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Genetic diversity, association and principle component analyses for agronomical and quality traits in genomic selection training population of groundnut (*Arachis hypogaea* L.)

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Abstract

Groundnut (*Arachis hypogaea* L.) is the world's third important source of oil. A Genomic Selection Training Population (GSTP) comprising 340 genotypes was evaluated over four locations for two seasons to study genetic variability and association among agronomical and quality traits. GSTP exhibited significant variation among the genotypes, seasons and G x E interaction. Moderate to high magnitude of genotypic coefficient of variation and phenotypic coefficient of variation coupled with high heritability was observed for most quality traits. The first 7 components of PCA analysis contributed more than 75% cumulative variability. The training population grouped into three clusters in both the seasons. The number of pods/plant, pod and seed yield/plant were significantly and positively associated with each other, while test weight had negative association with number of pods/plant and had positive association with pod and seed yield during rainy season of 2015. The significant positive correlation was also observed between oil, linoleic acid and stearic acid; similarly, linoleic acid had positive association with stearic acid and palmitic acid. Significant negative correlation was observed between oil and protein content, oleic acid and linoleic acid content. The superior genotypes, namely, ICG 5221, ICGV 01393, ICGV 07220, ICGV 97120, ICGV 06420, ICG 9507, ICGV 06188 and ICGV 00440 were best performer for yield, yield components and nutritional quality traits while ICG 2381 and ICG 5221 recorded a better performance for oil content. The rainy season was found to have an advantage for vegetative, physiological growth, oil content, oleic and oleic to linoleic ratio while the post-rainy season led to forced pod filling and reduced maturity.

Key words: Genomic selection, GCV, PCV, genetic variability, correlation.

Introduction

Cultivated tetraploid groundnut (*Arachis hypogaea* L.) is an important oil seed crop grown in tropical, subtropical and warm temperate regions of the world. It is cultivated mostly in dryland in India, and is more suitable crop for diversification of farming systems to ensure productivity. It is also used as an important source of vegetable protein and used as fodder crop for animal feed. The groundnut production is largely confined to Asian and African countries, in which, Asia accounts for about 50% of area and 60% of worlds groundnut production with largest share of India followed by China in area. However, in total production, China accounts highest (42.5%) in the world followed by India (14.5 %). According to SEA report in 2018-19, the area under groundnut was 40.12 lakh ha with productivity of 931 kg/ha as compared to previous year with area of 41.31 lakh ha, production, 52.75 lakh tonnes and proctivity, 1269 kg/ha (https://pjtsau.edu.in). Groundnut yields remained low (~ 975 kg/ha) in India contrasting to its potential that can reach over 4000 kg/ha in intensive agriculture systems like that of USA and China. Several constraining factors, including diseases and pests, erratic rainfall, drought, poor soils, market instability and lack of locally adapted high-yielding varieties may be assigned for this low level of productivity (Narh et al. 2014).

The improvement of yield, disease resistance and quality traits largely depends on the magnitude of

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genetic variability and the extent to which its determining characters are heritable. However, the progress in breeding through selection ride on genetic variability and groundnut has a challenge due to inherent low genetic variability Direct selection for groundnut yield improvement is often misleading because yield is polygenic trait controlled by many genes with small effects. It has been indicated by several researchers that the genetic variability in groundnut is low and hence it poses a bottleneck for its improvement. Therefore, efforts are needed to enlarge the genetic variability by breeding for high yield and improvement in oil, protein and fatty acids. To make better understanding of the variability and heritability components of the material along with that association among the traits towards the improvement of groundnut, ICRISAT has developed a Genomic Selection Training Population (GSTP) representing 21 countries. Having high protein content, a healthy oil profile may serve as a source of a key micronutrients including magnesium thus, groundnut has high medicinal value (Tidey 2012) and therefore, used by UNICEF to treat acute malnutrition among children and women. For confectionary purpose cultivars with high O/L ratio and higher protein content are preferred (Nigam et al. 1989; Bandyopadhyay et al. 2000). Oil quality in terms of high proportion of oleic acid is desirable to increase product shelf life (Bolton et al. 2002) and provide several health benefits to consumers.

Therefore, the genetic variability in the groundnut should be enlarged and used for breeding programme for the improvement in yield and other contents, *viz.,* oil, protein and fatty acids. Useful genetic resource and its broadening can facilitate the fast tracking variety development and release. Considering the above points, the present study was undertaken to evaluate the genotypes for yield and its components and different quality traits to estimate the genetic variability and to work out the inter-relationship among different characteristics in groundnut.

Materials and methods

Experimental material consisted of 340 diverse genotypes (Supplementary Table S1) which include sub-species and botanical varieties of cultivated groundnut to study agronomic and economically important traits and the quality characteristics. The same set of genotypes was also considered for genomic selection training population.

