The Pharma Innovation Journal 2023; 12(12): 1540-1543

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(12): 1540-1543

www.thepharmajournal.com
Received: 22-10-2023
Accepted: 30-11-2023

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Assessment of the genetic diversity in groundnut (*Arachis hypogaea* L.)

DM Suthar, DG Patel, PR Patel, NV Soni and HN Zala

Abstract
Genetic diversity among 42 genotypes of groundnut was estimated for ten characters using Mahalanobis D^2 statistics. Tocher's approach was used to divide genotypes into groups. The genetic diversity analysis revealed the formation of eight clusters suggested the presence of considerable genetic diversity among the 42 genotypes. Inter-cluster distances were higher than intra-cluster distances for mostly cluster, indicated the existence of substantial diversity among the genotypes. Among 8 clusters, cluster II was the largest having fifteen genotypes followed by cluster III (11) and cluster I (9), while cluster V, VI and VIII were solitary. Cluster IV and V has the maximum divergence because they contain desirable mean values for different characters. While, harvest index (52.03%) contributed the highest for divergence followed by pod yield per plant (20.56%) and number of mature pod per plant (12.89%). So, selection for divergent parents based on these characters would be useful for developing potential hybrids.

Keywords: Genetic diversity, D^2 statistics, clusters, groundnut

Introduction
Groundnut (*Arachis hypogaea* L.) is major and most famous oilseed crop not only in India but also across tropical and subtropical regions worldwide. The name "groundnut" comes from two Greek words "Arachis" which means legume and "hypogaea" which means below ground (the production of pods in the soil). Groundnut is highly self-pollinated legume crop and it comes under the Fabaceae family along with 2n=4x=40 chromosomes. Natural cross-pollination rates range from less than 1 to 6 percent as a result of typical flowers or bee activity (Duke, 1981 and Coffelt, 1989) [3, 2]. Because of high geographical area, China is the largest producer of groundnut. While, India ranked second as producer. Gujarat's primary oilseed crop is groundnut. Generally, groundnuts are rich source of healthy fats likes, monounsaturated and polyunsaturated fats. The oil content varied from 47% to 54%. They are also good source of plant-based protein range between 22-30%, valuable for vegetarians and vegan peoples. Minerals including magnesium, phosphorus, potassium, zinc, and iron are all present in groundnuts. These minerals are essential to the body's ability to produce energy, maintain healthy bones, and support the immune system. However, it's crucial to eat them in a responsible manner, particularly for people with nut allergies or those looking for to manage their calorie intake. Symbiotic bacteria play a major role in the nitrogen fixation process occurring within the root nodules of groundnut plants. These specific bacteria (*Rhizobium* sp.), displayed a mutualistic relationship with the plant and actively convert atmospheric nitrogen into biologically available forms that enrich the soil's nitrogen content. The ability of peanuts to fix nitrogen makes them crucial in crop rotations because they reduce the need for nitrogen-containing fertilizers and boost soil fertility. This crop exerted one unique characteristic which is positive geotropism. In which pods formation and development take place in underground. Assessing the degree and amount of variation within germplasm, as well as among the various groundnut cultivars that have been both released and also in pre-release stages, holds paramount importance in progressing rainfed groundnut production and also in improvement. The understanding of diversity serves as an essential foundation for enhancing the cultivation of groundnut in conditions dependent on rainfall for irrigation. In crop enhancement, assessing genetic diversity play greater impact on parent selection, as well as hybrids from diverse parents show greater heterosis than those between more closely related parents. (Harrington, 1940; Arunachalam 1981) [5, 1] This critical step involves searching genetic variability to advantageously combine traits, development of robust hybrids. By uniting distinct genetic variation, breeders cultivate robust and high-performing cultivar and also adapting to various challenges and optimizing productivity.

Hence, it necessitates studying the genetic divergence among the existing varieties and genotypes for the identification of parents and also some good donor for efficient hybridization programme. The D^2 statistics is a useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murty and Arunachalam 1966) [7]. In order to organize hybridization programmes to create groundnut varieties with high pod production, the current study was conducted to ascertain the type and extent of genetic divergence among the forty-two groundnut genotypes for ten characters.

