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Assessment of Genetic Diversity in Peanut (*Arachis hypogaea* L.) Genotypes Using Quantitative Traits by Cluster Analysis Method

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Abstract: In order to study genetic diversity of the genotypes of peanut, an experiment was carried out with 23 genotypes of peanut by using randomized complete block design with three replications in the City Astaneh Ashrafieh, North of Iran at 2010. The results of the analysis of variance showed that there was significant difference between different genotypes in term of the plant height, total number of pods, total weight of pods, 100 pods weight, 100 seed weight, biomass ($p<0.05$) total number of seeds and seed yield ($p<0.01$). It is indicated that there is diversity between studied genotypes in respect of studied quantitative characteristics. Cluster analysis by using the method of average distance between groups, set 23 genotypes in 3 separate groups. Second cluster with 7 genotypes regarding yield components with yield of 3001.04 kg h^{-1} was allocated in first place compared to other cluster. Also, second and third clusters compared to first group had most characteristics with similar average and close to each other. There was the least distance between the genotype ICGV92267 and ICGV03060 and the most genetic distance between ICGV00441 and ICGV92033, there was for we can probably use these two genotypes in breeding programs in cross breeding as parents.

Key words: Peanut, genetic diversity, cluster analysis, genotypes, cross breeding, Iran

INTRODUCTION

Diversity and selection are two major principles of each improvement program and selection has high efficiency when there is desired genetic diversity in studied characteristics.

Genetic diversity is one of basic requirements of development in plant breeding (Hallauer and Miranda, 1998). Peanut (*Arachis hypogaea* L.) is sub-species of cereals and it is an annual plant with two types standing and creeping (Khajehpour, 2007). Peanut is one of the most important oil grains which is planted because of its grains are rich in oil and protein. The oil of peanut is one of the most important plant oils in the regions where other oily plants can not grow (Saeidi-Mehrvarz, 2002). In spite of high morphological diversity in germ plasm of peanut, this diversity has not been used sufficiently in improvement programs of peanut and many available agricultural varieties has been produced usually on the basis of one or multiple common parents.

This may be due to lack of sufficient informations about morphological and agricultural characteristics of peanut (Badigannavar *et al*., 2002). So in order to exploit available diversity in germ plasm of peanut, it is necessary to evaluate its morphological and agricultural characteristics. Swamy *et al*. (2003) while comparing germ plasm of peanut observed that many characteristics like total number of pods, ripe pods and pegs in both groups were very different. Lopez *et al*. (2004) in their study, a 10 Spanish going varieties of peanut stated that lateness which is measured at the basis of the percent of ripe pods in each plant is correlated with yield and Olin's variety is a suitable line for high yield.

Sodaric (2002) studied the genotypes of soybean reported low diversity coefficients for the characteristics like seed yield in plant, the number of nodule in plant and the number of seed in plant.

Grouping genotypes at the basis of studied characteristics is one of the suitable methods for determining nearness, distance and closeness of them (Alexandra, 2005). Nadaf *et al*. (1986) used multi-variable analysis of cluster for grouping 83 genotypes of peanut from 18 countries at the basis of plant yield in a plot and 6 other agricultural characteristics that these genotypes formed 9 clusters which did not depend on grouping of their geographical region. Diversity of pod yield for 88% of total variance between clusters had been calculated. The number of complete pods, days until 50% fertilizing and 1000 seed weight were important in calculating the diversity in clusters. Sunchez *et al*. (2006) measured the number of ripe pods, seed weight, pod length, plant height, biological yield and percent of peel between 64 varieties of peanut which had been planted in two regions. They categorized varieties into 4 groups by

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cluster analysis and concluded that farming different groups was due to difference in their genotypes thus, categorizing germ plasm in case of the effect of genetic components and interaction of the genotypes of environment would be more complete. Aalami *et al.* (2007) in order to estimate the diversity of germ plasm of peanut in Iranian national plant gen bank in respect of important morphological characteristics, performed an experiment with 76 genotypes of peanut in 2002 and the results indicated high similarity between studied samples (average Euclid distance is 0.19). Sadhu and Khehra (1997) studied a series of 27 varieties of peanut for genetic diversity that the results indicated the difference between varieties and the characteristics of pod yield, length of primary stem and also number of pods per plant had the most share of diversity. For purpose, present study was performed to recognize available genetic diversity of peanut at the basis of important agricultural characteristics for development and assistance to next research projects.

