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Research Article

CAPTURING GENETIC DIVERSITY IN GENOMIC SELECTION PANEL OF GROUNDNUT FOR FOLIAR DISEASE RESISTANCE, YIELD AND NUTRITIONAL QUALITY TRAITS

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Abstract- Diversity among the genotypes for important target traits is essential to achieve crop improvement goals. A set of 340 groundnut genotypes included in Genomic Selection Panel (GSP) was evaluated at disease hotspot location to capture genetic diversity for resistance to foliar fungal diseases, yield and nutritional quality traits. The results revealed significant genotypic variation for all the traits under study. Cluster analysis based on phenotypic data of 19 traits grouped 340 genotypes into 15 clusters. The inter-cluster distance was high between clusters XIV and XV (894.73) while the intra-cluster distance was high for cluster XIII (120.21). Maximum contribution towards total divergence was by hundred kernel mass (24.42%), followed by days to maturity (15.95%), disease severity scores of rust (9.18%) at 90 DAS, plant height (8.87%) and disease severity scores of late leaf spot (7.37%) at 90 DAS. The performance of different botanical varieties revealed that var *vulgaris* (Spanish bunch) had high yield potential; var *peruviana* had an early maturity and var *hypogaea* (Virginia runner) had high Oleic/Linoleic acid ratio. A total of 50 genotypes identified resistant against both the diseases, of which 36 including 25 from ssp. *fastigiata* var *vulgaris* and 11 from ssp. *hypogaea* var *hypogaea* were advance breeding line that can be used in breeding program without tedious efforts of pre-breeding. Pod yield of resistant advance breeding lines varied from 1230 to 3560 kg/ha. The genotypes ICGVs 01274, 01361, 03043,05155, 05163, 06142, 07120 and 07235 recorded pod yield ≥ 2500 kg/ha with the disease severity score ≤ 3 for both the diseases. The genotypes ICGV 05155 (101 days) and ICGV 86699 (103 days) reported early maturing with disease severity score ≤ 3 for both the diseases are suggested to use in breeding program to combine diseases resistance with early maturity along with high pod yield potential.

Keywords- Genetic diversity, Foliar disease resistance, Multivariate analysis, Clustering, Peanut.

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Introduction

Groundnut (*Arachis hypogaea* L.) is a grain legume and oilseed, presently cultivated in more than 100 countries throughout tropical, subtropical and warm temperate regions of the world with an annual production and productivity of 42.32 m tons and 1654 kg/ha nuts-in-shell, respectively [1]. In some countries such as the USA and Europe, it is widely used as a food source while in developing countries it is used as food as well as oil extraction. Groundnut belongs to the genus *Arachis* which has 80 described species, grouped into nine sections based onthe morphology, geographic distribution and crossability [2, 3]. Except for *A. hypogaea* and *A. monticola* in Section *Arachis*and certain species in Section *Rhizomatosae* which are tetraploids (2n=4x=40), all the remaining species are diploids with 2n=2x=20 or 2n=2x=18 genome constitution [3].

Cultivated groundnut is believed to have developed from a single hybridization event between two of its diploid wild progenitors *A. duranensis*(contributor of "A" genome), and *A. ipaensis* (contributor of "B" genome) followed by polyploidization [4]. On the basis of morphological features, crossability and seed protein electrophoretic profiles, two subspecies (ssp.), fastigiated Waldron and ssp. *hypogaea* Krap. Rig were distinguished by Krapovickas and Gregory (1994) [2]. The ssp. *fastigiata* contains four (*vulgaris*, *fastigiata*, *peruviana* and *aequatoriana*), where as ssp. *hypogaea* contain two botanical varieties (*hypogaea* and *hirsute*) with different expression in plant, pod and seed characteristics[2].

Groundnut suffers from several diseases, which causes wide fluctuations in annual production and productivity, particularly in the rainfed condition that cover about 80% of total groundnut area in the country [5]. The yield losses in groundnut due to two major foliar fungal diseases *viz.,* late leaf spot (LLS) (*Phaeoisariopsis personata* Berk and Curt) and rust (*Puccinia arachidis* Speg.) can vary from 50-70%, and also affects the quality of the produce[6]. Beside yield, changes in kernel mass, total oil and protein contents and fatty acid composition are common due to both the diseases [7].

