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Research Article

Identification of multi-trait donor sources in groundnut (*Arachis hypogaea* L.) for yield and seed quality improvement

B. Sukrutha[1], Srividhya Akkareddy[2*], L. N. Vemireddy[1], A. R. Nirmal Kumar[1], P. Latha[2] and K.V. Nagamadhuri[2]

[1]S.V. Agricultural College, Acharya NG Ranga Agricultural University (ANGRAU), Tirupati, Andhra Pradesh, India
[2]Institute of Frontier Technology, Regional Agricultural Research Station, ANGRAU, Tirupati, Andhra Pradesh, India
*E-Mail: a.srividhya@angrau.ac.in

Abstract
Identification/availability of potent trait-specific donors is core-step towards a targeted crop improvement program, especially in groundnut. For identification of multi-trait donors, 24 ANGRAU released and other popular genotypes that are grown in India were studied for yield, seed-biochemical and micronutrient-quality. ANOVA showed significance for all the characters indicating the availability of sufficient variability among genotypes. The characters primary-branches/plant, secondary-branches/plant, pod yield/plant, sucrose content, Total Free Aminoacids (TFA), Total Soluble Solids (TSS) and iron content (IC) exhibited high GCV and PCV which indicates that selection for these characters is effective. High heritability and genetic advance as per cent of mean were recorded for plant height, primary branches, secondary branches, pod yield, hundred-pod weight, sucrose content, TFA, TSS and IC indicates that these are under the control of additive gene-action. Significant positive associations were observed for primary branches, secondary branches, 100-pod weight, shelling per cent, protein and zinc content. Cluster analysis also revealed the availability of ample diversity that can be used in trait-improvement programmes. HeatMap revealed that Bheema, Kadiri-7, Nithya Haritha and Kadiri-8 can be used as potential multi-trait donor sources for different yield and quality-related traits *viz*., pod yield, 100-pod weight, 100-kernal weight, primary branches, oil content, Fe and Zn content. Further, it is observed that more number of uniformly maturing pod bearing primary branches is a potent yield contributing trait in groundnut. Hence, the identification of multi-trait donors will improve breeding strategy and provide an advantage of selection at the enhancement of yield through multi-traits along with kernel quality improvement.

Keywords: Groundnut, Multi-trait donor, correlation, heatmap, variability, cluster analysis

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) belongs to *Papilionaceae* subfamily of the *Fabaceae* family which consists of important and edible oilseed crops in the world. It is an allotetraploid (AABB;2n=4x=40), commonly known as Peanut and Monkey nut (UK). It is most preferable as an excellent source of nutrition to both humans and also animals due to its high content of digestible proteins

(22-30%), vitamins (E, K and B group), minerals (phosphorus, calcium, magnesium and potassium) and phytosterols. The oil content of the seed varies from 44 to 50%, which varies among the varieties and agronomic conditions. As groundnut is an important oilseed crop, there is also a need to improve the quality traits of groundnut. Value addition of groundnut through quality

enhancement results in huge foreign exchange. Hence, selection for quality traits in groundnut is necessary in breeding programmes.

The reports are scanty on directional trait specific donor identification in groundnut, one of the major oilseeds of India, when compared to staple cereals like rice, maize, wheat etc. Hence, the current study is focused on the identification of trait specific donors. Genetic variability is a prerequisite for any crop improvement programme to obtain high yielding varieties by the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficient of variability (GCV and PCV), heritability and genetic advance. In genetic studies, characters with a high genotypic coefficient of variation indicate the potential for an effective selection. Heritability and genetic advance are useful parameters for the plant breeders to determine the direction and

magnitude of selection. Therefore, the present study was planned to estimate the genetic parameters for yield and seed quality traits in groundnut. Cluster analysis and HeatMaps help in the selection of donor parents across traits through graphical representation.

MATERIALS AND METHODS
The experiment was carried out with 24 genotypes of Groundnut that were released from RARS (Regional Agricultural Research Station), ANGRAU, Tirupati and ARS (Agricultural Research Station), ANGRAU, Kadiri and a few other popular varieties that are grown across India (**Table 1**). The experiment was laid out in a Randomized Block Design with three replications during *kharif,* 2019 at Dry land farm, Regional Agricultural Research Station, Tirupati. In each replication every genotype was sown in three rows of 5 m length with a spacing of 30 cm between the rows and 10 cm between the plants within the row.

