Genetic variability analyses for yield and physiological traits in groundnut (*Arachis hypogaea* L.) genotypes

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ABSTRACT

Twenty different groundnut genotypes were evaluated in a randomized block design with three replications during *kharif* 2012 to study the variability parameters, heritability, genetic advance, correlation coefficient and path analysis for ten characters. Analysis of variance revealed highly significant differences among genotypes for all the traits except stability of soil plant analytical development (SPAD) and Chlorophyll Meter Reading 45 days after sowing indicating that adequate variability was found in the genotypes studied for most of the characters. The characters like 100 kernel weight, SPAD Chlorophyll Meter Reading 75 days after sowing, specific leaf area 75 days after sowing and rust resistance had high heritability with high genetic advance as per cent of mean and medium genotypic coefficient of variation indicating greater role of additive gene effects on these traits. While pod yield had moderate genotypic coefficient of variation and heritability along with high genetic advance as per cent of mean revealed that this character is also governed by additive gene effects and selection would be effective even in the early generation. Days to maturity, shelling outturn and specific leaf area 45 days after sowing had moderate heritability accompanied with low genotypic coefficient of variation and genetic advance indicating these traits are governed by non-additive gene effects. Selection may be practiced in later generations for improving these traits. The results on genotypic correlation coefficients revealed that pod yield had significant highly positive correlation with days to maturity, 100-kernel weight, and SPAD Chlorophyll Meter Reading 45 days after sowing while it was negative and significant for days to flower initiation and rust disease. SPAD Chlorophyll Meter Reading 45 days after sowing and SPAD Chlorophyll Meter Reading 75 days after sowing had highly significant negative correlation with specific leaf area 45 days after sowing and specific leaf area 75 days after sowing. Specific leaf area 45 days after sowing had highly significant negative correlation with rust. Therefore, SPAD Chlorophyll Meter Reading value could be used to identify genotypes with low specific leaf area and rust resistance. Path analysis indicated that 100-kernel weight had high positive direct effect with highly significant positive correlation with pod yield. Hence, this character may be effective for selection of high pod yield.

Keywords: Correlation, Genotypic coefficient of variation, Groundnut, Heritability, Phenotypic coefficient of variation

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 is valued as a rich source of oil (48-50%), protein (25-28%), carbohydrates (10-20%) and provides 564 kcal of energy for every 100 g of kernels (Arya *et al.,* 2016). 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; Ajay *et al.,* 2016). Groundnut haulm is a very important nutritious feed for animals, it is more palatable and is a rich source of protein (8-15%), lipids (1-3%), minerals (9-17%), and carbohydrates (38-45%) as compared to cereal fodder. Nutrient digestibility of groundnut haulm for animals is about 53 per cent and that of crude protein is 88 per cent. It releases energy up to 2.337 cal/kg of dry matter (Singh and Diwakar, 1993; Narendra Kumar *et al.,* 2017).

There is large gap between potential pod yield and the realized pod yield in most of the situations (Johansen and Rao, 1996; Devasena *et al.,* 2017). Under rainfed situations, groundnut is attacked by several biotic and abiotic stresses that contribute to yield gap. Among the biotic stresses, foliar fungal diseases, late leaf spot (LLS) caused by *Phaeoisariopsis personata* (Berk. & Curt.) Van Arx and rust caused by *Puccinia arachidis* Speg. are the most widespread and major production constraints in groundnut growing regions. When they come together, it causes 50 to 70 per cent reduction in pod yield depending on severity of the disease incidence besides having an adverse effect on seed quality (Subrahmanyam *et al.,* 1984; McDonald *et al.,* 1985). Physiological parameters like specific leaf area (SLA) and soil plant analytical development (SPAD) chlorophyll meter reading (SCMR), which are easy to measure, are highly correlated with each other. Both traits have considerable genetic variation in groundnut (Serraj *et al.,* 2004; Upadhyaya, 2005; Lal *et al.,* 2006).