Groundnut kernels are good source of vegetable oil(40–60%), protein (20–40%) and carbohydrates (10–20%). Its 100 g of kernels provides 567 kcal of energy (USDA nutrient database). Beside these, it also contains Vitamin E, many important B-complex groups of thiamin, pantothenic acid, vitamin B-6, foliates, niacin and antioxidants like p-coumaric acid and resveratrol [8].Groundnut oil has 45-50% monounsaturated fatty acids, 30-35% polyunsaturated fatty acids and 17-18% saturated fatty acids [9]. Groundnut kernels with high monounsaturated fatty acid(Oleic acid) offer's remarkable health benefits to consumers; longer shelf life of oil and food products to processing industries and enhances profitability to groundnut farmers, leading to increased demand of groundnut cultivars with the high Oleic trait. For oil purpose, cultivars with high oil content and high Oleic/ Linoleic acid (O/L) ratio are preferred, whereas, for confectionary purpose cultivars with low oil content, high O/L ratio and high protein content are preferred. Several efforts were made in the past to screen germplasm to identify source of foliar disease resistant in groundnut for use in breeding program across the world

[10-13]. However, most of the identified resistant sources belonged either to Valencia landraces or interspecific derivatives of Virginia with several undesirable features like poor adaptation, reticulated, thick shell, highly constricted, beaked pods and late maturity that are commercially unacceptable [14]. Finding the durable source of foliar disease resistance along with desired pod and kernel features, and nutritional quality traits in different botanical groups is very important. Genetic variability is of greater interest to the plant breeder as it plays a vital role in framing a successful breeding program to achieve desired genetic gain. The cross involving genetically diverse parentsis likely to produce more variability in the segregating generations. Therefore, genetic diversity in Genomic Selection Panel (GSP) was assessed for disease resistance, yield and nutritional quality traits to enable identification of suitable genotypes for use in breeding.

Materials and Methods

A set of 340 diverse groundnut genotypes called GSP representing collection from 21 countries. Of these 51 genotypes representing 20 countries whereas 289 genotypes bread/originated at 11 breeding center across India with a major contribution of 189 genotypes by International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India. The GSP included genotypes from all six botanical varieties of cultivated groundnut *viz.*, *vulgaris* (212), *fastigiata* (10), *peruviana* (4), *aequatoriana* (1), *hypogaea* (111), *hirsuta* (1) and a single genotype belongs to unknown botanical type. The GSP was evaluated under field condition in hotspot location at Coconut Research Station, Aliyarnagar, Tamil Nadu, India ($10^0$29' N, $76^0$58' E, 288 m MSL) to assess genetic diversity for two major foliar diseases *i.e.,* rust and LLS, yield and nutritional quality traits during the rainy season of 2015. The trial was planted in Alpha Lattice Design (incomplete block design) with two replications; each replication was divided into 20 equal sized blocks with 17 genotypes in each to reduce intra-block variation and to maintain homogeneity in the trial. Each genotype was planted in a single row of four-meter length with inter and intra-row spacing of 30 and 10 cm, respectively. The trial was conducted under natural disease pressure in the disease-screening nursery to evaluate the reaction of genotypes against rust and LLS along with yield and nutritional quality traits. To ensure uniform disease pressure during crop growth stage, infector rows of a highly susceptible cultivar TMV 2 was planted around and in between the experimental plot. The genotypes were evaluated for LLS and rust through visual screening observation and a modified 9 point scale as given by Subrahmanyam *et al.,* (1995) [15]. A disease score of 1 indicates resistance with no or very little infection, while a score of 9 represents >80% leaves severely infected and defoliated in the case of LLS, whereas burning like appearance in the case of rust. Scoring of genotypes for rust and LLS was carried out at three different stages of crop growth at 15 days interval *viz.,* 75, 90 and 105 days after sowing (DAS). Observation were also recorded on 10 yield and its contributing traits (days to 50% flowering, number of primary branches, plant height, number of mature pods per plant, pod yield per plant, kernel yield per plant, shelling percent, hundred kernel mass, days to maturity, pod yield per hectare) and seven nutritional quality traits (oil content, protein content, Oleic acid, linoleic acid, palmitic acid, stearic acid, O/L ratio). Data on yield and its contributing traits were recorded from five randomly selected plants from each replication. Phenotyping for nutritional quality traits *i.e.,* oil and protein content, and fatty acid composition was done using near-infrared reflectance spectroscopy (NIRS Systems model XDS monochromator, FOSS Analytical AB, Sweden, Denmark). Calibration equations were developed in the groundnut breeding lab at ICRISAT and validated for the estimation of oil content, protein content and fatty acid composition in whole seeds of groundnut (Unpublished data). Standard agronomic management practices were followed to raise a good crop with optimum plant population. Protection was taken against insects whereas no protection measure applied to control foliar fungal diseases.

Analysis of variance was done using general linear mixed model (GLM) through proc glm function of SAS version 9.2 [16]. Best linear unbiased predictions (BLUPs) or adjusted means were estimated for each genotype for every trait except disease severity scores of rust and LLS because higher severity score among both the replications was considered as the final score of genotype. Genetic distance among the genotype was calculated using Mahalanobis's D^2 statistics described by Rao (1952) [17]. Clustering of genotypes into different clusters was done using Mahalanobis Euclidian distance [18] following Tochers's method through Window stats version 9.1.