The experiment was laid out in alpha (α) lattice design with two replications. Each genotype was sown in single row of 4 m at ICRISAT Patancheru, whereas 2 m at Agriculture Research Station, Kawadimatti, UAS, Raichur and UAS, Dharwad with the spacing of 30 cm and 10 cm between rows and plants, respectively. Each replication was divided into 20 blocks to reduce soil heterogeneity. The seeds were planted at uniform depth. All recommended agronomic package of practices were followed to raise good crop stand at all locations. Observations on agronomic traits, namely, days to 50 % flowering, plant height (cm), number of pods per plant, pod yield per plant (g), seed yield per plant(g) were recorded considering five randomly selected plants, shelling per cent and pod yield per hectare (kg) were calculated using formulae and 100 seed weight (gm). The data was analysed using SAS 9.2 v;software for analysis of variance (ANOVA) and variability, SPSS 16.0 v; for correlation and XL.STAT for Principal Component Analysis (PCA) and ward's clustering.

The observation on nutritional quality traits (oil, protein, oleic acid, linoleic acid, palmitic acid and stearic acid) were estimated by near infrared spectroscopy (NIRS) (Panford 1990; Misra et al. 2000 and Upadhyaya et al. 2012) at Deptt. of Groundnut Breeding, ICRISAT, Hyderabad, India. The O/L ratio was calculated by per cent of oleic acid/per cent of linoleic acid. The replicated data over 10 seasons for these traits were subjected for statistical analysis using SAS ver.9.2 and association analysis using SPSS ver.16.0.

Results and discussion

Genetic variability

The analysis of variance indicated that that genotypes were genetically diverse. This could be attributed to their divergent pedigree, origin and different botanical groups of germplasm lines. The mean performance for the days to 50 % flowering, plant height and no. of pods/plant were better expressed in *kharif* as compared to *rabi* season, while remaining traits such as pod and seed yield per plant, shelling per cent and 100 seed weight performed better in *rabi*. The phenotypic variance (σ2P) of all the agronomical traits was higher than the genotypic variance (σ2G) (Table 1). The range in heritability values was also wide but the heritability percentage differed as per season. Genetic advance as per cent of mean (GAM) was recorded high for all the studied traits except for

Table 1. Variability parameters for yield and related traits of genomic selection training population at UAS, Raichur during *rabi* 2014 and *kharif* 2015

Source of variation	Seasons	Days to 50% flowering	Plant height (cm)	No. of pods/ plant	Pod yield/ plant (gm)	Seed yield/ plant (gm)	Shelling per cent (%)	Pod yield/ ha (kg)	100-seed weight (gm)
GCV	*Rabi* 2014	3.194	13.349	22.518	20.550	20.767	5.318	32.421	21.504
	Kharif 2015	3.705	19.432	32.471	31.142	31.569	2.773	33.287	23.908
PCV	*Rabi* 2014	4.070	18.054	23.254	21.524	21.731	6.855	33.985	22.589
	Kharif 2015	4.653	20.858	33.360	32.201	32.870	4.101	37.443	24.055
Hbs (%)	*Rabi* 2014	61.593	54.677	93.770	91.151	91.322	60.194	91.006	90.626
	Kharif 2015	63.408	86.787	94.741	93.531	92.243	45.714	79.029	98.783
GAM	*Rabi* 2014	5.163	20.334	44.919	40.416	40.882	8.500	63.713	42.171
	Kharif 2015	6.078	37.291	65.108	62.043	62.460	3.862	60.958	48.951
GA	*Rabi* 2014	2.501	4.330	8.826	7.790	5.172	5.552	1233.669	18.169
	Kharif 2015	2.015	9.653	14.117	11.799	7.232	2.480	913.045	17.977
Mean	*Rabi* 2014	48.432	21.293	19.648	19.275	12.651	65.32	1936.305	43.085
	Kharif 2015	33.147	25.886	21.683	19.017	11.579	64.21	1497.828	36.725
Range	*Rabi* 2014	37.5-54.5	13.5-32.5	11.47-40	9.92-37.02	6.37-25.31	56.26-73.17	800-4799.54	24.19-87.9
	Kharif 2015	28-38	12.5-50.2	12.5-56.6	11-48.65	7-29.97	54.74-72.83	646.67-3703.34	21.85-87.55

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variaiton; Hbs = Heritibality in broad sense; GAM = Genetic advance as per cent of mean and GA = Genetic advance

days to 50% flowering and shelling per cent in both the seasons. To study the genetic variability in respect of quantitative characters is essential for selection of suitable genotypes. An assessment of heritable and non-heritable components in the total variability observed is indispensable in adopting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation. Since the measured genetic variability was of high magnitude in present study, individual plant selection could be practiced for the above mentioned characters to get high yielding genotypes. Several researchers have earlier studied genetic parameters in groundnut and reported similar findings for different agronomical traits (Narth et al. 2014; Upadhyay 2003; John et al. 2008, 2009). Zaman et al. (2011) reported highly significant variations among the groundnut genotypes for various agronomic characters studied. The highest GCV was observed for karnel yield/ha, karnel yield/plant, no. of branches/ plant, no. of nuts/plant, 100 kernal weight and plant height. The highest heritability was also observed for these traits. Solanki et al. (2020) also observed similar results in their study on a different set of groundnut varieties.

