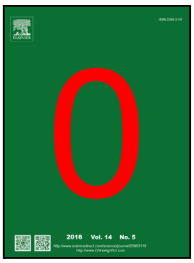
Journal of Integrative Agriculture 2017, 16(0): 60345-7

Available online at www.sciencedirect.com

ScienceDirect



RESEARCH ARTICLE

Characterization of groundnut (*Arachis hypogaea* L.) collection using quantitative and qualitative traits in the Mediterranean Basin

Engin Yol[1], Seymus Furat[2], Hari D Upadhyaya[3], Bulent Uzun[1]

[1] *Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya 07058, Turkey*
[2] *West Mediterranean Agricultural Research Institute, Antalya 07058, Turkey*
[3] *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Telangana 502324, India*

Abstract

This study was conducted to determine the genetic diversity and relationship among 256 groundnut genotypes of which 132 belong to subspecies (Subsp.) *Arachis hypogaea* L. and 124 to Subsp. *Arachis fastigiata* L. The collection was evaluated for eight quantitative and five qualitative traits during three consecutive years under Mediterranean climate conditions. Coefficient of variation (CV) significantly differed among the genotypes for all the studied quantitative traits ranged from 9.10 to 33.98%, while the highest CV was recorded for seed yield. The subspecies, *A. hypogaea* L. and *A. fastigiata* L., displayed significant differences for quantitative traits except for numbers of pods per plant and seed yield. Principal component analyses showed that the first three principal components accounted for 68.14% variation for quantitative traits. Major traits that accounted for the variation by the three PCs include days to the first flowering, days to 50% flowering, number of pods per plant and shelling percentage. The groundnut collection also offers wide seed coat color diversity which affects the crop marketability. The information on variations in quantitative and qualitative traits identified in the present investigation provided useful genotypes which would be serving parents. These parental genotypes can be used in groundnut breeding programs to develop desirable cultivars in Mediterranean basin and globally.

Keywords: evaluation, genetic diversity, peanut, agronomic selection

1. Introduction

Groundnut, also known as peanut, is an annual allotetraploid crop (2n=4x=40) and belongs to Fabaceae family. The genus, *Arachis* contains about 80 species including *Arachis* monticola, which is another tetraploid species. Differing from other flowering plant genera, the genus produces fruits below the ground but flowers, leaves and stems form above ground (Krapovickas and Gregory 1994). Groundnut is a native of South America (Gregory and Gregory 1976) and spreads worldwide from Chaco region between southern Bolivia and northwestern Argentina after a long journey (Upadhyaya *et al*. 2005). Systematic nomenclature of *Arachis hypogaea* L. shows that it is divided into two subspecies based on the presence/absence of flowers on the main axis and branching pattern (Krapovickas and Gregory 1994). Subspecies (Subsp.) *hypogaea* is divided into two botanical varieties, var *hypogaea* and var *hirsuta*, while Subsp. *fastigiata* includes the four varieties, var *fastigiata*, var *vulgaris*, var *aequatoriana* and var *peruviana.*

Received 23 November, 2016 Accepted 19 January, 2017
Correspondence Bulent Uzun, E-mail: bulentuzun@akdeniz.edu.tr

doi: 10.1016/S2095-3119(17)61675-7

Worldwide, groundnut was produced 45.22 million tons from 25.44 million ha with an average yield of 1.77 t ha^{-1} (FAO 2013). The crop is the second most important cultivated food legume and the fourth largest edible oilseed crop in the world (Shilman *et al*. 2011). The seeds have palmitic, oleic and linoleic acids accounting for about 90% of total fatty acids at seed maturity (Sekhon *et al*. 1972; Young and Waller 1972). Groundnut seeds with high oleic acid provide lower rate of oxidation and less painty flavor in storage causing higher acceptability for marketing (Mozingo *et al*. 2004). Groundnut is also valuable source of vitamins E, K, and B (the richest source of thiamine and niacin) and other essential minerals (Kassa *et al*. 2009). Groundnut cake after oil extraction is especially used for animal feeding with high protein content (Savage and Keenan 1994). Studies indicated that consuming groundnut at least four times a week showed a 37% reduced risk of coronary heart disease (Suchoszek-Lukaniuk *et al*. 2011) and anticancer activity with 50% inhibition of the proliferation of related leukemia cells (Hwang *et al*. 2008).

