Assessment of Genetic Diversity Among Groundnut (*Arachis Hypogaea* L.) Genotypes

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Abstract

In present experiment the genetic diversity studied among 30 genotypes of groundnut using D^2 statistic during *kharif* - 2014 in a randomized block design with three replications at the Instructional Farm, College of Technology and Engineering, Maharana Pratap University of Agriculture and Technology, Udaipur for thirteen agro-morphological characters including days to 50% flowering, days to maturity, plant height (cm), number of branches plant[-1], number of mature pods per plant, dry pod yield plant[-1] (g), kernel yield per plant (g), 100-kernel weight (g), sound mature kernels (%), shelling percentage, biological yield per plant, harvest index (%) and oil content (%). The analysis of variance revealed significant differences among the genotypes for all characters except days to 50% flowering and days to maturity. Based on Ward's method, 30 genotypes were grouped into two clusters. Cluster I was containing 29 genotypes while cluster II contained only 1 genotype i.e. UG-179. Inter cluster distance between these two clusters was observed 159.68, which proved UG-179 genotype sufficiently different from the rest 29 genotypes. Cluster means revealed that genotypes from these two clusters may be used for future hybrid groundnut breeding programs with special reference to dry pod yield, 100-kernel weight, biological yield, harvest index and oil content. The diversity present among the genotypes helps in producing better high oil groundnut genotypes for the developing countries while low oil genotypes having high confectionary quality also produced as per the demand of groundnut in the developed countries for food purposes.

1. Introduction

Groundnut (*Arachis hypogaea* L.) is the sixth most important oilseed crop in the world and grown for its high amount of oil (45-50%) and digestable protein (25-30%) throughout the world (Namrata et al., 2016; Dhakar et al., 2017). Groundnut is also known as "King of Oilseed" because it contains poly unsaturated fatty acids (PUFA) (40-50%) and mono unsaturated fatty acids (MUFA) like linoleic acid (25-35%) in right proportion which makes groundnut oil stable and nutritive (Rani, 2017; Gantait et al., 2017; Wang, 2018). Rancidity development in the oil is prevented by the presence of an antioxidant (tocopherol content approximately 0.9 mg/g oil) (Kushwah et al., 2016). Groundnut is also used for food purposes like groundnut butter, roasted groundnut and salted groundnut etc. in western part of the world (Nigam et al., 2004; Janila, 2016). So, in groundnut breeding cultivars with high oil for oil production and also cultivars with low oil for confectionary purposes are very important. Common problem faced by breeders in groundnut breeding is that most groundnut cultivars have a narrow genetic base that is due to recent polyploidization, self-pollination and lack of

sufficient informations about morphological and agricultural characteristics of groundnut (Badigannavar et al., 2002; Nigam et al., 2004). Precise information about the nature and degree of genetic diversity present in a population is must for the plant breeder because it helps in selection of most diverse parents which results in a hybrid with high heterosis (Kumari et al., 2015; Reddy, 2017). Knowledge of pre-existing genetic diversity is the basic need of any crop improvement programme (Bhakal, 2015). Hence, the present investigation was made to study the genetic divergence in 30 genotypes of groundnut *(Arachis hypogaea* L.) to identify potential genotypes for various yield traits which could be utilized in the hybridization programme as parents.

2. Materials and Methods

2.1. Experimental site and design

The experimental material composed of 30 groundnut genotypes including three checks namely Pratap Raj Mungphali, Pratap Mungphali-2, TG-37A (Table 1), were planted in a Randomized Block Design with three replications during *kharif,* 2014 at the Instructional Farm, College of

