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Multivariate Analysis, Genetic Diversity and Phenotypic Correlation of Nineteen Exotic Groundnut Accessions

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ABSTRACT

19 Groundnut (*Arachis hypogaea L.*) genotypes received from International Crops Research Institute for Semi Arid Tropics (ICRISAT) India were evaluated in a non replicated trial and the characters were subjected to multivariate analysis to study the variability within the genotypes. The first 5 axes of the principal component analysis captured 78% of the total variability and identified yield parameters such as number of pods per plant, pod weight per plant and growth parameters such as number of branches per plant, plant spread, and pod characteristics as the characters contributing most to total variation. Phenotypic correlation analysis revealed that the yield has positive correlation with the characters such as number of pods per plant and number of branches per plant. Wards clustering method has grouped the genotypes into 3 distinct clusters. The results can be applied in order to strengthen the breeding program.

Keywords: Correlation, Diversity, Genetic, Phenotypic, Groundnut

INTRODUCTION

Groundnut (*Arachis hypogaea L.*) is one of the chief oil seed crop in Sri Lanka, belonging to the family fabaceae. Around 11609 ha are (DOA, 2013) being cultivating annually in the country, majority is cultivating during the Maha season. Groundnut seeds contain about 40-50% oil and 18% carbohydrates in addition to minerals and vitamins (Singh et *al*., 2015).

The department of Agriculture of Sri Lanka has released 05 groundnut varieties, namely Indi,Tissa, Tikiri, Walawa and ANKG1. As well as these varieties farmers used to cultivate their own landraces. Average yield in the country is about 1.89 t/ha and further improvements are needed in order to address the current issues in the sector, such as quality improvements and remedies for biotic and abiotic stresses. ICRISAT, India is the primary groundnut germplasm provider for Sri Lanka. With these valuable germplasm, a successful evaluation under local conditions is vital, as it forms the base for the crop improvement. Identification of genetic diversity in a collection of germplasm can be used in selecting parental combinations for hybridization programmes. Ability to differentiate between cultivars in respect of genetic parameters is critical for further crop improvement. Characterization and quantification of genetic diversity and information on the genetic diversity within and among closely related crop varieties is essential for a rational use of plant genetic resources (Adeoluwa, 2011 and Singh et *al*., 2015). Statistical methods of classification of genotypes is usually done by multivariate methods and these includes Principal Component Analysis (PCA) and Cluster analysis (Odewale *et al*., 2012) Therefore, the objective of the present study is to identify the genetic diversity among the set of germplasm received from ICRISAT, India and to differentiate genotypes in to different groups.

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MATERIALS AND METHODS

19 accessions received from International Crops Research Institute for the Semi- Arid Tropics, India (ICRISAT) were used for the study at Grain Legumes and Oil Crops Research and Development Center, Angunakolapelessa, Sri Lanka during 2014 yala season. 10 seeds of each accession were planted in a line of 1.5m as a non replicated trial. All the recommended agronomic practices were carried out throughout the cropping season and supplementary irrigation provided when required. Plant qualitative and quantitative characters such as height to main stem at maturity, number of Days to maturity, Plant spread, Leaflet Length, Leaflet Width, Pod Length, Pod width, Seed Width, Seed Length, Number of pods/plant, Pod weight/plant and number of branches/plant were recorded in 5 random plants according to the descriptors of oil seed crops published by plant genetic resources center, Department of Agriculture, 1995. Data were subjected to multivariate analysis, Correlation and Wards cluster analysis using the SPSS 16 statistical package.

RESULTS AND DISCUSSION

The principal component analysis (Table 1) of agronomic and reproductive characters revealed that the principal axis 1 to 10 accounted for more than 98% of the total variability observed among the groundnut lines evaluated. Axes 1, 2, 3, 4 and 5 had eigen values greater than 1 and those axes summarized around 78% of the observed variation. Among those axes 1 contributed 30% of the variation. According to Makindes (2010) previous studies on groundnut germplasm, he also found that first five axes together explain more than 70% of the total variation among the genotypes.

In the first principal axis (Table 2) number of pods/plant, pod weight/plant and number of branches/plant had contributed majority of the variation with positive

significant coefficients of 0.871, 0.806 and 0.819 respectively. Plant spread also recorded positive coefficient (0.557) which had contributed to the principal axis one. Pod characters and 100 seed weight has negatively contributed to the principle axis one.

