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Phenotypic Diversity among the Virginia Breeding Lines of Groundnut

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ABSTRACT

An attempt has been made to study the genetic variability and classifying the 210 Virginia breeding lines along with five checks evaluated across two years. Significant differences observed among Virginia breeding lines for all traits except days to maturity. Moderate heritability coupled with high genetic advance as per cent of mean for hundred pod weight and hundred kernel weight suggesting the additive gene control and effectiveness for selection. Low heritability coupled with low genetic advance as per cent of mean for days to flowering and kernel characteristics suggests more environmental influence on their expression. Pod yield per plant correlated significantly and positively with primary branches per plant, hundred pod weight and kernel weight, SMK, shelling out turn, kernel length and kernel width. Cluster analysis based on Euclidean distance using Wards criteria, grouped 210 Virginia bunch breeding lines and four checks into three major clusters. Three major clusters consist each of 119 breeding lines in cluster I, 44 breeding lines and three checks in cluster II and 47 breeding lines and two check varieties in cluster III, respectively. Cluster I and cluster II contains high yielding breeding lines, where as cluster III had low yielding breeding lines. Sub cluster IIA had breeding lines with higher pod yield and kernel characteristics, which will be useful donors for Virginia groundnut improvement.

Keywords: Phenotypic diversity, Virginia breeding lines, hundred kernel weight, cluster analysis

Introduction

Groundnut (*Arachis hypogea* L.) is a major oilseed legume crop of arid and semi arid tropical of the world. It covers an area of 61 lakh hectares and production of 99 lakh tonnes with productivity of 1631 kg/ha in India (FAOSTAT, 2020). India has the highest area under groundnut cultivation. The six major states growing groundnut in India are Gujarat (39%), Rajasthan (15%), Andhra Pradesh (14%), Karnataka (9%), Madhya Pradesh (6%) and Maharashtra (5%) (IOPEPC, 2019). Botanically there are six distinct groups of groundnuts cultivated. The Virginia type is the predominant groundnut type grown in Gujarat and Rajasthan states of India and in small packets in southern states of India. In Gujarat, about >80% of the total area is under the six districts in the Saurashtra regions (Junagadh, Rajkot, Dwaraka, Amreli, Bhavanagar and Jamnagar). In Rajasthan, the groundnut is mainly cultivated in Bikaner, Jodhpur, Churu and Jaipur districts. In Tamil Nadu, about 10% area of groundnut area is occupied by Virginia type (TMV 10 and ALR1 of Virginia bunch and TMV 1 and TMV 4 of Virginia runner) particularly in some packets of Salem, Dharmapuri, Tiruvannamalai, Villupuram and Cuddalore districts under rainfed conditions (http://ikisan.com/tn-groundnut-history.html). Virginia runners varieties viz., Kadiri 771-1 and Kadiri-3 and Virginia bunch type Kadiri-2 are cultivated in Rayalaseema districts like Anantapur, Chitture, Cuddaph and Kurnool (Krishna, 2010). In Maharashtra, Virginia runner type grown in Marathwada region, Osmanabad and Bhid districts using the moisture gained from southeast and northwest monsoons.

Virginia groundnut belongs to sub species of *hypogaea* var. *hypogaea*, characterized by no floral axes on main stem in Virginia (*hypogaea*) compared to presence of floral axes in main stem in Spanish and Valencia types belongs to sub species *fastigiata* var. *vulgaris* and subspecies *fastigiata* var *fastigiata* respectively. Virginia groundnut is characterized by longer maturity duration, spreading growth habit, large kernel, high oleic acid and tolerance to biotic and abiotic stresses (Erickson and Ketring 1985; ICRISAT 1992). Attempts have been made in the past to estimate the genetic variability, correlation and divergence based morpho-agronomic traits in Virginia groundnut (Gupta et al. 2015; Shinde et al. 2019 and Dudhatra et al. 2022). Using Mahalnobis D^2 statistics 35 Virginia runner genotypes were grouped into seven clusters and found lack of relationship between genetic and geographic diversity (Golakia and Makne 1992). The significant positive correlation of pod yield per plant with hundred pod weight and shelling percentage was observed by Gupta et al. (1992) and Gangadhara et al. (2020). High heritability accompanied with high genetic advance as per cent of mean was recorded by Bhargavi et al. (2017) for pod yield per plant and 100 kernel weight. Coffelt et al. (1989) studied reproductive efficiency in 14 Virginia cultivars and suggested that yield increase can be accomplished by developing the variety in combination with high harvest index and reproductive efficiency.

Hence an attempt has been made to assess the genetic variability and classifying the Virginia breeding lines based on pod yield and kernel characteristics, which will be useful for identifying the diverse parents for hybridization and genetic improvement of Virginia groundnut.

Materials and Methods

Experimental location: The material for present study consists of two hundred and ten Virginia advanced breeding lines and four checks of groundnut obtained from Plant Breeding Section of ICAR-DGR, Junagadh. An experiment was laid out in the Augmented Randomized Complete Block Design at the Experimental plots of ICAR-Directorate of Groundnut Research (DGR) Station, Junagadh, Gujarat, India during *Kharif* 2017 (E1) and *Kharif* 2018 (E2). ICAR-Directorate of Groundnut Research is situated between 21.49°N latitude and 70.44°E longitude at an elevation of 107 meters above mean sea level. Each breeding line was sown in a single row of 3 m length and with a spacing of 60 × 10 cm and standard agronomic practices was followed to raise healthy crop.

