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## Research Article

# Assessment of genetic variability for yield and quality traits in groundnut genotypes

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### Abstract

Twenty groundnut genotypes were evaluated for 14 characters to study the genetic variability parameters, correlation coefficient and path analysis. Analysis of variance showed highly significant differences among genotypes for all the studied characters indicating that adequate variability was found among the genotypes studied for these characters. Days to 50% flowering, number of pods/plant, 100 pod weight, 100 sound mature kernel and sound mature kernel had high heritability coupled with high genetic advance as per cent of mean and medium to high genotypic coefficient of variation indicating selection would be rewarding for improving these traits because of greater control of additive gene effects, while the traits like primary branches per plant, pod yield and kernel yield had moderate GCV and heritability along with high genetic advance as per cent of mean revealed heritable component of genetic variance playing greater role in expression of these traits and selection would be effective. For seed size and quality related traits, medium heritability along with low genetic advance as per cent of mean was observed for KL/KW ratio, protein content, oil content and sugar content indicating high influence of environment on expression of these traits. Genotypic correlation coefficients revealed that pod yield had significant and highly positive correlations with plant height, primary branches per plant, pods per plant, 100 pod weight, 100 sound mature kernel, kernel yield and harvest index, while negative and significant for days to 50% flowering, 100 sound mature kernel and pods per plant had high positive direct effect and also highly significant positive correlation with pod yield. Therefore, selection for both component traits may helpful in identifying genotypes with high pod yield in groundnut.

### Key words

Variability, GCV, PCV, heritability, genetic advance, correlation

### Introduction

Groundnut (*Arachis hypogaea* L.) is an important self-pollinated oilseed crop grown in about 5.0 million ha area with the production and productivity of 7.72 million tons and 1537 kg/ha, respectively during 2015-16 to 2017-18 (Anonymous, 2018). Groundnut kernels are a source of high-quality edible oil (44–56%), easily digestible protein (22–30%), carbohydrates (10–25%), vitamins (E, K, and B complex), minerals (Ca, P, Mg, Zn and Fe) and fiber (Variath and Janila, 2017). It is also a rich source of several micronutrients and health-enhancing components, including minerals, antioxidants and vitamins along with some biologically active polyphenols, flavonoids and isoflavones (Janila *et al.*, 2013).

Genetic variability is the prerequisite for initiating an effective and successful breeding programme. Genetic variability in the cultivated groundnut is substantial due to single hybridization event between the diploid progenitors (*A. duranensis* and *A. ipaensis*, contributed “AA” and “BB” genomes, respectively) followed by chromosome doubling and thought to be originated at Southern Bolivia and Northern Argentina (Kochert *et al.*, 1996). To

exploit available genetic variability, requires lot of resources for the development of cultivars by selection and hybridization to adapt in to different environmental conditions. Effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the breeding material for the target trait. Genotypic coefficient of variability estimate gives good implication for genetic potential in crop improvement through selection (Johnson *et al.*, 1955).

Heritability is the squared correlation between predicted (phenotypic) value and actual genetic or genotypic value. Heritability ( $h^2$ ) can be used to predict the response to selection ( $R$ ) as  $R = h^2S$ , where  $S$  is the selection differential (Falconer and Mackay, 1996). Heritability is a very important parameter because it determines the response to selection. It is defined as the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects known as narrow sense heritability while proportion of phenotypic variance that is attributable to an effect for the whole genotype,

comprising the sum of additive, dominance and epistatic effects known as broad sense heritability (Nyquist, 1991; Falconer and Mackay, 1996). Heritability and genetic advance are very useful biometrical tool for breeders in determining the direction and magnitude of selection. High heritability alone is not enough to make efficient selection in the advanced generations and unless accompanied by substantial amount of genetic advance. The study of genetic advance with heritability estimates further clarify the nature of gene action controlling character, which deciding the breeding methodology for the genetic improvement of the character. Artificial selection for characters having low heritability and genetic advance should be practiced in advanced generations with reduced frequency of heterozygosity (Allard, 1999).