Table 1: List of genotypes used in present study and their pedigree

Sl. No.	Name of genotypes	Pedigree
1.	UG-158	J 63×TPG 41
2.	UG-159	JSSP 15×JSSP 24
3.	UG-160	GG 2×B 95
4.	UG-161	GG 8×TKG 19 A
5.	UG-162	GG 2×TPG 41
6.	UG-163	GG 20×PBS 24030
7.	UG-164	ICGX 090018
8.	UG-165	GG 21×R-2001-3
9.	UG-166	GG 8×TKG 19 A
10.	UG-167	GG 2×TG 26
11.	UG-168	GG 20×TAG 24
12.	UG-169	GG 20×ICGV 86325
13.	UG-170	GG-7×R-2001-3
14.	UG-171	GG-7×JL 501
15.	UG-172	TG-37 A×GG 20
16.	UG-173	GG 2×ICGV 91114-1
17.	UG-174	TG 40×ICGV 86325
18.	UG-175	PBS 24030×TG 37 A
19.	UG-176	ICGX 070067
20.	UG-177	J 11×TPG 41
21.	UG-178	ICGV 76×ICGV 86305
22.	UG-179	ICGV 86564×TPG 41
23.	UG-180	TG 37 A×CS 19
24.	UG-181	ICGV 86590×PBS 24030
25.	UG-182	UG 20×ALR-3
26.	UG-183	GG 5×Faizapur-2
27.	UG-184	GG 5×TPG 41
28.	Pratap Mungphali -2	ICGV- 86055×ICG- (FDRS 10)
29.	Pratap Raj Mungphali	Selection from ICGV 98223
30.	TG-37A	TG 25×TG 26

Technology and Engineering, Maharana Pratap University of Agriculture and Technology, Udaipur. In each replication, genotypes were sown in a plot of 5×0.9 m² accommodating 3 rows of 5 m length, spaced 30 cm apart with a plant to plant spacing of 10 cm. Recommended agronomic practices were followed to raise a healthy crop.

2.2. *Recording of data*

The data were recorded on five randomly selected competitive plants of each genotype for thirteen agro-morphological characters, except days to 50% flowering, days to maturity and 100-kernel weight, which were recorded on plot basis.

2.3. *Biochemical analysis*

Two random samples of kernels were drawn from bulk harvest of five randomly selected plants under each replication and oil content of kernels was determined by the Soxhlet's Method (A.O.A.C., 1965) and average oil content in per cent was worked out.

2.4. *Statistical analysis*

The mean value of the recorded data was subjected to analysis of variance (ANOVA) using the statistical method suggested by Fisher (1918). Multivariate analysis of D^2 was done for all thirteen characters by using Mahalanobis Statistics (1936) and clusters were formed by following the Ward (1963) method.

3. Results and Discussion

The significant treatment mean square indicated adequate variability among the genotype for almost all characters, except days to 50 per cent flowering and days to maturity (Table 2) which indicated the presence of considerable

Table 2: Mean square for various characters in Groundnut

Sl. No.	Characters	Replica-tion	Genotype	Error
	d.f.	[2]	[29]	[58]
1.	Days to 50% flowering	10.5333	4.1471	4.453
2.	Days to maturity	3.2444	5.3870	3.336
3.	Plant height (cm)	5.2724	10.9413**	2.444
4.	No. of branches plant⁻¹	0.2111	1.4410*	0.7513
5.	No. of mature pods plant⁻¹	3.2333	13.2034**	2.44
6.	Dry pod yield plant⁻¹ (g)	0.2111	16.7697**	1.659
7.	Kernel yield plant⁻¹ (g)	0.4767	7.7246**	1.194
8.	100-Kernel weight (g)	1.4333	110.6299**	0.9391
9.	Sound mature kernels (%)	1.9111	27.1249**	2.256
10.	Shelling percentage	6.6778	29.3444**	8.069
11.	Biological yield plant⁻¹	33.6333	62.3126**	26.21
12.	Harvest index (%)	17.1700	65.2100**	22.13
13.	Oil content (%)	1.2444	18.9962**	0.5433

[] Figures in parenthesis are degrees of freedom;
*, **: Significant at (p=0.05) and (p=0.01) level of significance, respectively

variability among the genotypes under study. On the basis of observed magnitude of the D^2 value, 30 groundnut genotypes were grouped into two clusters, in such a manner that the genotypes within the cluster had smaller D^2 value than the genotype from different cluster. Cluster I contain almost all genotypes i.e. 29, included in the experiment while cluster II contains only single genotype i.e. UG-179 (Table 3). Clustering pattern revealed that genotypes from quite different pedigree fall into a single cluster I which could be explained by the presence of unidirectional selection pressure for development of the genotypes which made them genetically similar as compared to their parents. The genotypes from the same origin may be present in same cluster or not, like UG-162 and UG-167 having one parent common (GG 2) are found in same cluster I while on other hand genotype UG-179 and UG-184 also having one parent common (TPG 41) but found in different clusters, cluster II and cluster I, respectively (Table 1) (Table 3). Looking at the pattern of varietal distribution in different clusters, it appeared that geographical distance between the varieties had no relation with the genetic divergence as the varieties

