



# Genetic Divergence Study in Groundnut Genotypes (*Arachishypogaea* L.)

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## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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## ABSTRACT

Employing the Mahalanobis  $D^2$  statistic, a divergence study was performed on 36 groundnut genotypes and 13 clusters were identified. Indicating that the genotypes of these groups may be more divergent from one another, the maximum inter-cluster distance (D) was found between cluster II and cluster XIII (315.56), followed by cluster III and cluster IX (289.56), cluster III and cluster XII (289.21), and cluster XII and cluster XIII (297.11). The genotypes in the mentioned clusters showed a significant difference in the means for traits that contribute significantly to yield, indicating that the genotypes in these clusters make ideal parents in a hybridization programme to produce transgressive segregants and improve groundnut.

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## 1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is the member of *Papilionaceae* subfamily of the *Fabaceae* family which included chief edible oil seed crops in the world. South America is where the domesticated peanut (*Arachis hypogaea* L.) first appeared. It is a significant source of food, fuel and oil. According to Jambunathan et al. [1], groundnut seeds (kernels) contain 35.6–54.2% oil, 16.2–36.0% protein [2] and 10–20% carbohydrates [3]. 100 g of the kernels provide 564 kcal of energy (Jambunathan, 1991). Additionally, the seeds are a good source of vitamins E, niacin, folacin, riboflavin, and thiamin as well as minerals including calcium, phosphorus, and iron. The success of a plant breeding programme is greatly influenced by the selection of suitable parents. It is anticipated that using divergent parents will produce hybrids with potential recombinants. Genetic improvement mostly depends upon the amount of genetic variability present in the population. When a plant breeder is concerned with a complicated trait like pod yield, the combined merit of many desired traits becomes more significant than any one character. In order to increase the pod and kernel yield, parents must be chosen based on the proportion of characters with quantitative divergence, which can be determined using the  $D^2$ -statistic developed by Mahalanobis [4]. The present study was conducted to determine the nature and magnitude of genetic divergence among the 36 bunch type groundnut genotypes, which will help to plan hybridization programmes to develop groundnut varieties with improved traits. Murty and Arunachalam [5] stressed the use of Mahalanobis's  $D^2$  statistic for estimating genetic divergence because it allows precise comparison among all the population in given any groups before executing actual crosses.

## 2. MATERIALS AND METHODS

At the Research Farm of the Department of Genetics and Plant Breeding, RVSKVV, College of Agriculture, Gwalior (M.P.), during the Kharif season 2018–19, an experiment involving 36 groundnut genotypes for 14 traits was carried out using a randomized block design (RBD) with three replications. Each genotype was sown in one row of 5 m length with a spacing of 30 cm x 10 cm for each replication. The 14 numerical characters include Days to Maturity, Number of Pods per Plant, Days to 50% Flowering, Number

of Primary Branches per Plant, Plant Height (cm), Number of Secondary Branches per Plant, and Days to 50% Fruiting. Five randomly chosen plants from each genotype in each replication were measured for their pod yield per plant (gm), 100 pod weight (gm), kernel yield per plant (gm), shelling percentage (%), pod yield per hectare (kg), sound mature kernel (%) and kernel yield per hectare (kg). Using Mahalanobis  $D^2$  [4], expanded by Rao [6], the genetic diversity between genotypes was calculated. According to Tocher's technique, the genotypes were categorized into clusters based on their  $D^2$  values [6]. The intra- and inter-cluster distances were calculated utilising Singh and Chaudhary's approach from 1985 [7]. The method of Singh was used to calculate the each character's contribution to divergence [8].