Analysis of variance showed significant variation among genotypes, seasons and genotypes X seasons for all the nutritional quality traits indicating the presence of abundant amount of variability in the material. Low to moderate PCV, GCV and GAM were recorded for nutritional quality traits as also reported earlier (Cholin et al. 2010) except O/L ratio. However the difference between GCV and PCV was more across the seasons indicating differential performance of genotypes in different seasons due to G x E interaction. Resultantly, it narrowed down the effectiveness of phenotypic selection, as also observed by Painawadee et al. (2009). High heritability was observed for all the traits except oil and protein in which moderate heritability was recorded in pooled analysis (Table 2), however, seasonal variations due to G x E interaction were recorded for per cent heritability (data not shown). However, low to moderate genetic advance as per cent of mean was recorded, whereas oleic acid, linoleic acid, stearic acid and O/L ratio had recorded high heritability coupled with moderate to high genetic advance as per cent mean but pooled analysis showed

Table 2. Genetic variability components, mean and range for oil, protein and fatty acid contents in Genomic Selection Training Population of groundnut in pooled over ten environments

Traits	GCV	PCV	Mean	Range	h^2.b (%)	GAM
Oil	3.01	4.08	49.45	46.60-58.25	54.57	4.59
Protein	2.95	5.23	24.94	22.77-27.42	31.89	3.44
Oleic acid (O)	7.73	9.57	43.48	36.83-74.69	65.27	12.87
Linoleic acid (L)	9.07	10.73	34.73	8.32-42.38	71.45	15.79
Palmitic acid	5.13	6.57	11.63	8.92-13.69	60.81	8.23
Stearic acid	10.76	14.72	2.34	1.60-3.47	53.45	16.21
O/L ratio	47.58	53.28	1.32	0.89-10.87	79.76	87.54

moderate heritability for oil content, protein content and stearic acid. Thus, simple selection for these traits would be more effective since the additive genetic component may be predominant in expression of these traits. (Paniwadee et al. 2009). G x E interactions have played a greater role to influence these parameters in many oilseed crops including groundnut (Jatti et al. 2008; Janila et al. 2016; Nowosad et al. 2017). An enhanced adaptation to suitable environmental conditions could provide higher seed quality and oil contents (Yole and Uzun 2019). It is not mandatory that high heritability associated with high genetic advance (Swarup and Chagule 1962) would always be effective for selection. If the heritability is governed by non-additive effects, the genetic advance will be low, same as if heritability is controlled by additive effects, it would be associated with high genetic advance (Panse, 1957).

Genetic correlations

The correlation values varied as per the season. No. of pods/plant showed strong positive correlation with pod yield/plant, seed yield/plant and pod yield//ha in *rabi* season (Table 3). Pod yield/ha displayed strong positive correlations with no. of pods/plant, pod yield / plant and seed yield/plant and thus these traits were observed to be positively correlated among them. This indicated that selection based on these traits will ultimately lead to high yielding genotypes. However during *kharif*, plant height showed positive correlation of pod yield/plant with seed yield/plant (Table 4) but not as strong as in *rabi*. Similarly, pod yield/plant and,

Table 3. Phenotypic and genotypic correlation matrix for yield and yield component traits of genomic selection training population at Raichur during *rabi* 2014

		DFF	PH	NPPP	PYPP	SYPP	SH	PYPHA
DFF	P G	1.00						
			1.00					
PH	PG	0.041	1.00					
			0.012	1.00				
NPPP	P G	0.060	-0.030	1.00				
			0.089*	-0.052	1.00			
PYPP	P G	0.027	-0.039	0.733**	1.00			
			0.033	-0.082*	0.752**	1.00		
SYPP	P G	0.040	-0.047	0.711**	0.978**	1.00		
			0.056	-0.084*	0.727**	0.980**	1.00	
SH	P G	-0.070	-0.052	-0.018	-0.011	-0.013	1.00	
			-0.206**	-0.020	-0.026	-0.028	-0.019	1.00
PYPHA	P G	-0.036	0.030	0.334**	0.546**	0.539**	0.029	1.00
		-0.024	0.077*	0.337**	0.551**	0.546**	0.025	1.00
HSW	P G	-0.044	-0.038	-0.007	0.065	0.060	-0.012	-0.001
		-0.046	-0.088*	-0.012	0.063	0.057	-0.037	-0.002

DFF = Days to 50% flowering; PH = Plant height; NPPP = No. of pods/plant; PYPP = Pod yield/plant; SYPP = Seed yield/plant; SH = Shelling per cent

Table 4. Phenotypic and genotypic correlation matrix for yield and yield component traits of genomic selection training population at Raichur during *kharif* 2015