Observations recorded: The observations on days to first flowering, days to 50% plants flowering, number of primary branches per plant, days to maturity, hundred pod and kernel weight, kernel width, kernel length and pod yield per plant were recorded on five random plants from each genotype. The SPAD chlorophyll meter reading (SCMR) a surrogate trait of water use efficiency was recorded at 60 days after sowing by collecting the second to third leaves from the top of the main stem of each plant by a Minolta handheld portable SCMR meter (SPAD- 502 plus Minolta, Tokyo, Japan) using four leaflets per sample and care was taken to ensure that the SPAD meter sensor fully covered the leaf lamina, avoiding any interference from veins and midribs. The weather conditions prevailing in growing years are presented in the Table 6.

Statistical analysis: Analysis of variance (ANOVA) for Augmented Randomized Block design was calculated using Proc GLM of SAS. Genotypic and phenotypic coefficients of variation were worked out as per the method suggested by Burton and De Vane (1953), heritability and genetic advance were calculated according to Johnson (1955) and Robinson et al. (1949). Pearson's correlation coefficients were calculated for each pair of traits to determine relationships among the yield and kernel traits. A cluster analysis was done on mean values of two years for 13 traits using Euclidean distance and dendrogram was constructed using R version 3.0.3.

Results and Discussion

Variability and genetic parameters

Analysis of variance (Table 1) showed significant differences among test genotypes for all the traits except days to maturity in two years. A wide range was observed for hundred pod weight (29-131g in E1 and 56-146 g in E2), hundred kernel weight (21-51 g in E1 and 18-63 g in E2), Sound mature kernel (26-58% in E1 and 38-80% in E2), Shelling out turned (53-83% in E1and 26-75%in E2) in both years (Fig. 1). Moderate range was observed in primary branches (3-16 in E1 and 2-20 in E2), days to 50 per cent flowering (24-40 days in E1 and 28-36 days in E2), days to maturity (112-125 days in E1 and 105-124 days in E2) and SPAD chlorophyll meter reading (25-45 in E1 and 27-44 in E2). Across years, Virginia breeding lines showed low variability for kernel width (6-9 mm in E1 and 6-10 mm in E2), kernel length (9-17 mm in E1 and 10-19 mm in E2) and kernel length to width ratio (1.2-2.4 in both E1 and E2).

The phenotypic and genotypic coefficient of variation and heritability along with genetic advance as percent of mean are presented in Table 2. Low heritability coupled with low genetic advance per cent of mean was observed for days to first flower initiation, days to 50% flowering and days to maturity in both environments suggesting that highly influence of environment and selection is ineffective for these traits. Similar results of low heritability and genetic advance as per per cent of mean was also observed by Saini and Sharma (2018) and Gangadhara et al. (2019). Temperature and photoperiod are two major environmental factors highly influencing the flowering and maturity duration. Cox (1979) and Nigam (1994, 1998) reported the effect of temperature and photoperiod on vegetative as well as reproductive growth of groundnut. Primary braches per plant exhibited low heritability and moderate genetic advance as per cent of mean in both E1 and E2.

Sound mature kernel (%) had high heritability in both E1 and E2 but genetic advance as per cent of mean was high in E1 and low in E2. Shelling percentage had high heritability coupled with high genetic advance as per cent of mean in E2 and high heritability with low genetic advance as per cent of mean in E1. High heritability in both E1 and E2 environments and low and high GAM in E1 and E2 indicates favourable environments in the form of rainfall in E2 compared to E1. Hundred pod and kernel weight showed moderate heritability and high genetic advance as per cent of mean both environments (E1 and E2). Moderate heritability coupled with high genetic advance as per cent of mean for hundred pod weight and hundred kernel weight suggests the additive gene control and effectiveness for selection. Pod yield per plant showed low heritability coupled with moderate genetic advance as per cent of mean in E2. A similar estimate of pod yield was recorded by Azharadheen and Gowda (2013). Kernel traits (Kernel width, Kernel length and Kernel length to width ratio) were showed low heritability coupled with low genetic advance as per cent of mean suggesting that complex nature and higher influence of environment and low scope for selection. Low heritability and genetic advance as per cent of mean for kernel width was also reported by Gangadhara et al. (2013).

Correlation and cluster analysis

Pod yield per plant correlated significantly and positively with primary branches per plant, hundred pod weight and kernel weight, SMK, shelling out turn, kernel length and kernel width. This kind of positive relationships between kernel traits with pod yield was also noticed by Gupta et al. (2015) and Gangadhara et al. (2020). Days to first flowering and 50 per cent flowering correlated significant negatively with sound mature kernel (%) and shelling out turn suggesting the influence of primary branches per plant and flowering time and duration with kernel maturity and pod yield. SCMR correlated significant positively with all kernel characteristics viz., hundred pod weight, hundred kernel weight, sound mature kernel (%), shelling out turn, kernel length and kernel length to width ratio. Kernel yield is an important economic yield, which in turn determined by hundred kernel weight, sound mature kernel (%) and shelling out turn, which are correlated positively with kernel length, kernel width and kernel length to width ratio. Size and shape of the kernel are the two important visible traits influencing the consumer preference, which in turn determined by kernel length and kernel width. Kernel length correlated positively with kernel length to width ratio, whereas kennel width correlated negatively with kernel length as well as kernel length to width ratio. Similar kind of relationship between kernel traits was also noticed by Gangadhara et al. (2019).