## 3. RESULTS AND DISCUSSION

Based on  $D^2$  value, the 36 groundnut genotypes were divided into 13 clusters (Table 2). Cluster I included the most genotypes (19), followed by Cluster IV (6), and the remaining clusters each contained a single genotype. According to Zaman et al. [9], the inter-cluster distance (Table 3) was greater than the intra-cluster distance, indicating that the genotypes of the distant group have more diversity. The inter-cluster distance analysis revealed that clusters II and XIII had the highest divergence (315.56), followed by cluster III and IX (289.56), cluster III and XII (289.21), and cluster XII and cluster XIII (297.11). Because these clusters had relatively high divergence in comparison to others, the genotypes in these clusters can be used to choose the parents for hybridization. Cluster III and Cluster V were next in line with a minimum inter-cluster distance of 27.81, followed by Cluster II and Cluster VI with a minimum inter-cluster distance of 47.89. While other clusters were mono-genotypic with no intra-cluster divergence, in cluster 4 (66.88) and cluster I (45.14) had the highest intra-cluster distances. Character's role in contributing to divergence (Table 1) were observed maximum in 100 pod weight(21.59%) followed by number of primary branches per plant(21.27%), number of secondary branches per plant(20.48%), pod yield per plant(18.10%), sound mature kernel(13.65%), plant height(1.90%), number of pods per plant(1.59%) whereas, magnitude of genetic divergence was less than one per cent for 100 kernel weight(0.79%), days to 50% flowering(0.16%), pod yield per hectare(0.16%), and kernel yield per hectare(0.32%). Days to

maturity, plant production of kernels per day, and shelling percentage do not influence divergence. These findings are in conformity with those reported earlier in groundnut by Vivekananda et al. [10]; Niveditha et al. [11]; Chavadhari et al. [12] and Saritha K et al. [13]. According to a suggestion, the character contributing the most

to divergence should be prioritized for future hybridization projects. The emphasis should be placed on genotypes belonging to clusters II, III, IX, XII, and XIII for choosing parents used for further crop development programmes, considering the cluster distances and cluster means in the current analysis.

**Table 1. Percent contribution of characters towards divergence in 36 groundnut genotypes**

S.N.	Characters	Times Ranked 1 <sup>st</sup>	% contribution of traits towards divergence
1	100 pod weight (gm)	136	21.59 %
2	Number of primary branches per plant	134	21.27 %
3	Number of secondary	129	20.48 %
4	Pod yield per plant	114	18.1 %
5	Sound mature kernel (%)	86	13.65 %
6	Plant height (cm)	12	1.9 %
7	Number f pods per plant	10	1.59 %
8	100 kernel weight (gm)	5	0.79 %
9	Kernel yield per ha(kg)	2	0.32 %
10	Days to 50% flowering	1	0.16 %
11	Pod yield per ha (kg)	1	0.16 %
12	Days to maturity	0	0.00 %
13	Kernel yield per plant (gm)	0	0.00 %
14	Shelling percentage	0	0.00 %

**Table 2. Distribution of groundnut genotypes in different clusters**

Cluster	Number of genotypes	Genotypes
I	19	ICGV -13562, ICGV-13554, ICGV-13560, ICGV-13575, ICGV-13557, ICGV-13214, ICGV-9895, ICGV-13219, ICGV-13226, ICGV-13227, ICGV-13220, ICGV-13233, ICGV-13235, ICGV-13240, ICGV-8010, ICGV-13246, ICGV-8110, ICGV-13545, Girnar 2
II	1	ICGV-13208
III	1	Girnar 3
IV	6	ICGV-13567, ICGV-13565, ICGV-13237, ICGV-13229, PBS-12200, PBS-12201
V	1	ICGV-13243
VI	1	ICGV-13555
VII	1	ICGV-13574
VIII	1	Mallika
IX	1	ICGV-8705
X	1	ICGV-13558
XI	1	ICG-X-1400-65-F <sub>2</sub>
XII	1	ICGV-13564
XIII	1	JGN-3