Materials and Methods

The experimental material consisted of 42 groundnut genotypes belonging to different botanical types *viz*; Spanish bunch and Virginia bunch evaluated in Randomized Block Design with four replications at Cotton Research Station, Sardarkrushinagar Dantiwada Agricultural University, Talod during *kharif* 2022. The sowing was done on 5th *July*, 2022. Each genotype was sown in each one rows of four meters length with optimum spacing of 45 cm × 10 cm. A total of 675.5 mm of rain fell during the course of the crop period and the temperature ranged from 25 °C to 35 °C with an average humidity of 91.5%. The agronomic practices and crop protection operations were carried out as per recommendation. The experimental material was evaluated for ten characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branch per plant, mature pods per plant, pod yield per plant (g), 100-kernel weight (g), shelling percentage (%), harvest index (%) and oil content (%). Data was collected from the five randomly selected plants within each genotype in each replication at appropriate development stage except days to 50% flowering and days to maturity. Oil content was estimated with the help of Nuclear Magnetic Resonance (NMR) machine. The data were subjected to statistical analysis. Mahalanobis (1928) [6] D^2 statistic was used for assessing the genetic divergence between different populations. Grouping of the genotypes in different clusters was done by using Tocher's method (Rao, 1952) [9]. Based on the genetic divergence the genotypes were grouped into different clusters. The inter cluster distance was calculated by measuring the distance between clusters I and cluster II, between clusters I and cluster III, between clusters II and cluster III and so on. Likewise, intra cluster distance also obtained by measuring the distance within clusters. While, cluster means and contribution towards the genetic divergence were obtained from the results of the analysis. All these parameters would help in selection of parents for hybridization programmes.

Results and Discussion

Genetic variation among 42 different genotypes was assessed by employing D^2 statistic for 10 distinct traits. To analyze this diversity, all the genotypes were grouped into different clusters by utilizing Tocher's method, technique introduced by Rao in 1952 [9].

Group constellation

Based on analysis results, all 42 groundnut genotypes were grouped into 8 different clusters. The distribution pattern of genotypes into 8 clusters was presented in table 1. Cluster II was the largest among 8 cluster contain fifteen genotypes followed by cluster III (11), cluster I (9), cluster IV and VII each having two genotypes and cluster V, VI and VIII were solitary. The development of solitary clusters may result from complete isolation, which prevents gene flow or from intense natural and human selection for various adaptive complexes.

Table 1: Distribution of forty-two groundnut genotypes into different clusters by Tocher's method

Cluster no.	Total no. of strain	Genotypes include in the cluster
I	9	JVB- 2551, IVK I 2021-9, JVB- 2523, IVK I 2021-4, ISK I 2021-3, NRC GCS- 623, JVB- 2552, IVK I 2021-5, GG- 20
II	15	GJG- 32, ISK I 2021-1, KDG- 128, ICGV- 16668, JSSP- 69, ICGV- 16697, TG- 37A, J- 108, ISK I 2021-7, JB- 1488, JVB- 2571, IVK I 2021-6, JVB- 2525, J- 114, JB- 1505
III	11	IVK I 2021-1, GJG- 22, JSSP- 73, JSSP- 68, J- 110, Kaushal, JSSP- 71, JSSP- 72, TG- 88, JVB- 2564, ISK I 2021-6
IV	2	JVB- 2565, JVB- 2577
V	1	JB- 1487
VI	1	GJG- 9
VII	2	JSSP- 70, J- 109
VIII	1	JL- 501