Table 1. Details of 24 groundnut genotypes used in the study

S.No.	Genotype	Pedigree	Habit Group SB/VB	Year of Release	Released Institute
1	JL-24	Selection from EC94943	SB	1979	ORS, Jalgaon
2	TPT-1	E.C.-106983 × 3	SB	1989	RARS, Tirupati
3	TPT-2	GAUG- 1 × Nc.Ac.FLA.14	SB	1989	RARS, Tirupati
4	TPT-3	Selection from TMV-10, a Virginia bunch variety with variegated testa	VB	1991	RARS, Tirupati
5	TAG 24*	TGS-2 × TGE-1	SB	1991	BARC, Mumbai
6	TPT-4	JL-24 × Ah316/S	SB	1995	RARS, Tirupati
7	Narayani	JL 24 × Ah316/S	SB	2002	RARS, Tirupati
8	Kalahasti	TCG1709 × TCG1518	SB	2002	RARS, Tirupati
9	Kadiri-6 (K-6)	JL-24 × Ah 316/s	SB	2002	ARS, Kadiri
10	Prasuna	TCG1717 × TCG1518	SB	2006	RARS, Tirupati
11	Abhaya	K-134 × TAG 24	SB	2006	RARS, Tirupati
12	Greeshma	TIR46 × JUG37	SB	2009	RARS, Tirupati
13	Kadiri-7(K-7)	{(ICGV 86522 × ICGV (FDRS) 10} × ICGV 91172	SB	2009	ARS, Kadiri
14	Kadiri-8 (K-8)	{(ICGV 86522 × ICGV (FDRS) 10} × ICGV 91172	VB	2009	ARS, Kadiri
15	Kadiri-9 (K-9)	Kadiri 4 × Vemana	SB	2009	ARS, Kadiri
16	KadiriHarithandra	91/57-2 × P I – 476177 (ICGX930181P3)	SB	2010	ARS, Kadiri
17	Rohini	Tirupati 4 × TIR 45	SB	2010	RARS, Tirupati
18	Bheema	TAG 24 × TG 19	SB	2010	RARS, Tirupati
19	ICGV-00350	ICGV-87290 × ICGV-87846	SB	2011	RARS, Tirupati
20	Dharani	VRI-2 × TCGP-6	SB	2012	RARS, Tirupati
21	Kadiri Amaravati	Kadiri 6 × Nc.Ac. 2242	SB	2016	ARS, Kadiri
22	TCGS-1073	Narayani × JAL30	SB	2018	RARS, Tirupati
23	TCGS-1157	TAG 24 × Jyothi	SB	2018	RARS, Tirupati
24	TCGS-894	TIR 46 × Kadiri 134	SB	2018	RARS, Tirupati

*hybridization with mutant TGS-2 obtained by irradiation with gamma rays (200 Gy) and mutant TGE-1 obtained by irradiation with X-rays (750 Gy).
ORS, Oil Seed Research Station; RARS, Regional Agricultural Research Station, Tirupati; BARC, Baba Atomic Research Station; ARS, Agricultural Research Station. SB, Spanish Bunch; VB, Virginia Bunch

Crop management was done as per the schedule. Harvesting was done 110 days after sowing.

Observations on seven quantitative parameters *viz.*, plant height (cm), the number of primary branches/plant, the number of secondary branches/plant, pod yield/plant (g), hundred pod weight (g), hundred kernel weight (g) and shelling percentage were recorded for all the genotypes of groundnut separately on randomly chosen five competitive plants in each genotype, in each replication. The analysis on six seed quality parameters *viz.*, protein content (μg/g) and oil content (μg/g) were done in grain analyser, Total Free Amino acids (TFA), Total Soluble Sugars (TSS), Total Sucrose content (Sadasivam and Manickam, 1961) and micronutrients *viz.* seed Fe (ppm) and Zn (ppm) content (using Atomic Absorption Spectrophotometer) were measured using standard protocols.

Data was subjected for analysis of variance (Panse and Sukhatme,1961) and genetic parameters *viz.* phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were estimated as per Lush (1940), Burton (1952), Allard (1960) and Johnson *et al*. (1955). Hierarchical cluster analysis was carried out using XLSTAT software employing 'Ward's method and clusters were formed on the basis of Euclidean distances. HeatMap was generated using XLSTAT software employing Red to Green through Black color scale and automatic color calibration and trait specific donor sources are visualized through the Map.

RESULTS AND DISCUSSION
Analysis of variance (ANOVA) showed significant differences for all the characters studied, indicating sufficient variability among the genotypes

(**Table 2**). The results of the analysis of variance were in accordance with the results obtained by Narasimhulu *et al.* (2012), John *et al.* (2013), Maurya *et al.* (2014), Vasanthi *et al.* (2015) Chandrashekhara *et al.* (2020), Jahanzaib *et al.* (2020), Shrotri *et al.* (2021) and Preeti *et al.* (2022). Hence, the availability of high trait variation among the genotypes suggests to utilize them in breeding programmes as donors or to release as commercial varieties.

Per se performance of yield and quality traits measured among the groundnut genotypes are presented in **Table 3**. The range of important yield governing traits viz. pod yield, shelling percentage and 100 seed weight were recorded as 10.40g-18.80g, 63.05-80.82%,38.67g-66g, respectively with mean values of 13.20g, 73.29% and 47.55g. Mean performance of 47 per cent for oil and 26 per cent for protein content were observed with values ranging from 45.87-48.87 and 25.57-26.80 per cent, respectively. These are in accordance with Jibrin *et al.* (2016), Mohammad Raza *et al.* (2018) and Aruna kumari *et al.* (2019). A similar range of oil (45-48%) and protein contents (25.5-26.8%) were reported by Noubissie *et al.* (2012) and Dwivedi *et al*. (1990). The ranges of micro nutrients Fe and Zn content were spread across 37.83 ppm- 206.67 ppm and 28.23 ppm- 57.33 ppm, respectively.

The characters *viz.*, the number of primary branches/plant (GCV-22.44 %; PCV-27.07 %), secondary branches/plant (GCV-97.34 %; PCV-119.90 %), pod yield/plant (GCV-22.41 %; PCV-28.66 %), sucrose content (GCV-38.61 %; PCV-39.25 %), total free amino acids (GCV- 29.00 %; PCV-29.13 %), total soluble sugars (GCV-38.54%; PCV-39.48%) and iron content

Table 2. Analysis of variance for yield and seed quality traits in groundnut

S.No.	Character	Mean sum of squares		
		Replications (df: 2)	**Treatments (df : 23)**	**Error (df : 46)**
1	Plant height	133.08	298.827**	27.71
2	Primary branches per plant	2.94	4.243**	0.56
3	Secondary branches per plant	0.13	2.660**	0.08
4	Pod yield per plant	4.97	30.948**	5.04
5	Hundred pod weight	285.89	1329.038**	217.79
6	Hundred kernel weight	36.15	144.416**	15.12
7	Shelling percentage	12.26	83.413**	16.33
8	Oil content	0.49	1.708**	0.06
9	Protein content	0.06	0.282**	0.07
10	Total Free Aminoacids (TFA)	6.31	22218.767**	64.76
11	Total Soluble Sugars (TSS)	0.02	0.062**	0.00
12	Total sucrose content	1.38	264.623**	2.91
13	Fe content	134.11	4359.679**	357.81
14	Zn content	48.76	194.429*	91.88