Results and Discussion

The analysis of variance revealed significant ($P<0.001$) difference among the genotypes for all the observed traits. The magnitude of D^2 values suggested that there was considerable diversity in the GSP for disease resistance, yield and nutritional traits. The range of variation allowed grouping of 340 genotypes into 15 clusters [Table-1].

Table-1 *Distribution of 340 genotypes of Genomic Selection Panel into different clusters*

Cluster	Cluster size	Genotypes
Cluster 1	163	ICGs 10053, 10185, 10701, 11088, 111, 11322, 11337, 11426, 11651, 12370, 12509, 12879, 14705, 14466, 14834, 14985, 15190, 15415, 1668, 1834, 2031, 1973, 2106, 2773, 2857, 3027, 3102, 3140, 3312, 3343, 3421, 3673, 434, 4343, 4527, 4729, 532, 5663, 8285, 875, 9315, 9507, 9961, ICGS 11, ICGS 44, ICGVs 00321, 00343, 00349, 00350, 00351, 00387, 01060, 01124, 01265, 01464, 02022, 02038, 02125, 02144, 02189, 02194, 02206, 02271, 02286, 02287, 02317, 02446, 03056, 03136, 03397, 03184, 03398, 04018, 04044, 04087, 04124, 04149, 05036, 06040, 06049, 06347, 06431, 07023, 07166, 07210, 07217, 07273, 09112, 13238, 13242, 13241, 13245, 86011, 86015, 86072, 86143, 86325, 86699, 87160, 87187, 87354, 87378, 87921, 88438, 89104, 90320, 91114, 91116, 92195, 92267, 93216, 93280, 93437, 93470, 93920, 94118, 94361, 95058, 95070, 95377, 95469, 96466, 97092, 97128, 97182, 97183, 97232, 97261, 97262, 98163, 98294, 99051, 99181, J 11, JL 24, Mutant 3, Somnath, SPS 10 , SPS 2, SPS 6, SPS 7, TAG 24, TDG 10, TDG 13, TDG 14, TG 39, 24 × 37-2275, 26 × 27-164, 26 × 37-IV- 9IR, 26 M- 119-1, 27 × 49- 12, 49 × 37-135, 49 × 39-21-1, 49 M-2-2, CSMG 84-1, DTG 15, DTG 3, Faizpur 1-5, Gangapuri
Cluster 2	38	ICGs 5745, ICGVs 00346, 6766, 00440, 01232, 01393, 02242, 05032, 05198, 05176, 06110, 06188, 07368, 94169, 97045, 96468, 97058, 99083, 99195, M 110-14, SPS 13, SPS 17, TG 41, TG 42, TG LPS 3, TG LPS 4, TG LPS 7, TPG 41, 26 × M-223-1, 27 × 49- 14, 27 × 49- 16, 27 × 49- 27-1, 39 × 49 -77, 39 × 49 -8, 49 × 27-13 (ii), 49 × 27-19, 49 × 37- 99(b) tall, 49 × 37-97-1
Cluster 3	1	ICG 12991
Cluster 4	90	ICG 13895, 156 (M 13), 3053, 5891, ICGVs 00005, 00068, 00191, 00246, 00248, 00290, 00362, 00371, 01273, 01274, 01276, 01361, 01495, 02266, 02298, 02321, 02323, 02411, 02434, 03042, 03043, 03064, 03207, 03128, 05057, 05100, 05141, 05155, 05161, 05163, 06042, 06099, 06100, 06175, 06142, 06420, 06422, 06423, 06424, 07120, 07145, 07148, 07168, 07220, 07223, 07227, 07235, 07246, 07247, 07359, 86564, 86590 , 97115, 97116, 97120, 97165, 98105, 98184, 98373, 99029, 99052, 99085, 99160, ICR 48, M 28-2, SPS 11, SPS 14, SPS 15, SPS 20, SPS 21, SPS 3, SPS 8, SPS 9, TG 19, TMV 2 NLM, 24 × 39-31 MR, 24 M-86, 39 × 49-81-1, 49 × 37-134, 49 × 37-90, 49 M-16, 49 × 39-8, 49 × 39-21-2, CS 39, GPBD 4
Cluster 5	1	ICG 10036,
Cluster 6	19	ICGs 14475, 442, 721, 5662, ICGS 76, ICGVs 01005, 01263, 07268, 88145, M 28-2, TG 49, 26 × M-95-1 RI, 26 M 156-2, 49 × 27-37, 49 × 37-91, 49 × 39-20-2, 49 × 39-21-2(a), DH 86, TMV 2
Cluster 7	1	ICG 8517
Cluster 8	1	ICGV 04115
Cluster 9	8	ICGVs 01478, 02251, 06234, 86352, 87846, 98432, 49 M- 1-1, BAU 13
Cluster 10	1	ICG 3746
Cluster 11	1	ICG 5221
Cluster 12	1	SPS 1
Cluster 13	12	ICGs 12276, 12625, 12672, 14482, 2381, 3584, 4955, 4543, 6646, 8751, ICGV 01328, MN1-35
Cluster 14	2	ICG 15419, ICG 6022
Cluster 15	1	SunOleic 95R

