped with number of immature pods per plant. Plant height, 100 seed weight, number of mature pods per plant and pod yield per plant were found to be closely associated with oleic acid content and oleic linoleic acid ratio, which indicated that breeding for both high kernel yield and high quality could be achieved indirectly through direct selection of such highly heritable and closely related traits. The second cluster consisted of palmitic acid content, linoleic acid content, free aminoacids, sound mature kernel per cent and protein content, which were placed closely to kernel yield per plant. Hence these traits could be given due consideration while breeding of kernel yield per plant. The third cluster consisted of eight traits namely, shelling percentage, days to 50% flowering, number of primary branches per plant, number of secondary

branches per plant, days to maturity, total soluble sugars, oil content and stearic acid content and were positioned far away from kernel yield per plant. Such traits are of less importance for breeding of high kernel yield per plant in groundnut. Similar findings were reported earlier by Yusuf *et al.* (2019).

The estimated genotypic and phenotypic association values for the characters were used to derive matching direct and indirect effects (**Table 2**). The magnitudes of genotypic path effects were higher than phenotypic path effects representing the masking effect of environment. Residual effect for genotypic and phenotypic path coefficient analysis were 0.635 and 0.554 respectively indicating that about 36.5% (genotypic) and 44.6% (phenotypic) of the variability in kernel yield per plant was contributed by 20 characters studied in path coefficient analysis. This indicated the moderate contribution of characters studied in this investigation.

The results revealed that the direct negative effect of pod yield per plant was predominant in influencing the kernel yield in peanut only at genotypic level, where as it positively influenced the kernel yield at phenotypic level. The direct positive effect of number of mature pods per plant, 100 seed weight, number of secondary branches per plant and sound mature kernel per cent were outstanding in regulating the kernel yield in peanut and also showed positive association with kernel yield both at genotypic and phenotypic levels, which suggested that these characters are the most important contributors for kernel yield and hence direct selection based on these traits for kernel yield would be rewarding. These results are in line with reports of Zaman *et al.* (2011) and Kumari and Sashidharan (2020). Direct positive effect of palmitic acid content both at genotypic and phenotypic levels and negative associations both at genotypic and phenotypic levels with kernel yield suggested that palmitic acid content would be an important contributor for increasing of kernel yield *via* other characters. Hence indirect selection might be rewarding for increment of kernel yield per plant. Number of mature pods per plant and 100 seed weight were showed positive indirect on kernel yield per plant *via* plant height, number of secondary branches per plant, pod yield per plant, stearic acid content and oleic acid content both at genotypic and phenotypic levels. Number of secondary branches per plant and sound mature kernel per cent showed positive indirect effect on kernel yield per plant *via* number of immature pods per plant, pod yield per plant, shelling percentage and palmitic acid content both at genotypic and phenotypic levels while palmitic acid content influenced the kernel yield per plant *via* days to 50% flowering, number of secondary branches per plant, shelling percentage, 100 seed weight, protein content, total soluble sugars and linoleic acid content. These results coincided with early reports made by Trivikramareddy *et al.* (2017), Kumari and Sashidharan (2020) and Yusuf *et al.* (2017).

Table 2. Direct (diagonal) and indirect effects of yield components on kernel yield per plant both at genotypic and phenotypic level in peanut