Improving the genetic potential of groundnut for qualitative and quantitative traits is one of the major objectives in most groundnut breeding programs (Upadhyaya *et al*. 2005). Wide genetic diversity for these traits is necessary for crop improvement. Commonly, the use of only few elite germplasm lines and/or cultivars in breeding programs reduces the genetic variation, leading to a narrow genetic base in the groundnut gene pool (Gupta *et al*. 2015). Sustainable groundnut improvement programs, therefore, need to discover and incorporate genes from germplasm with high genetic variability for desired traits. Many genetic diversity studies have been conducted in groundnut for different regions (Holbrook *et al*. 1993; Swamy *et al*. 2003; Upadhyaya *et al*. 2003, 2005, and 2006; Holbrook and Dong 2005; Kassa *et al*. 2009; Bishi *et al*. 2013; Jiang *et al*. 2014; Garba *et al*. 2015). New desirable traits and genotypes have been revealed in these studies to select specific cultivars for growing in the target regions of the crop.

Mediterranean areas offer suitable climate regimes for both vegetative and reproductive growth of groundnut (Caliskan *et al*. 2008b). Especially under irrigated conditions groundnut production could be remarkably increased (Smartt 1994). Wheat is a very common crop traditionally planted in fall or spring and harvested in summer in Mediterranean areas and groundnut is an important alternative crop for second-crop production (Isik and Gul 2004). However genetic diversity of cultivated gene pools of groundnut is narrow especially for these regions (Caliskan *et al*. 2008b). Thus, there is a need for studies to determine useful groundnut variability for the Mediterranean conditions. The evaluation of morphological traits for economic importance could be useful for choosing the appropriate initial materials for crop improvement in these areas. Therefore to better understand and effectively utilize groundnut germplasm in Mediterranean basin, it is important to evaluate global collections for desirable agronomic traits such environment. From this perspective, this present study was conducted to (i) assess the agro-morphological diversity of groundnut collections, which includes the mini core collece tion (Upadhyaya *et al*. 2002), breeding lines, local landraces, and registered cultivars, (ii) determine the relationship of important yield traits, and (iii) select desirable genotypes from different botanical varieties useful for breeding in Mediterranean areas and similar environments elsewhere.

2. Materials and methods

2.1. Genetic materials, experimental area and climate conditions

The plant material included 256 groundnut (*A. hypogaea* L.) genotypes representing over 25 countries across Asia, America and Africa (Appendix A). The field trials were set up at the West Mediterranean Agricultural Research Institute (36°52′N, 30°50′E, and altitude 15 m) during 2011, 2012, and 2013 growing seasons in Antalya, Turkey (Fig. 1). The experimental area has a coastline of the Mediterranean Sea

Fig. 1 Map of the Mediterranean Basin. ◆, experimental area.

(Fig. 1) with a typical Mediterranean climate conditions. The monthly mean temperature, sum precipitation and moisture during the growing seasons (May to September) were presented in Table 1. The average temperature had a similar trend during the three year growing periods. The highest temperatures were recorded in August and the lowest in May in the three consecutive years. The long term averages indicate that the temperatures tend to rise in the Mediterranean basin. A precipitation level during the growing period in May reached 107.2, 44.0, and 60.4 mm as the maximum in 2011, 2012, and 2013 growing seasons, respectively. No rainfall was recorded in July in the three different years. Humidity was generally similar in the three growing periods. The soil type in the experimental areas was silt and clay.