Cluster with 163 genotypes (47.94% of the population) was the largest followed by cluster IV and cluster II with 90 and 38 genotypes, respectively. The clustering of the genotypes was based on the performance of the genotypes for the different target traits. Therefore, genotypes of different pedigree and geographic origin but with the same level of performance for the trait were grouped into the same cluster. This could be attributed to lack of relationship between genetic and geographic diversity arose from genetic drifts and selection in a particular environment [19]. Therefore, selecting parents on the basis of genetic divergence analysis would be more rewarding than the choice made on the basis of geographic diversity [20].The present findings are in accordance with Makinde and Ariyo, (2010) [21].Eight genotypes *viz.,* ICG 12991, ICG 10036, ICG 8517, ICGV 04115, ICG 3746, ICG 5221, SPS 1 and Sun Oleic 95R formed their separate solitary clusters III, V, VII, VIII, X, XI, XII and XV, respectively. Such distinct solitary clustering of genotypes might be due to their superior/inferior performance for few traits or due to intensive natural/human selection for diverse adaptive gene complex. For example, SunOleic 95R is the only high Oleic line (74% oleic acid) among the entries and hence it grouped separately based on its performance for nutritional quality. Previous studies on genetic divergence in groundnut have reported 3 to 15 clusters based on Mahalanobis D^2 statistic and principal component analysis [22-26].

Table-2 *Average inter- and intra-cluster distances among 15 clusters formed by 340 groundnut genotypes*

Clusters	CI	CII	CIII	CIV	CV	CVI	CVII	CVIII	CIX	CX	CXI	CXII	CXIII	CXIV	CXV
CI	**36.73**	92.03	53.19	84.90	52.26	62.61	60.51	135.12	151.48	59.70	79.30	64.63	96.54	199.97	626.40
CII		**48.71**	153.35	115.86	108.98	88.56	135.42	176.41	87.16	161.56	170.98	157.03	143.02	202.71	658.83
CIII			**0.00**	140.34	66.79	94.03	51.45	186.52	229.98	20.29	49.44	83.20	114.23	199.34	683.93
CIV				**64.00**	89.73	100.05	114.71	84.77	137.62	125.29	127.04	82.32	114.99	210.20	648.57
CV					**0.00**	76.08	70.41	153.51	154.14	91.32	102.26	81.20	111.59	161.28	658.56
CVI						**78.61**	100.42	159.86	141.13	105.35	118.30	103.45	116.18	205.58	628.56
CVII							**0.00**	183.31	210.75	60.55	18.06	26.60	95.89	170.03	676.45
CVIII								**0.00**	159.26	132.89	177.24	137.69	168.79	283.99	760.91
CIX									**75.21**	212.11	245.57	225.13	187.06	231.56	718.55
CX										**0.00**	60.76	75.43	110.82	211.05	711.35
CXI											**0.00**	40.60	100.38	165.71	685.27
CXII												**0.00**	93.26	218.39	619.40
CXIII													**120.21**	172.64	627.15
CXIV														**35.80**	894.73
CXV															**0.00**

Where CI to CXV= Cluster I to Cluster XV; Diagonal values represents intra-cluster distances

Cluster distance and cluster means are important to generate information on genotypic variation for different traits and to identify suitable genotypes for crossing program. The average inter- and intra-cluster D^2 values are given in [Table-2]. Inter-cluster average D^2 values ranged from 18.06 (between cluster VII and XI) to 894.73 (between cluster XIV and XV) [Table-2]. The genotypes from the clusters having higher D^2 value can be utilized as parents for hybridization which would result in better transgressive segregants for traits of interest in advanced filial generations. The minimum inter-cluster distance between clusters VII and XI (18.06) followed by VII and XII (26.60) and between XI and XII (40.60) indicated that most of the genotypes had similar values for different traits in these clusters. The maximum intra-cluster distance was observed in cluster XIII (120.21) followed by cluster VI (78.61) and IX (75.21). Thus, selection of genotypes from cluster XIII might be fruitful to produce good recombinants from the same cluster.