Genetic variability for a trait in available genetic stock is the basic requirement for crop improvement. Effectiveness of selection is dependent upon the nature, extent and

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magnitude of genetic variability present in the breeding material for the target trait. Heritability is an important parameter because it determines the response to selection. It is 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 tools 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. Correlation measures the level of dependence among traits, but it is often very difficult to determine the actual mutual effects among traits if correlation values are similar for certain pairs of traits, direct effects for some of them and especially indirect effects via other traits can differ for some traits (Ikanovic *et al.,* 2011; Vaithiyalingan, 2016). Path coefficient analysis is very important technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable. Path coefficient analysis takes into account the casual relationship in addition to degree of relationship (Mahajan *et al.,* 2011). The present study was undertaken using 20 diverse groundnut genotypes to estimate genetic variability parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2), genetic advance (GA), genetic advance as percentage of mean (GAM), trait associations and path coefficient for yield and physiological 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. 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 row of 5 m length at 45 cm spacing between rows and 10 cm between plants. Recommended package of practices were followed for raising the crop. Supplementary irrigation was given as and when required to protect the crop. Chemical spraying of insecticide was done to prevent damage from insects-pests as and when required and no control measures were used to control foliar diseases. The observations were recorded on days to flower initiation, days to maturity, 100-kernel weight

(g), shelling outturn (%), pod yield (kg/ha), stability of soil plant analytical development (SPAD), Chlorophyll Meter Reading (SCMR) at 45 and 75 days after sowing (DAS), specific leaf area (cm^2/g) at 45 and 75 DAS and rust incidence. Observations on SCMR and SLA were recorded on third leaflets from top on the main stem of five randomly selected competitive plants in each genotype at 45 and 75 days after sowing.

Scoring of the each genotype for rust was carried out at 105 days after sowing. Observations for rust taken through visual score on a modified 1 to 9 point scale as given by Subrahmanyam *et al.* (1995). A disease score of 1 indicates resistance with no or very little disease infection while a score of 9 indicates highly susceptible with >80% severely infected leaves and defoliation in case of LLS, whereas burning like symptoms in case of rust. Observation on yield and its component traits were recorded on ten randomly selected plants in each genotype in each replication except days to flower initiation were recorded on plot basis. The data were subjected to statistical analysis and calculated analysis of variance (Panse and Sukhatme, 1961). Genotypic variance (V_g) and phenotypic variance (V_p) were estimated for the character having significant mean square due to the genotypes. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated formula suggested by Burton (1952). Heritability (h^2) was estimated in broad sense by formula suggested by Lush (1940). Genetic gain (GAM), the per cent expected genetic advance over the population mean, was computed by formula suggested by Johnson *et al.* (1955). Phenotypic (rp) and genotypic (rg) correlations between characters were estimated using the method described by Miller *et al.* (1958). Path coefficient analysis was estimated as per method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among genotypes for all the traits *viz.,* days to flower initiation, days to maturity, 100-kernel weight, shelling outturn, pod yield, SCMR 75DAS, SLA 45 and 75DAS and rust incidence/resistance except SCMR 45DAS (Table 1) indicating that adequate variability was found in the genotypes studied for these characters because of diverse pedigree of the advanced breeding lines and botanical types. Variability is a pre requisite for any breeding programme for improving the yield and other characters. Therefore, information on phenotypic coefficient of variation and heritability are helpful in prediction of the possible genetic advance by selection of genotypes for a character (Bhagasara *et al.,* 2017). Wider difference and reduction in the mean value of SLA from 45DAS to 75DAS could be due to water deficit stress at this stage resulting in deposition of cuticle wax on the leaf surface that increase leaf thickness and

weight and causes reduced SLA in later stage (Kalaria *et al.*, 2017).

Genotypic coefficient of variability estimate offers good implication for genetic potential in crop improvement through selection (Johnson *et al.*, 1955) and it also provides information on genetic variability present in the available genotypes. Results of phenotypic coefficient of variation (PCV) were found higher than genotypic coefficient of variation (GCV) for all the characters (Table 2) indicating the predominant role of environment in the expression of all the characters. High value of PCV than GCV for above characters was also observed by Zaman *et al.* (2011), Vasanthi *et al.* (2015), Patil *et al.* (2015), Bhargavi *et al.* (2016) and Chaudhari *et al.* (2017).

The wider difference between PCV and GCV were observed for pod yield, SCMR 45DAS, SLA 45DAS, SLA 75DAS and rust indicating that these characters were highly influenced by environmental factors. Some characters like days to flower initiation, days to maturity, 100 kernel weight, shelling outturn and SCMR 75DAS showed very low differences between phenotypic and genotypic coefficient of variation suggesting the less influence of environment on the expression of these traits and hence these characters could not be improved much by providing favourable environmental conditions and there would be an opportunity to use these characters in breeding programs for trait improvement. These results are in agreement with those reported by Zaman *et al.* (2011), Bhargavi *et al.* (2016) and Chaudhari *et al.* (2017). GCV values was found to be moderate for 100-kernel weight (19.7), pod yield (18.3), SCMR 75DAS (13.5), SLA 75DAS (12.5) and rust (15.1) while low GCV was found for days to flower initiation (8.9), days to maturity (2.3), shelling outturn (4.9), SCMR 45DAS (3.6) and SLA 45DAS (7.1). Genetic variability is a basic requirement of any breeding programme on which selection acts to evolve superior genotype. Thus, the higher the amount of genetic variation in these characters greater is the scope for its improvement through selection.