Chemical fertilizers were applied before seeding at the rate of 30 kg ha^{-1} using an $N/P_2O_5/K$ formula at 18/46/0. Plots were sown at the end of May in all three years in a randomized complete blocks design with two replications. Each accession was grown in two rows of 5 m length with a row to row distance of 70 cm and plant to plant within a row of 20 cm. Care was taken to ensure uniform depth of planting. Standard agronomic practices were applied for all plots in all three years.

2.2. Data collection

Morphological characterization was carried out using the groundnut descriptor (IBPGR and ICRISAT 1992). Eight quantitative traits were recorded on plot basis for all genotypes. The traits of the days to the first flowering and days to 50% flowering were recorded on plot basis as number of d from sowing to the first and 50% flower opening, respectively. The number of branches, plant height and number of pods per plant traits were recorded on five plants at harvest. The traits of thousand seed weight (g) and seed yield (kg da^{-1}) were measured after pods were dried. A 200-g mature pod sample was used to estimate shelling percentage.

Five qualitative traits were also measured during the growing period. Growth habit was recorded after flowering as: erect, semi erect and spreading. The traits of stem pigmentation, stem hairiness and leaf hairiness were classified as presence/absence from randomly selected five plants per plot. After harvest, seeds were dried and evaluated with respect to seed coat color.

2.3. Statistical analysis

Combined analysis of variance (ANOVA) of the three year data was performed for quantitative traits. Means were compared for all traits with least significance differences (LSD) test at the 0.05 and 0.01 levels using SAS 9.3 (SAS Institute 2011). The calculations for minimum, maximum, standard deviation, standard error, coefficient of variation and correlation analysis were conducted for quantitative traits. Qualitative data were analyzed using percentage distribution. Means of the Subsp. *fastigiata* and Subsp. *hypogaea*. were compared using *t*-test for all the traits. The standard analyses were conducted using MINITAB ver. 16.1 (Minitab, Pennsylvania).

Principal component analysis (PCA) was performed with the eight quantitative trait data using the “princomp” function from the “stats” package of R-project version 3.3.0 (R DevelopmentCore Team 2016). The first and the second principal component axes scores were plotted by the R “ggbiplot” package to aid visualization of 256 genotypes grouped by two subspecies and six botanical varieties. Cluster analysis was performed with the computer package NTSYS pc 2.1 (Rohlf 2000) using quantitative traits. Interval data option and distance coefficient were selected to calculate similarity and distance coefficients, respectively. Dendrogram was produced using UPGMA clustering of pair-wise similarity distances among the genotypes.

3. Results

3.1. Quantitative and qualitative traits

The combined ANOVA revealed significant variation among the genotypes for days to the first flowering, days to 50% flowering, number of branches, plant height, number of pods per plant, shelling percentage, thousand seed weight

Table 1 Monthly temperature, humidity and rainfall mean values in the growing periods of 2011, 2012 and 2013

Months	Temperature (°C)				Humidity (%)				Rainfall (mm)			
	2011	2012	2013	Long term averages[1)]	2011	2012	2013	Long term averages[1)]	2011	2012	2013	Long term averages[1)]
May	20.2	20.6	22.8	20.5	64.7	69.6	66.4	63.0	69.6	55.7	45	31.8
June	25.4	26.3	25.5	25.4	58.4	63.2	63.2	59.0	23.8	0	19.3	7.9
July	28.7	30.3	28.8	28.4	61.7	52.4	54.6	56.0	0	0	0	3.0
August	29.6	30.4	29.5	28.2	50.6	42.8	53.8	59.0	35.6	0	0	2.4
September	26.9	26.6	25.8	24.7	49.5	54.8	53.6	60.0	59.2	29.9	0	13.7

[1)] 1953–2013.