The mean of different clusters for various traits is given in [Table-3]. Among the clusters, cluster IV with 90 genotypes recorded lowest disease severity score for LLS (3.80) and rust (3.31)at 90 DAS coupled with higher number of mature pods per plant (18.32), kernel yield per plant (13.03 g) and pod yield per hectare (1930.61 kg). Thus, the genotypes in this cluster have high to moderate resistance to rust and LLS along with high yield potential. In terms of performance, cluster VIII with a single genotype (ICGV 04115) discriminated itself with higher number of mature pods per plant (31), pod yield per plant (21.15 g), shelling percent (71%%), higher yield (2223kg), with resistance to LLS (3.02) and rust (3.02) at 90 DAS, but had the longest maturity duration of 121 days. Cluster IX comprised of eight genotypes with a mean hundred kernel mass of 51 g, suitable for use in developing bold seeded varieties that can be used for confectionery purpose. Clusters I, II, V, VI, XII, XIII and XIV had moderate values for rust and LLS at 90 DAS as well as for most of the yield contributing traits while clusters III, VII, X, XI and XV are characterized by high disease scores for rust and LLS at 90 DAS and low performance for yield and its contributing traits. Cluster means together with information on the traits that contribute maximum towards divergence would help in the selection of parents.

Table-3 *Cluster means for disease severity scores to rust and LLS, and yield traits used for assessment of genetic diversity at Aliyarnagar*

Clusters	DFF	LLS90	RUST90	PH	NPB	NPP	PYPP	SYPP	SH	HKM	DM	PYH
Cluster I	29.50	5.75	6.17	36.70	4.74	13.89	9.65	6.04	62.87	29.14	105.89	1135.47
Cluster II	29.76	5.62	5.89	36.07	4.80	10.56	10.02	5.84	58.08	46.65	108.47	1234.56
Cluster III	27.50	7.59	7.94	46.00	3.70	15.50	8.80	5.60	63.67	22.10	105.00	443.87
Cluster IV	31.25	3.80	3.31	35.30	5.41	18.32	13.03	7.75	58.79	31.89	111.94	1930.61
Cluster V	29.00	5.50	4.47	42.60	4.10	12.80	13.30	7.30	54.70	25.02	103.50	1387.82
Cluster VI	29.47	5.62	6.17	35.12	4.78	15.36	11.63	6.60	57.47	33.85	106.00	1305.90
Cluster VII	28.50	5.50	6.61	47.90	3.60	7.40	5.80	3.60	62.31	24.25	105.50	675.70
Cluster VIII	31.50	3.02	3.02	35.70	5.40	30.95	21.15	14.88	70.46	33.45	121.50	2223.34
Cluster IX	32.06	5.75	5.13	38.74	6.09	15.25	18.43	10.76	60.54	50.95	116.00	1987.98
Cluster X	28.00	6.61	7.94	43.90	4.00	13.90	8.20	5.90	70.54	21.99	114.00	536.09
Cluster XI	27.50	5.01	7.08	52.00	4.30	18.40	10.20	6.10	60.12	23.30	106.00	805.27
Cluster XII	30.00	4.47	4.47	39.38	3.90	11.40	6.60	3.95	59.49	20.14	108.00	1100.00
Cluster XIII	30.04	4.79	5.62	41.52	4.60	10.63	8.71	4.98	57.94	29.25	109.50	1505.87
Cluster XIV	28.25	3.89	4.79	62.90	3.70	7.45	10.35	5.50	53.06	37.54	106.50	1171.24
Cluster XV	29.00	6.61	6.03	29.80	5.30	10.30	7.10	4.00	56.39	28.70	104.50	877.57

Where, DFF= Days to 50% flowering, LLS90 &RUST90= Disease severity score of late leaf spot and rust recorded at 90 days after sowing respectively, PH = Plant height (cm), NPB= Number of primary branches plant^{-1}, NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g), KYPP= Kernel yield plant^{-1} (g), SH = Shelling percent, HKW= Hundred kernel mass (g), DM= Days to physiological maturity, PYH= Pod yield hectare^{-1} (kg)

Cluster means for nutritional quality traits summarized in [Table-4], showed that genotypes of cluster XIV (ICG15419 and ICG 6022) had higher oil content (62.57%) in comparison to the other clusters. Asingle genotype of cluster XV (Sun Oleic 95R) maintained its own separate identity as a high Oleic line with Oleic acid

content of 74.38%, linoleic acid content of 5.30%, palmitic acid content of 8.47% and O/L ratio of 14.03. Sun Oleic 95R was the first high Oleic line to be released in USA [27]. Over the years it has successfully been used as a parent in different breeding programs across the world. The high Oleic trait was successfully introgressed from Sun Oleic 95R into three elite cultivars (ICGV's 06420, 06142 and 06110) at International Crops Research Institute for the Semi-Arid Tropics, Patancheru [28].