MATERIALS AND METHODS

This study was performed in Astaneh Ashrafieh located in the North of Iran in crop year of 2010. This experiment was performed by using randomized complete block design with 3 replications. Plant materials included 23 samples of available genotypes collection in Iranian national plant Genbank (Table 1).

Table 1: Names of genotypes and varieties in this study

No.	Names of genotypes
1	ICGV01260
2	ICGV02312
3	ICGV92052
4	ICGV92040
5	ICGV03060
6	ICGV93095
7	ICGV93125
8	ICGV00351
9	ICGV92033
10	ICGV91155
11	ICGV93232
12	ICGV00441
13	ICGV95148
14	ICGV92267
15	ICGV99235
16	ICGV93269
17	ICGV01263
18	ICGV96177
19	ICGV92054
20	ICGV93382
21	ICGV93134
22	Chico
23	NC_2 (North Carolina 2, native variety in Astaneh Ashrafieh, North of Iran)

After ploughing and disking the peanut farm in Spring, 150 kg ha^{-1} nitrogen fertilizer from urea source, 38 kg ha^{-1} phosphorous fertilizer from potassium sulfate source were distributed in the farm and was mixed with the soil beneath the plant.

In order to supply the need of plants to calcium and sulfur, 220 kg ha^{-1} chalk was used as the mixture with the soil under the pant. Combating with weeds was performed, using glyphocyte in the edge and between blocks and manual weeding was performed between plots. Sampling of plant was done after eliminations marginal trace. In this study, 11 quantitative characteristics related with yield and yield components and morphological characteristics in each block were measured and average data were used in multi-variable statistical analysis.

The plant height, number of secondary stems and length of mid-nodule in the step of complete ripeness were measured. The characteristics of yield seed, number of seed total per plant, pod weight, pod number, 100 seeds weight, 100 pods weight, pod length and biomass were estimated after harvesting. Variance analysis was performed on genotypes used in experiment using single variable method. In order to group studied genotypes, multi-variable Method of Clustering Analysis, UPGMA based on Euclid distance and the matrix of the coefficients of un-similarity on the characteristics of yield and yield components was used since for using clustering analysis. It is necessary to determine the amount of inter-group similarity and determining a method to form clusters which have been measured at the basis of the amount of similarity. For statistical analysis of one-variable was used from SAS software. Also, for multi-variable statistical methods of clustering analysis was used from DARwin 5.1 and Mega 3.1 software.

RESULTS

Single-variable analysis: The results of variance analysis of estimated characteristics are shown in Table 2. The characteristics of number of secondary stem, pod length and length of mid-nodule have not significant difference but the difference between genotypes for characteristics of plant height, total number of pods, total weight of pods, 100 pods weight, 100 seeds weight and biomass in 5% possibility level and for characteristics of total number seeds and yield in the 1% possibility level become significant.

Cluster analysis: In order to group studied varieties in respect of quantitative characteristics related to yield and yield components and morphological characteristics, the Method of Cluster Analysis, UPGMA (average distance

Table 2: Variance analysis of components yield and yield in 23 genotypes of peanut (*Arachis hypogaea* L.)