		DFF	PH	NPPP	PYPP	SYPP	SH	PYPHA
DFF	P G	1.00						
		1.00						
PH	P G	-0.059	1.00					
		-0.090*	1.00					
NPPP	P G	0.010	0.163**	1.00				
		0.054	0.169**	1.00				
PYPP	P G	0.013	0.183**	0.753**	1.00			
		0.068	0.196**	0.799**	1.00			
SYPP	P G	0.020	0.161**	0.745**	0.987**	1.00		
		0.091*	0.175**	0.805**	0.996**	1.00		
SH	P G	0.059	-0.126**	-0.079*	-0.094*	0.055	1.00	
		0.318**	-0.235**	-0.112**	-0.175**	-0.093*	1.00	
PYPHA	P G	-0.048	0.192**	0.475**	0.706**	0.691**	-0.088*	1.00
		0.014	0.220**	0.536**	0.821**	0.815**	-0.172**	1.00
HSW	P G	0.036	-0.149**	-0.172**	0.096*	0.106**	0.073	0.126**
		0.057	-0.169**	-0.176**	0.104**	0.120**	0.155**	0.160**

seed yield/plant were found positively correlated during *kharif*. Remaining traits showed low to moderate or negative correlations with yield/ha. It pointed out that seasonal fluctuations may also affect the correlation values among certain traits. The days to 50 % flowering during *kharif* 2015 at UAS Raichur followed the same trend as in *rabi* 2014 at same location. The correlations of plant height with other traits might have been affected due to congenial weather during *kharif*.

Extent and nature of relationship among different characters determines the direction of selection for desirable traits (Nunes da Luz et al. 2011). Phenotypic and genotypic correlations were estimated among all quantitative traits that are closely related to grain yield using BLUPs. The findings in present study followed the similar trends as reported earlier. The seed yield/plant has been reported to have highly significant and positive association with nut size, no. of nuts/plant, karnel size and days to 50% flowering (Zaman et al. 2011). Pod yield/plant in virginia groundnut has been reported significantly and positively correlated at both genotypic and phenotypic levels with no. of matured pods/plant, no. of pods/plant, 100-kernel weight, biological yield/plant and harvest index (Solanki et al. 2019). Matured pods per plant, 100-kernel weight, biological yield and harvest index showed high positive direct effects on pod yield per plant. Correlation and path co-efficient studies undertaken by Vasanthi et al. (2015) during *kharif* season indicated that the characters, number of mature pods/plant, no. of primary branches/plant and 100-seed weight may be given major emphasis for the selection of high yielding genotypes of groundnut.

Table 5. Association pattern among the nutritional quality traits in pooled over ten environments of groundnut Genomic Selection Training Population

	OIL	PRO	OA	LA	PA	SA	O/L
OIL	1						
PRO	-0.287**	1					
OA	-0.097	-0.027	1				
LA	0.229**	-0.031	-0.963**	1			
PA	0.047	0.043	-0.608**	0.509**	1		
SA	0.361**	0.09	-0.262**	0.286**	-0.154**	1	
O/L	-0.067	0.007	0.747**	-0.770**	-0.377**	-0.131*	1

Pro = Protein; OA = Oleic acid; LA = Linoleic acid; PA = Palmitic acid; SA = Stearic acid and O/L = Oleic/Linoleic ratio

To study association pattern among the nutritional quality traits the data was pooled over ten environments for Genomic Selection Training Population (Table 5). Oil content had negative association with protein content in training population in all seasons and across the locations. Increase in oil content would be at the cost of protein content and *vice-a-versa* (Dwivedi et al. 1990; Cholin et al. 2010). Oil content had positive association with linoleic acid content, but oleic acid and linoleic acids had inverse relationship. Groundnut breeding programme generally aims at getting genotypes which contain high oil, high protein content and heaving better oil quality parameters. Here desirable traits like oil content, protein content and oleic acid had inverse relationship among themselves in all seasons. It is difficult to get genotypes having these traits in combination (Cholin et al. 2010; Mukri et al. 2012). The oleic acid had significant positive association with O/L ratio in all seasons and locations, while negatively associated with linoleic acid, palmitic acid and steric acid content. Therefore, the palmitic acid and stearic acid content could be targeted to increase oleic acid content (Alt et al. 2005). The inverse relationship of oleic acid with palmitic and linoleic acid was also evident from the earlier studies (Cholin et al. 2010; Gangadhara et al. 2015). Interestingly, the association between linoleic acid and palmitic acid, linoleic acid and stearic acid were positive. Significant negative association between linoleic acid and O/L ratio were also observed (Table 3). Selection for reduced palmitate and stearate also facilitate indirectly to select the genotype with reduced linoleic acid (Rebertzke et al. 2001; Cardinal et al. 2007; Cholin et al. 2010).