Correlation allows indirect selection for quantitative character having low heritability by measures the degree and direction of association between two characters, which sometime may leads to faster progress than direct selection for the desired character. Correlation result hampered by direction, importance of character, effect of two or more characters and environmental effect on expression of the character. Correlation does not allow provide information regarding cause and effect. Path coefficient analysis is very important biometrical technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable. Hence, it is necessary to study path coefficient analysis, which takes in to account the casual relationship in addition to degree of relationship. The present study was undertaken using 20 diverse groundnut genotypes including advanced breeding lines and improved cultivars to estimate genetic variability parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ( $h^2_{bs}$ ), genetic advance (GA), genetic advance as percentage of mean (GAM), correlation coefficient and path coefficient analysis for yield and quality traits in groundnut.

### Materials and Methods

The experimental material consisted of 20 genotypes including five Spanish and 11 Virginia advanced breeding lines with four high yielding popular groundnut varieties *viz.*, GG 7, TG 37A, GG 20 and Somnath as check varieties. The experiment was laid out in a randomized complete block design with three replications during *kharif* 2012 at ICAR-Directorate of Groundnut Research, Junagadh, Gujarat (Lat. 21°31' N, Long. 70°36' E) in medium black calcareous soil. The seeds of each genotype were sown in five rows of 5m length at

45cm spacing between rows and 10cm between plants. Recommended package of practices were followed for raising of the crop. Supplementary irrigation was given as and when required to protect the crop. The observations were recorded on days to 50% flowering, plant height (cm), number of primary branches per plant, number of pods per plant, 100 pod weight (g), 100 sound mature kernel, sound mature kernel (%), kernel length/width ratio, kernel yield (kg/ha), pod yield (kg/ha), harvest index (%) on ten randomly selected competitive plants in each genotype in each replication except days to 50% flowering, which was recorded on plot basis. The data on quality parameters were recorded on protein content (%), oil content (%) and sugar content (%) by NIR (Dickey John, Instalab 700). The data were subjected to statistical analysis and analysis of variance was calculated (Panse and Sukhatme, 1976) and following genetic parameters were estimated for the character having significant mean square due to the genotypes. Phenotypic and genotypic coefficient of variation was calculated as suggested by Burton (1952), heritability (broad sense) by Lush (1940), genetic gain by Johnson *et al.* (1955), phenotypic (rp) and genotypic (rg) correlations by Miller *et al.* (1958) and path coefficient analysis as per method suggested by Dewey and Lu (1959).

### Results and Discussion

The analysis of variance for all characters (Table 1) revealed highly significant differences among all the twenty genotypes for all the characters *viz.*, days to 50% flowering, plant height (cm), number of primary branches per plant, number of pods per plant, 100 pod weight (g), 100 sound mature kernel, sound mature kernel (%), kernel length/width ratio, kernel yield (kg/ha), pod yield (kg/ha), harvest index (%), protein content (%), oil content (%) and sugar content (%). It indicating that adequate variability was found among the characters studied. It could be due to diverse pedigree of the advanced breeding lines and botanical types. The genetic variability in the material was considered for further analysis. Mean values of 20 genotypes for 14 characters revealed (Table 2) that advanced breeding line PBS 22080 was found significantly superior over the best check variety GG 20 (1339kg/ha, 1877kg/ha, 28%, 24.8%, 4.4%) for kernel yield (1770kg/ha), pod yield (2563kg/ha), harvest index (39%), protein content (32%) and sugar content (5.5), respectively. This advanced breeding line could be used in breeding programme for improving these characters.

The component of variance revealed that phenotypic coefficients of variance were higher

than the genotypic coefficients of variance for all the characters studied (Table 3), indicating the role of environment in the expression of these characters. Similarly higher phenotypic coefficients of variation than genotypic coefficients of variation for traits studied were also observed by Zaman *et al.* (2011), Patil *et al.* (2015), Bhargavi *et al.* (2016) and Chaudhari *et al.* (2017). The wider differences between PCV and GCV were also observed for plant height, primary branches per plant, pods per plant, kernel yield, pod yield, harvest index and sugar content indicating that these characters were highly influenced by environmental factors to greater extent. Some characters like days to 50% flowering, 100 pod weight, 100 sound mature kernel, KL/KW ratio, protein and oil content exhibited very low differences between phenotypic and genotypic coefficients of variation suggesting less influence of environment on the expression of these traits. The narrow differences between PCV and GCV were also observed for days to 50% flowering and 100 pod weight as reported earlier by Chavadhari *et al.* (2017). The wider differences between PCV and GCV were also reported in the literature for plant height by Yusuf *et al.* (2017), for primary branches per plant by Zaman *et al.* (2011), Vasanthi *et al.* (2015), Yusuf *et al.* (2017) and Sab *et al.* (2018), for pod yield by Vasanthi *et al.* (2015) and Bhargavi *et al.* (2016), for harvest index by Bhargavi *et al.* (2016) and Yusuf *et al.* (2017) and for kernel yield by Bhargavi *et al.* (2016).