Table 3: Groundnut genotypes included in each cluster

Clusters	No. of geno-types	Name of genotypes
I	29	UG-158, UG-159, UG-160, UG-161, UG-162, UG-163, UG-164, UG-165, UG-166, UG-167, UG-168, UG- 169, UG-170, UG-171, UG-172, UG-173, UG-174, UG-175, UG-176, UG-177, UG-178, UG-180, UG-181, UG-182, UG-183, UG-184, Pratap Mungpha-li -2, Pratap Raj Mungphali, TG-37A
II	1	UG-179

from same source had fallen into different clusters as well as the same cluster contained varieties from different sources. The similar results were found by Islam et al. (2005). On considering mean of characters with respect to these two clusters, significant difference was observed for most of the traits under study (Table 4). Genotypes belonging to cluster II having higher mean values for number of mature pods plant^{-1} (6.67), dry pod yield plant^{-1} (15.67 g), kernel yield plant^{-1} (10.66 g), 100 kernel weight (60.00 g), sound mature kernel (90.33 %), biological yield plant^{-1} (42.00 g), harvest index (37.47) and oil content (41.67 %). This revealed that the genotypes from these two clusters able to produce desirable transgressive segregates for above mentioned characters upon hybridization and can provide an opportunity for selection of better genotypes in succeeding generations of groundnut breeding programmes. This enables breeder to produce genotypes with high oil content for developing countries and low oil genotypes used in confectionary

Table 4: Cluster mean values of 13 different characters of 30 genotypes

Character/ Cluster	Cluster I	Cluster II
DF	28.57	29.33
DM	100.40	105
PH	29.53	29.20
NBP	5.09	8
NMP	11.18	6.67
DPY	11.89	15.67
KYP	8.36	10.66
KW	42.83	60
SMK	88.63	90.33
SP	70.43	68
BYP	36	42.00
HI	33.35	37.47
OC	37.76	41.67

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; NBP: No. of branches plant^{-1}; NMP: No. of mature pods plant^{-1}; DPY: Dry pod yield plant^{-1}; KYP: Kernel yield plant^{-1}; KW: 100-Kernel weight; SMK: Sound mature kernel; SP: Shelling percentage; BY: Biological yield plant^{-1}; HI: Harvest index; OC: Oil Content

purposes for developed countries.

Although adequate amount of variability present among the genotypes but it was not evenly distributed so we obtained only two clusters. Average intra cluster distance observed within cluster I was 51.35 while in cluster II it was 0 because it contains only single genotype UG-179, these finding are in contrast with Verma et al. (2006), Peshattiwar et al. (2009). While considering inter cluster distances, cluster I and cluster II exhibited very high inter- cluster distance (159.68), these finding are in close agreement with Dolma et al. (2010), Zaman et al. (2010), Yadav et al. (2014) and Dhakar et al. (2017). This revealed that only one genotype under study, UG 179 significantly different from others so it is strongly advised to use this genotype in hybridization with the members of cluster I for groundnut improvement programs (Table 5).

Table 5: Average intra and inter-cluster D^2 values in 30 genotypes of groundnut

Cluster	I	II
I	51.35	159.68
II	159.68	0.00

4. Conclusion

Genotypes from cluster I and II could be used for the production of the desirable transgressive segregants with

special reference to characters like dry pod yield, 100-kernel weight, biological yield, harvest index and oil content which helps in producing better groundnut genotypes with high oil according to the demand of developing countries for oil production or low oil genotypes having high confectionary quality according to the demand in the developed countries for food purposes which ensures better future of groundnut improvement programs.

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