Table 3. *Per se* Performance of 24 groundnut genotypes for yield and seed quality traits

Genotype	Yield traits									Seed quality traits				
	PH (cm)	PBP (No.)	SBP (No.)	PYP (g)	100 PW (g)	100 KW (g)	SP- %	Oil %	Protein %	Sucrose µg g⁻¹	TFA µg g⁻¹	TSS g g⁻¹	Fe content ppm	Zn content ppm
Abhaya (TPT 25)	45.12	5	0	13.73	102.00	42.67	77.04	48.40	26.33	36.46	322.40	0.25	64.70	41.18
Bheema (TG 47)	53.01	7	2	18.80	149.33	66.00	71.25	47.50	26.20	38.22	239.33	0.21	68.13	43.67
Dharani (TCGS1043)	50.87	4	0	10.80	98.00	44.00	77.27	47.67	26.37	32.22	258.53	0.15	60.60	36.37
Dheeraj (TCGS1073)	50.61	4	1	12.93	112.67	52.67	72.17	48.70	26.33	16.19	370.87	0.51	64.30	28.23
Greeshma (TCGS-APNL-888)	47.14	5	1	13.20	88.00	46.67	78.95	48.67	25.57	29.52	226.05	0.43	65.57	45.23
ICGV00350	55.00	4	1	12.67	91.33	45.33	66.85	48.67	25.80	28.62	385.53	0.35	71.93	31.20
JL-24	47.07	5	1	13.80	112.47	48.62	72.68	48.40	26.27	13.36	255.02	0.35	62.97	29.98
Kadiri Amaravati	52.27	6	1	10.67	111.33	48.00	65.22	46.87	25.83	22.75	290.95	0.47	60.50	41.25
Kadiri Harithandra	50.03	5	0	11.73	95.33	43.33	69.91	47.77	25.93	26.33	358.72	0.35	64.70	34.27
Kadiri-6 (K6)	55.62	5	1	12.93	100.00	49.33	73.67	48.03	26.50	27.17	208.49	0.14	55.10	41.83
Kadiri-7 (K7)	44.54	7	2	18.00	141.33	56.67	70.24	45.87	26.53	31.39	407.87	0.33	69.96	40.41
Kadiri-8 (K8)	47.22	8	1	15.11	117.78	48.00	74.48	46.53	26.47	13.37	259.22	0.25	54.52	57.33
Kadiri-9 (K9)	48.41	5	0	13.47	91.33	43.33	80.82	47.50	26.37	19.97	239.76	0.21	71.57	48.99
Kalahasti (TCGS320)	46.54	5	2	13.20	148.67	55.33	63.05	47.33	26.40	27.19	328.81	0.60	63.77	49.72
Narayani (TCGS 29)	64.49	5	0	13.20	105.33	46.67	71.55	47.93	26.40	28.49	586.60	0.50	72.17	52.42
Nithya Haritha (TCGS1157)	44.57	6	1	14.93	116.00	48.00	71.75	47.60	26.80	36.93	309.90	0.56	62.13	49.03
Pragati (TCGS894)	49.15	3	1	12.84	113.33	49.56	69.72	48.10	25.87	9.81	290.13	0.55	37.83	35.27
Prasuna (TCGS 341)	52.01	4	0	13.60	110.00	44.67	76.15	48.50	26.30	11.79	196.80	0.59	74.77	43.11
Rohini (TCGS-APNL-913)	51.27	4	0	10.67	97.33	45.33	73.93	48.87	26.07	13.01	236.52	0.44	61.65	33.00
TAG24	43.83	7	0	12.87	93.93	43.98	75.80	48.50	25.73	36.80	311.34	0.26	66.80	35.66
TPT-1 (TCG 1704)	45.14	4	0	10.93	76.00	38.67	79.82	48.10	26.27	15.53	230.95	0.56	49.50	47.35
TPT-2 (TCG1706)	39.29	4	0	13.87	93.33	44.67	74.91	48.73	26.03	30.16	214.16	0.24	75.40	29.41
TPT-3 (TCG 1518)	42.76	6	0	12.56	87.76	42.44	76.84	47.43	25.87	8.86	237.79	0.34	76.67	45.58
TPT-4 (TCGS 30)	51.23	4	0	10.40	106.00	47.33	74.81	48.40	25.87	26.47	346.07	0.29	49.88	50.60
General Mean	49.05	5	1	13.20	106.61	47.55	73.29	47.92	26.17	24.19	296.33	0.37	63.55	41.30
Maximum	64.49	8	2	18.80	149.33	66.00	80.82	48.87	26.80	38.22	586.60	0.60	76.67	57.33
Mimimum	39.29	3	0	10.40	76.00	38.67	63.05	45.87	25.57	8.86	196.80	0.14	37.83	28.23
C.D.	8.679	1.23	0.47	3.701	24.333	6.41	6.662	0.39	0.44	2.81	13.27	0.05	31.19	15.81
SE(m)	3.039	0.43	0.17	1.296	8.52	2.245	2.333	0.14	0.15	0.98	4.65	0.02	10.92	5.53
SE(d)	4.298	0.61	0.23	1.833	12.05	3.174	3.299	0.19	0.22	1.39	6.57	0.03	15.45	7.83
C.V.	10.924	15.08	32.02	17.003	14.176	8.201	5.546	0.49	1.02	7.05	2.72	8.56	22.77	23.21
Kurtosis	2.24	0.87	2.32	1.48	0.29	1.28	1.71	0.95	-0.51	-1.22	4.44	-1.23	3.21	0.06
Skewness	-0.95	0.67	1.51	0.96	0.46	1.08	0.25	-0.96	-0.15	-0.18	1.75	0.11	1.65	0.08