Cluster analysis based on Euclidean distance using Wards criteria, grouped 210 Virginia bunch breeding lines and four checks into three major clusters. Three major clusters consist each of 119 breeding lines in cluster I, 44 breeding lines and three checks in cluster II and 47 breeding lines and two check varieties in cluster III respectively. Cluster I and cluster II contains high yielding as well as higher ranges for hundred pod and kernel weight where as cluster III had low yielding breeding lines. Sub cluster IIA had breeding lines with higher pod yield and kernel characteristics, which will be useful donors for Virginia groundnut crop improvement.

Identification of trait specific breeding lines

Early flowering and high SCMR are important traits for drought tolerance in groundnut. SPAD Chlorophyll meter reading is more pertinent trait for drought tolerance associated with leaf nitrogen and drought tolerance (Kalariya et al. 2017). Breeding lines showing higher SCMR (>42) are PBS 25107, PBS 25090, PBS 25091 and PBS 25081. Breeding lines viz., PBS 21095, PBS 21089, PBS 21108, PBS 25062, PBS 25064, PBS 25076, PBS 25100, and PBS 25114 flowered early (27 days). Advanced breeding lines with high sound mature kernel (>63%) are PBS 25106, PBS 24142, PBS 24022, PBS 25077, PBS 25101, PBS 21105, PBS 21108, PBS 25116, PBS 25096, PBS 26061, PBS 26043, PBS 24148, PBS 25115 and PBS 25022. For confectionery use, large seeded type and high shelling per centage are preferred. Breeding lines PBS 21105, PBS 21120, PBS 26057, PBS 26061, PBS 24145, PBS 26056, PBS 24133, PBS 24152 and PBS 26052 had higher shelling per centage (>70%). Seed size had highly positive correlation with seed weight (Chiow and Wynne 1983), which in turn increases yield, nutritional content as well as seedling vigour. Two traits, kernel shape and size are important visible features for consumer's preference. Kernel length to width ratio (>2) are preferred as large seed with uniform shape. Advance breeding lines viz., PBS 21115, PBS 21108, PBS 25022, PBS 21086, PBS 26031, PBS 21087, PBS 25044, PBS 26047, PBS 21084, PBS 21085, PBS 26015, PBS 25059, PBS 26050 and PBS 25077 showed high kernel length to width ratio (>2mm).

Conclusions

The present study exhibited significant differences among the genotypes for pod yield and its component traits. Moderate heritability coupled with high genetic advance as per cent of mean for hundred pod weight and hundred kernel weight suggested the additive gene control and effectiveness for selection. Promising trait specific superior Virginia breeding lines identified will serve as donors for the development of large seeded and higher pod yield in Virginia groundnut.

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Table 1. ANOVA for yield and kernel characteristics 210 Virginia breeding lines.

Character	Blocks (df=6)	Entries (df=214)	Tests (df=209)	Controls (df=4)	Tests Vs Controls (df=1)	Error (df=24)
***Kharif* 2017 (E1)**						
Primary branches per plant	0.89	4.49*	4.48*	5.75*	1.2	1.65
Days to first flower initiation	3.32	6.96*	6.52*	19.19*	48.86*	2.34
Days to 50% flowering	2.72	11.39*	10.62*	46.90*	31.74*	2.87
Days to maturity	5.99	6.06	6.14	3.26	0.49	3.66
SPAD Chlorophyll meter reading	10.0	13.7*	13.9*	3.7	20.5	4.5
Hundred pod weight (g)	66.72	207.6*	179.3*	1544.1*	767.2*	39.2
Hundred kernel weight (g)	26.76*	34.3*	30.06*	159.57*	419.2*	3.15
Pod yield per plant (g)	14.52	6.61	5.83	5.75	172.8	6.69
Sound mature kernel (%)	16.44*	39.41*	33.32*	246.64*	482.28*	3.29
Shelling percentage (%)	13.82*	22.51*	20.16*	1.10	599.1*	0.98
Kernel width (mm)	0.723*	0.445*	0.413*	2.04*	0.931*	0.176
Kernel length (mm)	1.14	1.69*	1.70*	0.75	4.14*	0.59
Kernel length to width ratio	0.017	0.03*	0.029*	0.055*	0.006	0.012
***Kharif* 2018 (E2)**						
Primary branches per plant	11.45	10.03*	9.92*	14.02*	16.55	4.77
Days to first flower initiation	1.18	1.980*	1.8*	5.24*	27.75*	0.85
Days to 50% flowering	1.03	2.14*	1.9*	7.0*	32.9*	0.82
Days to maturity	18.02	17.98	17.74	32.47	10.45	13.25
SPAD Chlorophyll meter reading	3.75	5.85*	5.98*	0.30	0.31	3.07
Hundred pod weight (g)	13.85	295.0*	268.2*	1484.7*	1125.0*	28.7
Hundred kernel weight (g)	10.09	51.58*	49.4*	138.0*	158.04*	7.5
Pod yield per plant (g)	4.89	6.78*	6.44*	3.61	90.13*	2.34
Sound mature kernel (%)	0.761*	23.94*	23.17*	0.85	276.9*	1.023
Shelling percentage (%)	16.85*	72.89*	71.15*	174.5*	30.86*	5.26
Kernel width (mm)	0.70*	0.634	0.612*	1.90*	0.194	0.397
Kernel length (mm)	0.53*	2.26*	2.23*	3.86*	0.044	0.63
Kernel length to width ratio	0.038*	0.044*	0.045*	0.024	0.0054	0.021

* Indicates the statistical significance of entries or treatments at 5% level.

