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Genetic divergence study for different traits in groundnut

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Abstract
The present investigation was conducted during summer 2018, to study the genetic divergence for different traits among F_5 progenies of eight crosses of groundnut. The investigation was conducted with 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.). Total forty genotypes were grouped in seven clusters. Cluster I with 12 genotypes emerged as the largest cluster followed by cluster V with 10 genotypes and cluster II and IV with 6 genotypes, cluster VI with 4 genotypes. Remaining two clusters (III and VII) were monogenotypic. Cluster V exhibited maximum intra cluster distance i.e. (D=14.37), followed by cluster VI, cluster I, cluster II and cluster IV. Being monogenotypic, remaining clusters showed no intra cluster distance. Maximum inter cluster distance was found between cluster II and V, followed by V and VII and IV and VI
It was observed that cluster II had the lowest cluster mean for days to 50% flowering and maturity. Cluster V had the highest cluster mean for number of branches per plant, number of matured pods per plant also lowest mean for number of immature pods per plant, highest shelling %, sound mature kernel (%) and dry pod yield per plant. Cluster VII had the mean for haulm yield per plot. Cluster IV had the highest mean for hundred kernel weight. Cluster III had the highest mean for traits oil percent and protein content.

Keywords: Compound growth rates, area, production, and productivity

Introduction
Groundnut (*Arachis hypogaea* L.), is an allotetraploid (2n=4x=40) species which likely evolved from two diploids (Kochert *et al.*, 1996) [7]. It belongs to the family *Leguminosae*, subfamily *Papilionoidae*, tribe *Aeschnomeneae*, sub-tribe *Stylosanthinae*, genus *Arachis* and species *hypogaea* (Isleib *et al.*, 1994) [4]. It is self-pollinated, annual, herbaceous legume growing upright or prostate, 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) [2]. 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 prostate and in bunch types they are more or less erect in the young plants but tend to become prostate 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) [10].
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. Further, majority of the economically importance characters including dry pod yield and it's components are emenable for genetic improvement through intense breeding among genetically diverse parent. The Mahalanobis's D^2 statistics is powerful tool for calculating the divergence between the population based on which genotype can be grouped into suitable clusters.

Materials and Methods

The material used in the present study consisted of 40 F_5 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.), 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 analysis of divergence was carried out by D^2 statistics of Mahalanobis (1936) [8] as described by Rao (1952) [12]. Analysis of variance for the individual characters studied was worked out as per RBD to test the significances of differences among the genotypes. The characters exhibiting significant differences were only used for further analysis of D^2 statistics. With the help of D^2 values between the clusters, a diagram showing the relationship between different genotypes was drawn.

Table 1: Number of genotype: 40 F_5 progenies of eight crosses

Sr. 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

Results and Discussion

The significant mean squares due to genotypes suggested the preface of ample variability. The genetic divergence among forty genotype of groundnut was estimated based upon observation of twelve characters. The D^2 values between all possible pairs, which indicated the presence of greater diversity among the genotypes for all the traits. The Mahalanobis D^2 statistics was computed for all possible pair of population under study.

Composition of cluster

The grouping of the genotypes was carried out by following Tocher's method, as described by Rao (1952) [12]. The fourty genotypes studied under investigation were grouped into seven clusters. The composition of cluster is given in Table 2. Cluster I was the largest having 12 genotypes followed by cluster V having 10 genotypes and cluster II and IV with 6 genotypes, cluster VI with 4 genotypes. Remaining two clusters *viz*, III and VII were monogenotypic (Table 2). The earlier worker Golakia and Makne (1992) [3], Katule (1992) [6], Reddy and Reddy (1993) [13], Rameshkumar *et.al* (1999) [11], Sonone and Thaware (2009) [16], Singh *et.al* (2010) [14].

Table 2: Grouping of forty genotypes of groundnut in various clusters on the basis of D^2 statistic

Cluster No.	No. of Genotypes	Name of Genotype		Pedigree
I	12	32	C_7-P_2	Phule -6021 X RHRG-6110
		35	C_7-P_5	Phule -6021 X RHRG-6110
		31	C_7-P_1	Phule -6021 X RHRG-6110
		34	C_7-P_4	Phule -6021 X RHRG-6110
		11	C_3-P_1	WRGS-15 X R-8808
		13	C_3-P_3	WRGS-15 X R-8808
		5	C_1-P_5	TAG 24 X Phule Unnati
		15	C_3-P_5	WRGS-15 X R-8808
		22	C_5- P_2	Phule -6021 X Phule Unnati
		2	C_1-P_2	TAG 24 X Phule Unnati
		25	C_5- P_5	Phule -6021 X Phule Unnati
		21	C_5- P_1	Phule -6021 X Phule Unnati
II	6	38	C_8- P_3	WRGS-15 X SB-XI
		40	C_8- P_5	WRGS-15 X SB-XI
		37	C_8- P_2	WRGS-15 X SB-XI
		39	C_8- P_4	WRGS-15 X SB-XI
		36	C_8- P_1	WRGS-15 X SB-XI
		12	C_3- P_2	WRGS-15 X R-8808
III	1	24	C_5- P_4	Phule -6021 X Phule Unnati