High heritability in broad sense was recorded (Table 2) for days to flower initiation (67.9), 100 kernel weight (86.4), SCMR 75DAS (73.6), SLA 75DAS (61.6) and rust (68.8) while moderate heritability was observed for shelling outturn (56.5), pod yield (39.4) and SLA 45DAS (29.8). High heritability increases when the genetic components contribute more to the variation as compared to non-genetic factors i.e., environmental conditions. High heritability of a trait does not mean that the trait is not influenced by environmental condition. Heritability can also change as a result of changes in the environment, migration, inbreeding, or the way in which heritability itself is measured in the population under study (Visscher *et al.*, 2008). Heritability gives an idea about the feasibility of selection. Therefore, high heritability for above characters indicated that genetic component is predominant with less influence by environmental effect and hence selection for these traits may lead to genetic improvement of these characters through selection.

Table 1 Analysis of variance for ten characters in different genotypes of groundnut

Source of variation	Df	DFI	DM	HKW	SOT	PY	SCMR45DAS	SCMR75DAS	SLA45 DAS	SLA75 DAS	Rust
Replication	2	4.31	26.9	26.4	19.9	431608.4	39.8	4.6	278.3	645.3	0.3
Genotype	19	18.85**	34.3*	165.9**	42.8**	399062.5**	17.4	45.7**	1109.9*	1547.8**	3.3**
Error	38	2.56	14.7	8.3	8.8	135445.2	13.6	5.1	490.9	265.2	0.4

*, ** Significant at 0.05 and 0.01 probability levels, respectively. Where, DFI- Days to flower initiation; DM-days to maturity; HKW-100 kernel weight (g); SOT- Shelling outturn (%); PY- Pod yield (kg/ha); SCMR45 & 75DAS-SPAD Chlorophyll Meter Reading 45 and 75 days after sowing; SLA-Specific leaf area (cm²/g).

Table 2 Genetic variability parameters for yield and other component traits in groundnut genotypes

Parameters	Mean	Range	CV (%)	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	h²(%)	Genetic advance	GAM
Days to flower initiation	26.2	22.6-30.0	6.1	8.0	5.4	10.8	8.9	67.9	4.0	15.1
Days to maturity	112.0	104.6-116.3	3.4	21.2	6.5	4.1	2.3	30.9	2.9	2.6
100 kernel weight (g)	36.9	25.1-49.5	7.8	61.0	52.7	21.2	19.7	86.4	13.9	37.7
Shelling outturn (%)	68.8	63.2-75.1	4.3	20.3	11.5	6.6	4.9	56.5	5.2	7.6
Pod yield (kg/ha.)	1620.7	1076.9-2563.1	22.7	223323.7	87896.4	29.2	18.3	39.4	383.2	23.6
SCMR45 DAS	29.1	23.6-32.6	12.6	14.8	1.1	13.2	3.6	7.6	0.6	2.1
SCMR75 DAS	27.5	18.7-33.9	8.2	18.7	13.8	15.7	13.5	73.6	6.6	23.8
SLA45 DAS	204.4	179.3-259.1	10.8	699.3	208.2	12.9	7.1	29.8	16.2	7.9
SLA75DAS	164.8	136.1-238.1	9.8	692.6	426.4	16.0	12.5	61.6	33.4	20.2
Rust	6.5	4.0-8.0	10.1	1.4	1.0	18.2	15.1	68.8	1.7	25.7

CV-Coefficient of variation, PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, h²- Heritability in broad sense, GAM-Genetic advance as per cent of mean

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 was found to be high for 100 kernel weight (37.7), pod yield (23.6), SCMR 75DAS (23.8), SLA 75DAS (20.2) and rust (25.7). It indicated that these characters are controlled by additive gene effects and selection could be effective for improvement of these characters in studied genotypes. 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 gives clear idea about the effectiveness of selection for improving characters (Mandal *et al.*, 2017).