Table-4 *Cluster means for different nutritional quality traits used for assessment of genetic diversity at Aliyarnagar*

Clusters	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Cluster I	52.85	19.98	41.34	39.94	11.70	2.13	2.09
Cluster II	51.12	21.25	43.82	37.70	11.29	2.07	2.19
Cluster III	53.58	15.44	48.16	35.40	10.56	1.61	2.40
Cluster IV	55.20	20.16	39.82	41.22	12.18	2.25	2.00
Cluster V	49.14	18.49	36.84	44.22	11.63	2.37	1.86
Cluster VI	52.85	20.25	43.96	37.95	11.02	2.22	2.19
Cluster VII	52.85	22.09	42.12	39.82	14.06	1.46	2.09
Cluster VIII	51.84	22.18	35.88	44.49	12.60	1.74	1.82
Cluster IX	50.27	21.90	45.43	36.12	10.76	2.34	2.29
Cluster X	56.10	17.39	45.70	37.33	10.96	2.10	2.24
Cluster XI	54.91	20.52	44.22	39.44	13.40	1.17	2.19
Cluster XII	58.06	22.56	36.84	43.56	14.82	2.02	1.91
Cluster XIII	58.06	19.01	47.06	37.09	10.76	2.07	2.34
Cluster XIV	62.57	17.31	49.00	41.60	7.84	3.39	2.24
Cluster XV	51.98	21.34	74.38	5.30	8.47	2.13	14.03

The numbers of times that each of the 19 traits appeared in first rank and its respective per cent contribution towards total genetic divergence is presented in [Table-5]. Among all the traits studied, hundred kernel mass contributed maximum (24.42%) towards the total diversity followed by days to maturity (15.95%), disease score of rust at 90 DAS (9.18%), plant height (8.87%), disease score of LLS at 90 DAS (7.37%) and yield per hectare (5.94%). Nutritional quality traits contributed least towards total genetic diversity present in GSP. The greater contribution of hundred kernel mass and least contribution of nutritional quality trait towards total genetic variation was also reported in earlier studies [29, 30]. It has been suggested that the traits with the maximum contribution towards divergence should be given importance for selection of genotypes in breeding program. Among the nutritional quality traits, Oleic acid had highest contribution (2.97%) followed by palmitic (2.92%) and linoleic acid (1.98%) towards total genetic diversity present in GSP. Cluster means together with information on the traits that contribute maximum towards divergence would help in the selection of parents. Considerable genetic diversity was reported for resistance to both the diseases, yield and major yield contributing traits.

Table-5 *Percent contribution of different traits towards total genetic divergence of genomic selection panel of groundnut evaluated at Aliyarnagar during rainy season 2015*

S. No.	Traits	Number of times ranked first	Percentcontribution towards divergence
1	Days to 50% flowering	2092	3.63
2	Disease score of late leaf spot at 90 DAS	4250	7.37
3	Disease score of rust at 90 DAS	5293	9.18
4	Plant height (cm)	5114	8.87
5	Number of primary branches plant^{-1}	865	1.50
6	Number of pods plant^{-1}	1863	3.23
7	Pod yield plant^{-1} (g)	1064	1.85
8	Seed yield plant^{-1} (g)	1540	2.67
9	Shelling percent	1589	2.76
10	Hundred kernel mass (g)	14071	24.42
11	Days to maturity	9193	15.95
12	Yield per hectare (kg)	3422	5.94
13	Oil content (%)	501	0.87
14	Protein content (%)	697	1.21
15	Oleic acid content (%)	1714	2.97
16	Linoleic acid content (%)	1142	1.98
17	Palmitic acid content (%)	1680	2.92
18	Stearic acid content (%)	836	1.45
19	O/L ratio	704	1.22