and seed yield (Table 2). The groundnut collection had two subspecies and six botanical varieties and all of them indicated wide variation except for var. *hirsuta*, var. *aequatoriana* and var. *peruviana* because they had fewer number of genotypes (Appendix A). Means of days to the first flowering varied from 17.3 to 40.3 d in the whole collection (Table 3). Subsp. *hypogaea*, Subps. *fastigiata*, var. *hypogaea*, and var. *fastigiata* had similar trends for the days to the first flowering, however, var. *hirsuta*, var. *aequatoriana* and var. *peruviana* indicated a narrow range. The variation for number of branches per plant was 3.8 to 14.3 for the whole collection and also in Subsp. *hypogaea* and var. *hypogaea* (Table 3). The genotypes in var. *hirsuta*, var. *vulgaris*, var. *aequatoriana* and var. *peruviana* had fewer number of branches per plant. Considerable variability in number of pods per plant was reflected by Subsp. *hypogaea*, Subsp. *fastigiata*, var. *hypogaea*, var. *fastigiata* within the range of 22.8 to 66.1, however, it was 29.8 to 38.9 as the minimum and the maximum for the genotypes included in var. *hirsuta*, var. *aequatoriana* and var. *peruviana*. There was also much variation for thousand seed weight and seed yield traits in the collection ranged from 311.0 to 759.0 g and from 52.4 to 527.7 kg da^{-1}, respectively (Table 3). Subsp. *hypogaea* showed higher range of variation compared to Subps. *fastigiata* for both these traits.

The groundnut collection examined in this study had 132 genotypes from Subsp. *hypogaea*, and 124 genotypes from Subsp. *fastigiata*. The *t*-test of significance for mean values indicated that there were significant differences between the subspecies for days to the first flowering, days to 50% flowering, number of branches, plant height, shelling percentage and thousand seed weight (Table 4). However, the number of pods per plant and seed yield showed no significant difference between the subspecies. The maturity traits (days to the first flowering and 50% flowering) and thousand seed weight were considerably higher in Subsp. *hypogaea* than Subsp. *fastigiata*. Coefficient values (%) of the two subspecies were relatively in a similar range except for thousand seed weight and seed yield (Table 4).

The frequency distribution of qualitative traits was presented in Fig. 2. Three different growth habits were observed in the collection as erect, semi-erect and spreading with the percentages of 58.2, 32.4 and 9.4%, respectively. The frequency of hairiness was detected for stem and leaf with the percentages of 35.5 and 46.1%, respectively. There was no pigmentation in more than half of the collection. Seed coat color varied from white to various shades of tan, red or purple (Fig. 3).

3.2. Principal component and cluster analyses

PCA using the eight quantitative traits including maturity, yield and yield components indicated that more than 68.14% variability was accounted for by the first three principal components (PCs) with eigenvalues ≥1 (Table 5). The 1st principal component (PC1) had an eigenvalue of 2.81 and explained 34.93% of the total variation. Days to the first flowering, days to 50% flowering and thousand seed weight

Table 2 Means, standard deviations and LSD values for quantitative traits in groundnut collection[1)]

Traits	Days of first flowering	Days of 50% flowering	Number of branches	Plant height (cm)	Number of pods per plant	Shelling percentage (%)	Thousand seed weight (g)	Seed yield (kg da^{-1})
Means and standard deviations	28.7±5.0	32.0±5.0	6.8±1.7	60.4±8.2	38.3±8.5	61.7±5.6	473.9±98.4	216.6±73.6
LSD	0.68**	0.1**	0.8**	2.3**	15.64**	8.02**	183.9**	182.67*

[1)] LSD, least significant differences.
*, **: Statistically significant at P=0.05 and P=0.01 level, respectively.