Table 1: Eigen values and proportion of the thirteen principal components for nineteen accessions of groundnut

Axes	Eigen value		Proportion	Cumulative %
1	3.907		30.052	30.052
2	2.432		18.707	48.759
3	1.432		11.016	59.776
4	1.408		10.833	70.609
5	1.001		7.700	78.309
6	0.827		6.360	84.670
7	0.714		5.490	90.160
8	0.512		3.941	94.101
9	0.411		3.162	97.263
10	0.149		1.150	98.413
11	0.111		0.853	99.265
12	0.055		0.427	99.692
13	0.040		0.308	100.000

In the second principal axis comparatively high positive coefficients were observed pod characteristics such as 100 pod weight (0.85), pod length (0.826), and pod width (0.719). Seed width, height to main stem and pod/weight/plant had contributed negatively on the second principle axis.

The third component axis had its largest co-efficient values in 100 seed weight (0.889) while height to main stem (-0.873) was shown highly negative contribution.

In the fourth principle component axis seed length (0.797) has contributed mainly for the variation and Days to maturity (0.847) had more weight in the principle component five.

Table 2: Principle component analysis for thirteen agronomic traits associated with nineteen accessions of groundnut

	PC1	PC2	PC3	PC4	PC5
Eigen Values	3.907	2.432	1.432	1.408	1.001
Proportion of variance	0.30	0.18	0.11	0.108	0.077
Cumulative Proportion of Variance	0.30	0.49	0.60	0.71	0.78
100 pod weight (g)	.067	.850	.205	-.049	.125
Days to maturity	.080	.174	.239	-.013	.847
Height to main stem (cm)	.019	-.281	-.873	.009	-.209
Plant spread	.557	.232	-.400	-.057	-.450
Leaflet width	-.055	-.568	.090	.282	.070
Pod length	-.269	.826	.302	.052	.044
Pod width	-.251	.719	.160	.078	.473
Seed width	.324	.137	.048	-.787	-.056
Seed length	.402	-.011	-.037	.797	-.061
No: of pods/plant	.871	-.131	-.245	.131	.016
Pod weight/plant	.806	-.270	-.210	.005	.118
No: branches/plant	.819	.108	.419	-.172	-.073
100 seed weight	-.167	.115	.889	-.055	-.097

Sample characters are generally inter correlated to varying degree, hence not all principal components are needed to summarize the data accurately (Jonah, 2014). Accordingly in this study, the first 5 principal components have explained 78% of the total variability observed. It showed that genetic variability showed more positive on characters such as 100 pod weight, 100 seed weight, number of pods/plant and number of branches/plant. Kumar (2010) findings also revealed that only first five of the fourteen principal components accounted 76% of the total variation among genotypes.

According to the phenotypic correlation analysis (Table 4), Pod weight per plant had high positive correlation (0.769) with number of pods per plant. Number of pods per plant also showed significant positive correlation (0.567) with number of branches per plant. Makinde (2013) also observed similar results in his study with groundnut, where yield per plant had positive correlation with number of pods per plant and number of branches per plant.100 seed weight and pod characteristics such as pod length and pod width shown positive significant correlation of 0.66 and 0.67 respectively. Accordingly pod length and pod width together had high positive correlation (0.75). Plant height to main stem was negatively correlated (-0.487) with pod length. When considering 100 seed weight, it was significantly but negatively correlated with the plant height to main stem (-.69) and leaflet length (-.47).

When considering results of principle component analysis and phenotypic correlation analysis, the characters with high positive loadings in same principle component has been getting a high significant correlation. In this study, the first principle component had high positive loadings on characters like number of pod/plant and pod weight/plant. These two characters has high positive correlation value (0.769**) according to the correlation analysis.

In principle component two, high positive loading was on 100 seed weight and high negative correlation was on height to main stem. The correlation analysis conform that result, as these two characters had high negative correlation (-.69**). Similar trend was observed in other characters which having significant correlation coefficients. According to Lezzoni and Pritts (1991), variables, which a have high positive loading on a PC, are positively inter-correlated as a group. Variables having a high negative loading are also correlated as a group, however, they are negatively correlated with those variables having positive loading.