Intra and inter relation of clusters

Generally, the distance between two clusters indicates the amount of diversity present in population. With the increasement of distance between two clusters, greater the divergence and *vice versa*. The genotypes in the same cluster were more closely related to each other than those belonging to another cluster. In other words, the genotypes grouped in one cluster was less divergent than those genotypes which was placed in a different cluster. The intra and inter cluster distances were given in table 2. The intra cluster distance (D^2) ranged between 28.20 (cluster I) to 47.85 (cluster VII). The cluster V, VI and VII were solitary clusters and therefore, their intra cluster distance were zero. The inter cluster distance (D^2) ranged between 50.28 to 380.24. The maximum inter cluster distance was observed between cluster I and VIII (380.84) followed by cluster IV and VIII (366.89), cluster V and VI (281.11), cluster VI and VIII (276.81), cluster I and V (255.27) and cluster II and VIII (218.95). The slightest inter cluster distance was observed between cluster I and IV (50.28) followed by cluster II and IV (61.67) and cluster III and VI (61.97). For the majority of clusters, inter-cluster distances were greater than intra-cluster distances, indicating the presence of significant genotypic variation. By crossing between genotypes from different clusters, there is chances to obtain offspring with traits that surpass the range of those parents (transgressive segregants), which is crucial in genetic improvement as it allows the development of new varieties with desirable characteristics that may not be present in the original parental lines.

Table 2: Average intra and inter cluster D^2 values of 42 genotypes of groundnut

Cluster	I	II	III	IV	V	VI	VII	VIII
I	28.20	93.33	76.12	50.28	255.27	80.44	194.87	380.84
II		31.03	86.57	61.67	86.69	136.67	137.90	218.95
III			41.66	99.28	160.87	61.97	78.82	189.93
IV				43.64	188.40	137.06	202.56	366.89
V					0	281.11	113.66	103.35
VI						0	153.18	276.81
VII							47.85	82.92
VIII								0

Cluster Means

Cluster means make it simple to compare several clusters. We can find differences or similarities in the average values of variables across clusters by comparing the cluster means of various clusters. Understanding the traits and behaviors of various groups within the data is aided by this comparison. Cluster means analyzed for ten traits in groundnut clearly indicate appreciable difference for most of the characters as shown in table 3. A considerable amount of inter cluster variation was observed among all the traits. Based on results, cluster V displayed desirable mean value for various characters like, number of fully developed pod (21.95), pod yield per plant (29.30g), oil content (49.20%), days to 50 *per cent* flowering (27.00 days) and days taken for fully maturation (118.00days). While, cluster IV having favourable mean value for plant height (44.53cm), primary branches per plant (6.38) and 100-kernel weight (49.16g). Cluster VIII and VI contain superior mean value for harvest index (63.48%) and shelling percentage (62.08%), respectively. This revealed that cluster IV and V has the maximum divergence. Inter crossing genotypes from these clusters might result in wide array of variability for exercising effective selection.

Table 3: Cluster means for yield and its component traits in groundnut

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branch/plant	Number of mature pod/plant	Pod yield/plant (g)	100-Kernel weight (g)	Shelling percentage (%)	Harvest index (%)	Oil content (%)
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
I	28.53	118.81	57.17	6.24	18.03	25.16	46.50	59.00	43.30	48.83
II	29.97	120.45	51.09	6.23	21.85	28.51	40.62	54.19	50.59	48.78
III	29.07	118.84	55.31	5.74	16.46	21.17	42.62	58.00	49.50	48.82
IV	30.50	120.13	44.53	6.38	18.95	28.41	49.16	53.75	45.43	49.10
V	27.00	118.00	45.95	5.90	21.95	29.30	43.17	59.39	59.68	49.20
VI	35.00	124.50	64.35	5.25	16.60	19.55	41.88	62.08	45.50	48.62
VII	28.13	118.88	48.95	5.95	14.98	18.88	41.49	60.08	56.39	48.33
VIII	29.75	120.25	60.15	5.35	17.05	20.70	33.96	47.65	63.48	49.04