High oil content groundnut varieties are currently in high demand from the oil-crushing factories. Recent studies have demonstrated the possibility to raise oil content to as much as 55% of seed composition, presenting up to 80% oleic (Chen et al. 2019; Varshney 2016). Oil quality in terms of high proportion of oleic acid is desirable to increase product shelf life (Bolton et al. 2002) and provide many health benefits to consumers. The challenge is to build on these advances in groundnut improvement for oil content and quality (Holbrook et al, 2016; Parsley and Anthony 2017) to put these traits together with other desirable agronomic traits (i.e. yield and disease resistance) in an ideal cultivar for stakeholders of the value chain. The present study identified the germplasm lines, ICG

Table 6. Percentage of variation explained by the first seven principal components (PCs) in genomic selection training population at Raichur *rabi* 2014

PC's	Eigenvalue	Variability	Cumulative (%)	DFF (%)	PH	NPPP	PYPP	SYPP	PYPHA	SH	HSW
F1	3.568	22.300	22.300	0.000	0.000	**0.546**	**0.830**	**0.815**	**0.646**	0.000	0.003
F2	2.212	13.826	36.126	0.018	0.001	0.005	0.014	0.014	0.007	0.000	0.008
F3	1.447	9.047	45.172	0.305	0.026	0.099	0.033	0.033	0.129	0.054	0.018
F4	1.380	8.626	53.798	0.028	0.214	0.005	0.002	0.001	0.011	0.005	0.000
F5	1.146	7.161	60.959	0.002	**0.226**	0.032	0.030	0.028	0.087	0.002	**0.458**
F6	1.051	6.569	67.528	0.034	0.073	0.003	0.000	0.000	0.004	**0.573**	0.016
F7	0.957	5.982	73.510	0.004	0.011	0.056	0.013	0.012	0.042	0.087	0.247

Table 7. Percentage of variation explained by the first seven principal components (PCs) in genomic selection training population at Raichur *kharif* 2015

PC's	Eigenvalue	Variability	Cumulative (%)	DFF (%)	PH	NPPP	PYPP	SYPP	PYPHA	SH	HSW
F1	4.104	25.649	25.649	0.000	0.063	**0.598**	**0.888**	**0.871**	**0.780**	0.009	0.009
F2	2.286	14.287	39.936	0.038	0.007	0.000	0.011	0.011	0.012	0.001	0.020
F3	1.574	9.837	49.772	0.002	0.212	0.038	0.000	0.003	0.004	0.203	**0.453**
F4	1.379	8.618	58.390	0.109	0.001	0.005	0.004	0.009	0.002	0.089	0.013
F5	1.185	7.408	65.798	**0.436**	0.165	0.006	0.006	0.012	0.002	0.071	0.015
F6	1.029	6.432	72.229	0.063	0.004	0.012	0.002	0.005	0.017	0.039	0.002
F7	0.961	6.003	78.233	0.018	0.018	0.153	0.007	0.017	0.051	0.120	0.311

DFF=Days to 50 per cent flowering, PH=Plant height (cm), NPPP=Number of pods per plant, PYPP=Pod yield per plant (g), SYPP=Seed yield per plant (g), SH=Shelling percent, PYPHA=Pod yield per hectare (kg) and HSW=100 seed weight (g)

2381, ICG 5221, ICGV 06420, ICG 14482 and ICG 14475 which are consistent across all the environments for nutritional and quality traits. Genotypes, ICG 2381 and ICG 5221 were highly stable for oil content and therefore, may be recommended for their utilization in breeding improvement of oil content in groundnut.

Cluster analysis

The PCA on the mean values of the entire training population was performed which provided a reduced dimension model that could indicate measured differences among the genotypes in the population. The results revealed the importance of the first seven Principal Components (PCs) in discriminating the groundnut genomic selection training population. Since first seven PCs had Eigen values greater than or equal to 1.0 during *rabi* and *kharif*, respectively (Tables 6 and 7). The percentage of total variance explained by the first seven PCs in each season was more than 70%. PC1 separates the genotypes for the traits for no. of pods/plant (0.546), pod yield/ plant (0.830), seed yield/ plant (0.815) and pod yield/ha (0.646) in *rabi* 2014. No. of pods/plant (0.598), pod yield/ plant (0.888), seed yield/plant (0.871) and pod yield/ha (0.780) in *kharif* 2015. The PC 1 was most important component and accounted for more variation in both seasons.

Seasonal variations were recorded for principal component analysis. A total 73.51 per cent variability was expressed in *rabi* season which is cumulative of first seven principal components. Three clusters were formed, in this season in which cluster I, II and III consists of 154, 185 and 1 genotypes, respectively. Cluster I showed better performance for protein content (25.63), palmitic acid content (11.99) and steric acid content (2.28) while Cluster II displayed for plant height (21.49), no. of pods/plant (21.72), pod yield (21.52) seed yield/plant (14.14), 100-seed weight (43.64) and oil content (50.67%), cluster III has out break for less number of days to 50% flowering (47.90), pod yield/ha (3383.00), shelling % (69.83), oleic acid content (76.73), linoleic acid content (4.63) and O/L ratio (16.56).