Genetic variability is a pre requisite for breeding programme on which selection acts to evolve superior genotype. GCV values (Table 3) were found to be high to moderate for days to 50% flowering (12.6), primary branches per plant (15.2), pods per plant (25.0), 100 pod weight (19.2), 100 sound mature kernel (19.0), sound mature kernel (24.4), kernel yield (19.3), pod yield (18.3) and harvest index (13.5). It indicated that higher the amount of genetic component of variation in these characters, greater the scope for its improvement through selection. High GCV values for these characters were also observed by Yusuf *et al.* (2017). High heritability was recorded (Table 3) for days to 50% flowering (66.4), pods per plant (63.9), 100 pod weight (82.5), 100 sound mature kernel (86.2), sound mature kernel (76.6), while moderate heritability was observed for plant height (31.1), primary branches per plant (52.7), KL/KW ratio (30.3), kernel yield (41.3), pod yield (39.4), harvest index (46.3), protein content (47.7), oil content (43.8) and sugar content (30.1). High heritability for days to 50% flowering was also observed by Zaman *et al.* (2011) and Patil *et al.* (2015), for 100 pod weight was in agreement with Zaman *et al.* (2011), Gupta *et al.* (2015) and Chavadhari *et al.* (2017).

High heritability for above characters indicated the least influence of environment hence, selection for improvement of these characters may not be much useful because sometime high heritability may be due to selective effect of favourable environment on trait expression therefore heritability along with genetic advance explains the degree of genetic gain obtained in a character at particular selection pressure. High genetic advance along with high heritability estimates provides most suitable opportunity for practice selection and suggest suitable breeding strategy for genetic improvement of such traits.

Genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in deciding an appropriate breeding method. Genetic advance as per cent of the mean (GAM) was found to be high for days to 50% flowering (21.1), primary branches per plant (22.7), pods per plant (41.2), 100 pod weight (35.9), 100 sound mature kernel (36.3), sound mature kernel (44.0), kernel yield (25.5), pod yield (23.6). It indicated that the characters were controlled by additive gene action and selection would be effective for improvement of these characters in genotypes studied. Genetic advance is a more reliable index for understanding the effectiveness of selection for improvement of traits because these estimates are derived by heritability, phenotypic standard deviation and intensity of selection. Therefore, genetic advance along with heritability provides better information on heritable component of variance for the control of a character and helpful in effectiveness of selection for improving characters. Similar findings of high genetic advance as per cent of the mean for primary branches per plant, kernel yield and pod yield were also reported by Hampannavar *et al.* (2018).

High heritability coupled with high genetic advance as per cent of mean and medium to high genotypic coefficient of variation was observed (Table 3) for days to 50% flowering (66.4, 21.1), number of pods per plant (63.9, 41.2), 100 pod weight (82.5, 35.9) 100 sound mature kernel (86.2, 36.3) and sound mature kernel (76.6, 44.0) indicating these characters were least influenced by environmental effect hence, selection would be rewarding for improving these traits due to additive gene effect. High heritability with high genetic advance findings for pods per plant was in agreement with Frimpong *et al.* (2017), Chaudhari *et al.* (2017) and Sab *et al.* (2018) and for 100 pod weight with Chavadhari *et al.* (2017).