Table 2. Genetic parameters for yield and kernel characteristics in Virginia breeding lines.

	Min	Max	Mean	σ^2_g	σ^2_p	GCV	PCV	$h^2_{(bs)}$	GAM
***Kharif* 2017**									
Primary branches per plant	3	16	6.94	0.40	2.06	9.16	20.68	19.63	12.01
Days to first flower initiation	22	35	27.58	0.66	3.00	2.95	6.28	22.03	4.93
Days to 50% flowering	24	40	30.80	1.22	4.08	3.58	6.56	29.82	8.15
Days to maturity	112	125	116.60	0.34	4.00	0.50	1.72	8.59	0.61
SPAD Chlorophyll meter reading	25.9	45.8	36.11	1.32	5.81	3.18	6.67	22.65	7.50
Hundred pod weight (g)	29	131	81.78	24.05	63.28	6.00	9.73	38.01	60.59
Hundred kernel weight (g)	21	51	34.23	4.45	7.60	6.16	8.05	58.55	26.78
Sound mature kernel (%)	26	58	40.70	5.16	8.45	5.58	7.14	61.05	26.12
Shelling out turn	53	83	69.33	3.08	4.06	2.53	2.91	75.78	9.14
Kernel length (mm)	9.9	17.1	13.62	0.16	0.75	2.91	6.37	20.83	2.37
Kernel width (mm)	6	9	7.76	0.04	0.21	2.53	5.97	17.92	1.02
Kernel length to width ratio	1.2	2.4	1.78	0.003	0.015	2.86	6.80	17.73	0.30
***Kharif* 2018**	**Min**	**Max**	**Mean**	σ^2_g	σ^2_p	**GCV**	**PCV**	$h^2_{(bs)}$	**GAM**
Primary branches per plant	2	20	8.07	0.75	5.53	10.77	29.22	13.58	19.22
Days to first flower initiation	25	33	28.57	0.16	1.02	1.41	3.54	15.78	1.16
Days to 50% flowering	28	36	30.68	0.19	1.01	1.41	3.28	18.54	1.26
Days to maturity	105	124	115.87	0.68	13.93	0.71	3.22	4.86	1.20
SPAD Chlorophyll meter reading	27.4	44.1	36.56	0.40	3.47	1.72	5.10	11.41	2.23
Hundred pod weight (g)	56	146	92.90	38.03	66.27	6.64	8.77	57.39	84.38
Hundred kernel weight (g)	18	63	37.49	6.32	13.29	6.71	9.73	47.59	34.77
Pod yield per plant	3	22	10.30	0.63	2.95	7.70	16.68	21.33	12.59
Sound mature kernel (%)	38	80	69.74	3.32	4.09	2.61	2.89	81.17	9.79
Shelling out turn	26	75	46.28	9.84	14.76	6.78	8.31	66.65	43.83
Kernel length (mm)	10	19	14.36	0.23	0.87	3.36	6.49	26.77	3.33
Kernel width (mm)	6	10	7.87	0.12	0.55	3.52	7.58	21.59	2.49
Kernel length to width ratio	1.26	2.4	1.84	0.0029	0.027	2.91	8.93	10.64	0.32

Min=Minimum, Max=Maximum, σ²g=Genotypic variance, σ²p=Phenotypic variance, GCV=Genetic coefficient of variation, PCV=Phenotypic coefficient of variation, h2(bs)=Heritability in broad sense, GAM=Genetic advance as per cent of mean

Table 3. Mean values of sub cluster for yield and kernel characteristics in Virginia breeding lines.

Cluster	No.	No.	ABL	PRIM	DFI	DFF	DM	SCMR	PYLP	HPW	HKW	SMK	SP	KL	KW	KLWR
I	119	20	Ia1	9	29	32	117	34	9	80	32	53	53	13.4	7.60	1.79
		36	Ia2	8	28	30	116	38	10	82	34	56	58	14.0	7.87	1.80
		19	Ib1	8	28	31	116	34	9	91	35	52	56	14.6	7.81	1.90
		44	Ib2	7	28	31	116	37	9	92	40	58	61	14.6	8.07	1.83
II	47	4	IIA	8	28	31	117	38	11	125	49	60	64	16.6	8.43	1.97
		27	IIb1	7	28	31	116	37	10	100	39	56	58	14.1	7.88	1.80
		16	IIb2	7	27	30	117	37	9	109	45	59	63	15.2	8.43	1.82
III	49	5	IIIA	7	28	31	115	36	7	54	23	49	49	12.2	6.94	1.76
		35	IIIb1	8	29	32	116	36	9	71	29	51	53	13.2	7.39	1.80
		9	IIIb2	6	26	29	115	34	6	64	27	53	55	11.4	7.53	1.54

PRIM=Primary branches per plant, DFI=Days to first flowering, DFF=Days to 50% flowering, DM=Days to Maturity, SCMR=SPAD Chlorophyll meter reading, PYLP=Pod yield per plant, HPW=Hundred pod weight, HKW=Hundred kernel weight, SMK=Sound mature kernel (%), SP=Shelling percentage, KL=Kernel length (mm), KW=Kernel width (mm), KLWR=Kernel length to width ratio

Table 4. Clustering pattern if Virginia breeding lines based on Euclidean distance.