Wards cluster analysis based on first seven principal component scores resulted in three clusters. The total 78.23% variability has been accounted by the first seven principal components. All the 340 genotypes in training population were distributed among clusters I, II and III with 125, 214 and 1 genotypes in each clusters, respectively (Supplementary Tables S1 and S2). Performance with respect to agronomic and quality traits varied. The clusters and mean of each clusters are presented in table 9 and 10 respectively. The present study on Principal Component Analysis suggested that, per cent variation was explained by the first seven principal components (PC) and the vector loading for each agronomic characters whose Eigen values greater than 1. The first seven PCs explained $\geq$ 75.00 % variation in genomic selection training population. Makinde and Ariyo (2010) and Kumar (2010) observed 76% of the total variation among genotypes from first five PCs and Upadhyaya et al. (2009) explained that first nine PCs accounted 79% of the total variation. Three clusters were formed in both the seasons and the genotypes of the common eco-geographic origin or same location included into different clusters without forming a single cluster indicated that geographic diversity was not related to genetic diversity (Zaman et al. 2011). The first and second principle components were more important because they contribute more than 50% of the total variation contributed by first seven PCs. Upadhyaya (2003) and Amarasinghe et al. (2016) reported that first PC contributes more variation. Plant breeding plays a key role in increase the groundnut acreage especially in arid region of Karnataka. Thus knowledge about genetic variability, trait associations and diversity is important for groundnut improvement strategies.

Authors' contribution

Conceptualization of research (KVP, HDU, RP); Designing of the experiments (KVP, HDU, RP); Contribution of experimental materials (KVP, HDU, SG); Execution of field/lab experiments and data collection (RP, RL, HK, SG, S); Analysis of data and interpretation (RP, HDU, KVP); Preparation of manuscript (KVP, RP).

Declaration

The authors declare no conflict of interest.

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Supplementary Table S1. Distribution of groundnut genotypes of genomic selection training population into Ward clusters for Raichur *Rabi* 2014

Cluster	Genotypes
I (154)	ICGV 00068, ICGV 00191, ICGV 00246, ICGV 00343, ICGV 00349, ICGV 00350, ICGV 00387, ICGV 01005, ICGV 01124, ICGV 01232, ICGV 01263, ICGV 01273, ICGV 01274, ICGV 01276, ICGV 01328, ICGV 01464, ICGV 02022, ICGV 02038, ICGV 02144, ICGV 02189, ICGV 02251, ICGV 02271, ICGV 02287, ICGV 02321, ICGV 02434, ICGV 02446, ICGV 03043, ICGV 03184, ICGV 03207, ICGV 05036, ICGV 05057, ICGV 05141, ICGV 06099, ICGV 06100, ICGV 06234, ICGV 06423, ICGV 06431, ICGV 07166, ICGV 07220, ICGV 07227, ICGV 07223, ICGV 07246, ICGV 07268, ICGV 07273, ICGV 09112, ICGV 13238, ICGV 13242, ICGV 86015, ICGV 86072, ICGV 86325, ICGV 86352, ICGV 86590, ICGV 86699, ICGV 87160, ICGV 87378, ICGV 87921, ICGV 89104, ICGV 92267, ICGV 93437, ICGV 94118, ICGV 95070, ICGV 