Medium heritability, GCV coupled with high genetic advance as per cent of mean was observed

for primary branches per plant (52.7, 22.7), kernel yield (41.3, 25.5) and pod yield (39.4, 23.6), respectively. It revealed that these characters were governed by additive gene effects and low and moderate heritability may be due to high effect of environment therefore, selection would be rewarding for improving these traits. These results are in agreement with those of Vasanthi *et al.* (2015) and Tirkey *et al.* (2018) for pod yield. Moderate heritability accompanied with medium genetic advance as per cent of mean was observed for plant height (31.1, 10.4) and harvest index (46.3, 18.9), which indicated that both additive and non-additive gene actions play important role in the expression of these traits and improvement can be done through diallel selective mating followed by selection in advanced generations. For seed size and quality related traits, medium heritability accompanied with low genetic advance as per cent of mean was observed for KL/KW ratio (30.3, 5.8), protein content (47.7, 8.9), oil content (43.8, 3.8) and sugar content (30.1, 7.8), respectively indicating these traits were highly influence by environmental effect and governed by non-additive gene action. The traits governed by non-additive gene action can be improved by inter-mating among selected plants in early generation and selection may be practiced in later generations. It provides limited scope for improvement of these traits through selection. Moderate heritability with low genetic advance for oil and protein content were also reported by Chaudhari *et al.* (2017). Yield is complex traits governed by several contributing traits and also have less variability in groundnut. Hence, improvement through direct selection is difficult hence it is important to understand the association of different characters with yield for enhancing the usefulness of selection criterion. These characters can be improved by indirect selection. The genotypic and phenotypic correlation coefficients are helpful in identification of component traits. In the present study in general, magnitude of genotypic correlation coefficients were higher than the phenotypic correlation coefficients (Table 4). It revealed that genes governing by two traits were similar but the environmental conditions involving the expressions of these traits have a small and similar effect. Genotypic correlation was found more significant than phenotypic correlation indicating that there was prevalence of environmental interaction and strong genetic association between characters and there was scope for selection for improving these traits.

The results (Table 4) of genotypic correlation coefficients revealed that pod yield had significant and highly positive correlation with plant height (0.38), primary branches per plant (0.46), pods per

plant (0.54), 100 pod weight (0.45), 100 sound mature kernel (0.33), kernel yield (0.99) and harvest index (0.55), while negative and significant for days to 50% flowering (-0.38). It suggesting that pod yield could be improved by selecting above highly positive correlated traits, while early flowering could be simultaneously selected for high yield. Results are in agreement with those of Vasanthi *et al.* (2015) for primary branches per plant and Hampannavar *et al.* 2018 for pods per plant and kernel yield.

Quality traits had no correlation with pod and kernel yield, but they had correlation with other component traits (Table 4). Protein and sugar contents had positive and significant correlations with days to 50% flowering (0.42, 0.35), primary branches per plant (0.67, 0.64) and KLWR (0.29, 0.46), respectively, whereas negative and significant correlations with plant height (-0.48, -0.37) and SMK (-0.50, -0.53), respectively. Oil content had significant positive correlations with plant height (0.34), 100 pod weight (0.40), HSMK (0.42) and SMK (0.40), whereas, it had significant and negative correlation with days to 50% flowering (-0.39), primary branches per plant (-0.66) and KLWR (-0.44). It revealed earlier flowering increases protein and sugar contents while decreases oil content. Oil content increases with plant height, 100 pod weight, HSMK, SMK and decreases with days to 50% flowering, pods per plant, KLWR and protein content in genotypes studied. Quality traits had very strong correlation with each other. Results revealed that oil content had strong significant negative correlation with protein content (-1.00) and sugar content (-1.00), while protein content had strong significant positive correlation with sugar content (0.99) indicating that there would be possibility of simultaneous improvement of protein content and sugar content in groundnut. Significant negative correlation of oil content with protein content was also reported by Chaudhari *et al.* (2017).

Correlation coefficients quantify the associations in magnitude and direction (direct or indirect) in the sum total effects, selection based on this value alone will be some time misleading unless the direct effect is very high in the same direction. Study of direct and indirect effects through path analysis is a better tool for identification of component traits. Direct and indirect effects of the different characters on pod yield were worked out at genotypic level (Table 5). The variability explained by path analysis is inversely proportional to the residual effect. Residual effect (0.13) indicated that 87% variability of pod yield was explained by all the traits. Path analysis results revealed that kernel yield had the highest positive

direct effect on pod yield followed by oil content, HSMK, pods per plant, sugar content and days to 50% flowering, while primary branches per plant, 100 pod weight, SMK and harvest index exhibited high negative direct effects on pod yield. It clearly indicated that kernel yield, HSMK and pods per plant had high positive direct effects and also highly significant positive correlations with pod yield. Therefore, selection for these component traits may increase pod yield in studied groundnut genotypes. Similar trend was also observed by Turkey *et al.* (2018) for kernel yield and by Zaman *et al.* (2011) for kernel yield and days to 50% flowering.