Cluster	Sub Cluster	No	Advanced Breeding Lines
I	Ia1	20	PBS 24131, PBS 25086, PBS 25053, PBS 24156, PBS 25075, PBS 25078, PBS 26031, PBS 26033, PBS 24102, PBS 24106, PBS 24107, PBS 24122, PBS 25059, PBS 25051, PBS 24114, PBS 25038, PBS 25108, PBS 25048, PBS 25047, PBS 26023
	Ia2	36	PBS 25061, PBS 25064, Girnar 2, PBS 21107, PBS 26062, PBS 25033, PBS 25034, PBS 25082, PBS 24002, PBS 25081, PBS 25091, PBS 21096, PBS 25090, PBS 21109, PBS 21085, PBS 24073, PBS 25111, PBS 24151, PBS 24155, PBS 24144, PBS 24153, PBS 25117, PBS 21091, PBS 25080, PBS 25118, PBS 25032, PBS 26019, PBS 24124, PBS 24140, KDG 123, KDG 128, PBS 21087, PBS 25125, PBS 25126, PBS 21118, PBS 24141
	Ib1	19	PBS 25043, PBS 21090, PBS 25104, PBS 25044, PBS 24118, PBS 24116, PBS 21116, PBS 25060, PBS 26039, PBS 26051, PBS 24112, PBS 24113, PBS 24115, PBS 24119, PBS 25098, PBS 26038, PBS 26049, PBS 21100, PBS 21113,
	Ib2	44	PBS 21115, PBS 26052, PBS 21084, PBS 21119, PBS 25110, PBS 26058, PBS 26056, PBS 26059, PBS 25022, PBS 25101, PBS 25115, PBS 25025, PBS 25107, PBS 21093, PBS 21086, PBS 24101, PBS 25077, PBS 25116, PBS 25084, PBS 25072, PBS 26026, PBS 21111, PBS 25119, PBS 25102, PBS 26053, PBS 24150, PBS 25050, PBS 25021, PBS 25100, PBS 21114, PBS 24075, PBS 26041, PBS 25024, PBS 25028, PBS 21106, PBS 26028, PBS 24145, PBS 24152, PBS 24154, PBS 26055, PBS 26057, PBS 24142, PBS 21105, PBS 26040,
II	IIA	4	PBS 21112, PBS 25094, PBS 24022, PBS 24133
	IIb1	27	PBS 26044, PBS 25103, PBS 21117, PBS 26047, PBS 21097, PBS 25026, PBS 26015, PBS 24110, PBS 24111, PBS 21110, PBS 24109, PBS 24085, PBS 25076, PBS 24008, PBS 25015, PBS 25017, PBS 6048, PBS 24117, PBS 24126, PBS 25027, PBS 24147, PBS 24146, PBS 26060, PBS 21102, PBS 4108, PBS 21103, PBS 25097
	IIb2	16	PBS 21095, PBS 21089, PBS 21088, PBS 21092, PBS 25029, PBS 21108, PBS 26043, PBS 25095, PBS 25096, GG 20, Somnath, PBS 24148, PBS 25106, PBS 21120, PBS 25023, PBS 26061
III	IIIA	5	PBS 25067, PBS 25099, PBS 26045, PBS 24125, PBS 25113
	IIIb1	35	PBS 24121, PBS 24120, PBS 24104, PBS 24105, PBS 24103, PBS 25070, PBS 24123, PBS 24127, PBS 25069, PBS 25054, PBS 24130, PBS 26042, PBS 25037, PBS 26050, PBS 24157, PBS 24158, PBS 24076, PBS 25122, PBS 25123, PBS 25124, PBS 25120, PBS 25121, PBS 21098, PBS 24132, PBS 21099, PBS 25035, PBS 24006, PBS 24038, PBS 24129, PBS 26022, PBS 24040, PBS 25089, PBS 26025, PBS 25045, PBS 25046
	IIIb2	9	PBS 21101, PBS 25062, PBS 25066, PBS 24135, PBS 24139, PBS 24134, PBS 25114, PBS 24137, PBS 24138

Table 5. Promising breeding lines identified for yield and kernel traits.