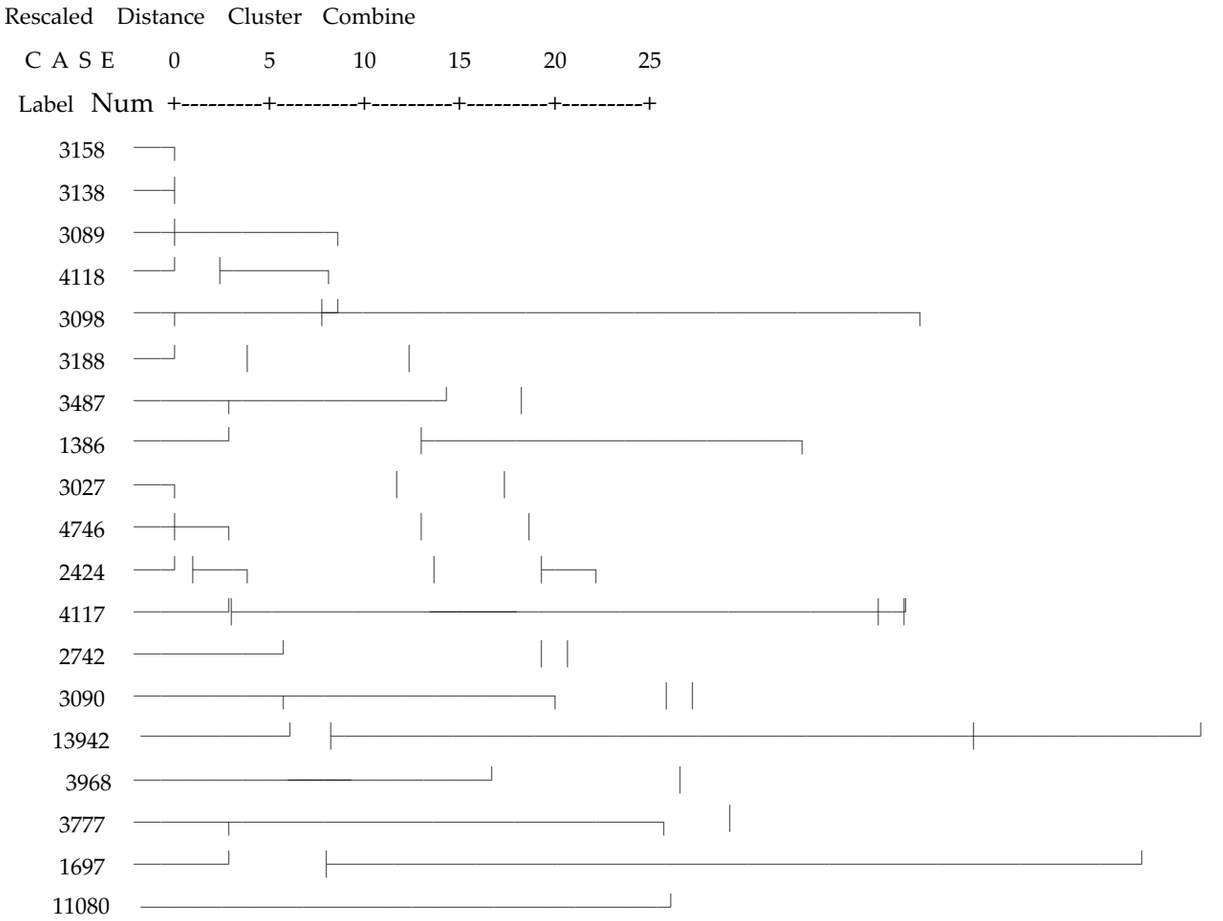

Fig. 1: The Dendrogram showing 19 genotypes of groundnut derived from Hierarchical cluster analysis (Wards method)

Wards hierarchical cluster analysis based on ten principal component scores resulted 3 clusters in the rescaled distance of 20 (Fig.1). The main cluster consists of 13 accessions and the other two clusters only include 3 accessions. The genotypes of the common eco-geographic origin or same location included into different clusters without forming a single cluster indicated that geographic diversity was not related to genetic diversity (Zaman *et al.*, 2010).Even though all these accessions were from ICRISAT; fair amount of diversity can be found. Maximum cluster distance can be observed between the accessions in cluster 1(ICGV3158, ICGV 3138, ICGV 3089, ICGV 4118) and the accessions in the cluster 3 (ICGV 3777, ICGV 1697, ICGV 11080). May be these genotypes can be chosen in hybridization program for getting the most variability. Even by visual look, as listed in the table 3; these accessions have fair amount of diversity. It can clearly see with the cluster analysis results where three distinct clusters have been formed.

Table 3: Accession number, and some qualitative characteristics of the groundnut germplasm used in the study