		Mean^2										
S.O.V	df	Mid-c nodule length	Total no. of pods	Total weight of pods	Yield	100 pods weight	Total no. of seed	Plant height	No. of secondary stem	100 seeds weight	Biomass	Pod length
Block	2	0.37^{NS}	16.78^{NS}	18.75^{NS}	143.62^{NS}	154.20^{NS}	13.85^{NS}	8.56^{NS}	4.23^{NS}	448.20^{NS}	97.93^{NS}	0.038^{NS}
Genotype	22	0.45^{NS}	112.42*	78.15*	798.13**	203.37*	381.60**	39.26**	3.77^{NS}	480.51*	591.36*	0.212^{NS}
Error	44	0.36	21.55	31.08	199.19	96.19	84.13	13.15	2.46	228.50	209.99	0.125
CV (%)		9.80	3.65	6.30	8.78	5.89	10.05	13.99	10.81	6.80	7.02	12.810

^{NS}Not significant; *Significant at $p<0.05$ and **Significant at $p<0.01$

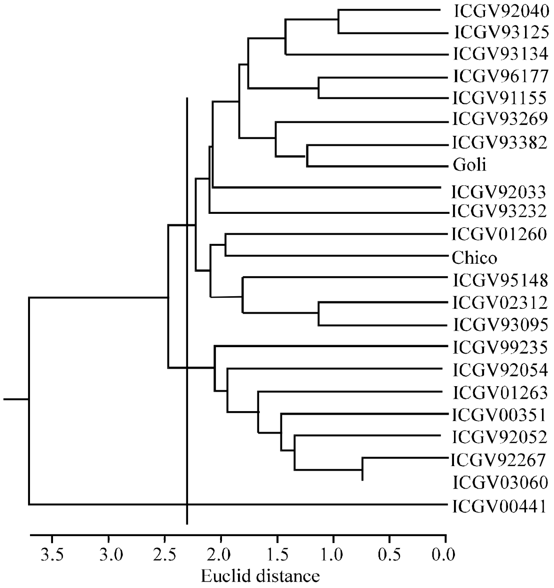

Fig. 1: Dendrogram of peanut genotypes with method of distance average between groups

between groups) based on the standard of Euclid distance was used that dendrogram section firstly divided the genotypes in the distance of 2.6-3.5 into 2 basic groups which in one, there was 1 and in another 22 genotypes but considering standard distance and calculating intra and inter-group matrix decreased the range from 2.6-2.3 distance and as a result, 23 studied genotypes were located in 3 separate groups (Fig. 1).

First cluster was the smallest and includes one variety. Second cluster includes 7 and third cluster includes 15 varieties (Table 3). To define the size of each studied characteristics in each group, the average of each group for each characteristic and its amount as compared to the average of main community for that characteristic was calculated (Table 4). First cluster was included on genotype called ICGV0041 for morphological characteristics of length of mid-nodule, plant height and number of secondary stem was in highest amount and in the light of 100 seeds weight, 100 pods weight and pod length compared to the average of other clusters had considerable preference (Table 4).

Table 3: No. of genotypes in each groups

No. of genotypes	Groups
1	1
7	2
15	3

Table 4: Comparison of clusters mean with total mean for yield components and yield of peanut (*Arachis hypogaea* L.)

	Groups			
Characteristics	1	2	3	Total mean
Mid-nodule length (cm)	3.96	2.87	3.01	3.01
Total no. of pods in plant	47.30	93.30	59.13	69.01
Total weight of pods (g m^{-2})	86.91	90.03	55.66	67.48
Yield (kg m^{-2})	2897.16	3001.04	1855.46	2249.41
100 seeds weight (g)	107.00	57.16	52.59	56.34
100 pods weight (g)	227.65	125.87	109.78	119.80
Total no. of seeds in plant	3.53	2.84	2.67	2.76
Biomass (g m^{-2})	60.50	138.72	79.42	96.64
Plant height	102.75	171.81	145.45	151.61
Pod length (cm)	90.15	61.39	57.40	69.64
No. of secondary stem in plant	10.50	7.93	7.74	7.91

Second cluster with seven genotypes in respect of the characteristics of total number of pods, total number of seeds, total weight of pods, biomass and the yield of 3001.04 kg ha^{-1} as compared to the average of other clusters was located in 1st order which this cluster had least amount in respect of characteristics of the length of mid-nodule and plant height as compared to the average of other clusters. Third cluster with 15 genotypes with the average yield of 1885.46 kg ha^{-1} as compared to other clusters had the least amount. Second and third clusters as compared to first group have most characteristics with similar average and close to each other (Table 4). Except for first cluster which has one genotype, the least diversity was observed in second cluster. Studies showed that there was least genetic distance between the varieties ICGV92267 and ICGV03060 and the highest genetic distance between the varieties ICGV00441 and ICGV92033.