S.No.	Character	G/PDFF	DM	PH	NPP	NSPP	NMPP	NMPPPYP	SMKP	SHP	KYP (r)	HSW	OC	PC	FAA	TSS	PAC	SAC	OAC	LAC	OLR	KYP (r)	
1	DFP	-0.882	0.034	0.393	-0.209	0.280	-0.006	0.007	0.245	-0.027	-0.048	-0.176	-0.295	0.078	0.229	0.010	-0.016	0.003	-0.028	0.089	-0.000	-0.031	-0.176
2	DM	-0.123	-0.002	-0.005	0.010	0.002	0.004	-0.000	-0.097	-0.004	0.051	-0.184*	-0.043	-0.007	-0.017	-0.003	0.003	-0.002	0.032	0.003	0.010	-0.184*	-0.153
3	PH	-0.082	0.367	0.208	-0.008	0.015	-0.034	0.013	0.075	-0.096	-0.010	-0.153	-0.322	0.095	-0.246	-0.001	-0.028	-0.001	0.037	-0.042	-0.005	0.028	-0.099
4	NPP	-0.005	-0.038	-0.003	0.002	0.001	-0.002	-0.002	-0.032	-0.023	0.002	-0.099	-0.048	-0.011	0.015	0.000	0.005	-0.001	0.002	-0.011	0.021	0.049	0.431**
5	NSPP	0.519	-0.114	-0.669	0.132	-0.085	0.479	-0.003	-0.500	0.091	0.036	0.431**	0.660	-0.068	-0.092	0.002	0.039	-0.002	0.015	-0.058	0.001	-0.014	0.322**
6	NMPP	0.047	0.008	0.012	-0.007	-0.001	0.053	0.000	0.166	0.016	-0.025	0.322**	0.082	0.008	-0.001	-0.001	-0.006	0.001	0.001	-0.017	-0.001	-0.182	0.203
7	NMPPPYP	-0.784	0.013	0.375	-0.235	0.618	0.771	0.046	-0.093	-0.060	-0.107	0.203	-0.129	0.005	0.250	0.007	-0.013	-0.012	-0.068	-0.191	-0.008	0.035	0.081
8	SHP	-0.053	-0.003	-0.003	0.024	0.004	0.047	-0.002	0.026	-0.005	0.052	0.081	-0.013	0.007	-0.008	-0.002	0.001	-0.004	-0.002	-0.040	0.019	-0.005	0.331**
9	SHP	-0.377	0.009	0.086	-0.222	0.655	0.540	0.041	-0.417	0.087	-0.028	0.331**	0.052	-0.047	0.028	0.004	0.004	0.004	-0.121	0.036	0.001	-0.005	0.234**
10	SHP	-0.037	-0.004	-0.001	0.013	0.007	0.050	-0.003	0.138	0.019	0.031	0.234**	0.007	0.008	0.000	-0.001	-0.001	0.006	-0.005	0.010	-0.005	0.001	0.234**
11	SHP	0.002	-0.005	-0.131	-0.074	0.144	2.447	0.079	-0.673	-0.003	-0.012	0.640**	0.095	-0.073	-0.282	-0.007	0.014	-0.029	-0.032	-0.495	-0.020	-0.307	0.640**
12	SHP	-0.002	0.000	0.003	0.005	0.002	0.233	-0.006	0.255	-0.001	0.011	0.512**	0.016	0.008	0.012	0.003	-0.002	-0.035	-0.002	-0.173	0.086	0.101	0.512**
13	SHP	-0.042	0.029	0.011	-0.069	0.171	1.225	0.157	-0.323	0.087	-0.024	0.387**	-0.097	0.198	-0.367	-0.004	0.020	-0.018	0.003	-0.291	-0.016	-0.266	0.387**
14	SHP	-0.004	-0.005	-0.000	0.004	0.001	0.105	-0.013	0.153	0.015	0.013	0.285**	-0.014	-0.023	0.021	0.002	-0.004	-0.023	-0.000	-0.095	0.067	0.086	0.285**
15	SHP	0.237	-0.030	-0.366	-0.024	0.298	1.799	0.055	-0.915	0.105	0.022	0.997**	0.495	-0.021	-0.445	0.000	0.026	-0.004	-0.048	-0.140	-0.003	-0.045	0.997**
16	SHP	0.023	0.002	0.004	0.001	0.002	0.113	-0.004	0.524	0.023	-0.025	0.732**	0.068	0.001	0.025	-0.005	-0.004	-0.002	-0.043	0.013	0.014	0.732**	
17	SHP	0.058	-0.085	-0.148	0.034	0.138	-0.015	0.033	-0.233	0.414	-0.035	0.407**	0.231	0.092	-0.347	0.010	0.005	0.015	0.037	0.125	0.004	0.074	0.407**
18	SHP	0.005	0.008	0.002	-0.001	0.001	-0.003	-0.002	0.108	0.113	0.038	0.334**	0.036	-0.008	0.021	-0.004	0.001	0.022	0.002	0.040	-0.016	-0.025	0.334**
19	SHP	-0.297	0.027	0.169	-0.177	0.129	0.204	0.026	0.140	0.102	-0.141	0.172	-0.106	0.142	0.043	0.001	-0.025	0.004	-0.022	-0.012	-0.006	-0.027	0.172
20	SHP	-0.033	-0.000	-0.002	0.007	0.001	0.014	-0.001	-0.070	0.023	0.189	0.122	-0.013	-0.015	-0.004	-0.001	0.004	0.004	-0.001	-0.013	0.024	0.010	0.122