Variability among the botanical varieties

Foliar disease resistance

In the present study, 20 out of 111 genotypes of var *hypogaea*; 30 out of 212 genotypes of var *vulgaris* identified resistant against LLS and rust with ≤3 disease severity score for both the diseases. A single genotype of var *aequatoriana* (ICG 12625) recorded resistant reaction against LLS whereas of var *peruviana* (ICG 8751) against rust. The genotypes reported resistant to LLS and rust in var *vulgaris* and var *hypogaea* possess high yield potential with desirable pod and kernel related traits with different maturity duration (101 to 121 days) that can effectively be used in breeding program to develop resistant lines with farmers, consumers and traders preferred traits. Similarly, sources of resistance to LLS and rust in different botanical varieties were earlier identified [11, 31] and used to develop breeding lines with resistance [32, 33]. An extensive screening of 13,000 accessions at ICRISAT identified 49 landraces and 20 other genotypes of var. *peruviana* as resistant against rust and LLS [34]. Among the identified resistant genotypes for both the disease, a total of 36 including 25 from ssp. *fastigiata* var *vulgaris* and 11 from ssp. *hypogaea* var *hypogaea* were advance breeding line breed by ICRISAT, Patancheru indicating that these lines can be used in breeding program without tedious efforts of pre-breeding. Pod yield of resistant cultivars of ssp *fastigiata* varied from 1230 to 3560 kg/ha. The genotypes ICGVs 01274, 03043, 05155, 05163, 06142, 07120 and 07235 recorded pod yield ≥ 2500 kg/ha with the disease severity score ≤ 3 for both the diseases. However, pod yield of resistant cultivars of ssp *hypogaea* varied from 995 to 2530 kg/ha with a single genotype ICGV 01361 recorded pod yield of ≥2500 kg/ha. The genotypes ICGV05155 (101 days) and ICGV 86699 (103 days) reported early maturing compared to other are suggested to use in breeding program. Superior resistant genotypes from ICRISAT mini core collection has earlier been identified by Sudini *et al.* (2015) [13].

Yield and its contributing traits

The mean performance of different botanical varieties revealed that cultivars belonging to ssp. *fastigiata* var *vulgaris* (Spanish Bunch) had higher number of mature pods per plant (18), pod yield per plant (12.7 g), shelling percent (63.2%) and pod yield per hectare (1511 kg) compared to other botanical varieties. The results suggested that cultivars of ssp. *fastigiata* var *vulgaris* had higher yield potential [Table-6] and [Fig-1]. The superior performance of ssp. *fastigiata* var *vulgaris* cultivars compared to other was earlier reported [22, 35]. Genotypes of ssp. *hypogaea* var *hirsute* followed by var *hypogaea* (Virginia runner and bunch) had higher hundred kernel mass suggested that most of the genotypes with large kernel size in GSP are Virginia type. Days to maturity of genotypes of different botanical varieties revealed that cultivars of ssp. *fastigiata* var *peruviana* were early maturing cultivars that can be used as a parent to develop early maturing genotypes [Table-6]. Early maturing genotypes from var *peruviana* were earlier identified by Upadhyaya *et al.* (2006) [24].

Table-6 *Mean performance of different botanical varieties for disease resistance, yield and nutritional quality traits evaluated at Aliyarnagar during rainy season 2015*

Subspecies	Botanical variety	Market type		Disease resistance		Yield and its contributing traits							Nutritional quality traits						
			Number	LLS90	Rust90	DFF	NPP	PYPP	SH	HKM	DM	PYH	OC%	PC%	OA%	LA%	PA%	SA%	O/L
fastigiata	*aequatoriana*	*UNK*	1	3.0	5.0	30	10	6.4	53.1	29.9	120	661.8	63.5	17.5	46.1	44.7	8.2	2.9	1.0
	fastigiata	*Valencia*	10	4.3	5.5	29	11	9.5	55.8	30.6	107	929.6	55.0	19.8	42.8	40.8	11.4	2.3	1.1
	peruviana	*UNK*	4	4.5	3.8	29	13	11.9	57.5	29.4	105	1407.0	53.2	18.8	41.2	41.0	11.4	2.3	1.0
	vulgaris	*Spanish Bunch*	212	4.9	5.1	29	18	12.7	63.2	31.9	108	1510.6	53.4	20.0	41.3	40.2	11.7	2.2	1.1
hypogaea	*hirsuta& UNK*	*UNK*	2	4.0	4.0	28	3	4.8	53.4	36.7	107	1257.8	62.1	19.0	48.5	42.2	7.5	3.5	1.2
	hypogaea	*Virginia Bunch*	100	4.2	4.5	32	15	11.6	60.2	34.5	110	1475.6	53.6	20.7	43.0	38.8	11.7	2.2	1.2
		Virginia Runner	11	4.7	5.0	31	13	9.0	61.6	30.6	106	956.4	51.1	21.1	43.8	37.2	11.1	2.2	2.1

Where, LLS90 & Rust90= Disease severity score of late leaf spot and rust at 90 days after sowing, respectively; DFF= Days to 50% flowering; PYPP= Pod yield plant^{-1} (g); SH= Shelling percent; HKM= Hundred kernel mass (g); DM= Days to physiological maturity; PYH=Pod yield hectare^{-1} (kg); OC%= Oil content (%); PC%= Protein content (%); OA%= Oleic acid content (%); LA% = Linoleic acid content (%); PA%= Palmitic acid content (%); SA%= Stearic acid content (%); O/L = Oleic/Linoleic acid ratio; UNK= Unknown

