Karnataka J. Agric. Sci., 27 (2): (219-221) 2014

Genetic diversity analysis based on nutritional, oil quality and yield component traits in mini core collection of groundnut (*Arachis hypogaea* L.)*

Groundnut (*Arachis hypogaea* L.) is an annual legume, grown primarily for high quality edible oil and easily digestible protein in its seeds. It is cultivated in 109 countries, in tropical, sub-tropical, and warm temperate regions of the world. In India during 2010-11 it was grown on 4.93 million ha with an estimated total production of 5.64 million tonnes (groundnuts in shell) and an average productivity of 1144 kg/ ha (FAO 2011).

The quantity and quality of edible oil or various food products of groundnut depends on the total oil and protein content in seeds and fatty acid composition of the commercially grown cultivars. The evaluation and screening of germplasm and wild species collections in US indicated low genetic variability for oil, protein content and fatty acid composition (Hammond *et al*., 1997). A total collection of 15445 accessions, representing global germplasm, are maintained at ICRISAT, Patencheru, Andhra Pradesh, India. When the size of the collection is too large, it becomes unmanageable to evaluate and identify the diverse and useful ones. A very small proportion of these large germplasm accessions are being used in groundnut breeding programmes. Alternatively, after constructing core collection of these world germplasm, a mini core collection (184 accessions) has been developed using taxonomical, geographical and morphological descriptors (Upadhyaya, 2003). The mini core collection represented variability present in core collection that represents variability of the entire germplasm collection. Evaluation of mini core collection has resulted in identification of diverse accessions with drought tolerance, high yield potential, high shelling out turn and 100-seed weight (Upadhyaya *et al*., 2005). But efforts towards breeding for improved oil quality is meager probably because of unavailability of diverse genetic sources for nutritional and oil quality traits. Due to the paucity of genetic diversity in the available germplasm and cultivars, only few of them are frequently used in groundnut improvement programmes. In the USA, the cultivar Dixie Giant was a germplasm source in all pedigree of runner market-type peanuts and Small White Spanish-1 cultivar in 90 per cent or more pedigrees. These two lines contributed nearly 50 per cent of the germplasm of runner cultivars. Chico is the most extensively used source of earliness in several breeding programs. It has been used 1180 times as a parent in developing early maturity lines at ICRISAT from1976 to 2002 (Upadhyaya *et al*., 2005). In US, a natural mutant for high oleic acid, F435 was the only one source that could be used for improving oil quality traits in groundnut, and it has been patented too (Norden *et al*., 1987). This has resulted in narrowing of genetic base of the cultivated groundnut. So there is an urgent need to identify diverse source, as a parent for oil quality improvement in groundnut.

The mini core consisted of 184 accessions of groundnut germplasm lines obtained from ICRISAT Patancheru, Hyderabad and three breeding lines (R 9227, MN 1-28 and MN 1-35) and four cultivars (GPBD 4, TAG 24, JL 24 and M 28-2) were evaluated in randomised complete block design with two replications in the 2008 rainy and 2008-09 post rainy seasons at UAS Dharwad in vertisols. Each genotype was sown in single line of 2.5 m length with spacing of 30 cm inter row and 10 cm inter plant. Data were recorded on a plot basis for days to 50 per cent flowering, pod yield (kg/ha), shelling percentage and 100- seed weight (g). The pod from entire plot was harvested and immature pods were removed, air dried, cleaned and weighed. The yield of five tagged plants was added to determine total plot yield. Matured pod sample of 200 g was used to estimate shelling percentage.

$$\text{Shelling per cent} = \frac{\text{Kernel weight (g)}}{\text{Pod weight (g)}} \times 100$$

A random sample of 100 seeds was used to record 100 seed weight and protein content, oil content and fatty acid composition were measured from seed sample drawn from each genotype with Near Infra Red Spectroscopy (Misra *et al*., 2000). D^2 analysis was carried out with data on 11 economic traits. A generalized distance (D^2) was calculated for each pair of genotypes using Mahalanobis (1936) D^2 - statistics.

The extent of contribution of each character to total diversity of mini core collection is presented in Table 1. The oleic acid ranked first (5936 times out of 19073 total numbers of combinations) and contributed 30.75 per cent to divergence of genotypes. This was followed by protein content which ranked first (5556 times out of 19073 total numbers of combinations) and contributed 28.78 per cent to divergence. Hence, oleic acid and protein content are the two major contributors towards divergence of genotypes and together they contributed 59.53 per cent towards diversity. Contributions from remaining traits to diversity were minor.