PH : Plant height; 100 KW : Hundred kernel weight; TFA : Total free amino acids; PBP: Primary branches per plant ; SP: Shelling percentage; TSS: Total soluble sugars; SBP: Secondary branches per plant; Oil: Oil content; Fe: Iron content; PYP: Pod yield per plant; Protein: Protein content; Zn: Zinc content; 100 PW: Hundred pod weight; Sucrose: Sucrose content

Table 4. Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as percent of mean for yield and seed quality traits in groundnut

Character	General mean	Range		Variance		Coefficient of variation (%)		Heritability (broad sense) (%)	Genetic advance	Genetic advance as per cent of mean
		Maxi-mum	Mini-mum	geno-typic	pheno-typic	Geno-typic	Pheno-typic			
Plant height (cm)	49.05	64.49	39.29	93.70	122.32	19.73	22.55	76.53	17.13	35.55
Number of primary branches	5.09	7.93	3.07	1.30	1.90	22.44	27.07	68.67	1.89	38.30
Number of secondary branches	0.69	2.13	0.00	0.45	0.69	97.34	119.92	65.89	1.46	162.78
Pod yield per plant (g)	13.20	18.80	10.40	8.76	14.29	22.41	28.66	61.15	4.75	36.10
Hundred pod weight (g)	106.61	149.33	76.00	388.48	617.03	18.49	23.30	62.97	31.46	30.22
Hundred kernel weight (g)	47.55	66.00	38.67	9.55	16.48	6.49	8.54	57.77	7.40	10.16
Shelling percentage (%)	73.29	80.82	63.05	117.29	255.68	14.78	21.81	45.94	15.56	20.64
Oil content (%)	47.92	48.87	45.87	0.55	0.61	1.55	1.63	90.60	1.46	3.04
Protein content (%)	26.17	26.80	25.57	0.07	0.14	1.01	1.44	49.64	0.39	1.47
Sucrose content ($\mu g\ g^{-1}$)	24.19	38.22	8.86	87.24	90.06	38.61	39.25	96.78	18.93	78.25
Total free aminoacids ($\mu g\ g^{-1}$)	296.33	586.60	196.80	7383.96	7449.42	29.00	29.13	99.13	176.25	59.48
Total soluble sugars (g/g)	0.37	0.60	0.14	0.02	0.02	38.54	39.48	95.30	0.29	77.51
Fe content (ppm)	83.09	206.67	37.83	1333.71	1691.68	43.96	49.50	78.85	66.81	80.41
Zn content (ppm)	41.30	57.33	28.23	34.22	126.11	14.16	27.19	27.12	6.27	15.19

(GCV-43.96 %; PCV-49.50 %) exhibited high GCV and PCV which indicates that selection for these characters is effective (**Table 4**).

Moderate GCV and high PCV was observed for plant height (GCV- 19.73 %; PCV-22.55 %), hundred pod weight (GCV-18.49 %; PCV-23.3 %), shelling percentage (GCV-14.78 %; PCV-21.81 %) and zinc content (GCV-14.16 %; PCV-27.19 %). Low GCV and PCV was recorded for hundred kernel weight (GCV- 6.49 %; PCV-8.54 %), oil content (GCV-1.55 %; PCV- 1.63 %) and protein content (GCV-1.01 %; PCV-1.44 %). The results of Zaman *et al*. (2011), Mahesh *et al.* (2018) and Bhargavi *et al.* (2016) and Shrotri *et al.* (2021) were similar to the present report of high GCV and PCV for the number of primary branches per plant. High estimates of GCV for total soluble sugars and sucrose content were also reported by Rathod and Toprope (2018). Heritability in the broad sense ranged from 27.12 per cent for zinc content to 99.13 per cent for TFA. High heritability coupled with high genetic advance as per cent of mean recorded for plant height (H-76.53 %; GAM-35.55), number of primary branches/ plant (H-68.67 %; GAM-38.30), the number of secondary branches/ plant (H-65.89 %; GAM-162.78), pod yield/plant (H-61.15 %; GAM-36.10), hundred pod weight (H-62.97 %; GAM-30.22), sucrose content (H-96.78 %; GAM-78.25), total free aminoacids (H-99.13 %; GAM-59.48), total soluble sugars (H-95.30 %; GAM-

77.51) and iron content (H-78.85 %; GAM-80.41) indicates that these are under the control of additive gene action. Moderate heritability and GAM were exhibited by shelling percentage (H-45.94 %; GAM-20.64) and hundred kernel weight (H-57.77%; GAM-10.16). High heritability and low GAM were recorded for oil content (H- 90.6%; GAM-3.04).

High heritability and high genetic advance as per cent of mean for pod yield/plant were observed which are in accordance with Narasimhulu *et al*. (2012), Singh *et al*. (2017), Kumar *et al*. (2019) and Shrotri *et al*. (2021). Moderate heritability and moderate genetic advance as per cent of mean for hundred kernel weight were similar to the reports of Patil *et al*. (2014). In the present study, protein content and oil content showed low estimates of GCV and PCV. These results were in conformity with the findings of Vasanthi *et al.* (2015), Omprakash and Nadaf (2017) and Mahesh *et al.* (2018). High heritability coupled with high genetic advance as per cent of mean for plant height was also reported by Zaman *et al*. (2011), Patil *et al*. (2014), Bhargavi *et al*. (2016), Chavadhari *et al*. (2017) and Mahesh *et al*. (2018) and Shankar *et al*. (2019).