Contribution of individual traits toward divergence

It had been suggested that the character who had the greatest impact and contributed the most towards divergence was thought to deserve special consideration for the hybridization programme. Contribution of each character to total genetic divergence was presented in table 4. Out of ten characters studied, harvest index (52.03%) contributed the maximum for divergence, taking first ranked 13 times out of 861 combinations, subsequently pod yield per plant (20.56%) with 8 times, number of mature pod per plant (12.89%) with 111 times, plant height (4.88%) with 42 times, number of primary branch per plant (3.48%) with 30 times and days to 50 *per cent* flowering (2.09%) with 18 times, oil content (1.51%) for 177 times and shelling percentage (1.28%) for 448 times ranked first. While, days to maturity (0.35%) and 100-kernel weight (0.93%) contributed negligible towards the total genetic divergence as depicted in table 4. Therefore, while choosing parents for hybridization harvest index, pod yield per plant and number of mature pod per plant should be taken into consideration to emphasize because they together contributing 85.48% to the total divergence. Similar higher contribution of harvest index, pod yield per plant and mature pods per plant were observed by Saini *et al.* (2020) [11]. Gantait *et al.* (2017) [4], Raza *et al.* (2018) [10], Tayade *et al.* (2018) [13] and Sudhishna *et al.* (2022) [12] recorded similar result of contribution for pod yield. While, observed similar result of contribution for number of mature pod per plant.

Table 4: Relative *per cent* contributions of various characters to divergence in groundnut

No.	Character	Time ranked 1st	Contribution to divergence %
1	Days to 50% flowering	18	2.09
2	Days to maturity	3	0.35
3	Plant height	42	4.88
4	Primary branches per plant	30	3.48
5	mature pods per plant	111	12.89
6	Pod yield per plant	8	20.56
7	100-kernel weight	11	0.93
8	Shelling percentage	448	1.28
9	Harvest index	13	52.03
10	Oil content	177	1.51

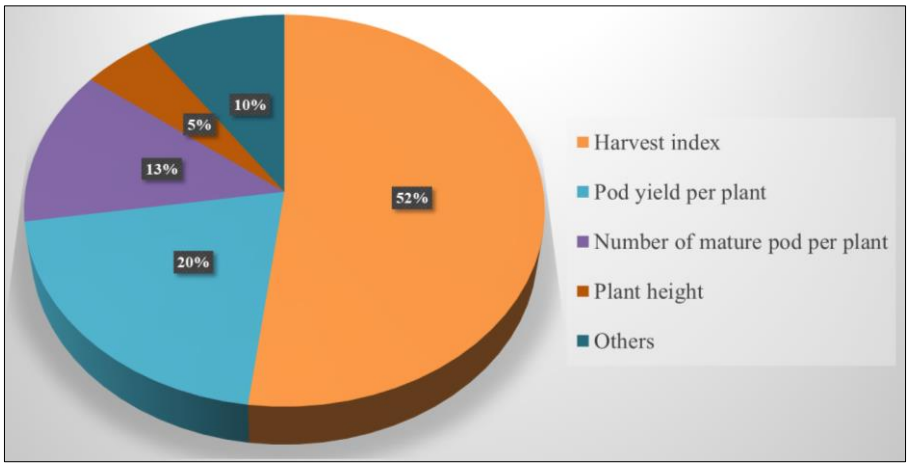

Fig 1: Graphical representation of percent contribution towards genetic divergence by the different characters in groundnut

Conclusion

The diversity study is prerequisite for hybridization programmes. The generation of transgressive segregantes or superior recombinants was aided by the selection of parents based on intra and inter cluster distance and cluster mean. The total 42 genotypes were grouped into eight clusters. The maximum intra-cluster distance was observed in cluster VII followed by cluster IV. The maximum inter cluster distance was observed between cluster I and VIII followed by cluster IV and VIII. Inter cluster distances were higher than intra cluster distances which indicated the existence of substantial diversity among the genotypes. While choosing parents for hybridization harvest index, pod yield per plant and mature pods per plant should be taken into consideration to emphasize because they together contributing 85.48% to the total divergence. This revealed that cluster IV and V has the maximum divergence. Intercrossing genotypes from these clusters may produce a large range of diversity, allowing for productive selection.

Acknowledgements

The authors are thankful to Dr. D. G. Patel, Assistant Research scientist, Cotton Research Station, S. D. Agricultural University, Talod, Gujarat for providing the facilities, genotypes and support for conducting of my experiment.

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