A total of 15 clusters were formed based on D^2 statistics, of which 12 clusters were solitary with single genotype. The formation of such large number of distinct solitary clusters may be due to intensive natural or human selection for diverse adaptive gene complex. The cluster I was the large with 100 germplasm accessions followed by cluster II and VII with 72 and 12 germplasm accessions, respectively (Table 2). The germplasm accessions originating from different countries were clustered randomly irrespective of their geographical origin. From this, it was

Table 1. Rank and per cent contribution of 11 quantitative traits towards diversity of groundnut in mini core collection

Source	Times Ranked 1st	Contribution (%)
Days to 50% flowering	944	4.89
Plant height (cm)	2842	14.72
Number of pods	216	1.12
100 seed weight	773	4.00
Shelling per cent	133	0.70
Kernel yield (g/plant)	160	1.03
Pod yield (g/plant)	170	1.88
Protein	5556	28.78
Oil	1541	7.98
Oleic acid	5936	30.75
Linoleic acid	802	4.15

*Part of Ph. D. thesis submitted by the first author to the University of Agricultural Sciences Dharwad - 580 005, India.

evident that geographic diversity was not a reasonable index of genetic diversity and Mahalnobis's D^2 analysis of quantitative traits including quality traits is a powerful tool for measuring genetic divergence amongst the material chosen, which could be even from the same geographic origin. Thus, geographic diversity, though important, may not be the only factor in determining genetic divergence and the factor other than geographic diversity such as genetic drift, selection pressure and environment may be responsible for differential grouping of genotypes.

Majority of the Spanish bunch accessions were grouped in cluster I that was relatively low in oleic acid content and high in protein content. Majority of the Virginia types with relatively

Table 2. Distribution of groundnut germplasm of minicore collections into different clusters

Cluster No.	No. of genotypes	ICG number of genotype
I	100	ICG434, ICG12988, ICG1137, ICG1711, ICG3421, ICG1519, ICG4684, ICG6236, ICG9249, ICG3102, ICG9507, ICG7963, ICG13491, ICG5236, ICG12879, ICG11687, ICG81, ICG3240, ICG14118, ICG9157, ICG4750, ICG4729, ICG3746, ICG1973, ICG5779, ICG2106, ICG13603, ICG11109, ICG334, ICG15042, ICG6703, ICG5195, ICG7906, ICG5494, ICG9809, ICG10384, ICG4716, ICG4538, ICG14466, ICG11515, ICG3343, ICG2019, ICG36, ICG626, ICG12921, ICG11249, ICG3584, ICG332, ICG297, JL24, GPBD4, ICG10554, ICG12189, ICG11651, ICG10092 ICG7969, ICG14985, ICG6402, ICG10474, ICG4543, ICG8567, ICG4911, ICG6407, ICG6888, ICG111, ICG2857 ICG13982, ICG14705, TAG24, ICG4670, ICG5827, ICG397, ICG14710, ICG7153, ICG13941, ICG7000 ICG10566, ICG8083, ICG11855, ICG14127, ICG6654, ICG8760, ICG118, ICG11322, ICG4527, ICG9961, ICG5891, ICG13723, ICG532, ICG9666, ICG76, ICG4389, ICG163, ICG13787, M28-2, ICG9777, ICG10036, ICG12682, ICG513, ICG11219.
II	72	ICG1415, ICG14523, ICG11144, ICG14106, ICG15309, ICG2738, ICG13856, ICG5609, ICG6201, ICG10565, ICG4955, ICG1142, ICG14630, ICG3673, ICG8517, ICG115, ICG13858, ICG1399, ICG188, ICG3681, ICG442, ICG4998, ICG12370, ICG7181, ICG12000, ICG3992, ICG3775, ICG2511, ICG4598, ICG10479, MN1-28, ICG14482, ICG4746, MN1-35, ICG14475, ICG4412, ICG9842, ICG6667, ICG5327, ICG12672, ICG9315, ICG15287, ICG8106, ICG11457, ICG14008, ICG12276, ICG5221, R9227, ICG11862, ICG3027, ICG12697, ICG13942, ICG3053, ICG4343, ICG8285, ICG5663, ICG15190, ICG721, ICG4156, ICG1668, ICG6057, ICG6892, ICG2772 , ICG5475, ICG875, ICG10185, ICG928, ICG1274, ICG8490, ICG13099, ICG9905, ICG7190.
III	1	ICG5662
IV	1	ICG6813
V	1	ICG2773
VI	1	ICG9037
VII	12	ICG862, ICG2925, ICG14482, ICG11088, ICG6022, ICG15419, ICG12625, ICG11426, ICG5286, ICG2381, ICG2777, ICG6913
VIII	1	ICG5745
IX	1	ICG1656-M-13
X	1	ICG6646
XI	1	ICG6766
XII	1	ICG6275
XIII	1	ICG9418
XIV	1	ICG7243
XV	1	ICG10890

Table 3. Cluster mean of 11 quantitative traits of groundnut in minicore collection

