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Genetic variability and association study for different traits in F₅ progenies of groundnut

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Abstract

The present experiment was conducted during summer 2018, to study variability and diversity among F₅ progenies of eight crosses of groundnut. The experiment was laid in compact family block design with two replication at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.). Analysis of variance revealed highly significant differences among the progenies of eight crosses for the characters studied, indicating appreciable amount of variability among the progenies for the characters studied. The estimation for phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. The number of branches per plant recorded the highest estimate of GCV and PCV followed by number of immature pods per plant, number of mature pods per plant, dry pod yield per plant. The moderate estimates of GCV and PCV were observed for haulm yield per plant and hundred kernel weight.

In correlation study, it was observed that dry pod yield per plot recorded significant positive correlation with days to maturity, number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling %, sound mature kernel and protein content at both genotypic and phenotypic levels while characters immature pods per plant and oil content, were negatively associated with dry pod yield per plot.

Keywords: Genetic variability, traits, F₅ progenies, groundnut

Introduction

Groundnut (*Arachis hypogaea* L.), is an allotetraploid (2n=4x=40) species which likely evolved from two diploids (Kochert *et al.*, 1996) [15]. It belongs to the family *Leguminosae*, subfamily *Papilionoidae*, tribe *Aeschnomeneae*, sub-tribe *Stylosanthinae*, genus *Arachis* and species *hypogaea* (Isleib *et al.*, 1994) [9]. It is self-pollinated, annual, herbaceous legume growing upright or prostrate and has an indeterminate growth habit. Natural cross pollination occurs at rates of less than 1 to 6 per cent due to a typical flowers or action of bees (Duke, 1981 and Coffelt, 1989) [8, 6]. The groundnut plant is sparsely hairy and generally grows 12 to 65 cm high. It has a central, upright stem and many lateral branches. In runner types, the laterals are prostrate and in bunch types they are more or less erect in the young plants but tend to become prostrate at a later stage. The fruit is a pod with one to five seeds that develops underground within a needle like structure called a peg, an elongated ovarian structure.

Groundnut is an important crop from the perspective of food and nutrition security of poor small holder farmers in developing countries, where it is grown widely. It is grown extensively in the developing countries of Asia, Africa and Latin America. About 62 per cent of the production comes from South, East and Central Asia. Africa and Asia produced 91 per cent of the world's total groundnut production (Nedumaran *et al.*, 2015) [17].

To meet the demand of increasing population and maintaining self sufficiency, there is need to increase the groundnut production. Successful establishment of germplasm collection and plant introduction for crop improvement as well as germplasm conservations requires studies in genetic variability within plant populations. Genetic variability and heterozygosity existed within population in both natural and cultivated populations.

The magnitude of variability and the knowledge of extent to which desirable characters are heritable is a pre-requisite for crop improvement. The variability available in the breeding material is very important in the selection of superior plant types, where selection of superior plant is based not only on yield alone but also on the yield contributing characters. For the reliable field selection, it becomes necessary to partition the relative amount of heritable and non-heritable variability exhibited by yield contributing characters. Pod yield in groundnut is quantitative in nature and polygenically controlled.

Selection on the basis of yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable. Knowledge of the associations between yield and its component characters and among the component characters themselves can improve the efficiency of selection in plant breeding. Correlation studies taken alone are often misleading and the actual dependence of pod yield on the correlated yield, component characters needs confirmation, which can easily and untangled and unravelled by path coefficient analysis.

Materials and methods

The material used in the present study consisted of 40 F₅ progenies of eight crosses of groundnut received from Groundnut Breeder, All India Co-ordinated Research Project on Groundnut, Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.).

Table 1: Number of genotype: 40 F₅ progenies of eight crosses

S. No	Name of cross	Number of progeny
1.	TAG-24 x Phule Unnati	5
2.	Phule Unnati x TPG-41	5
3.	WRGS-15 x RHRG-8808	5
4.	Phule 6021 x ICGV-00350	5
5.	Phule 6021 x Phule Unnati	5
6.	Phule Unnati X SB-XI	5
7.	Phule 6021 x RHRG-6110	5
8.	WRGS-15 X SB-XI	5
	Total	40

Experiment was conducted by Compact Family Block Design with two replications during summer 2018. Each progeny was sown in eight rows of 3 m length in each replication. The inter and intra row to row spacing was 30 cm and 10 cm, respectively. Full dose of the recommended dose of nitrogen along with the entire dose of phosphorus were applied at the time of sowing. Observation were recorded from each replication on ten randomly selected plant from each progeny, viz., days to 50% flowering, days to maturity, number branches per plant, number mature pod per plant, number of immature pod per plant, pod yield per plot, haulm yield per plant, 100 kernel weight, shelling percentage, sound mature kernel, oil content and protein content. The mean values of five randomly selected observational plants for 12 different traits were used for statistical analysis. The genotypic and phenotypic coefficient of variation were calculated by the formulae as suggested by Burton and De vane (1953) [5]. Analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic covariances were calculated as per the formulae given by Singh and Chaudhari (1977) [21].