A correlation study reveals the association between trait pairs which in-turn give information to the breeder that helps in directional/anti-directional improvement of the multitude of traits at a time. The phenotypic (r_p)

and genotypic (r_g) correlation coefficients are furnished in **Table 5**. The pod yield per plant showed positive and significant correlation with plant height (r_g =0.314), primary branch number (r_p = 0.789; r_g = 0.926), secondary branch number (r_p = 0.501; r_g=0.721), hundred pod weight (r_p=0.524; r_g=0.720), shelling percent (r_p=0.532; r_g=0.819) and quality parameters *viz*., protein content (r_p=0.330; r_g=0.683) and zinc content (r_p=0.238; r_g=0.600) which suggests that increase or improvement in these characters lead to improvement in pod yield/plant.

Similar kinds of results i.e. significant positive correlation of pod yield/plant with hundred pod weight, shelling per cent, protein content was observed by Kumar *et al*. (201), Bhargavi *et al*. (2016) and Shoba *et al*. (2012). Similar results were also reported by Surbhi *et al*. (2016), Yusuf *et al*. (2017), Mahesh *et al*. (2018) and Preeti *et al*. (2022). A significant and positive correlation of pod yield/ plant and secondary branch number/ plant was reported by John *et al*. (2009), Vasanthi *et al*. (2015), Mahesh *et al*. (2018) and Preeti *et al*. (2022). A positive correlation of pod yield and primary branch

Table 5. Phenotypic and genotypic correlation analysis for yield and seed quality traits in groundnut

Character		PH	PBP	SBP	PYP	100 PW	100 KW	SP %	Oil %	Protein %	Sucrose	TFA	TSS	Fe	Zn
		Yield and its component traits								**Seed quality parameters**					
PH	r_p	1.000	0.204	-0.135	0.211	0.103	-0.188	0.078	-0.110	0.187	-0.184	0.149	-0.005	0.355**	0.183
	r_g	1.000	0.293*	-0.065	0.314**	0.188	-0.281*	0.169	-0.090	0.191	-0.212	0.163	0.008	0.451**	0.260*
PBP	r_p		1.000	0.539**	0.789**	0.548**	-0.167	0.525**	-0.660**	0.255*	0.089	0.000	-0.124	0.080	0.300*
	r_g		1.000	0.790**	0.926**	0.661**	-0.358**	0.672**	-0.825**	0.587**	0.134	0.006	-0.171	0.043	0.721**
SBP	r_p			1.000	0.501**	0.375**	-0.388**	0.234*	-0.544**	-0.006	-0.053	0.019	-0.033	0.149	0.190
	r_g			1.000	0.721**	0.623**	-0.599**	0.502**	-0.733**	0.246*	-0.042	0.021	-0.044	0.196	0.555**
PYP	r_p				1.000	0.524**	-0.101^NS	0.532**	-0.428**	0.330**	0.033	-0.024	-0.153	0.029	0.238*
	r_g				1.000	0.740**	-0.282*	0.819**	-0.618**	0.683**	0.074	-0.025	-0.232*	0.023	0.600**
100 PW	r_p					1.000	-0.341**	0.938**	-0.464**	0.311**	0.188	0.151	0.077	-0.039	0.166
	r_g					1.000	-0.659**	0.951**	-0.607**	0.686**	0.249*	0.225	0.131	-0.123	0.441**
100 KW	r_p						1.000	-0.007	0.295*	0.006	0.152	-0.245*	-0.277*	-0.180	0.046
	r_g						1.000	-0.404**	0.452**	-0.023	0.228	-0.334**	-0.364**	-0.242*	-0.016
SP %	r_p							1.000	-0.374**	0.330**	0.243*	0.070	-0.039	-0.097	0.178
	r_g							1.000	-0.542**	0.849**	0.384**	0.142	-0.016	-0.239*	0.502**
Oil %	r_p								1.000	-0.366**	-0.044	-0.145	0.097	0.092	-0.357**
	r_g								1.000	-0.424**	-0.067	-0.150	0.100	0.126	-0.649**
Protein%	r_p									1.000	0.063	0.097	0.017	-0.188	0.263*
	r_g									1.000	0.132^NS	0.126	0.035	-0.194	0.392**
Sucrose	r_p										1.000	0.278*	-0.358**	-0.076	0.005
	r_g										1.000	0.280*	-0.360**	-0.094	0.066
TFA	r_p											1.000	0.217	0.035	0.065
	r_p											1.000	0.216	0.041	0.122
TSS	r_g												1.000	0.030	0.094
	r_p												1.000	0.026	0.121
Fe	r_g													1.000	-0.006
	r_p													1.000	-0.153
Zn	r_p														1.000
	r_g														1.000

rp: phenotypic correlation, rg: genotypic correlation. p ≤ 0.05 (*) and 0.01(**)

PH : Plant height; 100 KW : Hundred kernel weight; TFA : Total free amino acids; PBP: Primary branches per plant ; SP: Shelling percentage; TSS: Total soluble sugars; SBP: Secondary branches per plant; Oil: Oil content; Fe: Iron content; PYP: Pod yield per plant; Protein: Protein content; Zn: Zinc content; 100 PW: Hundred pod weight; Sucrose: Sucrose content

number was reported by Vasanti *et al*. (2015) and Kumar *et al*. (2019). Among the quality traits, protein content showed a significant and negative correlation with oil content (r=-0.366) whereas, hundred kernel weight was positively correlated with oil content (r_p = 0.295; r_g = 0.452). Non-significant and positive correlation was recorded for sucrose content (r_p= 0.033; r_g = 0.74) and iron content (r_p= 0.029; r_g= 0.033). Similar kinds of results of negative correlation of protein content with oil content and positive correlation of hundred kernel weight with oil content were reported by Noubissie *et al*. (2012).