Cluster Means	Days to 50% flowering	Plant height (cm)	No. of pods	Test weight	Shelling per cent	Kernel yield (g/plant)	Pod yield (g/plant)	Protein %	Oil %	Oleic acid %	Linoleic acid %
Cluster I	34.58	36.2	21.44	45.42	70.34	13.86	19.39	27.60	46.29	45.18	33.13
Cluster II	36.15	36.88	18.31	48.38	68.73	12.04	17.31	19.14	46.33	52.50	27.93
Cluster III	39.75	34.13	16.00	63.75	72.75	12.33	16.81	26.91	44.13	58.11	22.72
Cluster IV	38.50	26.00	17.38	36.38	73.25	9.40	12.82	22.44	42.20	48.86	30.39
Cluster V	36.75	24.50	16.25	38.50	77.75	11.68	15.01	23.58	42.98	53.67	26.08
Cluster VI	39.25	26.00	16.63	36.38	72.13	7.38	10.14	25.88	41.13	52.58	28.51
Cluster VII	36.96	31.67	16.47	49.94	63.20	15.88	23.86	17.55	43.28	62.84	20.97
Cluster VIII	40.25	25.38	16.25	55.25	67.75	11.14	16.11	26.76	45.18	63.33	18.87
Cluster IX	38.75	42.88	17.00	70.38	72.75	12.38	17.02	26.51	47.07	56.91	23.85
Cluster X	32.75	45.25	18.75	60.63	71.75	24.33	33.95	25.05	43.83	60.57	22.54
Cluster XI	41.25	43.88	15.75	59.38	65.00	8.62	13.13	22.61	47.88	62.93	18.08
Cluster XII	31.75	46.25	14.25	27.38	74.75	10.88	14.41	20.25	44.74	61.56	20.03
Cluster XIII	34.00	36.38	20.38	42.13	72.25	13.24	18.19	19.66	45.34	33.60	43.74
Cluster XIV	37.25	30.25	14.88	52.00	56.00	13.30	35.97	24.60	42.89	57.70	24.03
Cluster XV	33.00	18.38	11.50	28.50	51.13	7.59	12.60	15.77	47.75	42.36	36.62

Table 4. Intra and inter cluster distance of mini core collection

Cluster Distances	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV
Cluster I	5.73														
Cluster II	9.24	7													
Cluster III	7.37	8.2	0												
Cluster IV	7.57	8.31	6.77	0											
Cluster V	7.52	8.14	6.07	2.57	0										
Cluster VI	7.69	9.21	6.44	2.77	3.35	0									
Cluster VII	12.05	8.7	9.36	9.56	9.05	9.97	7.74								
Cluster VIII	9.35	8.94	4.5	7.33	5.67	6.73	8.88	0							
Cluster IX	7.89	7.99	4.1	9.56	9.01	9.52	10.16	7.09	0						
Cluster X	8.55	8.56	6.9	10.09	9.55	9.88	9.33	9.37	6.15	0					
Cluster XI	10.76	8.24	7.23	11.01	10.25	11.27	9.85	7.64	5.33	9.12	0				
Cluster XII	10.02	7.99	10.06	9.92	9.25	10.4	9.54	10.54	9.47	8.03	8.4	0			
Cluster XIII	7.62	8.76	10.39	7.91	9.05	8.97	12.02	12.33	10.35	10.26	12.56	10.56	0		
Cluster XIV	8.77	8.77	7.31	7.63	7.01	7.63	9.81	7.62	8.44	9.08	9.84	9.96	9.69	0	
Cluster XV	11.4	9.57	12.18	8.67	8.39	9.88	10.54	10.8	13.23	13.42	13.15	11.36	9.25	10.53	0

higher oleic acid content were grouped in cluster II (Table 2). This pattern supported the fact that oleic acid content contributed most for genetic divergence.

The germplasm accession included in cluster I (Table 3) had more number of pods per plant with high protein content. Cluster IX with control Virginia runner cultivar (ICG 1656/M-13) had high test weight, whereas, shelling percentage was high in germplasm accession ICG 2773 grouped in cluster V. Higher kernel yield was recorded by germplasm accession ICG 6646 and highest pod yield was recorded in germplasm accession ICG 7243 that were grouped clusters X and XIV respectively. ICG 2381 with high oleic acid and low linoleic acid content was grouped in cluster VII. The reports of the earlier works have indicated that ratio of oleic acid to linoleic acid matters a lot from the point of both oxidative stability and nutritional value (Lopez *et al*., 2001). With respect to these aspects germplasm accession grouped in different clusters with desired nutritional and oil quality and yield component traits can be selected. For increased oleic acid content germplasm accessions, *viz*.ICG862, ICG2925, ICG14482, ICG11426, ICG5286, ICG2381, ICG2777, ICG6913, ICG6766, ICG5475 of spp. *hypogaea* and ICG11088, ICG6022, ICG15419, ICG12625, ICG6646, ICG6275 of spp. *fastigiata* can be utilized in further oil quality improvement program in groundnut.

Cluster VII had maximum intra cluster distance followed by cluster II and cluster I indicating wide genetic divergence among the constituent germplasm accessions (Table 4). Inter cluster distance was maximum between cluster X and cluster XV, followed by cluster IX and XV, XI and XV, XI and XIII. Hence, the germplasm accessions included in the cluster IV, V, VI, IX, X, XI, XIII and XV, *i.e*., ICG 6813, ICG 2773, ICG 9037, ICG 156, ICG 6646, ICG 6766, ICG 6275, M-13 may be chosen for effective hybridization program that would result in wide spectrum of variability, especially for oil quality traits to operate effective selection in segregating generation.

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(Received: August, 2011 ; Accepted: June, 2014)

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