Results and discussion

Analysis of variance revealed highly significant differences among the families (crosses) and progenies within family for the characters studied, indicating appreciable amount of variability among the genotypes for the studied characters Table 1. Aghav (2010) [1], Atak (2014) [2], Kadam (2016) [14], Rao (2016) [18], Sardar (2017) [20] and Wadikar (2018) [25] also observed appreciable amount of variability among the genotypes.

Variability parameters

Adequate variability was observed among the genotype under

study. Further, wide range was observed for number of mature pods per plant, dry pod yield per plant and number of branches per plant.

The estimation for phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. The number of branches per plant recorded the highest estimate of GCV and PCV followed by number of immature pods per plant, number of mature pods per plant, dry pod yield per plant. The moderate estimates of GCV and PCV were observed for haulm yield per plant and hundred kernel weight.

In present investigation, the characters number of branches per plant, number of immature pods per plant, number of mature pods per plant, hundred kernel weight and dry pod yield per plot expressed high estimates of heritability (broad sense) accompanied with high genetic advance and percent of mean indicating that these traits were predominantly governed by additive gene action and could be improved through simple selection only.

Coefficient of genotypic and phenotypic variation

It was observed that the estimates of phenotypic coefficient of variation (PCV) were magnitudinally higher than the genotypic coefficient of variance (GCV) for all the characters studied indicating the influence of environment of these traits. The highest estimate of GCV and PCV recorded by number of branches per plant (42.71, 44.09) followed by number of immature pods per plant (41.11, 45.46), number of mature pods per plant (29.0, 29.80) and dry pod yield per plant (23.90, 24.36) respectively. The moderate low to estimates of GCV and PCV was observed for the characters haulm yield per plant (16.88, 17.12), hundred kernel weight (14.31, 14.94). However, the low estimates of GCV and PCV were observed by characters viz., days to 50% flowering (9.83, 10.37), sound mature kernel (6.22, 6.34), days to maturity (6.11, 6.19), oil content (3.95, 4.07), protein content (3.75, 3.83) and shelling percentage (1.56, 1.61) respectively. Similar results were recorded by John *et al.* (2008, 2009, 2011a) [11, 12, 13], Korat (2009) [16], Zaman *et al.* (2011) [26] and Vishnuvardhan *et al.* (2012) [24].

Correlation coefficient

In present study, it was observe that dry pod yield per plot recorded significant positive correlation with days to maturity, number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling %, sound mature kernel and protein content at both genotypic and phenotypic levels while characters immature pods per plant and oil content, were negatively associated with dry pod yield per plot.

The dry pod yield had highly significant and positive correlation at both genotypic and phenotypic levels with number of mature pods per plant (rg = 0.865, rp =0.818), number of branches per plant (rg = 0.785, rp =0.742), sound mature kernel percent (rg = 0.678, rp =0.647), shelling percent (rg = 0.576, rp =0.552), hundred kernel weight (rg = 0.301, rp =0.288) and significant positive with days to maturity (rg = 0.220, rp =0.209) and protein content (rg = 0.178, rp =0.176). Venkataramana *et al.* (2000a) [23], John *et al.* (2009) [13], Raut *et al.* (2010) [19], Dhakar *et al.* (2017) [17], Bhargavi *et al.* (2015) [14], Babariya and Dobariya (2012) [3] were observed significant and positive correlation for these characters. However number of immature pods per plant (rg = -0.523, rp = -0.452) and oil content (rg = -0.306, rp = -0.296) had highly significant with negative correlation with dry pod yield at both level. Similar results were recorded by Sumathi

and Muralidharan (2007) [22] and Jeyaramraja and Fantahun (2014) [10]. Days to 50% flowering ($rg = 0.142$, $rp = 0.142$) had positive and non-significant correlation whereas, haulm yield

($rg = -0.011$, $rp = -0.018$) had negative and non significant correlation at both levels with dry pod yield.