21	SHP	0.252	-0.114	-0.426	0.029	0.033	0.224	-0.015	-0.437	0.092	0.015	0.464**	1.036	-0.002	-0.201	0.010	0.016	0.003	-0.067	-0.053	-0.000	0.071	0.464**
22	SHP	0.031	0.010	0.006	-0.002	0.000	0.022	0.001	0.208	0.024	-0.015	0.417**	0.171	0.000	0.012	-0.004	-0.003	0.003	-0.004	-0.020	0.002	-0.025	0.417**
23	SHP	0.079	-0.040	-0.073	0.001	0.035	0.206	-0.036	-0.032	-0.044	0.023	-0.061	0.002	-0.867	0.812	-0.023	0.016	-0.055	-0.081	0.004	0.005	0.014	-0.061
24	SHP	0.007	0.003	0.001	0.001	0.000	0.014	0.002	0.005	-0.007	-0.022	0.044	0.000	0.129	-0.048	0.004	-0.003	-0.011	-0.004	0.003	-0.018	-0.013	0.044
25	SHP	0.173	0.077	-0.053	0.050	-0.016	0.589	0.049	-0.348	0.123	0.005	0.327**	0.178	0.601	-1.171	0.012	-0.002	0.005	0.019	0.025	0.001	0.009	0.327**
26	SHP	0.022	-0.006	-0.000	-0.002	0.000	0.030	-0.003	0.142	0.025	-0.007	0.259**	0.021	-0.066	0.094	-0.004	0.001	0.009	0.001	0.006	-0.003	-0.001	0.259**
27	SHP	-0.140	-0.005	-0.027	-0.028	0.043	-0.264	-0.010	-0.002	0.070	-0.002	0.045	0.174	0.182	-0.225	0.060	0.014	0.000	-0.003	0.067	0.005	0.046	-0.045
28	SHP	-0.017	0.001	0.000	0.002	0.000	-0.026	0.001	0.003	0.019	0.004	-0.034	0.028	-0.023	0.015	-0.024	-0.003	0.001	-0.000	0.026	-0.023	-0.017	-0.034
29	SHP	0.165	0.115	0.288	-0.033	-0.027	-0.368	-0.034	0.260	-0.025	-0.039	-0.191	-0.180	0.155	-0.025	-0.009	-0.090	0.001	-0.006	-0.022	-0.003	0.016	-0.191
30	SHP	-0.021	-0.010	-0.004	0.002	-0.000	-0.034	0.002	-0.120	-0.007	0.039	-0.174	-0.030	-0.019	0.003	0.004	0.020	0.002	-0.000	-0.010	0.015	-0.006	-0.174
31	SHP	-0.039	-0.005	0.019	0.046	0.050	-1.214	-0.047	0.066	0.108	-0.009	0.004	0.045	0.161	-0.106	0.000	-0.002	0.058	0.024	0.510	0.020	0.311	0.004
32	SHP	-0.004	0.000	0.000	-0.001	0.001	-0.093	0.003	-0.026	0.028	0.008	-0.009	0.006	-0.017	0.010	-0.000	0.001	0.088	0.001	0.173	-0.086	-0.101	-0.009
33	SHP	-0.082	-0.046	0.034	-0.054	0.265	0.259	-0.002	-0.148	-0.051	0.011	0.123	0.233	-0.235	0.074	0.001	-0.002	-0.005	-0.299	0.100	0.005	0.087	0.123
34	SHP	0.011	0.004	-0.001	0.002	0.002	0.024	-0.000	0.051	-0.012	0.011	0.087	0.034	0.024	-0.003	-0.000	0.000	-0.002	-0.020	0.033	-0.021	-0.028	0.087
35	SHP	0.100	0.020	-0.050	-0.057	0.030	1.547	0.058	-0.164	-0.066	-0.002	0.219	0.070	0.005	0.037	-0.005	-0.003	-0.038	0.038	-0.783	-0.033	-0.426	0.219
36	SHP	0.013	-0.001	0.001	0.003	-0.000	0.133	-0.004	0.074	-0.015	0.008	0.173*	0.011	-0.001	-0.002	0.002	0.001	-0.050	0.002	-0.305	0.153	0.151	0.173*
37	SHP	0.010	-0.051	-0.013	0.051	0.024	-1.354	-0.068	0.083	0.041	0.024	-0.197	-0.012	-0.109	-0.024	0.008	0.008	0.033	-0.041	0.725	0.036	0.433	-0.197
38	SHP	0.002	0.005	0.000	-0.003	0.000	-0.118	0.005	-0.041	0.011	-0.027	-0.167	-0.002	0.014	0.002	-0.003	-0.002	0.045	-0.002	0.275	-0.170	-0.157	-0.167
39	SHP	-0.054	0.063	0.064	-0.084	0.006	1.470	0.082	-0.081	-0.060	-0.008	0.171	-0.144	0.074	0.022	-0.005	0.003	-0.036	0.051	-0.652	-0.030	-0.511	0.171
40	SHP	-0.007	-0.006	-0.001	0.005	0.000	0.127	-0.006	0.039	-0.015	0.010	0.151	-0.023	-0.009	-0.001	0.002	-0.001	-0.048	0.003	-0.248	0.143	0.185	0.151