Among the yield component traits, significant positive correlations were observed for primary branches/ plant, secondary branches/ plant, hundred pod weight and shelling per cent at both phenotypic and genotypic levels whereas plant height showed a significant positive correlation at a genotypic level only.

Cluster analysis is used to group/ungroup the genotypes that are most similar/divergent towards the parameters under study. Clustering promotes the selection process and become effective and easy to the breeder in understanding and utilizing of the genotypes under study. Hierarchical cluster analysis revealed that 24 genotypes of groundnut were grouped into two main clusters i.e. Cluster A and Cluster B (**Fig.1**).

Cluster B contains five genotypes, whereas cluster A contains nineteen genotypes. Cluster A is a major one and is further divided into two sub-clusters Cluster A1 and A2. Sub-cluster A1 contains eight genotypes and sub-cluster A2 contains eleven genotypes. Genotypes from clusters A2 and B are more divergent and can be selected to utilize as potential parents for the improvement of positive characters exhibited by the respective genotypes.

The genotype Bheema with the highest pod yield/plant (18.80 g), hundred pod weight (149.33 g) and hundred kernel weight (66.0 g); Kadiri – 8 with the highest Zn content (57.33 ppm) and Nitya Haritha with the highest protein content (26.80 %) belongs to cluster B (**Fig. 1 & Table 3**). The genotypes Kadiri-9 showed the highest value for shelling per cent (80.82%) and TPT-3 had the highest Fe content (76.67 ppm) belongs to cluster A1. The genotype Rohini had the highest oil content (48.87 %) belongs to cluster A2. Hence, these genotypes that fall in divergent clusters are promising donor sources for improving respective traits.

HeatMaps generates complex values into easily understandable colored graphical forms. Color gradients (red to green through black) were given to analyze the similarity as well as divergence among genotypes across the traits. Red color indicates the lower value of a particular genotype with respect to a particular trait,
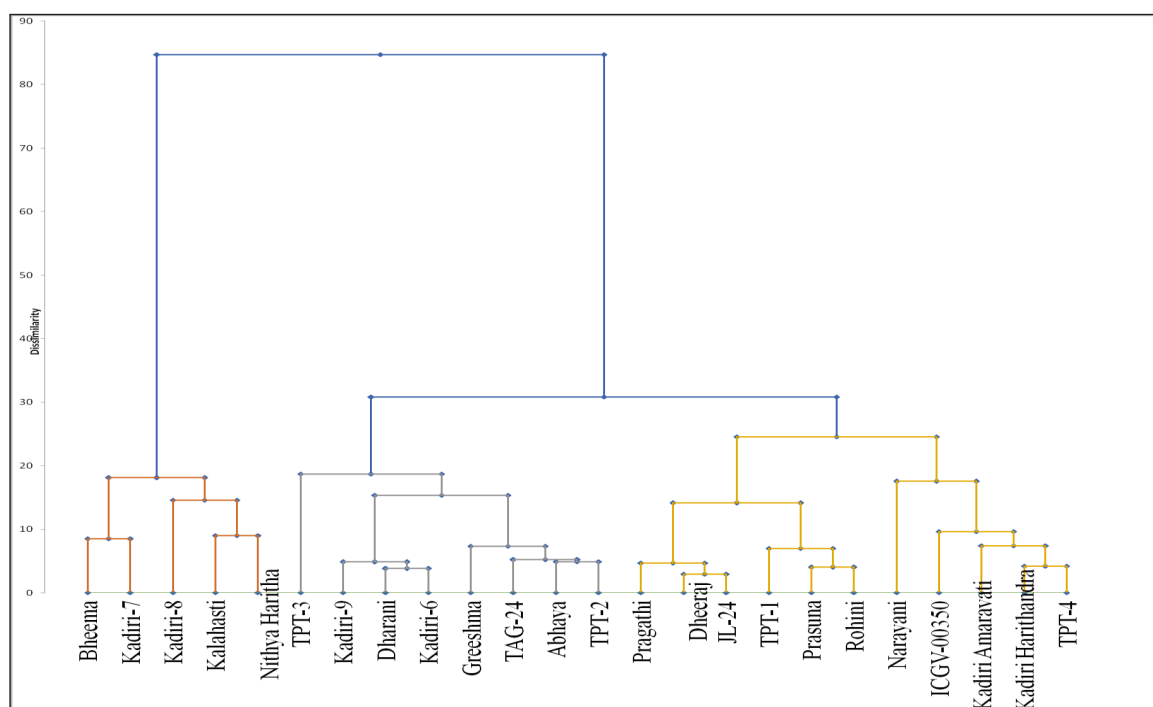