Table 2: Mean, range of variation, phenotypic and genotypic variances and coefficients of variation, heritability (bs.), genetic advance and genetic advance expressed as per cent of mean for twelve characters in groundnut genotypes

S. No.	Character	Mean	Range	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Genotypic coefficient of variation GCV (%)	Phenotypic coefficient of variation PCV (%)
1	Days to 50% flowering	48.18	40.50-54.50	22.45	24.98	9.83	10.37
2	Days to maturity	126.90	113.5-139.0	60.21	61.80	6.11	6.19
3	Number of branches/plant	7.15	4.00-16.00	9.33	9.94	42.71	44.09
4	Number of matured pods/plant	29.06	12.50-48.50	71.02	74.98	29.00	29.80
5	Number of immature pods/plant	6.15	1.50-12.50	6.39	7.82	41.11	45.46
6	Haulm yield/plot (kg)	8.56	4.35-10.65	2.09	2.15	16.88	17.12
7	100 kernel weight (g)	33.81	27.50-48.50	23.42	25.52	14.31	14.94
8	Shelling %	68.77	67.15-72.30	1.14	1.23	1.56	1.61
9	Sound mature kernel (%)	89.80	80.50-98.50	31.25	32.39	6.22	6.34
10	Oil content (%)	47.45	44.20-51.00	3.52	3.74	3.95	4.07
11	Protein Content (%)	22.22	20.05-23.95	0.70	0.72	3.75	3.83
12	Dry pod yield /plot (kg)	1.386	0.82-1.97	0.110	0.114	23.90	24.36

Table 3: Genotypic (Above diagonal) and phenotypic (Below diagonal) correlation coefficient among twelve characters in summer groundnut genotypes

S. No.	Character	Days to 50% flowering	Days to maturity	No. of branches /plant	No. of matured pods/ plant	No. of immature pods/ plant	Haulm yield/ plot (kg)	100 kernel weight (g)	Shelling (%)	Sound mature kernel (%)	Oil content (%)	Protein Content (%)	Dry pod yield/ plot (kg)
1	Days to 50% flowering	1.000	0.758**	-0.078	0.129	0.022	0.155	0.125	0.167	0.165	0.389**	0.073	0.142
2	Days to maturity	0.717**	1.000	-0.060	0.198*	-0.184*	0.079	0.476**	-0.043	-0.038	0.368**	0.169	0.220*
3	Number of branches/ plant	-0.052	-0.047	1.000	0.788**	-0.451**	-0.043	-0.131	0.257*	0.642**	-0.350**	0.081	0.785**
4	Number of matured pods/ plant	0.125	0.199*	0.748**	1.000	-0.359**	0.024	0.127	0.471**	0.688**	-0.229*	0.212*	0.865**
5	Number of immature pods/ plant	0.038	-0.164	-0.388**	-0.307**	1.000	0.157	-0.168	-0.221*	-0.332**	0.165	-0.414**	-0.523**
6	Haulm yield/plot (kg)	0.144	0.071	-0.052	0.026	0.142	1.000	0.047	0.244*	0.013	-0.247*	0.163	-0.011
7	100 kernel weight (g)	0.098	0.440**	-0.144	0.122	-0.145	0.046	1.000	0.119	-0.277**	-0.202*	0.155	0.301**
8	Shelling percent	0.143	-0.032	0.230*	0.440**	-0.176*	0.235*	0.117	1.000	0.555**	-0.324**	0.232*	0.576**
9	Sound mature kernel (%)	0.145	-0.043	0.595**	0.663**	-0.304**	0.022	-0.253*	0.535**	1.000	0.016	0.171	0.678**
10	Oil content (%)	0.362**	0.363**	-0.324**	-0.208*	0.159	-0.228*	-0.194*	-0.305**	0.027	1.000	-0.027	-0.306**
11	Protein Content (%)	0.055	0.161	0.080	0.190*	-0.364**	0.162	0.140	0.227*	0.169	-0.023	1.000	0.178*
12	Dry pod yield /plot (kg)	0.142	0.209*	0.742**	0.818**	-0.452**	-0.018	0.288**	0.552**	0.647**	-0.296**	0.176*	1.000

*, ** significant at 5 and 1%, respectively

Conclusions

Analysis of variance revealed highly significant differences among the F₅ progenies of eight crosses for all the characters studied, indicating appreciable amount of variability among the genotypes for the studied characters. The dry pod yield had positive and significant association with days to maturity, number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling per cent, sound mature kernel and protein content at both genotypic and phenotypic levels. Rigorous selection could be effected to have good genotype for both season in F₆ progenies of Groundnut.

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