Trait	Promising Virginia Breeding Lines
Pod yield per plant (13g)	PBS 25111, PBS 25033, PBS 21114, PBS 24110, PBS 24085, PBS 26055, PBS 21118, PBS 21112, PBS 21095, PBS 21115
Days to 50% flowering (27 days)	PBS 21095, PBS 21089, PBS 21108, PBS 25062, PBS 25064, PBS 25076, PBS 25100, PBS 25114
SPAD Chlorophyll meter reading (>42)	PBS 25107, PBS 25090, PBS 25091, PBS 25081
Hundred pod weight (>112g)	PBS 24022, PBS 24133, PBS 21112, PBS 25094, PBS 21089, PBS 21088, PBS 21095, PBS 24148
Hundred kernel weight (>47g)	PBS 25029, PBS 24133, PBS 24022, PBS 21112, PBS 21108, PBS 25106, PBS 25096, PBS 26043
Sound mature kernel (>63%)	PBS 25106, PBS 24142, PBS 24022, PBS 25077, PBS 25101, PBS 21105, PBS 21108, PBS 25116, PBS 25096, PBS 26061, PBS 26043, PBS 24148, PBS 25115, PBS 25022
Shelling out turn (>66%)	PBS 21105, PBS 21120, PBS 26057, PBS 26061, PBS 24145, PBS 26056, PBS 24133, PBS 24152, PBS 26052
Kernel length (>15mm)	PBS 24133, PBS 24022, PBS 25095, PBS 21115, PBS 21108, PBS 26061, PBS 25044, PBS 21092
Kernel length to width ratio (>2mm)	PBS 21108, PBS 25022, PBS 21087, PBS 211086, PBS 21115, PBS 26031, PBS 26050, PBS 21115, PBS 26047, PBS 26015, PBS 25044, PBS 21084, PBS 24127, PBS 21085, PBS 25059, PBS 24022, PBS 25113

Table 6. Weather parameters recorded at Junagadh during Kharif 2017 and Kharif 2018.

Month	June		July		August		September		October	
Year	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
Max temperature (°C)	37	37.1	30.9	30.7	31.3	30.5	32.4	32.1	36.5	37.4
Min temperature (°C)	26.6	28.1	25.4	25.8	24.6	25	24.5	23.5	22.9	21.5
Mean temperature (°C)	31.8	32.6	28.1	28.3	28	27.7	28.5	27.8	29.7	29.5
Relative humidity (%)	69	65	85	85	84	83	79	71	51	47
Wind speed (Km/h)	23.9	12.5	25	9.3	25.3	9.3	27.4	5.2	20.2	2.7
Evaporation (mm)	6.8	8.2	2.4	2.9	3	2.9	3.9	4.3	5.9	5.5
Total rainfall (mm)	147.8	7.4	330.5	641.9	282.6	88.6	43.5	51.5	0	0
Total rainy days	10	1	18	14	10	5	4	0	0	0