G- Genotypic level; P- Phenotypic level ; Residual effect of genotypic and phenotypic paths, respectively- 0.635, 0.554

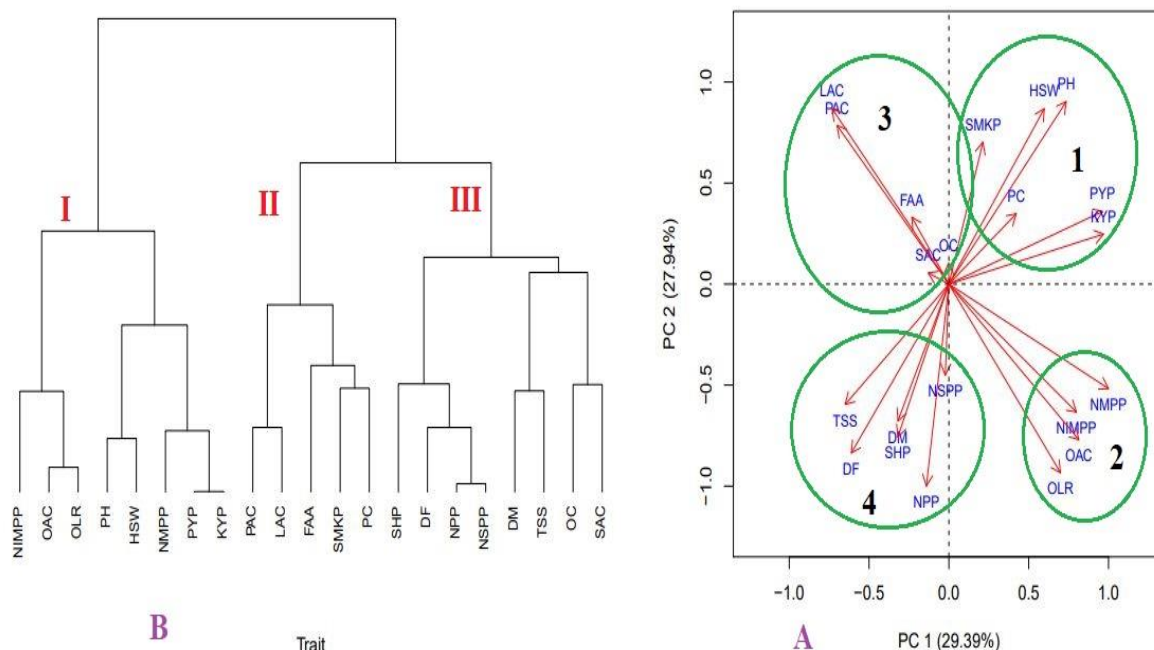


Fig. 1. A). Biplot showing the relation between PC1 and PC2 for 21 traits of 65 peanut genotypes B). Dendrogram of 21 traits in 65 peanut genotypes

Days to 50% flowering was observed to have direct negative effect on kernel yield per plant and negative association both at genotypic and phenotypic levels. These results are in harmony with Trivikramareddy *et al.* (2017), Kumari and Sashidharan (2020) and Shruti (2020). All the characters were observed to have indirect effect on kernel yield per plant through number of mature pods per plant, 100 seed weight, number of secondary branches per plant and sound mature kernel per cent, which indicated that selection for these traits would result in substantial improvement in kernel yield per plant. High residual effects of both genotypic and phenotypic paths (0.614, 0.558) for kernel yield revealed that there might be other important characters which were not studied in the current study. Foregoing evidences indicate that number of mature pods per plant, 100 seed weight, number of secondary branches per plant and sound mature kernel per cent might prove as efficient alternate criteria of selection for kernel yield per plant. In other words, selection indices may be formed by considering all these characters for improvement of kernel yield per plant in groundnut.

