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## Studies on character association and path analysis in groundnut (*Arachis hypogaea* L.)

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### Abstract

The study was undertaken to estimate the character association, direct and indirect effects by path analysis for pod yield and its components by using 39 groundnut genotypes. The genotypic correlation coefficients were found to be relatively closer to the corresponding phenotypic correlations coefficients, representing strong inherent association between the traits. Pod yield was significant positively correlated with Kernel yield, Shelling percent and hundred kernel weight and significant negative association with day to 50% flowering, days to maturity and dry haulm yield. Path coefficient analysis revealed that the direct positive effect of kernel yield followed by days to maturity.

**Keywords:** Correlation path analysis and groundnut

### Introduction

The cultivated groundnut *Arachis hypogaea* L. is one of the most important oil and protein producing legume crop of the semi-arid tropics. Groundnut kernel contains 46-52% high quality oil more than 25% assumable protein and Vitamin B and E. It is one the most important edible oil in the world. The breeding objective in groundnut is to develop varieties with high yield, early maturity, high protein and oil content, resistant to diseases and insect pests. Since the economic part of groundnut known as pod is developed under the soil, prediction of its performance based on aerial morphological characters is almost difficult (Weiss, 2000) [1]. As it is a highly self pollinated crop, the variability observed within the habit groups reported to be very low (Emery and Wynne, 1976) [5]. In fact, greater interest to the plant breeder is pod yield. Genetic improvement of pod yield, alone, is not possible through phenotypic selection because of polygenic nature and low heritability. Hence, resorting to selection through correlated response entailing several contributing factors which influence pod yield both directly and indirectly shall be most appropriate. The path coefficient analysis is one of the effective technique to sought out inter relationship between different yield characters and their direct and indirect effect on yield through correlation values. The present study was undertaken to understand variability and the relationship between various characters and their contribution to yield.

### Materials and Methods

The material in the present investigation consists of 39 genotypes including two checks were sown in randomized complete block design (RBD) with two replications at Professor Jayashankar Telangana State Agricultural University, Regional Agricultural Research Station, Jagtial during *Rabi* 2011-12. Each genotype was raised in 5m length with spacing of 30 X 10 cm. Recommended agronomic practices were followed to raise a good crop. Observations were recorded on days to 50% flowering, days to maturity, shelling percent, hundred kernel weight(g), dry pod yield(kg/ha), kernel yield(kg/ha) and dry haulm yield(kg/ha). The data were recorded on five randomly selected plants in each entry in each replication. The mean values were used for analysis of variance. The correlation coefficients and path analysis were carried out following the methods of Al-Jibouri *et al.*, (1958) [1] and Dewey and Lu (1959) [3] respectively.

### Results and discussion

The analysis of variation revealed highly significant differences among the genotypes for all the characters studied *viz.*, days to 50% flowering, days to maturity, shelling percent, hundred kernel weight(g), dry pod yield(kg/ha), kernel yield(kg/ha) and dry haulm yield(kg/ha) indicating the existence of considerable genetic variation in the experimental material. Pod yield is a complex character governed by several contributing traits. Hence, it is important to

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understand the association of different characters with pod yield for enhancing the usefulness of selection criterion to be followed while developing varieties. In the present investigation the genotypic and phenotypic correlations are on par with each other suggesting the less influence of environment. Hence, in this paper the genotypic correlations only discussed (Table 1). Invariably pod yield was significant positively correlated with Kernel yield, Shelling percent and hundred kernel weight and significant negative association with day to 50% flowering, days to maturity and dry haulm yield. Chishti *et al.*, (2000)<sup>[2]</sup> reported positive and significant correlations between pod yield and the number of pods in plant, grain to pod weight, 100-grain weight and per cent oil as well as a negative and significant correlation between pod yield and the number of days to maturity. Sumati *et al.*, (2007) and Dhaliwal *et al.*, (2010)<sup>[4]</sup> also reported that pod yield was significant positive association with kernel yield and hundred kernel weight that supports present findings. Thirumala rao *et al.*, (2012)<sup>[9]</sup> reported that pod yield positively associated with kernel yield, hundred kernel weight, shelling percent and number of pods per plant. Shankar *et al.*, (2018)<sup>[6]</sup> reported that pod yield positively associated with kernel yield, hundred kernel weight and number of pods per plant. Days to 50% flowering was significant positive association with dry haulm yield and non significant positive association with days to maturity and significant negative association with Shelling percent, Kernel

yield and hundred kernel weight. Days to maturity was significant positive association with dry haulm yield and significant negative association with Shelling percent, Kernel yield and hundred kernel weight. Shelling percent was significant positive association with Kernel yield, hundred kernel weight and negative association with dry haulm yield. Hundred kernel weight was significant positive association with Kernel yield and positive association with dry haulm yield. Kernel yield was significant negative association with dry haulm yield.

In view of the fact that correlation coefficients do not take into account extremely complex interrelationships between various characters., Path coefficient analysis was applied to partition the correlation into direct and indirect effects. Path coefficient analysis (Table 2) discovered that the direct positive effect of kernel yield followed by days to maturity and negative effect of shelling percent, days to 50% flowering, dry haulm yield and hundred kernel weight revealed on pod yield. Thirumala Rao *et al.*, (2014)<sup>[10]</sup> reported that direct positive effect of kernel yield days to maturity, no of pods per plant and hindered kernel weight on pod yield. P.B.Singh *et al.*, (2017)<sup>[7]</sup> reported that kernel yield, oil content, shelling percent have direct and positive effect on pod yield. Shankar *et al.*, (2018)<sup>[6]</sup> reported that direct positive effect of kernel yield and number of pods per plant on pod yield.

**Table 1:** Genotypic correlation coefficients between different traits in Groundnut

Character	DF	DM	S%	HKW	KY	DHY	Seed Yield/Plant
Days to 50% flowering(DF)	1.0000	1.1409	-0.4471**	-0.2499*	-0.3310**	0.4014**	-0.3080**
Days to maturity(DM)		1.0000	-0.7380**	-0.1899	-0.3081**	0.7656**	-0.2518*
Shelling (S%)			1.0000	0.2614*	0.5186**	-0.0020	0.3970**
Hundred Kernel weight(HKW)				1.0000	0.2895*	0.1021	0.2724*
Kernel yield(KY)					1.0000	-0.2282*	0.9902**
Dry haulm yield(DHY)						1.0000	-0.2508*

\*, \*\* Significant at P=0.05 and P = 0.01 level respectively

**Table 2:** Direct (diagonal) and indirect effects of yield contributing characters in Groundnut

Character	DF	DM	S%	HKW	KY	DHY	Seed Yield/Plant
Days to 50% flowering(DF)	-0.0552	-0.0630	0.0247	0.0138	0.0183	-0.0222	-0.3080**
Days to maturity(DM)	0.0301	0.0264	-0.0195	-0.0050	-0.0081	0.0202	-0.2518*
Shelling (%)	0.0707	0.1166	-0.1580	-0.0413	-0.0820	0.0003	0.3970**
Hundred Kernel weight(HKW)	0.0004	0.0003	-0.0004	-0.0014	-0.0004	-0.0001	0.2724*
Kernel yield(KY)	-0.3511	-0.3268	0.5502	0.3071	1.0608	-0.2420	0.9902**
Dry haulm yield(DHY)	-0.0028	-0.0063	0.0000	-0.0007	0.0016	-0.0070	-0.2508*

Residual effect (G) = 0.0247 G = Genotypic

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