DISCUSSION

The effect of genotype on seed yield was significant. Since, characteristics related to seed yield components like the 100 pods weight, total number of seeds, 100 seeds weight and biomass become significant, it seems that effect of these characteristics led to significant of seed yield. These characters can be used as determinant factors of yield in peanut. In addition, significant of the characteristics related to the yield components and yield has shown the availability of diversity between studied genotypes from the studied quantitative characteristics point of view because genotypes were different regarding growth and ripening.

In experiment performed by Singh and Kaur (1993) and Foundra *et al.* (2000) on peanut characteristics like total number of seed, 100 pods weight, 100 seeds weight and biomass have been reported as important and effective characteristics in yield and also the main characters in study of genetic and morphological diversity of peanut. Grouping genotypes at the basis of studied principles is one of the suitable ways to define their closeness, distance and nearness (Farshadfar, 2005). According to the fact that the method of average distance between groups which was done the basis of Euclid distance had divided genotypes into 3 groups but each one of groups were divided into sub-groups, sub-groups of third cluster have high diversity of intermediate ripeness, fast-ripening, resistant to dryness and dried nuts types which are distributed along third cluster but the maximum diversity in cluster is related to Spanish bunch with intermediate type of ripeness.

Perhaps, the distribution of these variants in different sub-groups of this cluster and their 100% lack of distinction was due to climatical conditions of studied region. As an example, since according to the distribution of genotype types of peanut in third cluster of intermediate ripeness type is dominant in this cluster, it seems that fast-ripening variants influenced by the conditions of region did not show the signs of fast-ripening and also other characteristics related to Virginia bunch with intermediate ripeness type have located in second cluster. In fact low diversity was seen in this cluster. Sigamani (1984) had categorized the types of Spanish, Valencia and Virginia that except for the kinds of Virginia, considerable genetic diversity was seen in other studied cases. Virginia variants previously have been selected in order to desirable breeding characters and probably for this reason, lower diversity has been observed in it as a result these variants must be considered in studies related to the prevention of epidemies of some important diseases of peanut. Dwinedi *et al.* (2001) have stated that this low diversity is due to self-fertility. Also, Badigannavar *et al.* (2002) reported relatively low genetic diversity for morphological characteristics of peanut. Second cluster was set in 1st order in respect of yield with 3001.04 kg ha^{-1} and least plant height, the length of mid-nodule and highest number of pods and total number of seeds has allocated to itself. Probably decreased mid-nodule length and plant height had led to more fertilized stype and as a result forming mor pods and producing more seeds and thus yield has been increased. Yavada *et al.* (1984) obtained positive correlation between height and the number of grains. Maiti and Wesche-Ebeling (2000) also observed positive correlations between the number of pods in plant and the number of seeds in plant.

CONCLUSION

Genotype ICGV00441 which was located separately in one cluster was different from other samples of other groups in respect of most morphological characteristics of the length of mid-nodule, plant height and the number of secondary stem. It was a reason for its separately grouping as compared to other genotypes. These studies were obtained from comparing average character related to each group total average, so that where the average of character in each group is higher than total average of community that group has more value for taking part in breeding programs as parents. Finally, genotypes of two groups with most distance from each other can be considered as the parents for crossbreeding for obtaining higher heterosis. Therefore, the genotypes ICGV00441 and ICGV92033 with most distance from each other can be used in optimal-species programs as parents in cross breeding. Overall we can conclude that there is significant genetic diversity between studied genotypes and some genotypes like ICGV99235, ICGV92054, ICGV01263 and ICGV92033 having high potential in the characters of yield and yield components can be suitable cases for use in breeding programs.

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