Table 3 Range of variation for different traits of subspecies and botanical varieties of groundnut collection in Mediterranean climate conditions

Groups	Days to the first flowering (d)	Days to 50% flowering (d)	Number of branches	Plant height (cm)	Number of pods per plant	Shelling percentage (%)	Thousand seed weight (g)	Seed yield (kg da^{-1})
Entire collection	17.3–40.3	21.0–45.0	3.8–14.3	34.2–80.9	22.8–66.1	45.3–73.1	311.0–759.0	52.4–527.7
Subsp. *hypogaea*	17.3–40.0	21.0–45.0	3.8–14.3	34.2–72.9	23.9–66.1	45.7–73.1	332.3–759.0	52.4–527.7
Subsp. *fastigiata*	18.3–40.3	21.0–42.0	4.0–10.4	37.3–80.9	22.8–54.7	45.3–72.2	311.0–611.6	55.0–502.9
var. *hypogaea*	17.3–40.0	21.0–45.0	3.8–14.3	34.2–72.9	23.9–66.1	45.8–73.1	332.3–759.0	52.4–527.7
var. *fastigiata*	19.7–40.3	21.0–42.0	4.0–10.4	37.3–80.9	22.8–54.7	45.3–72.2	313.8–595.8	90.8–393.2
var. *hirsuta*	28.0–28.0	31.0–31.0	6.0–6.0	63.2–63.2	36.2–36.2	58.1–58.1	476.3–476.3	208.6–208.6
var. *vulgaris*	18.3–30.3	21.0–35.0	4.0–8.8	42.2–74.3	24.5–53.8	46.1–71.1	311.0–611.6	55.0–502.9
var. *aequatoriana*	28.0–28.0	31.0–31.0	6.3–6.3	68.6–68.6	38.9–38.9	56.9–56.9	518.8–518.8	170.1–170.1
var. *peruviana*	24.0–27.0	27.0–30.0	4.3–5.8	54.6–57.1	29.8–31.5	50.7–51.4	433.4–513.7	303.8–353.6

Table 4 Means, coefficient of variation and standard error for eight quantitative traits for two different subspecies in the groundnut collection

Characters	Subsp. *hypogaea*[1)]			Subsp. *fastigiata*[1)]			Differences
	Mean±SE	SD	CV (%)	Mean±SE	SD	CV (%)	
Days of the first flowering (d)	32.1±0.32	3.70	11.53	25.00±0.31	3.41	13.63	**
Days of 50% flowering (d)	35.5±0.33	3.80	10.76	28.42±0.31	3.48	12.26	**
Number of branches	7.4±0.15	1.72	23.29	6.06±0.12	1.29	21.25	**
Plant height (cm)	57.18±0.67	7.68	13.43	63.84±0.66	7.35	11.52	**
Number of pods per plant	38.8±0.88	10.08	25.99	37.92±0.58	6.48	17.09	NS
Shelling percentage (%)	60.80±0.49	5.64	9.27	62.68±0.49	5.45	8.69	**
Thousand seed weight (g)	519.12±9.21	105.87	20.39	425.67±5.40	60.18	14.14	**
Seed yield (kg da^{-1})	208.96±6.82	78.38	37.51	224.67±6.06	67.60	30.04	NS

[1)] SE, standard error; SD, standard deviation; CV (%), coefficient of variation. Differences between means of Subsp. *hypogaea* and Subsp. *fastigiata* were tested by *t* test.
**, significant at the 0.01 probability level; NS, non-significant.

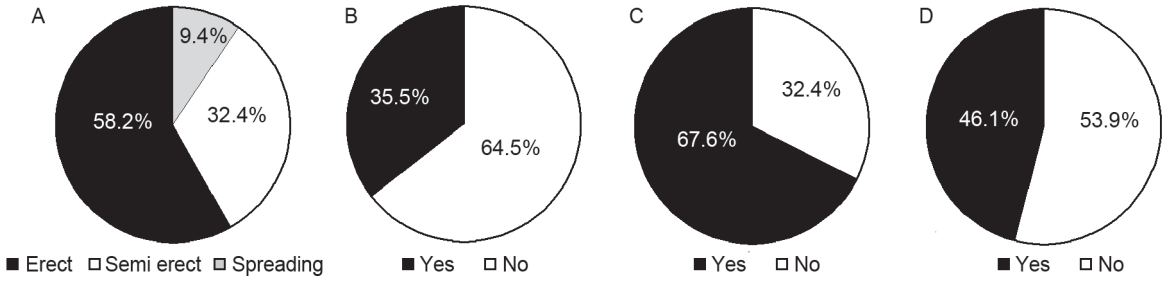


Fig. 2 Frequency distribution of 256 groundnut genotypes for growth habit (A), stem pigmentation (B), stem hairiness (C), leaf hairiness (D).