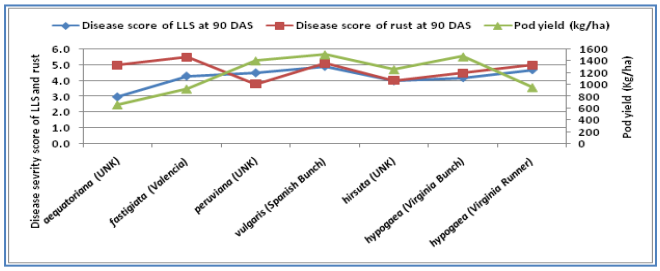

Fig-1 Disease reaction of different botanical varieties of cultivated groundnut against late leaf spot and rust at 90 days after sowing (DAS) with yield potential

Nutritional quality traits

Wide range of variability for oil content was observed among all the botanical varieties of groundnut. The ssp. *fastigiata* var *vulgaris* cultivars had oil content varied 45 to 62%, *fastigiata* from 49 to 62%, *peruviana* from 48-58 whereas ssp. *hypogaea* var *hypogaea* (Virginia bunch) varied from 44 to 63% and Virginia runner from 48 to 56%. A single cultivar belonging to ssp. *Fastigiata* var*aequatoriana* (ICG 12625) recorded high oil content (63%) followed by ssp. *hypogaea* var *hirsute* (ICG 15419) (62.0%) compared to other botanical varieties. The protein content of genotypes of different botanical varieties varied from 16 to 28%. Genotypes of Virginia runner had high oil content coupled with high hundred kernel mass are suggested to use in breeding program. There was wide range of variability in different varieties *viz, vulgaris* (29-54%), *fastigiata* (37-49%), *peruviana* (36-46%) and *hypogaea* (31-60% for virginia bunch and 34-74% for virginia runner) was reported for Oleic acid content. The Virginia runners had high Oleic acid, low linoleic acid and high O/L ratio compared to others [Fig-2]. A single genotype in GSP, Sun Oleic 95R identified as high Oleic line with >74% Oleic acid pointing towards to the need to develop high Oleic lines in groundnut. Significant variability within and among the different botanical varieties for oil and protein content along with fatty acid was earlier reported [35, 36]. They concluded that the Oleic acid concentration was higher in the genotypes belonging to Virginia runner, followed by that of Virginia bunch and a minimum in the Spanish bunch type. A reversed trend was observed with respect to linoleic acid concentration [35].

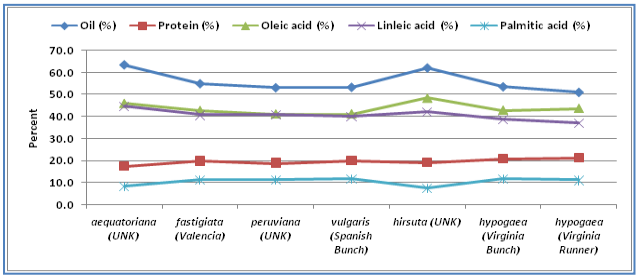

Fig-2 Variation in different botanical varieties of cultivated groundnut for nutritional quality traits

Conclusion

In order to make groundnut crop more resilient to biotic and abiotic stresses, assessment of genetic diversity is a pre-requisite to find the source of resistance/tolerance to biotic and abiotic stresses along with yield and nutritional quality traits. The present study is the most comprehensive evaluation of a diverse collection of genotypes. There was sufficient genetic diversity observed for different traits in all the botanical varieties of cultivated groundnut. The identified advanced breeding lines in both the subspecies (25 in *fastigiata* and 11 in *hypogaea*) will be useful for the breeder to use in breeding programs skipping the linkage drag with undesirable traits and tedious pre-breeding work. Pieces of information generated on cluster distance together with cluster mean will be fruitful to select the better parent in breeding program for development of improved cultivars with disease resistance, high yield potential and improved nutritional quality. The genotypes grouped based on their phenotypic performance can be selected for trait-specific breeding. Looking towards the emerging demand of high Oleic groundnut from industry traders and consumers, there is a strong need to focus on the development of high Oleic lines in groundnut.

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Author Contributions: The study was conducted by Sunil Chaudhari. He has taken all the data, carried out data analysis and written manuscript. Dr. Dhirendra Khare has provided guidance to conduct the study and Dr Sundravadna has managed trial at Aliyarnagar and helped to get disease score for rust and LLS. Mr Surrendra Singh has generated layout of the experiment and prepared seed material of GSP. Dr Murali TV has provided valuable guidance during the course of present investigation and reviewed manuscript.

Abbreviations: GSP- Genomic selection panel, LLS- Late leaf spot, NIRS- Near-infrared reflectance spectroscopy, DAS- Days after sowing

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Conflict of Interest: None declared

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