High heritability coupled with high genetic advance as per cent of mean and medium genotypic coefficient of variation was observed (Table 2) for 100 kernel weight (86.4, 37.7), SCMR 75DAS (73.6, 23.8), SLA 75DAS (61.6, 20.2) and rust (68.8, 25.7) indicating these characters are least influenced by environmental effect and hence, selection would be rewarding for improving these traits due to additive gene effects. Genetic coefficient of variance estimates along with heritability would provide the best information of the amount of advance to be expected from selection (Burton and Devane, 1953). High heritability with high genetic advance findings for 100 kernel weight was in agreement with Zaman *et al.* (2011), Bhargavi *et al.* (2016), Yusuf *et al.* (2017), Chavadhari *et al.* (2017) and for SLA it was in agreement with Sab *et al.* (2018) and for rust with Chaudhari *et al.* (2017).

High heritability accompanied with moderate genetic advance as per cent of mean was observed for days to flower initiation (67.9, 15.1) indicating that the selection for improvement of this character may be rewarding because 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 to exploit additive effects. Moderate heritability coupled with high genetic advance as per cent of mean was observed for pod yield (39.4, 23.6). It revealed that pod yield is governed by additive gene effects and low and moderate heritability may be due to the greater effect of environment on expression of trait and therefore selection would be rewarding for improving pod yield in studied genotypes. Results of moderate heritability with high genetic advance for pod yield are in agreement with Chavadhari *et al.* (2017). Moderate heritability accompanied with low genetic advance as per cent was recorded for days to maturity, shelling outturn and SLA 45DAS indicating these traits are highly influenced by environmental effects 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 was also reported by Zaman *et al.* (2011) and Chavadhari *et al.* (2017) for days to maturity and Yusuf *et al.* (2017) and Kademani and Herakal (2017) for shelling outturn. Variability parameters helps in identifying the characters having high response to selection while characters like yield governed by several contributing traits and also have less variability in groundnut. These characters can be improved by indirect selection through identification of component traits. Hence, genotypic and phenotypic correlation coefficients are helpful in identification of these component traits.

In the present study, magnitude of genotypic correlation coefficients were higher than the phenotypic correlation coefficient (Table 3). It revealed that genes governing two traits are 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 low contribution of environment in the expression of these traits and there would be scope of improving these traits through indirect selection. The results on genotypic correlation coefficients revealed that the pod yield was significant and positive with days to maturity (0.68), 100 kernel weight (0.41), SCMR 45DAS (0.67) while it was significant and negative with days to flower initiation (-0.26) and rust incidence (-0.30). It suggested that pod yield could be improved by simultaneously selecting for long duration, high 100 kernel weight and high SCMR value in the studied groundnut genotypes. Similar findings were also reported for 100 kernel weight and days to maturity (Vasanthi *et al.*, 2015; Gaikpa *et al.*, 2015; Zongo *et al.*, 2017), for rust (Chaudhari *et al.*, 2017) and for SCMR (Nigam and Aruna, 2008).

Physiological parameters (SCMR and SLA) also play important roles in disease resistance. SLA is an indicator of leaf thickness, low SLA (thick leaves) usually having higher chlorophyll per unit leaf area and hence a greater photosynthetic capacity. The SCMR is an indicator of the photo-synthetically active light-transmittance characteristics of the leaf, which is dependent on the unit amount of chlorophyll per unit leaf area (chlorophyll density). In general genotypes having dark green leaves are more tolerant to leaf spot and rust. SLA 45DAS had highly significant negative correlation (-0.39) with rust. It revealed that higher leaf thickness reduced the rust incidence. Hence it could be used as a reliable parameter of indirect selection for rust resistance in groundnut. SCMR 45DAS had high significant negative correlation with SLA 45DAS (-0.86) and SLA 75DAS (-0.30) while SCMR 75DAS also had negative highly significant correlation with SLA 45DAS (-0.83) and SLA 75DAS (-0.41). It indicated that SCMR could be used

as a reliable parameter to identify genotypes with low SLA in groundnut. SCMR and SLA were significantly negatively correlated with each other irrespective of the time of observation and therefore can be recorded at any time after 50 days of crop growth (Nigam and Aruna, 2008) and similar findings are in agreement with those reported by Rao et al. (2001) and Upadhyaya (2005). Pod yield exhibited significant positive correlation with SCMR also reported by Sab et al. (2018).