Fig. 1. Dendrogram generated through cluster analysis of groundnut genotypes

whereas the gradient of green color indicated higher value and black indicates a moderate value approximately (**Fig. 2**). For instance, the genotypes Bheema (TG 47) possessed higher values for pod yield/plant, hundred pod weight and hundred kernel weight. Kadiri – 9 showed the highest shelling percentage among all the genotypes. For oil content, Rohini possessed the highest value followed by Greeshma and TPT-3, which showed higher values for 'Fe' content, whereas Kadiri – 8 for the highest Zn content. Hence, the genotypes *viz*., Bheema, Kadiri 9, Rohini and Kadiri 8 are identified as valuable sources in breeding programs. Further, at the farmer level they generate more income, whereas at the consumer level they are found to be nutritive sources. (**Fig. 2 & Table 3**).
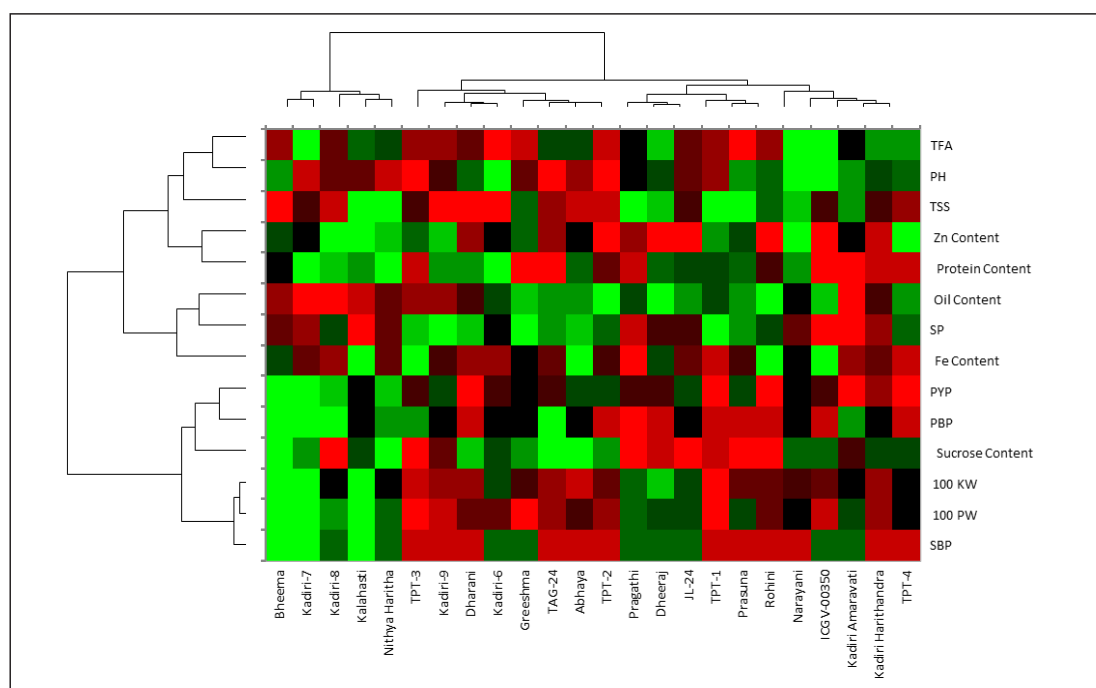
Fig. 2. HeatMap generated through cluster analysis

Table 6. Genotypes identified as potent donor sources for major yield and quality traits

S.No.	Genotype	Major yield traits	Quality traits
1	Bheema (TG 47)	Pod yield per plant (18.80 g) 100 pod weight (149.33 g) 100 kernel weight (66.00g) Primary branches/plant (7) Secondary branches/plant (2)	Oil content (47.50 %) Protein content (26.20 %) Sucrose (38.22 μg g^{-1}) Fe content (68.13 ppm) Zn content (43.67 ppm)
2	Kadiri-7 (K 7)	Pod yield per plant (18.00 g) 100 pod weight (141.33 g) 100 kernel weight (56.67g) Primary branches/plant (7) Secondary branches/plant (2)	Protein content (26.53 %) Sucrose (31.19 μg g^{-1}) TFA (407.87 μg g^{-1}) Fe content (69.96 ppm)
3	Nithya Haritha	Pod yield per plant (14.93g) Primary branches/plant (6) 100 pod weight (116.00g) 100 kernel weight (55.33g)	Oil content (47.93 %) Protein content (26.80 %) Sucrose (36.93 μg g^{-1}) TFA (309.90 μg g^{-1}) TSS (0.56 g g^{-1}) Fe content (62.13 ppm) Zn content (49.03 ppm)
4	Kadiri-8 (K 8)	Pod yield per plant (15.11g) 100 pod weight (117.88g) Primary branches/plant (8)	Protein content (26.47 %) Zinc (57.33 ppm)