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**Table 1. Analysis of variance for 14 characters in 20 genotypes of groundnut**

Source of variation	d. f.	Days to 50% flowering	Plant height (cm)	Primary branches/plant (no.)	Pods/plant (no.)	100 pod weight (g)	100 sound mature kernel (g)	Sound mature kernel (%)
Replications	2	23.3	54.1	0.31	5.6	138.7	47.6	48.4
Genotypes	19	53.2**	44.0**	1.89**	22.0**	907.5**	335.5**	574.8**
Error	38	7.6	18.1	0.31	3.1	59.3	17.6	53.2

\*, \*\* Significant at 5% and 1% levels, respectively

**Table 1. (Continued)**

Source of variation	d. f.	Kernel length/width ratio	Kernel yield (kg/ha)	Pod yield (kg/ha)	Harvest index (%)	Protein content (%)	Oil content (%)	Sugar content (%)
Replications	2	0.04	187813.7	431608.4	38.2	34.2	49.6	15.6
Genotypes	19	0.03**	205874.6**	399062.4**	71.8**	12.6**	8.2**	0.55*
Error	38	0.01	66244.2	135445.1	20.0	3.3	2.4	0.23

\*, \*\* Significant at 5% and 1% levels respectively



**Table 2. Estimates of mean, range, CD and coefficients of variation of 20 genotypes for 14 characters in groundnut**

Genotypes	DFE	PH	PB	PPP	HPW	HSMK	SMK	KLWR	KY	PY	HI	PC	OC	SC
PBS 12180	30	37	3	11	59	35	66	1.9	1005	1337	34.9	27.4	50.6	4.5
PBS 12181	25	36	3	14	59	35	59	1.9	1064	1439	32.9	27.7	50.3	4.6
PBS 12183	28	33	4	11	57	37	60	1.7	835	1171	25.8	30.0	47.9	5.1
PBS 12185	25	33	4	11	80	48	43	1.7	1102	1573	38.0	28.2	50.4	4.6
PBS 12186	25	34	4	13	87	54	65	1.7	1499	2190	42.2	26.1	52.1	4.2
PBS 22075	35	28	5	7	71	47	43	1.9	1005	1484	26.5	24.7	53.1	3.8
PBS 22076	28	33	4	7	109	66	73	1.7	1163	1583	31.3	25.8	52.1	4.1
PBS 22077	28	33	5	8	111	70	67	1.8	1327	1868	28.1	25.9	52.1	4.3
PBS 22080	31	35	5	15	88	55	53	1.9	1770	2563	38.7	32.0	47.2	5.5
PBS 22081	32	30	6	12	86	54	55	1.9	1431	2109	31.1	29.7	49.0	5.0
PBS 22082	36	29	5	8	83	55	40	1.8	693	1077	25.4	27.8	50.8	4.6
PBS 22083	32	26	5	9	94	53	35	1.9	962	1455	27.6	30.7	48.3	5.3
PBS 22084	34	32	5	10	88	51	32	1.9	1097	1713	29.8	29.8	49.2	5.1
PBS 22086	35	28	5	8	95	58	31	1.8	978	1514	33.4	29.1	50.2	5.0
PBS 22088	38	28	5	5	101	70	55	1.7	782	1234	27.7	28.5	50.3	4.4
PBS 22091	36	28	5	13	81	51	47	1.7	1072	1463	27.1	30.7	48.7	5.0
GG 7	27	40	4	10	101	59	81	1.5	1331	1826	34.6	27.1	51.3	4.5
TG 37 A	33	28	4	10	78	55	58	1.6	950	1416	30.8	29.3	50.0	4.8
GG 20	28	38	5	8	117	67	66	1.8	1339	1877	28.0	24.8	53.2	4.5
Somnath	32	31	5	6	105	68	49	1.9	980	1522	24.0	27.0	49.6	4.8
Mean	31	32	5	10	88	54	54	1.8	1119	1621	30.9	28.1	50.3	4.7
Range	25-38	26-40	3.2-5.6	5-15	57-117	35-70	31-81	1.5-1.9	693-1770	1077-2563	24-42.1	24.7-31.9	47.1-53.1	3.7-5.4
CD at 5%	4.5	7.0	0.9	2.9	12.7	6.9	12.0	0.2	425.0	608.0	7.3	3.0	2.5	0.8
CV (%)	8.9	13.5	14.4	18.8	8.8	7.6	13.5	7.7	23	22.7	14.5	6.5	3.1	10.5