From the above mentioned results, it could be concluded that the characters plant height, number of secondary branches per plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, 100 seed weight and protein content were the yield

components positively associated with kernel yield per plant. Results of both PCA and dendrogram pattern together implied that plant height, number of mature pods per plant, number of immature pods per plant, pod yield per plant, 100 seed weight, oleic acid content and oleic linoleic acid ratio were found to be closely associated with kernel yield. Number of mature pods per plant, 100 seed weight, number of secondary branches per plant and sound mature kernel per cent were the most important in governing the kernel yield in peanut through direct positive effect and indirect positive effect *via* different yield attributing traits.

REFERENCES

- Ajay, B.C., Gowda, M.V.C., Rathnakumar, A.L., Kusuma, V.P., Abdul, F.R., Prasanna, H., Ramya, K.T., Govindaraj, G. and Prashanthbabu. H. 2012. Improving genetic attributes of confectionary traits in peanut (*Arachis hypogaea* L.) using multivariate analytical tools. *Journal of Agricultural Science*, 4(3): 247-258. [Cross Ref]
- Banfield, C.F. 1978. Principal component analysis for genstat. *Journal of Statistics and Computer Simulation*, 6: 211-222. [Cross Ref]
- Bhargavi, G., Rao, S.V., Babu, D.R. and Rao, N.K.L.

2017. Character association and path coefficient analysis of pod yield and yield components in Virginia bunch groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **8**(1): 262-268. [Cross Ref]
- Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**: 515-518. [Cross Ref]
- FAO, 2019. Food and agricultural organization statistical database available at www.faostat.org.
- Godhani, P.P., Jivani, L.L., Patel, B.M. and Raval, L.J. 2020. Character association and path coefficient analysis studies for quantitative traits in F₃ generation of groundnut (*Arachis hypogaea* L.). *Indian Journal of Pure and Applied Biosciences*, **8**(6): 190-199. [Cross Ref]
- Kumari, K. and Sashidharan, 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. [Cross Ref]
- Palanisingh, V., Vijayalakshmi, R., Sathishkumar, R. and Palanichamy, V. 2020. Groundnut exports of India direction and trends. *International Journal of Scientific and Technology Research*, **9**(6): 397-400.
- Pavankumar, C., Rekha, R., Venkateswarulu, O. and Vasanthi, R.P. 2014. Correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.). *International Journal of Applied Biology and Pharmaceutical Technology*, **5**(1): 8-11.
- Rahman, M.H., Sinha, P.K. and Basu, M.S. 1995. Birsa Bold 1, A promising new confectionery variety of groundnut. *International Arachis Newsletter*, **15**: 12.
- Sadasivam, S. and Manickam, A. 1961. Biochemical methods for Agricultural Sciences, Wiley Eastern Limited, New Delhi, 187-188.
- Shruti, K. 2020. Stability analysis in groundnut (*Arachis hypogaea* L.), Ph.D. (Agri.) Thesis, Acharya N.G. Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India.
- Singh, R.K. and Chaudhary, B.D. 1977. *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi.
- Trivikramareddy, A., Reddisekhar, M., Vijayabharathi, A.T., Lakshmi, P., Lakshmikantha, G.R. 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. [Cross Ref]
- Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*, **20**: 557-585.
- Yusuf, Z., Hugo, A., Hussein, S., Mohammed, W. and Zeleke, H. 2019. Agromorphological and biochemical markers selection in groundnut (*Arachis hypogaea* L.) cultivars. *Merit Research Journal of Agricultural Science and Soil Sciences*, **7**(1): 15- 20.
- Yusuf, Z., Zeleke, H., Mohammed, W., Hussein, S. and Hugo, A. 2017. Estimate of genetic variability parameters among groundnut (*Arachis hypogaea* L.) genotypes in Ethiopia. *International Journal of Plant Breeding. Crop Science*, **4**(2): 225-230.
- Zaman, M.A., Khatun, M.T., Ullah, M.Z., Moniruzzamn, M. and Alam, K.H. 2011. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). *A Scientific Journal of Krishi Foundation*, **9**(1&2): 29-36. [Cross Ref]