

**STUDY OF GENETIC VARIABILITY AND CORRELATIONS IN SELECTED
GROUNDNUT GENOTYPES.**

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ABSTRACT: Genetic variation and association among nine characters were studied in eighteen selected groundnut genotypes. Analysis of variance revealed highly significant differences among the genotypes for all the characters studied. The PCV was generally higher than the GCV for all the characters but in some cases, the two values differed slightly. The lowest values were shown by SMK percent and shelling percentage and the highest values were shown by pod yield per plant, kernel yield per plant, test weight and three diseases. High heritability along with the GAM was high for pod yield per plant, kernel yield per plant, test weight, shelling percentage and three diseases, indicated the importance of additive gene action and the ample scope for improvement in these traits through simple selection. The correlation study revealed that pod yield per plant had significant positive association with kernel yield per plant, shelling percentage and SMK percent at both genotypic and phenotypic levels. *Aspergillus* seed colonization exhibited significant desirable negative association with test weight revealing that the resistant genotypes in general had higher seed size.

Key words: Genetic variability, heritability, correlations, *Aspergillus* seed colonization and groundnut.

INTRODUCTION

The cultivated peanut (*Arachis hypogaea* L.) is a major crop in most tropical and subtropical regions of the world and in India it ranks first among edible oilseed group. Peanut seeds are of high value because of their high contents of oil (43-54%) and protein (25-30%). Genetic variability is the prerequisite for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and the extent to which it is heritable. Hence, in present investigation an attempt was made to determine the performance of some selected groundnut genotypes to assess the variability of the important traits, and to determine correlations between these traits.

MATERIAL AND METHODS

The experimental material comprised of eighteen selected groundnut genotypes of different botanical groups were screened under *in vitro* condition for reaction to *Aspergillus* seed colonization. The pure culture of *A. flavus* strain Af 11-4, a highly aggressive and toxigenic strain was used for *in vitro* seed colonization following the procedure and 1-4 seed colonization severity scale of Thakur *et al.*, (2000). The experiment was conducted by following Randomized Complete Block Design with three replications during post rainy 2007, at Botanical garden of University of Agricultural Sciences, Dharwad. Each entry was grown in three rows of 2.25 meter length with row to row distance was 30 cm and plant to plant distance was 10 cm. All recommended agronomic practices were followed for reaping good crop. The modified 9- point scale for rust and late leaf spot (Subbarao *et al.*, 1990) was used for screening genotypes in field. The yield and yield components namely plant yield per plant, kernel yield per plant, hundred kernel weight, shelling percentage and SMK percent were recorded. The various genetic parameters like variability, GCV, PCV, heritability and genetic advance as percentage of mean were calculated by adopting the formulae given by Johnson *et al.*, (1955).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the genotypes for all the traits indicating thereby sufficient variability present in the material studied (table I). The nature and magnitude of the variation was assessed by phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (H %) and genetic advance over mean (GAM) as presented in table II. The estimates of phenotypic coefficient of variation were always higher than genotypic coefficient of variation signifying the influence of environmental factors, while in certain cases low magnitude of difference observed indicated that these characters were less influenced by the environments. Genotypic coefficient of variation measures the amount of variation present in a particular character. However, it does not determine the proportion of heritable variation present in the total variation. Therefore, heritability which represents the heritable variation existing in the character was calculated.

Table I. Analysis of variance for productive parameters and disease reactions in groundnut.

Source	D.F.	Pod yield (kg/ha)	Pod yield / plant (g)	Kernel yield / plant (g)	Test weight (g)	Shelling percentage	Sound mature kernel (%)	<i>A. flavus</i> score (1-4 scale)	Late leaf spot (1-9 scale)	Rust (1-9 scale)
Genotype	17.00	597209.41**	17.73**	14.38**	342.34**	109.92**	46.14**	3.01**	7.18**	7.67**
Error	17.00	202191.06	2.95	1.64	16.19	7.04	11.34	0.01	0.23	0.25

*, **: Significant at 5% and 1% level of probability, respectively

Table II. Components of variation for different traits in selected genotypes.