Where; DFE: Days to 50% flowering; PH: plant height; PB: number of primary branches per plant; PPP: number of pods/plant; HPW: 100 pod weight (g); HSMK: 100 sound mature kernel (g); SMK: sound mature kernel (%); KLWR :Kernel length/width ratio; KY: kernel yield (kg/ha); PY: pod yield (kg/ha); HI: harvest index (%); PC: protein content (%); OC: oil content (%); SC: sugar content (%).



**Table 3. Genetic variability parameters for yield and quality traits in groundnut genotypes**

Parameters	Mean	Phenotypic Variance	Genotypic Variance	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability (%)	Genetic Advance	Genetic Advance as % of mean
Days to 50% flowering	31.0	22.8	15.2	15.4	12.6	66.4	6.5	21.1
Plant height (cm)	32.1	27.3	8.5	16.3	9.1	31.1	3.3	10.4
Primary branches/plant (no.)	4.6	0.9	0.5	20.9	15.2	52.7	1.0	22.7
Pods/plant (no.)	10.0	9.8	6.2	31.3	25.0	63.9	4.1	41.2
100 pod weight (g)	87.6	343.1	283.0	21.1	19.2	82.5	31.5	35.9
100 sound mature kernel (g)	54.4	123.3	106.3	20.4	19.0	86.2	19.7	36.3
Sound mature kernel (%)	54.0	227.1	173.9	27.9	24.4	76.6	23.8	44.0
Kernel length/width ratio	1.8	0.0	0.0	9.3	5.1	30.3	0.1	5.8
Kernel yield (kg/ha)	1119.3	112786.8	46540.1	30.0	19.3	41.3	285.5	25.5
Pod yield (kg/ha)	1620.8	223323.7	87896.4	29.2	18.3	39.4	383.2	23.6
Harvest index (%)	30.9	37.3	17.3	19.8	13.5	46.3	5.8	18.9
Protein content (%)	28.1	6.5	3.1	9.0	6.2	47.7	2.5	8.9
Oil content (%)	50.3	4.4	1.9	4.2	2.8	43.8	1.9	3.8
Sugar content (%)	4.7	0.3	0.1	12.5	6.9	30.1	0.4	7.8



**Table 4. Genotypic (lower left) and phenotypic (upper right) correlation coefficients among ten characters of groundnut genotypes**

Characters	DFE	PH	PB	PPP	HPW	HSMK	SMK	KLWR	KY	PY	HI	PC	OC	SC
DFE		-0.46**	0.39**	-0.25	0.04	0.14	-0.43**	0.17	-0.38**	-0.28*	-0.43**	0.25	-0.10	0.12
PH	-1.00**		-0.23	0.23	-0.01	-0.16	0.51**	-0.06	0.50**	0.38**	0.37**	-0.22	0.18	-0.06
PB	0.60**	-0.71**		-0.17	0.35**	0.36**	-0.34*	0.21	0.00	0.05	-0.38**	0.19	-0.17	0.26
PPP	-0.46**	0.39**	-0.32*		-0.41**	-0.52**	0.07	0.12	0.35**	0.32*	0.36**	0.29*	-0.28*	0.26*
HPW	0.07	0.07	0.53**	-0.65**		0.86**	0.14	-0.16	0.18	0.22	-0.14	-0.21	0.24	-0.05
HSMK	0.28*	-0.12	0.57**	-0.69**	1.00**		0.08	-0.22	0.09	0.15	-0.18	-0.17	0.15	-0.10
SMK	-0.69**	0.87**	-0.47**	0.09	0.16	0.16		-0.30*	0.33**	0.21	0.15	-0.39**	0.37**	-0.34*
KLWR	0.38**	-0.31*	0.52**	0.05	-0.28	-0.34**	-0.68**		0.00	0.04	-0.03	-0.08	0.05	-0.04
KY	-0.51**	0.50**	0.30**	0.64**	0.38**	0.24	0.43**	0.05		0.97**	0.64**	-0.08	0.11	-0.01
PY	-0.38**	0.38**	0.46**	0.54**	0.45**	0.33**	0.28	0.11	0.99**		0.62	-0.05	0.09	0.01
HI	-0.62**	0.52**	-0.51**	0.73**	-0.13	-0.27*	0.32*	-0.31*	0.59**	0.55**		-0.01	0.09	-0.08
PC	0.42**	-0.48**	0.06	0.67**	-0.36	-0.34**	-0.50**	0.29*	0.07	0.16	0.14		-0.91**	0.86**
OC	-0.39**	0.34**	-0.04	-0.66**	0.40**	0.42**	0.40**	-0.44**	-0.07	-0.16	-0.05	-1.00**		-0.84**
SC	0.35**	-0.37**	0.10	0.64**	-0.20	-0.23	-0.53*	0.46**	0.18	0.30	0.06	0.99**	-1.00**	