Correlation coefficients quantify the associations in magnitude and direction (direct or indirect) in the sum total effects, selection based on this value alone will sometimes be 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 4). The variability explained by path analysis is inversely proportional to the residual effect. Residual effect (0.91) indicated that 9% variability of pod yield was explained by all the traits. Path analysis results revealed that shelling outturn (1.26) had highest positive direct effect on pod yield followed by days to flower initiation (1.0) and 100 kernel weight (0.94) while rust (-1.18) followed by days to maturity (-0.69) and SLA 45DAS (-0.49) exhibited high negative direct effects on pod yield. It clearly indicated that 100 kernel weights had high positive direct effect and highly significant positive correlation with pod yield. Therefore selection for high kernel weight may increase pod yield in studied groundnut genotypes. High positive direct effect on pod yield for shelling outturn was also reported by Zaman et al. (2011) and Tirkey et al. (2018).

Table 3 Genotypic (lower left) and phenotypic (upper right) correlation coefficient among ten characters of groundnut genotypes

Characters	DFI	DM	HKW	SOT	PY	SCMR45DAS	SCMR75DAS	SLA45DAS	SLA75DAS	Rust
DFI		0.33*	0.04	-0.53**	-0.09	0.05	0.34**	-0.11	0.10	0.00
DM	0.85**		0.31*	-0.40**	0.19	0.20	0.14	-0.19	-0.06	-0.22
HKW	0.13	0.67**		-0.08	0.19	0.39**	0.49**	-0.39**	-0.12	0.09
SOT	-0.82**	-0.47**	-0.07		0.10	0.03	-0.07	0.05	-0.18	0.29*
PY	-0.26*	0.68**	0.41**	0.13		0.20	0.08	-0.04	-0.06	-0.30*
SCMR45DAS	0.46**	1.11	1.79	-0.55**	0.67**		0.32*	-0.76**	-0.19	0.13
SCMR75DAS	0.46**	0.61**	0.57**	-0.16	0.11	1.81		-0.35**	-0.32*	0.21
SLA45DAS	-0.42**	-0.61**	-0.81**	0.55**	0.09	-0.86**	-0.83**		0.24	-0.20
SLA75DAS	0.17	-0.03	-0.17	-0.15	0.01	-0.30*	-0.41**	0.27*		-0.12
Rust	-0.05	-0.31*	0.12	0.29*	-0.40**	0.18	0.25	-0.39**	-0.14	

*, ** Significant at 0.05 and 0.01 probability levels, respectively. Where, DFI- Days to flower initiation; DM-days to maturity; HKW-100 kernel weight (g);
SOT- Shelling outturn (%); PY- Pod yield (kg/ha); SCMR45 & 75DAS-SPAD Chlorophyll Meter Reading 45 and 75 days after sowing; SLA-Specific leaf area (cm²/g).

Table 4 Direct and indirect effects at genotypic level of ten characters to determine the effect of other characters on pod yield of groundnut genotypes

Characters	DFI	DM	HKW	SOT	SCMR45DAS	SCMR75DAS	SLA45DAS	SLA75DAS	Rust	rg
DFI	**1.089**	-0.594	0.120	-1.040	-0.093	-0.012	0.205	0.009	0.055	-0.26*
DM	0.926	**-0.698**	0.627	-0.595	-0.223	-0.016	0.301	-0.001	0.363	0.68**
HKW	0.139	-0.466	**0.941**	-0.083	-0.360	-0.014	0.397	-0.009	-0.136	0.41**
SOT	-0.897	0.330	-0.062	**1.262**	0.111	0.004	-0.271	-0.008	-0.338	0.13
SCMR45DAS	0.503	-0.774	1.684	-0.695	**-0.201**	-0.046	0.423	-0.016	-0.212	0.67**
SCMR75DAS	0.500	-0.425	0.534	-0.199	-0.363	**-0.025**	0.408	-0.021	-0.294	0.11
SLA45DAS	-0.455	0.429	-0.762	0.698	0.174	0.021	**-0.490**	0.014	0.465	0.09
SLA75DAS	0.187	0.019	-0.158	-0.192	0.061	0.010	-0.130	**0.052**	0.161	0.01
Rust	-0.050	0.215	0.108	0.361	-0.036	-0.006	0.193	-0.007	**-1.181**	-0.40**

Residual effect at genotypic level= 0.91, Where, DFI- Days to flower initiation; DM- Days to maturity; HKW- 100 kernel weight (g); SOT- Shelling outturn (%);
PY- Pod yield (kg/ha); SCMR45 &75DAS- SPAD Chlorophyll Meter Readings 45 & 75 days after sowing; SLA- Specific leaf area (cm²/g), rg- Genotypic correlation

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