had the highest positive eigenvectors in PC1, while the plant height had the highest negative eigenvector. The 2nd component (PC2) explained 20.90% of the total variance with an eigenvalue of 1.61 and mainly correlated to number of pods per plant and seed yield, positively (Table 5). The 3rd principal component's (PC3) eigenvalue was 1.0 explaining 12.31% of the total variation with positive eigenvector for shelling percentage (Table 5).

The genotypes in the collection were grouped by subspecies and botanical varieties onto PC1 and PC2. The majority of genotypes of Subsp. *hypogaea* were distributed on the right half of the plot which was positively related PC1 (Fig. 4). Similarly, genotypes of var. *hypogeea* were distributed on the right of the plot (Fig. 5). The genotypes of Subsp. *fastigiata*, var. *vulgaris* and var. *fastigiata* were mainly located on the left part of plot which was mainly correlated with PC2. The varieties of *peruviana*, *aequatoriana* and *hirsuta* had few genotypes in the collection and they were related with PC2 (Fig. 5).

A dendrogram was constructed with distance matrix using the UPGMA clustering procedure (Fig. 6). The 256 genotypes were grouped in five main clusters. Distance estimates based on the eight agronomic traits ranged from 2.31 to 103.46 (Fig. 6). The second cluster contained maximum genotypes (122) while there are only four genotypes in fifth cluster. The genotypes ACG 45, ACG 193, ACG 206 and ACG 256 consituted a definite cluster (fifth cluster) differing from the remaining genotypes based on quantitative traits.

3.3. Phenotypic correlation

Table 6 showed significant correlation coefficients among the phenotypic traits. The combined data over three years indicated that there was a strong and positive correlation between days to the first flowering and days to 50% flowering. These two maturity traits also positively and significantly correlated with the number of branches and thousand seed weight while negatively correlated with plant height. Number of branches had negative association only with plant height however positively correlated with number of pods per plant and thousand seed weight. The important yield component trait, number of pods per plant, showed positive correlations with seed yield and thousand seed weight. There was a negative correlation between shelling percentage and thousand seed weight.

3.4. Evaluation of the groundnut collection

A total of 256 genotypes were evaluated with analysis of variance. LSD values were also calculated for each quantitative

trait to identify desirable genotypes in this study. Results showed that the earliest flowering genotype was ACG 94 (about 17 days after sowing) from Subsp. *hypogaea* var. *hypogaea* (Appendix A). There were several other early-flowering genotypes including ACG 51, ACG 65, ACG 45 and ACG 88 with means of 18 to 19 days after planting. The most late flowering genotype was ACG 255 with a mean of 40.3 d from Subsp. *fastigiata* var. *fastigiata*. The check cultivars NC-7 (Subsp. *hypogaea*) and Florispan (Subsp. *fastigiata*) had 28 and 25 days to the first flowering, respectively (Appendix A). ACG 94 and ACG 177 had the minimum and the maximum values for the days to 50% flowering, respectively. ACG 232 from Subsp. *hypogaea* var. *hypogaea* having high number of branches than other genotypes and controls. The genotypes ACG 97 and ACG 86 produced the tallest plants, while ACG 194 produced the shortest plant stature in the collection. The most desirable genotypes possessing number of pods per plant were ACG 221, ACG 202, ACG 7 and ACG 220 with the values of about 66, 65, 65 and 64, respectively.