Table 7. Genotypes identified with high performance for specific traits

1	Greeshma	Shelling percentage (78.95 %)	Oil content (48.67 %) Sucrose (29.52 µg g^{-1}) Fe Content (65.57 ppm) Zn Content (45.23 ppm)
2	Abhaya	Shelling percentage (77.04 %)	Oil content (48.40 %) Protein content (26.33 %) Sucrose (36.46 µg g^{-1}) TFA (322.40 µg g^{-1})
3	TPT-1	Shelling percentage (79.82 %)	Oil content (48.10 %) Protein content (26.27 %) TSS (0.56 g g^{-1}) Zn Content (47.35 ppm)
4	Kadiri-9 (K 9)	Shelling percentage (80.82%)	Protein content (26.37 %) Fe Content (71.57 ppm) Zn Content (48.99 ppm)
5	TPT-3	Primary branches/plant (6) Shelling percentage (76.84 %)	Fe content (76.67 ppm) Zn Content (45.58 ppm)
6	Dharani	Shelling percentage (77.27 %)	Protein content (26.37 %) Sucrose (32.22 µg g^{-1})
7	Dheeraj	100 pod weight (112.67 g) 100 kernel weight (52.67 g)	Oil content (48.70 %) Protein content (26.33 %) TFA (370.87 µg g^{-1}) TSS (0.51 g g^{-1})
8	Prasuna	100 pod weight (110.00 g) Shelling percentage (76.15 %)	Oil content (48.50 %) Protein content (26.30 %) TSS (0.59 g g^{-1}) Fe Content (74.77 ppm) Zn Content (43.11 ppm)
9	TPT-4	100 pod weight (106.00 g) 100 kernel weight (47.33 g)	Oil content (48.40 %) Sucrose (26.47 µg g^{-1}) TFA (346.07 µg g^{-1}) Zn Content (50.60 ppm)
10	JL 24	100 pod weight (112.47 g) 100 kernel weight (48.62 g)	Oil content (48.40 %) Protein content (26.27 %)
11	Kadiri 6	100 kernel weight (49.33 g)	Oil content (48.03 %) Protein content (26.50 %) Sucrose (27.17µg g^{-1})
12	Pragathi	100 pod weight (113.33 g) 100 kernel weight (49.56 g)	Oil content (48.10 %)
13	Kalahasthi	100 pod weight (148.67 g)	Protein content (26.40 %) Sucrose (27.19 µg g^{-1}) TFA (328.81 µg g^{-1}) TSS (0.60 g g^{-1})
14	Kadiri Amaravathi	100 pod weight (111.33 g) 100 kernel weight (48.00 g) Primary branches/plant (6)	-
15	ICGV00350	-	Oil content (48.67 %) Sucrose (26.62 µg g^{-1}) TFA (385.53 µg g^{-1}) Fe Content (71.93 ppm)
16	TAG 24	-	Oil content (48.50 %) Sucrose (36.80 µg g^{-1}) TFA (311.34 µg g^{-1})
17	Narayani	-	Protein content (26.40 %) Sucrose (28.49 µg g^{-1}) TFA (586.60 µg g^{-1}) TSS (0.50 g g^{-1}) Fe Content (72.17 ppm)
18	TPT 2	-	Sucrose (30.16 µg g^{-1}) Fe Content (75.40 ppm)
19	Kadiri Harithandra	-	Sucrose (26.33 µg g^{-1}) TFA (358.72 µg g^{-1})

Note: bold font shows the higher values for respective traits

The list of genotypes that could be used as donor sources for the multitude of traits governing yield and quality in peanut are detailed in **Table 6**. Bheema, Kadiri -7, Nithya Haritha and Kadiri -8 were identified as better donor sources pertaining to both yield and quality traits. Interestingly, it is observed that the genotype having the highest number of primary branches (6- 8) per plant, also bears more number of uniformly matured pods (at least 3-5 numbers/branch). Hence, these genotypes can be considered as the potential donor sources to increase yield level along with uniform maturity. However, when considered specific yield related and as well quality traits v*iz*., shelling per cent, 100 pod weight, 100 seed weight, oil, sucrose and Fe and Zn contents (**Table 7**) the genotypes that recorded higher values includes Greeshma (shelling: 78.95 %; oil: 48.67 %), Abhaya (shelling: 77.04 %; oil: 48.40 % and sucrose: 36. 46µgg^{-1}), TPT-1 (shelling: 79.82 %; oil: 48.10 % and Zn: 47.35 ppm), Kadiri-9 (shelling: 80.82% and Fe: 71.57 ppm), TPT-3 (shelling: 76.84% and Fe: 76.67 ppm), Dharani (shelling: 77.27% and sucrose: 32.22µgg-1), Dheeraj (100 pod weight: 112.67 g, 100 kernal weight: 52.67g, oil: 48.70% and TFA: 370.87µg g^{-1}), Prasuna (shelling: 76.15%; oil: 48.50 % and Fe: 74.77 ppm), TPT-4 (oil: 48.40% and Zn: 50.60 ppm), JL24 (100 pod weight: 112.47g, 100 kernal weight: 48.62 g and oil: 48.40%), Kadiri 6 (100 kernal weight: 49.33 g and oil: 48.03 %), Pragathi (100 pod weight: 113.33 g; 100 kernal weight : 49.56 g; oil: 48.10 %) and Kalahasthi (100 pod weight: 148.67g), Whereas for quality traits *viz*. high oil content, Fe, Sucrose and TFA the genotypes ICGV00350 (Oil: 48.67%; Fe: 71.93ppm), TAG 24 (Oil: 48.50%, Sucrose: 36.80µgg-1), Narayani (TFA: 586.60µg g-1; Fe: 72.17ppm) and TPT-2 (Fe: 75.40ppm) recorded higher values. The identified list of genotypes can be used for further improvement of high yielding varieties with moderate seed quality traits.

Of the 24 genotypes studied eight genotypes viz., TPT-3, TPT-4, Rohini, Bheema, Nithya Haritha, Kadiri -7, Kadiri 8 and Kadiri 9 are identified as potential donors for yield traits, kernel quality, Fe and Zn content. Thus, heatmap studies can be considered as a ready reckoner in identifying very valuable donor sources especially to use in the improvement of desired trait combinations of recipient parents, as shown in the study.

Development of any crop for the desirable traits, depends on the analysis of variability that exists among the genotypes and understanding of their relation. GCV, SCV, GAM and heritability are basic genetic parameters to measure before using a genotype as the donor and as well to understand the inheritance pattern in segregating populations towards selection. The current study revealed the existence of potential diversity among the genotypes through ANOVA and cluster analysis. High heritability and GCV, SCV and GAM of traits measured under study showed their importance in downstream breeding applications. Through the understanding of

association study, improvement of the multitude of traits is possible using the genotype panel. The genotypes Bheema, Kadiri -7, Nithya Haritha and Kadiri -8 were identified as potential donor sources for the majority of yield and quality related traits in groundnut. Hence, these can be used in breeding programs and as donors to improve a multitude of traits and as well at farmer-consumer level to meet their expectations apart from gaining nutritional security.

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