95377, ICGV 96466, ICGV 96468, ICGV 97120, ICGV 97165, ICGV 97182, ICGV 97183, ICGV 97261, ICGV 97262, ICGV 98163, ICGV 98184, ICGV 98294, ICGV 99029, ICGV 99051, ICGV 99085, ICGV 99160, ICGV 99181, ICR 48, J 11, M 28-2, Mutant 3, TAG 24, TDG 10, TDG 13, TDG 14, TG 41, TG 42, TG LPS 4, TGLPS7, TKE 19A, TMV 2 NLM, TMV2, 24 M-86, 24 x 39-31 MR, 26 M- 119-1, 26 M 156-2, 26 X 37-IV- 9IR, 26 X M-95-1 RI, 26X 27-164, 27 x 49- 14, 27 x 49- 27-1, 39 x 49 -77, 39x 49-81-1, 49 M-2-2, 49 x 27-37, 49 x 37-135, CS 39, Dharwad11, Dharwad13, Dharwad14, Dharwad2, Dharwad3, Dharwad5, Dharwad6, Dharwad9, DTG 3, ICG 10053, ICG 10185, ICG 11088, ICG 11651, ICG 12276, ICG 12370, ICG 12625, ICG 12879, ICG 12991, ICG 13895, ICG 13941 (ICGS 44), ICG 14475, ICG 14482, ICG 14705, ICG 14834, ICG 14985, ICG 15190, ICG 15415, ICG 1668, ICG 2031, ICG 2738 (Gangapuri), ICG 3140, ICG 3421, ICG 3584, ICG 3673, ICG 442, ICG 4955, ICG 532, ICG 5663, ICG 5745, ICG 8285, ICG 6022, ICG 8517, ICG 8751, ICG 9507, ICG 9961, ICGS 11,
II (185)	ICGV 00005, ICGV 00248, ICGV 00290, ICGV 00321, ICGV 00346, ICGV 00351, ICGV 00362, ICGV 00371, ICGV 00440, ICGV 01060, ICGV 01265, ICGV 01361, ICGV 01393, ICGV 01478, ICGV 01495, ICGV 02125, ICGV 02194, ICGV 02206, ICGV 02242, ICGV 02266, ICGV 02286, ICGV 02290, ICGV 02298, ICGV 02317, ICGV 02323, ICGV 02411, ICGV 03042, ICGV 03056, ICGV 03064, ICGV 03136, ICGV 03128, ICGV 03397, ICGV 03398, ICGV 04018, ICGV 04044, ICGV 04087, ICGV 04115, ICGV 04124, ICGV 04149, ICGV 05032, ICGV 05100, ICGV 05155, ICGV 05161, ICGV 05163, ICGV 05176, ICGV 05198, ICGV 06040, ICGV 06042, ICGV 06049, ICGV 06110, ICGV 06142, ICGV 06175, ICGV 06188, ICGV 06347, ICGV 06420, ICGV 06422, ICGV 06424, ICGV 07023, ICGV 07120, ICGV 07145, ICGV 07148, ICGV 07168, ICGV 07210, ICGV 07217, ICGV 07235, ICGV 07247, ICGV 07359, ICGV 07368, ICGV 13241, ICGV 86011, ICGV 86143, ICGV 86564, ICGV 87187, ICGV 87354, ICGV 87846, ICGV 88145, ICGV 88438, ICGV 90320, ICGV 91114, ICGV 91116, ICGV 92195, ICGV 93216, ICGV 93280, ICGV 93470, ICGV 93920, ICGV 94169, ICGV 94361, ICGV 95058, ICGV 95290, ICGV 95469, ICGV 97045, ICGV 97058, ICGV 97092, ICGV 97115, ICGV 97116, ICGV 97128, ICGV 97232, ICGV 98105, ICGV 98373, ICGV 98432, ICGV 99052, ICGV 99083, ICGV 99195, ICGV 99233, ICG 10036, ICG 10701, ICG 111, ICG 11322, ICG 11337 , ICG 11426, ICG 12509, ICG 12672, ICG 13942 (ICGS 76), ICG 14466, ICG 15419, ICG 156 (M 13), ICG 1834, ICG 1973, ICG 2106, ICG 2381, ICG 2773, ICG 2857, ICG 3027, ICG 3053, ICG 3102, ICG 3343, ICG 3312, ICG 3746, ICG 434, ICG 4343, ICG 4527, ICG 4543, ICG 4729, ICG 5221, ICG 5662, ICG 5891, ICG 6646, ICG 6766, ICG 721, ICG 875, ICG 9315, ICGC 13245, JL 24, M 110-14, M 28-2, MN1-35, Somnath, TG 19, TG 39, TG 49, TG LPS 3, TPG 41, 24 x 37-2275, 26 X M-223-1, 27 x 49- 12, 27 x 49- 16, 39 x 49 -8, 49 M- 1-1, 49 M-16, 49 x 27-13 (ii), 49 x 27-19, 49 x 37- 99(b) tall, 49 x 37-134, 49 x 37-90, 49 x 37-91, 49 x 37-97-1, 49 x 39-20-2, 49 X 39-21-1, 49 x 39-21-2, 49 X 39-21-2(a), 49 x 39-74, 49 x 39-8, BAU 13, CSMG 84-1, DH 86, Dharwad1, Dharwad10, Dharwad12, Dharwad15, Dharwad4, Dharwad7, Dharwad8, DTG 15, Faizpur 1-5, GPBD 4
III (1)	SUN OLEIC 95 R