Characters	MEAN	RANGE	GCV	PCV	H (%)	GA M
Pod yield (kg/ha)	2505.75	1732.00 – 4018.00	17.74	25.23	49.40	25.68
Pod yield / plant (g)	13.96	8.50 – 20.65	19.48	23.04	71.50	33.96
Kernel yield / plant (g)	9.70	3.58 – 15.53	26.03	29.19	79.50	47.85
Test weight (g)	56.02	35.94 – 81.85	22.79	23.90	91.00	44.78
Shelling percentage	68.20	42.46 – 74.91	10.52	11.21	88.00	20.32
Sound mature kernel (%)	90.65	77.97 – 96.79	4.60	5.91	60.50	7.38
<i>A. flavus</i> score (1-4 scale)	2.11	1.00 – 4.00	57.97	58.23	99.10	118.96
Late leaf spot (1 - 9 scale)	4.00	2.00 – 7.00	46.60	48.11	93.80	93.00
Rust (1 - 9 scale)	6.03	2.00 – 8.00	31.96	33.02	93.70	63.70

GCV – Genotypic Coefficient of Variation; PCV – Phenotypic Coefficient of Variation; H (%) – Estimate of broad sense heritability
GAM – Genetic advance as percent of mean

High heritability and genetic advance expressed as percentage of mean was high for pod yield per plant, kernel yield per plant, test weight and shelling percentage. It revealed that the characters are governed by additive gene effects and hence, selection would be effective in improvement of this trait. The present findings are in conformation with the findings of John *et al.*, (2007) and Khote *et al.*, (2009). Whereas high heritability along with low GAM and GCV was observed for sound mature kernel (%) indicated the role of non-fixable genetic variance in the expression of this trait and selection for this trait would be ineffective. The estimates of high heritability for *Aspergillus* seed colonization was in conformation with Upadhyaya *et al.*, (1997) and late leaf spot and rust also showed high heritability.

The genetic and phenotypic correlations among the various characters are presented in Table III. The pod yield per plant showed strong and positive association with kernel yield per plant, shelling percentage and SMK percent at both genotypic and phenotypic levels indicating that pod yield per plant could be used as preliminary criteria for selecting high yielding genotypes. A similar result of significant positive association of pod yield per plant with shelling per cent was reported by Abhay-Darshora *et al.*, (2002). While, the significant positive association of pod yield per plant with sound mature kernel per cent was reported by Francis and Ramalingam (1997) and Vasanthi *et al.*, (1998). The Shelling per cent had significant positive association with sound mature kernel per cent as reported by Vasanthi *et al.*, (1998). The late leaf spot also showed positive association with rust indicate that some of the genotypes have resistance to both the diseases. *Aspergillus* seed colonization exhibited significant desirable negative association with test weight revealing that the resistant genotypes in general had higher seed size.

Table III. Phenotypic correlation coefficients among yield attributes and disease resistance traits in groundnut

Character	Pod yield (Kg/ha)	Pod yield / plant (g)	Kernel yield / plant (g)	Test weight (g)	Shelling percentage	Sound mature kernel (%)	<i>A. flavus</i> score (1-4 scale)	Late leaf spot (1 - 9 scale)	Rust (1 - 9 scale)
Pod yield (Kg/ha)	1.00	0.54*	0.57*	0.29	0.47	0.45	0.19	0.01	0.07
Pod yield / plant (g)	0.66**	1.00	0.97**	-0.04	0.59**	0.54*	0.42	0.13	0.27
Kernel yield / plant (g)	0.70**	0.97**	1.00	-0.05	0.75**	0.64**	0.48*	0.16	0.28
Test weight (g)	0.28	-0.18	-0.15	1.00	0.05	-0.01	-0.65**	0.20	0.16
Shelling percentage	0.66**	0.67**	0.81**	0.06	1.00	0.69**	0.39	0.17	0.26
Sound mature kernel (%)	0.84**	0.65**	0.80**	-0.05	0.97**	1.00	0.33	0.18	0.20
<i>A. flavus</i> score (1-4 scale)	0.29	0.51*	0.55*	-0.68**	0.41	0.45	1.00	0.10	0.13
Late leaf spot (1 - 9 scale)	0.00	0.14	0.18	0.20	0.22	0.21	0.12	1.00	0.78**
Rust (1 - 9 scale)	0.08	0.28	0.29	0.17	0.30	0.27	0.14	0.81**	1.00

Below diagonal - Genotypic correlation, Above diagonal – Phenotypic correlation

*, ** indicate the significance of 5% and 1% level of probability, respectively

These relationships indicate that the trait, pod yield per plant, which was found to show higher heritability and positively correlated with kernel yield per plant, shelling percentage and SMK percent, can be a good criterion to be used in selection programmes to improve yield of peanuts. Test weight, although giving a high heritability estimate, however did not show good correlations with the yield traits, and thus, is not a good criterion for selection.

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