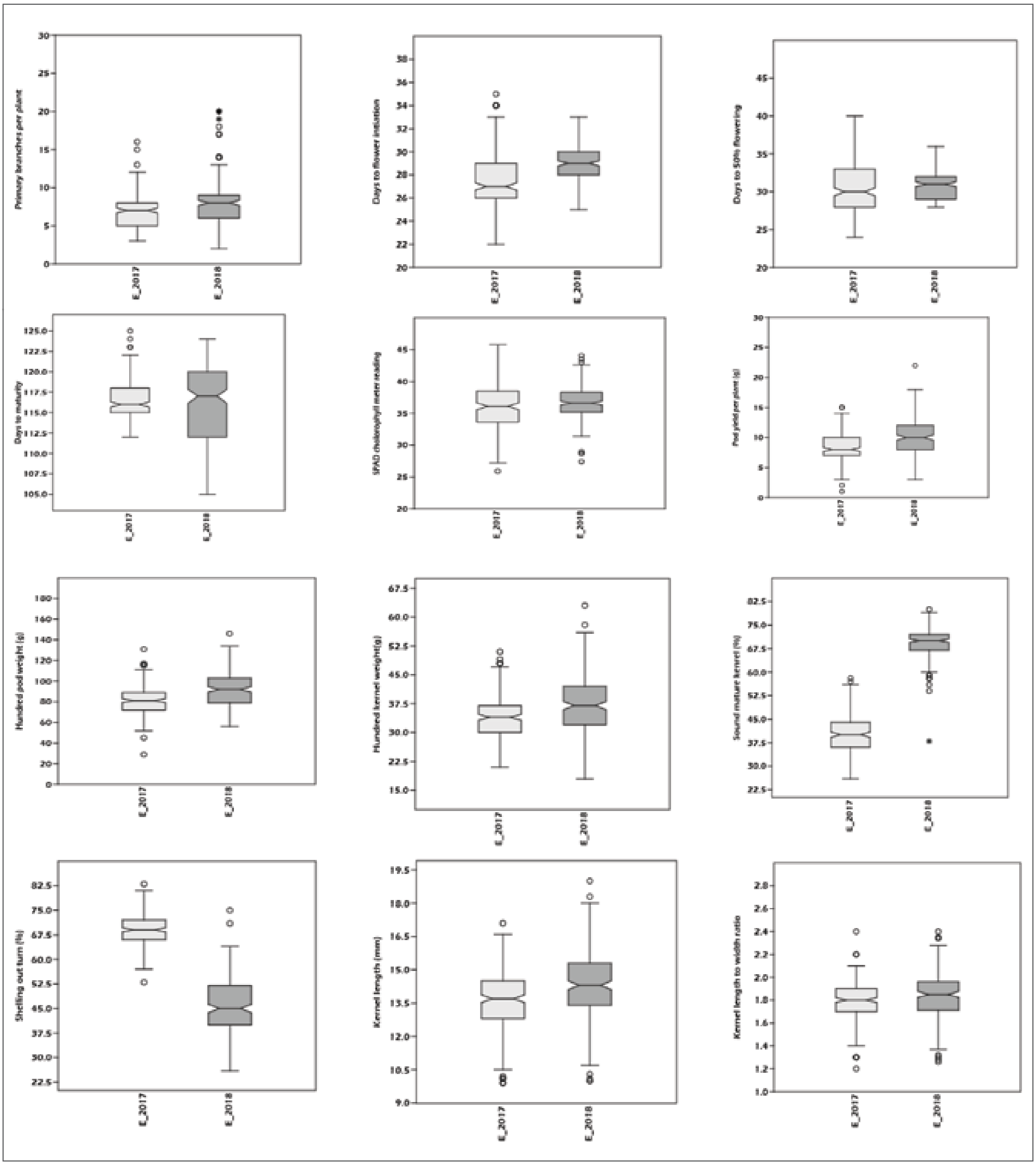

Figure 1. Box plot variation for pod yield and attributing traits in 215 Virginia breeding lines.

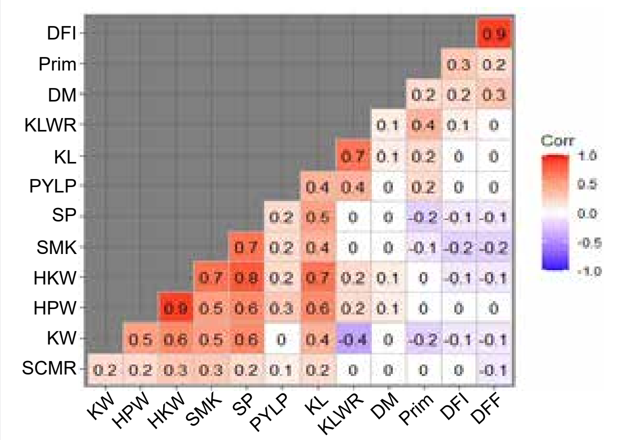

Figure 2. Relationship between pod yield, flowering and kernel characteristics.

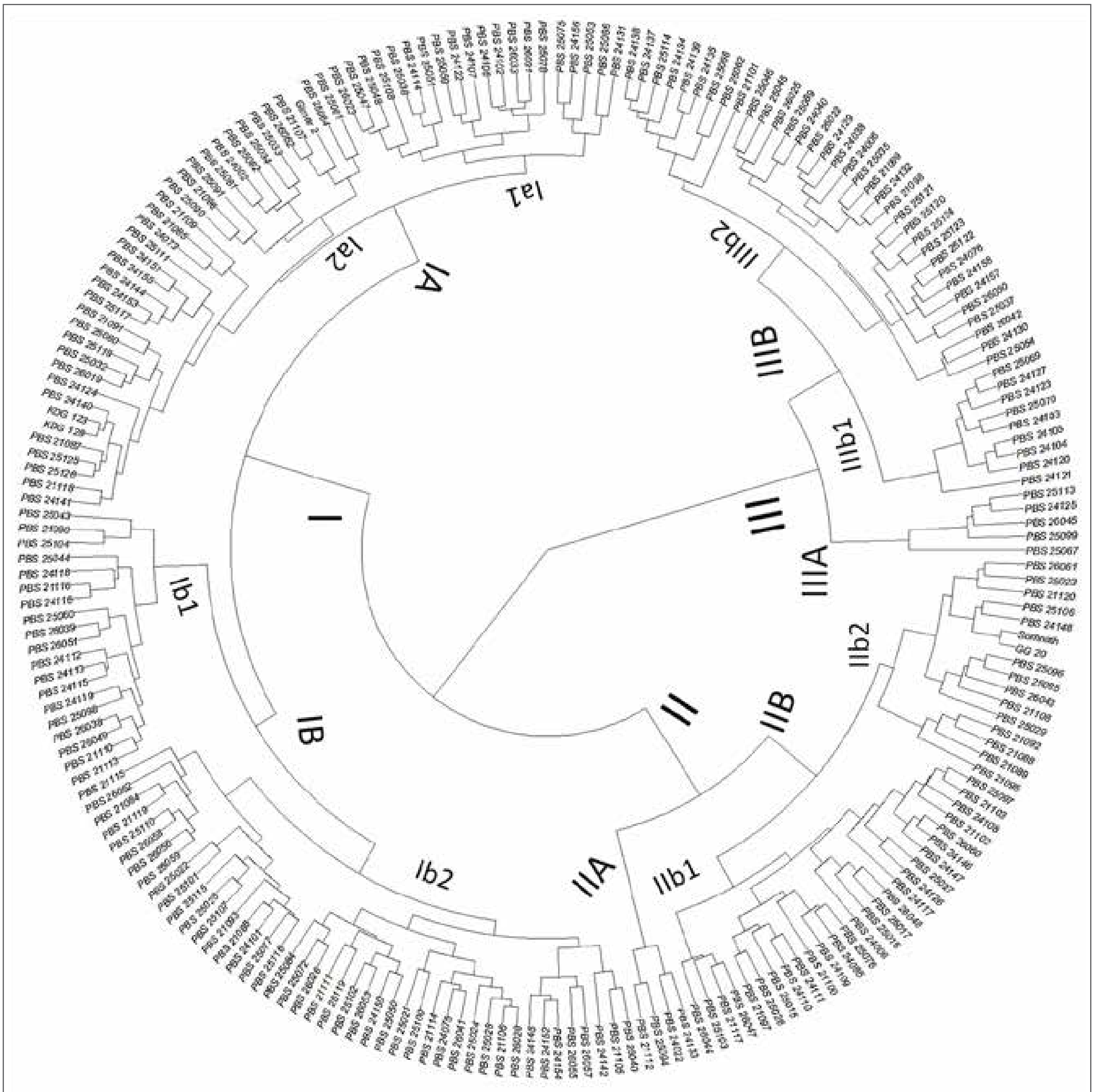

Figure 3. Dendrogram showing three major clusters among 215 Virginia breeding lines based on Euclidean distance.