IV	6	6	C_2- P_1	Phule Unnati X TPG-41
		10	C_2- P_5	Phule Unnati X TPG-41
		8	C_2- P_3	Phule Unnati X TPG-41
		7	C_2- P_2	Phule Unnati X TPG-41
		9	C_2- P_4	Phule Unnati X TPG-41
		23	C_5- P_3	Phule -6021 X Phule Unnati
V	10	17	C_4- P_2	Phule 6021 X ICGV-00350
		19	C_4- P_4	Phule 6021 X ICGV-00350
		16	C_4- P_1	Phule 6021 X ICGV-00350
		20	C_4- P_5	Phule 6021 X ICGV-00350
		18	C_4- P_3	Phule 6021 X ICGV-00350
		26	C_6- P_1	Phule Unnati X SB-XI
		30	C_6- P_5	Phule Unnati X SB-XI
		28	C_6- P_3	Phule Unnati X SB-XI
		27	C_6- P_2	Phule Unnati X SB-XI
		29	C_6- P_4	Phule Unnati X SB-XI
VI	4	1	C_1- P_1	TAG 24 X Phule Unnati
		4	C_1- P_4	TAG 24 X Phule Unnati
		3	C_1- P_3	TAG 24 X Phule Unnati
		14	C_3- P_4	WRGS-15 X R-8808
VII	1	33	C_7- P_3	Phule -6021 X RHRG-6110

Percent contribution of various characters for divergence

The analysis of per cent contribution of twelve characters towards the expression of total genetic divergence (Table 3) indicated that dry pod yield per plot (23.85) followed by haulm yield per plot (17.18), protein content (13.08), days to maturity (12.82), sound mature kernel (9.23), shelling per cent (8.46), 100 kernel weight (6.28), oil content (4.23), number of branches per plant (3.85) contributed maximum towards divergence. However, the contributions of number of matured pods per plant (0.51), days to 50 % flowering (0.38) and number of immature pods per plant (0.13) were of low magnitude. Which supports the earlier findings of Reddy and Reddy (1993) [13], Sonawane (2010) [15].

Table 3: Percentage contribution of various characters towards total divergence

Sr. No.	Characters	Number of times appearing first	% contribution toward divergence
1	Days to 50 % flowering	3	0.38
2	Days to maturity	100	12.82
3	Number of branches/plant	30	3.85
4	Number of matured pods/plant	4	0.51
5	Number of immature pods/plant	1	0.13
6	Haulm yield/plot (kg)	134	17.18
7	100 kernel weight (g)	49	6.28
8	Shelling (%)	66	8.46
9	Sound mature kernel (%)	72	9.23
10	Oil content (%)	33	4.23
11	Protein Content (%)	102	13.08
12	Dry pod yield /plot (kg)	186	23.85

Intra and inter cluster distance

The intra and inter cluster D^2 values were worked out using Mahalanobis D^2 statistics. The mean D^2 values of cluster elements were used as measure of intra and inter cluster distance and are presented in.

Cluster V exhibited maximum intra cluster distance i.e. (D=14.37), followed by cluster VI (D=13.2) cluster I (D=10.86) cluster II (D=10.63) and cluster IV (D=9.88). Being monogenotypic, remaining clusters showed no intra cluster distance.

The maximum inter cluster distance was observed between cluster II and cluster V (D=24.92), followed by cluster V and cluster VII (D=24.58), cluster V and cluster VI (D=23.78) and cluster IV and cluster VI (D=23.16). The lowest inter cluster distance was observed between cluster III and cluster IV (D=11.94). The earlier worker Katule *et al.* (1992) [6], Rameshkumar *et.al* (1999) [11], Johan Joel and Mylsamy (1998), Sonawane (2010) [15], had been reported similar finding which supports to the above findings.

Cluster means

The cluster means for twelve characters studied are given in Table 4. It revealed wide range of variability for most of the characters. It was observed that cluster II had the lowest mean for early days to 50% flowering (42.67) and early maturity (118.50). Cluster V had the highest mean for number of branches per plant (11.10) and number of matured pods per plant (40.90) also lowest mean for number of immature pods per plant (4.90), highest shelling per cent (69.88 %), sound mature kernel per cent (96.80 %) and dry pod yield (1.82). Cluster VII had the highest mean for haulm yield per plot (9.70). Cluster IV had the highest mean for 100 kernel weight (42.25). Cluster III had the highest cluster mean for traits oil percent (50.30) and protein content (23.55). The lowest dry pod yield mean was observed by cluster II (0.94). On the basis of per cent performance, inter cluster distance and cluster mean the six progenies of different crosses *viz*,C1-P3, C2-P4, C3-P4, C4-P3, C6-P3 and C8-P2 were identified for advancing in F_6 and then will be selected for crossing

programme for the genetic improvement in Groundnut. Similar finding were corroborated with Katule *et al.* (1992) [6] and Nadaf *et al.* (1986) [9]

Table 4: Average inter and intra–cluster distance values for groundnut genotypes

Cluster No.	I	II	III	IV	V	VI	VII
I	10.86	15.45	12.5	14.93	21.1	16.39	14.62
II		10.63	18.37	19.64	24.92	18.24	14.16
III			0	11.94	22.77	21.52	20.25
IV				9.88	20.07	23.16	20.16
V					14.37	23.78	24.58
VI						13.2	19.84
VII							0

Conclusions

The total forty genotypes were grouped into seven clusters. Maximum inter cluster distance was found between cluster II and V and V and VII cluster V had the highest cluster mean for majority of characters including dry pod yield per plot. The dry pod yield was contributed highest for genetic divergence followed by haulm yield, protein content, days to maturity, sound maturity kernel and shelling per cent On the basis of perse performance, inter cluster distance and cluster mean the progenies *viz,* C1-P3 (TAG-24 x Phule Unnati), C2-P4 (Phule Unnati x TPG-41), C3-P-4 (WRGS-15 x RHRG-8808), C4-P3 (Phule-6021 x ICGV-00350), C6-P3 (Phule Unnati x SB-XI) and C8-P2 (WRGS-15 x SB-XI) are suggested for further crossing programme and genetic improvement in Groundnut..

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