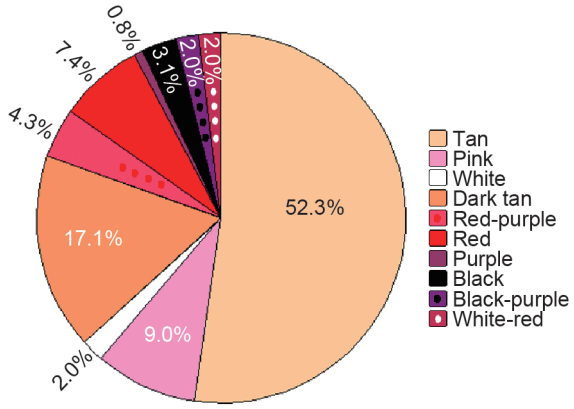


Fig. 3 Frequency distribution of 256 groundnut genotypes for seed coat color.

They belong to Subsp. *hypogaea* var. *hypogaea* and were superior to control NC-7 (Subsp. *hypogaea* var. *hypogaea*) which had about 37 pods per plant. Genotype ACG 224 from Subsp. *hypogaea* had the highest shelling percentage (73.1%). Several other genotypes from Subsp. *hypogaea*, ACG 204, ACG 205 and ACG 192 had also higher values for shelling percentage. ACG 200 from Subsp. *hypogaea* var. *hypogaea* produced the maximum thousand seed weight in the collection followed by ACG 217 and ACG 216 from the same systematic group. ACG 181 had the highest value for this trait from Subsp. *fastigiata*, Subsp. *vulgaris* with about 611 g however lowers about 150 g than ACG 200. The most desirable genotype for the seed yield was ACG 206 with respect to overall means of the three years. This genotype belongs to Subsp. *hypogaea* var. *hypogaea* with the value of about 670 kg da^{-1}, and ACG 45 has the highest value for seed yield in Subsp. *fastigiata* var. *vulgaris*. The lowest seed yield was observed in ACG 151 and ACG 108.

4. Discussion

This study demonstrated wide variation for yield and yield components useful for selection of elite genotypes as desirable parents for groundnut breeding. The traits for the days to the first flowering and days to 50% flowering contributed mostly to genetic diversity of the collection with a large range of variation because of the different responses of each genotype to the growing environment. Flowering traits are an important components for early maturity (Upadhyaya and Nigam 1994) and likely for early harvest. The latter helps in avoidance of late season biotic and abiotic stress factors and also makes possible for a second crop following harvest of wheat which is important for profitable and sustainable farming (Poehlman and Sleper 1995). Furthermore, Nigam and Aruna (2008) indicated that short plant

Table 5 Eigenvectors for the first three principal components of traits associated with yield and agronomic performance in 256 groundnut genotypes

	PC axis[1)]		
	PC1	PC2	PC3
Eigenvalues	2.81	1.61	1.00
Explained proportion of variation (%)	34.93	20.90	12.31
Cumulative proportion of variation (%)	34.93	55.83	68.14
Traits (eigenvectors)			
Days to first flowering (d)	0.545	–0.094	0.249
Days to 50% flowering (d)	0.543	–0.080	0.251
Number of branches	0.357	0.325	–0.121
Plant height (cm)	–0.309	0.269	–0.085
Number of pods per plant	0.138	0.624	–0.099
Shelling percentage (%)	–0.126	0.302	0.837
Thousand seed weight (g)	0.385	0.085	–0.362
Seed yield (kg da^{-1})	–0.033	0.562	–0.096

[1)] PC, principal components; PC1, PC2, and PC3, the 1st, the 2nd and the 3rd PC, respectively.