Supplementary Table S2. Distribution of groundnut genotypes of genomic selection training population into Ward clusters for Raichur *Kharif* 2015

Cluster	Genotypes
I (125)	ICGV 00246, ICGV 00371, ICGV 00387, ICGV 01124, ICGV 01232, ICGV 01276, ICGV 01464, ICGV 01495, ICGV 02022, ICGV 02189, ICGV 02194, ICGV 02206, ICGV 02242, ICGV 02271, ICGV 02286, ICGV 02290, ICGV 02317, ICGV 02323, ICGV 02434, ICGV 03043, ICGV 03064, ICGV 03056, ICGV 03128, ICGV 03184, ICGV 03397, ICGV 03398, ICGV 04018, ICGV 04044, ICGV 04115, ICGV 04149, ICGV 05036, ICGV 05057, ICGV 05100, ICGV 05161, ICGV 05163, ICGV 05176, ICGV 05198, ICGV 06040, ICGV 06100, ICGV 06188, ICGV 06234, ICGV 06347, ICGV 06422, ICGV 06423, ICGV 07120, ICGV 07145, ICGV 07220, ICGV 07227, ICGV 07235, ICGV 07247, ICGV 07273, ICGV 07368, ICGV 09112, ICGV 13242, ICGV 86011, ICGV 86352, ICGV 86564, ICGV 86590, ICGV 87160, ICGV 87354, ICGV 87378, ICGV 91114, ICGV 91116, ICGV 92195, ICGV 92267, ICGV 93470, ICGV 94169, ICGV 94118, ICGV 94361, ICGV 95377, ICGV 95469, ICGV 96466, ICGV 96468, ICGV 97116, ICGV 97120, ICGV 97183, ICGV 97232, ICGV 98105, ICGV 98294, ICGV 98373, ICGV 99029, ICGV 99052, ICGV 99083, ICGV 99160, ICGV 99233, ICG 10701, ICG 12509, ICG 13895, ICG 13941 (ICGS 44), ICG 15415, ICG 1834, ICG 2031, ICG 3312, ICG 3584, ICG 3746, ICG 4729, ICG 8285, ICG 8517, ICG 9507, ICG 9961, Mutant 3, Somnath, TG 19, TG 39, TG 41, TMV 2 NLM, 26 M- 119-1, 26 M 156-2, 27 x 49- 12, 27 x 49- 27-1, 39 x 49 -8, 49 M- 1-1, 49 M-16, 49 x 27-13 (ii), 49 x 27-19, 49 x 39-21-2, CS 39, CSMG 84-1, Dharwad13, Dharwad14, Dharwad3, Dharwad4, Dharwad8, Dharwad9, DTG 15,
II (214)	ICGV 00005, ICGV 00068, ICGV 00248, ICGV 00191, ICGV 00290, ICGV 00321, ICGV 00343, ICGV 00346, ICGV 00349, ICGV 00350, ICGV 00351, ICGV 00362, ICGV 00440, ICGV 01005, ICGV 01060, ICGV 01263, ICGV 01265, ICGV 01273, ICGV 01274, ICGV 01328, ICGV 01361, ICGV 01393, ICGV 01478, ICGV 02038, ICGV 02125, ICGV 02144, ICGV 02251, ICGV 02266, ICGV 02287, ICGV 02298, ICGV 02321, ICGV 02411, ICGV 02446, ICGV 03042, ICGV 03136, ICGV 03207, ICGV 04087, ICGV 04124, ICGV 05032, ICGV 05141, ICGV 05155, ICGV 06042, ICGV 06049, ICGV 06099, ICGV 06110, ICGV 06142, ICGV 06175, ICGV 06420, ICGV 06424, ICGV 06431, ICGV 07023, ICGV 07148, ICGV 07166, ICGV 07168, ICGV 07210, ICGV 07217, ICGV 07223, ICGV 07246, ICGV 07268, ICGV 07359, ICGV 13238, ICGV 13241, ICGV 86015, ICGV 86072, ICGV 86143, ICGV 86325, ICGV 86699, ICGV 87187, ICGV 87846, ICGV 87921, ICGV 88145, ICGV 88438, ICGV 89104, ICGV 90320, ICGV 93216, ICGV 93280, ICGV 93437, ICGV 93920, ICGV 95058, ICGV 95070, ICGV 95290, ICGV 97045, ICGV 97058, ICGV 97092, ICGV 97115, ICGV 97128, ICGV 97165, ICGV 97182, ICGV 97261, ICGV 97262, ICGV 98163, ICGV 98184, ICGV 98432, ICGV 99051, ICGV 99085, ICGV 99181, ICGV 99195, ICR 48, J 11, JL 24, M 110-14, M 28-2, M 28-2, MN1-35, TAG 24, TDG 10, TDG 13, TDG 14, TG 42, TG 49, TG LPS 3, TG LPS 4, TGLPS7, TKE 19A, TMV2, TPG 41, 24 M-86, 24 x 37-2275, 24 x 39-31 MR, 26 X 37-IV- 9IR, 26 X M-223-1, 26 X M-95-1 RI, 26X 27-164, 27 x 49- 14, 27 x 49- 16, 39 x 49 -77, 39x 49-81-1, 49 M-2-2, 49 x 27-37, 49 x 37- 99(b) tall, 49 x 37-134, 49 x 37-135, 49 x 37-90, 49 x 37-91, 49 x 37-97-1, 49 x 39-20-2, 49 X 39-21-1, 49 X 39-21-2(a), 49 x 39-74, 49 x 39-8, BAU 13, DH 86, Dharwad1, Dharwad10, Dharwad11, Dharwad12, Dharwad15, Dharwad2, Dharwad5, Dharwad6, Dharwad7, DTG 3, Faizpur 1-5, GPBD 4, ICG 10036, ICG 10053, ICG 10185, ICG 11088, ICG 111, ICG 11322, ICG 11337 , ICG 11426, ICG 11651, ICG 12276, ICG 12370, ICG 12625, ICG 12672, ICG 12879, ICG 12991, ICG 13942 (ICGS 76), ICG 14475, ICG 14466, ICG 14482, ICG 14705, ICG 14834, ICG 14985, ICG 15190, ICG 15419, ICG 156 (M 13), ICG 1668, ICG 1973, ICG 2106, ICG 2381, ICG 2738 (Gangapuri), ICG 2773, ICG 2857, ICG 3027, ICG 3053, ICG 3102, ICG 3140, ICG 3343, ICG 3421, ICG 3673, ICG 434, ICG 4343, ICG 442, ICG 4527, ICG 4543, ICG 4955, ICG 5221, ICG 532, ICG 5662, ICG 5663, ICG 5745, ICG 5891, ICG 6022, ICG 6646, ICG 6766, ICG 721, ICG 875, ICG 8751, ICG 9315, ICGC 13245, ICGS 11,
III (1)	SUN OLEIC 95 R