\*, \*\* Significant at 5% and 1% levels respectively. Where; DFE: Days to 50% flowering; PH: plant height; PB: number of primary branches per plant; PPP: number of pods/plant; HPW: 100 pod weight (g); HSMK: 100 sound mature kernel (g); SMK: sound mature kernel (%); KLWR: Kernel length/width ratio; KY: kernel yield (kg/ha); PY: pod yield (kg/ha); HI: harvest index(%); PC; protein content(%); OC: oil content(%); SC: sugar content (%).

**Table 5. Direct (bold) and indirect effects at genotypic level of ten characters to determine the effect of other characters on pod yield of groundnut genotypes**

Characters	DFF	PH	PB	PPP	HPW	HSMK	SMK	KLWR	KY	HI	PC	OC	SC	rg
DFF	0.334	-0.001	-0.243	-0.157	-0.021	0.158	0.120	0.065	-0.595	0.090	-0.020	-0.232	0.126	-0.38**
PH	-0.346	0.001	0.284	0.131	-0.019	-0.068	-0.153	-0.053	0.586	-0.075	0.023	0.201	-0.133	0.38**
PB	0.202	0.000	-0.402	-0.108	-0.148	0.321	0.082	0.089	0.350	0.074	-0.003	-0.027	0.035	0.46**
PPP	-0.155	0.000	0.128	0.339	0.180	-0.393	-0.016	0.008	0.747	-0.104	-0.033	-0.395	0.233	0.54**
HPW	0.025	0.000	-0.214	-0.220	-0.278	0.566	-0.028	-0.049	0.448	0.019	0.018	0.241	-0.073	0.45**
HSMK	0.093	0.000	-0.228	-0.235	-0.278	0.567	-0.028	-0.058	0.281	0.038	0.017	0.249	-0.084	0.33**
SMK	-0.230	0.001	0.188	0.031	-0.045	0.091	-0.175	-0.116	0.503	-0.046	0.025	0.239	-0.191	0.28
KLWR	0.126	0.000	-0.210	0.015	0.079	-0.192	0.119	0.171	0.060	0.045	-0.014	-0.261	0.168	0.11
KY	-0.171	0.000	-0.121	0.217	-0.107	0.137	-0.075	0.009	1.165	-0.085	-0.003	-0.043	0.067	0.99**
HI	-0.209	0.000	0.207	0.247	0.037	-0.151	-0.055	-0.054	0.692	-0.144	-0.007	-0.032	0.020	0.55**
PC	0.140	0.000	-0.025	0.229	0.101	-0.191	0.088	0.050	0.079	-0.019	-0.049	-0.594	0.358	0.16
OC	-0.130	0.000	0.018	-0.224	-0.112	0.237	-0.070	-0.075	-0.083	0.008	0.049	0.597	-0.375	-0.16
SC	0.117	0.000	-0.039	0.218	0.056	-0.131	0.092	0.079	0.215	-0.008	-0.048	-0.618	0.362	0.3

Residue= 0.137; Where; DFF: Days to 50% flowering; PH: plant height; PB: number of primary branches per plant; PPP: number of pods/plant; HPW: 100 pod weight (g); HSMK: 100 sound mature kernel (g); SMK: sound mature kernel (%); KLWR :Kernel length/width ratio; KY: kernel yield (kg/ha); PY: pod yield (kg/ha); HI: harvest index (%); PC: protein content (%); OC: oil content (%); SC: sugar content (%), rg: genotypic correlation