**Table 3. Average intra and inter cluster D2 values of 36 groundnut genotypes**

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	45.14	92.78	78.79	101.23	79.37	64.99	97.61	105.50	187.12	103.93	114.15	197.05	139.64
II		0.00	217.07	98.04	223.88	47.89	49.74	79.27	106.31	128.23	233.72	121.33	315.56
III			0.00	203.11	38.71	111.54	189.46	163.52	289.41	135.24	92.57	289.21	94.24
IV				66.88	131.91	85.83	126.17	196.04	100.50	203.51	180.87	188.94	203.82
V					0.00	119.09	210.24	233.09	228.65	173.51	73.90	279.29	67.93
VI						0.00	72.65	100.28	79.04	147.16	155.44	143.34	169.93
VII							0.00	27.81	112.62	60.70	137.53	59.54	223.72
VIII								0.00	213.03	49.48	156.05	113.08	240.39
IX									0.00	246.70	219.89	98.17	276.45
X										0.00	79.28	93.56	215.24
XI											0.00	139.51	63.19
XII												0.00	297.11
XIII													0.00

**Table 4. Cluster means value for 14 traits in groundnut genotypes**

Cluster	Plant height(cm)	Days to 50% flowering	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	Pod yield per plant	100 pod weight (gm)	Kernel yield per plant	100 kernel weight (gm)	Shelling %	Sound mature kernel (%)	Pod yield per ha.(kg)	Kernel yield per ha.(kg)
I	26.69	36.12	111.11	3.49	3.77	21.95	9.59	112.26	6.36	34.16	64.11	85.14	3192.26	2114.30
II	26.43	36.00	111.00	4.10	4.50	25.00	14.73	<b>145.00</b>	9.73	36.00	62.72	85.00	4906.33	3241.33
III	<b>20.40</b>	<b>39.00</b>	<b>114.00</b>	<b>3.00</b>	3.20	24.67	<b>7.77</b>	82.00	5.37	32.00	<b>70.07</b>	<b>80.00</b>	<b>2586.00</b>	1787.33
IV	28.17	33.11	108.11	3.59	3.67	22.61	13.12	142.33	8.69	<b>45.33</b>	66.18	90.72	4407.17	2895.22
V	22.47	36.67	111.67	3.03	2.53	<b>20.00</b>	8.03	106.00	<b>5.30</b>	38.00	69.58	86.00	2675.00	<b>1765.00</b>
VI	25.80	34.67	109.67	3.33	4.00	30.33	15.13	125.00	9.93	31.00	<b>61.74</b>	83.00	5039.00	3308.00
VII	27.20	34.33	109.33	4.60	4.40	34.00	14.93	102.00	9.97	36.00	66.33	91.00	4972.67	3309.00
VIII	27.83	34.33	110.33	4.50	<b>4.77</b>	36.67	12.13	87.00	8.20	33.00	69.03	84.00	4040.67	2730.33
IX	28.07	36.00	111.00	4.03	3.50	35.00	<b>20.03</b>	144.0	<b>13.50</b>	45.00	67.48	<b>92.00</b>	<b>6671.00</b>	<b>4495.67</b>
X	25.50	36.00	111.00	5.00	3.40	27.67	10.20	92.00	6.87	35.00	63.54	86.00	3396.67	2286.67
XI	32.90	36.00	111.00	4.27	<b>2.40</b>	30.00	9.77	82.00	6.33	36.00	65.68	89.00	3252.33	2109.00
XII	32.20	35.00	110.00	<b>5.40</b>	3.20	<b>37.00</b>	17.73	118.00	11.67	40.00	65.53	90.00	5905.00	3885.00
XIII	<b>34.10</b>	<b>31.00</b>	<b>106.00</b>	3.07	2.93	<b>37.00</b>	7.97	<b>80.00</b>	5.37	<b>27.00</b>	69.40	89.00	2653.00	1781.00

#### 4. CONCLUSION

JGN-3 of cluster XIII, ICGV-13564 of cluster XII, ICGV-13558 of cluster IX, Girnar-3 of cluster III, and ICGV-13208 of cluster II were found to be diverse and superior for kernel yield and the majority of the attributing features based on genetic diversity study. These genotypes might be used in upcoming breeding programmes for advancement.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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