Accession number	Growth habit	Stem branching pattern	Stem pigmentation of mature plant	Peg pigmentation	Pod reticulation	Seed color	Number of seeds/pod
ICGV 4118	Decumbent-2	alternate	present	present	prominent	Pink	1/2
ICGV 3089	erect	alternate	present	present	prominent	Pink	2
ICGV 3090	erect	alternate	absent	present	moderate	Pink	1/2
ICGV 3777	Decumbent-2	alternate	present	present	slight	Dark puple	2/3
ICGV 3158	erect	alternate	absent	present	moderate	Pink	1/2
ICGV 1697	erect	alternate	absent	present	very prominent	Pink	2/3
ICGV 3027	Decumbent-2	alternate	present	present	moderate	Pink	1/2
ICGV 4117	erect	sequential	present	present	prominent	Pink	1/2
ICGV 3968	Decumbent-2	alternate	present	present	moderate	Pink	1/2
ICGV 4746	Decumbent-3	alternate	present	present	prominent	Light pink	1/2
ICGV 11080	erect	alternate	absent	absent	very prominent	Pink	3/4
ICGV 3138	erect	Irregular with flowers on main stem	absent	present	prominent	Pink	1/2
ICGV 3098	Decumbent-3	Irregular with flowers on main stem	present	present	moderate	Pink	2
ICGV 2742	erect	Irregular with flowers on main stem	present	present	slight	Pink	1/2
ICGV 13942	Decumbent-2	alternate	present	present	prominent	Pink	2/3
ICGV 3487	erect	Irregular with flowers on main stem	present	present	moderate	Light red	2/3
ICGV 3188	Decumbent-3	alternate	absent	absent	prominent	Pink	2
ICGV 2424	Decumbent-3	alternate	absent	present	moderate	Pink	2/3
ICGV 1386	Decumbent-2	Irregular with flowers on main stem	absent	present	moderate	Pink	2

Table 4: Simple phenotypic correlation among 14 traits of groundnut genotypes

	100 PW	DTM	HtMS	PS	LL	LW	PL	PW	SW	SL	NPP	PWP	NBP	100 sw
100 PW		.250	-.395	.111	-.271	-.261	.666**	.674**	.223	-0.051	-0.084	-0.289	0.239	.25
DTM			-.179	-.086	-.372	-.051	.162	.336	-.022	0.004	-0.082	0.048	0.043	.36
HtMS				.424	.510*	.213	-.487*	-.435	.032	0.118	0.257	0.219	-0.392	-.69**
PS					.303	-.107	-.056	-.371	.182	0.115	0.404	0.398	0.381	-.28
LL						.337	-.198	-.379	-.184	0.203	0.205	0.085	-0.297	-.47*
LW							-.326	-.248	-.197	0.125	0.054	0.048	-0.112	.03
PL								.753**	.006	-0.126	-0.428	-0.396	0.042	.43
PW									-.005	-0.103	-0.232	-0.33	-0.123	.17
SW										-0.319	0.166	0.176	0.355	.11
SL											0.429	0.29	0.117	-.08
NPP												0.769**	0.567*	-.43
PWP													0.448	-.34
NBP														.19

100 PW= 100 pod weight, DTM= Days to maturity, HtMS= height to main stem, PS= Plant spread, LL= Leaflet Length, LW= Leaflet Width, PL= Pod Length, PW= Pod width, SW=Seed Width, SL= Seed Length, NPP=No:of pods/plant, PWP=Pod weight/plant, 100 Sw= 100seed weight, NBP=No;of branches/plant

** Correlation significant at the 0.01 level

* Correlation significant at the 0.05 level

Table 5: Mean values of characters of 19 groundnut genotypes in 3 clusters

Cluster	Number of genotypes	DTM	HM (cm)	PS (cm)	100PW (g)	100 SW(g)	PL mm)	PW (mm)	NBP	NPP	PWP
1	13	110	31.8	56.6	76.2	38.7	26.2	4.1	5.9	27	16.2
2	03	110	24.7	68.6	96.6	44	28.1	4.3	9.3	46	30.9
3	03	113	33.9	68.3	98	35.3	33.7	5.3	5.6	28	22.1

100 PW= 100 pod weight, DTM= Days to maturity, HM= height to main stem, PS= Plant spread, PL= Pod Length, PW= Pod width, NPP=No: of pods/plant, PWP= Pod weight/plant, NBP= No: of branches/plant, 100 Sw= 100seed weight,

The maximum number of pods per plant was recorded in the Cluster 2 (Table 4). Also it has recorded the highest number of branches per plant (9.3) and highest pod weight per plant. Cluster 1 and 3 recorded pod weight per plant values as 16.2 and 22.1 respectively. Cluster 2 recorded highest mean values for 100 seed weight (44g). Mean value for number of days to maturity in these three clusters was ranged between 110 to 113 days (Table 5).

CONCLUSIONS

The principal component analysis can be successfully used in describing the variability of groundnut genotypes as it has captured considerable variation within the genotypes in higher number of axes. In this technique the main characters which considered in describing the total variation were number of pods/plant, pod weight/plant, number of branches/plant, pod characteristics and 100 seed weight. The correlation analysis revealed that characters such as number of pod/plant and number of branches/plant can be considered in selecting for the yield performance of groundnut. 3 clusters were identified where considerable amount of diversity was observed within the genotypes used for the study.

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