References

Azharudheen TPM and Gowda MVC, (2013). An assessment of prospects of developing confectionery grade genotypes with multiple disease resistance in groundnut (*Arachis hypoageae* L.). Inter J of Biotechn and Bioengineering Research 4:347-354

Bhargavi G, Satyanarayana Rao V, Ratna Babu D and Narasimha Rao KL (2017). Genetic variability studies in Virginia bunch groundnut (*Arachis hypogaea* L.). Agric. Sci. Digest. 37(4): 310-313

Burton GW and De vane EM (1953). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron. J. 45: 479-481

Chiow HY and Wynne JC (1983). Heritabilities and genetic correlations for yield and quality traits of advanced generations in a cross of peanut. Peanut Sci. 37:13-17

Coffelt A, Seaton ML and VanScoyoc SW (1989). Reproductive efficiency of 14 Virginia-type peanut cultivars. Crop Sci. 29:1217-1220

Cox FR (1979). Effect of temperature treatment on peanut vegetative and fruit growth. Peanut Sci. 6(1): 14-17

Dudhatra RS, Viradiya YA, Joshi KB, Desai TA, Vaghela GK (2022). Genetic divergence analysis in groundnut (*Arachis hypogaea* L.) genotypes. Emer Life Sci Res. 8(1):114-118. Groundnut Crop Survey Report, IOPEPC, 2019

Erickson PI and Ketring DL (1985). Evaluation of genotypes for resistance to water stress in situ. Crop Sci. 25:870-876

FAO of United Nation, FAOSTAT, (2020). https://www.fao.org/faostat/en/#data/QCL http://www.fao.org/faostat/en/#data/QC, (Accessed 5 July 2020)

Gangadhara K, Dagla MC, Praveen Kona, Narendra Kumar, Ajay BC, Rathnakumar AL and Gor HK, (2019). Evaluation of large seeded groundnut advanced breeding lines for components of pod yield and water use efficiency. Int.J.Curr. Microbiol.App.Sci. 8(10): 835-844

Gangadhara K, Rathnakumar AL, Praveen Kona, Ajay BC, Narendra Kumar, Sushmita and Gor HK, (2020). Evaluation of groundnut germplasm for pod yield and its attributes in summer J. Oilseeds Res. 37:39-40

Golakia PR and Makne VG (1992). D^2 analysis in Virginia runner groundnut genotypes Indian J. Genet**.** 52 (3): 252-256

Gupta RP, Vachhani JH, Kachhadia VH, Vaddoria MA and Barad HR, (2015). Correlation and path analysis in Virginia groundnut (*Arachis hypogaea* L.) Electronic Journal of Plant Breeding 6(1):248-252

ICRISAT (1992). Annual report. International Crop Research Institute for Semi arid Tropics, Patencheru, India

Ikisan Agroinformatics and services, Groundnut, http://ikisan.com/tn-groundnut-history.html (Accessed 28 August 2020)

Johnson HW, Robinson HF and Comstock RE, (1955). Estimates of genetic and environmental variability in Soybean Agronomy J. 47:314-318

Kalariya KA, Singh AL, Chakraborty K, Ajay BC, Zala PV, Patel CB, Nakar RN, Goswami N and Mehta D, (2017). SCMR: A more pertinent trait than SLA in peanut genotypes under transient water deficit stress during summer. Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci. 87(2):579-589

Krishna KR, (2010). Agro ecosystems of South India: Nutrient dynamics, ecology and productivity, Brown Walker Publishers, Bocaraton, Florida, USA

Nigam SN, Nageswara Rao RC, Wynne JC, Williams M, Eitzner M and Nagabhushanam GVS, (1994). Effect and interaction of temperature and photoperiod on growth and partitioning in three groundnut (*Arachis hypogaea* L.) genotypes. Ann. App. Biol. 125:541-552

Nigam SN, Nageswara Rao and Wynne JC, (1998). Effects of temperature and photoperiod on vegetative and reproductive growth of Groundnut (*Arachis hypogaea* L.) J Agron and Crop Sci. 181:117-124

Robinson HF, Comstock RE and Harvey PH, (1949). Estimates of heritability and degree of dominance in corn. Agron. J. 41:353-359

Saini H and Sharma MM, (2018). Genetic variability and character association study in a RIL population for yield and quality traits in groundnut (*Arachis hypoagea* L.). Inter. J. of chemical studies. 6(6):2179-2185

Shinde HN, More SR, Pawar SV, Amolic VL, Shinde GC and Nimbalkar CA (2019). Genetic divergence study for different traits in groundnut. J Pharmacognosy and Phytochemistry 8(5):1501-1504