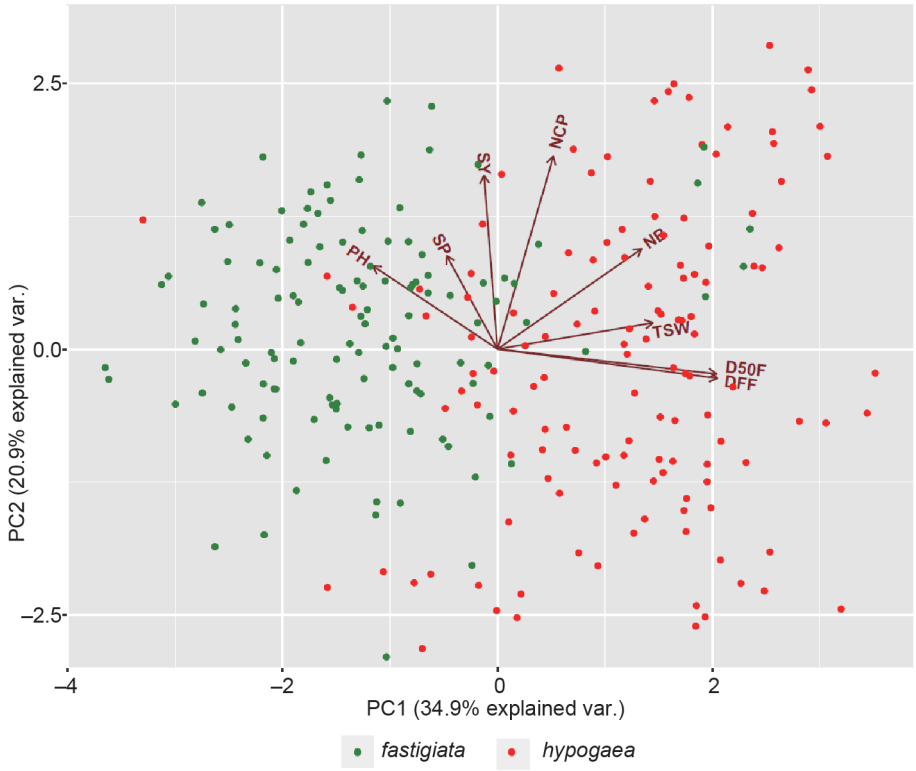


Fig. 4 Associations among 256 *Arachis hypogaea* L. genotypes between the two subspecies using the first two principal coordinates (the 1st principal component (PC1), and the 2nd principal component (PC2)) obtained from a principal component (PC) analysis. PH, plant height; SP, shelling percentage; SY, seed yield; NCP, number of pods per plant; NB, number of branches; TSW, thousand seed weight; D50F, days to 50% flowering; DFF, days to the first flowering.

stature, fewer days to the first flowering, and accumulation of maximum numbers of early flowers are important traits to develop short duration groundnut cultivars. In the collection evaluated in our study, we have identified many genotypes which had early flowering and shorter plant stature from different subspecies and botanical varieties (Appendix A) which have high potential for development of early maturity cultivars for Mediterranean areas. Selection in specific regions for flowering traits is important because flowering is highly variable depending on genotype, environment and temperature (Rao and Murty 1994; Craufurd *et al*. 2000). The genotypes, ACG 13 and ACG 65, had 21 and 22 d for days to 50% flowering in the collection however they showed later flowering characteristic in rainy and post-rainy growing season in India (Upadhyaya *et al*. 2014) showing an enviromental effect on flowering time. Taxanomic differences also affect the flowering in groundnut and generally the genotypes belong to Subsp. *hypogaea* have late maturity compared to Subsp. *fastigiata* (Mothilal 2012). Correlatively, almost all early flowering genotypes in the collection belong to Subsp. *fastigiata* especially var. *vulgaris* (Appendix A).

Branching is one of the most important characteristic to distinguish the two subspecies of groundnut (Krapovickas and Gregory 1994). The trait also plays an important role for seed yield (Rehman *et al*. 2001; Kumar *et al*. 2010) and showed significant differences among genotypes and subspecies in the groundnut collection evaluated (Tables 2 and 4). Upadhyaya (2003) examined the ICRISAT core collection of 1704 accessions consisting of 794 Subsp. *hypogaea* and 910 belonging to Subsp. *fastigiata* for mean number of branches and observed them as 5.5 and 4.2, respectively. Further, Swamy *et al*. (2003) evaluated 504 accessions of which 230 belonging to Subsp. *hypogaea* and 274 to Subsp. *fastigiata* and obtained mean number of branches of 2.8 to 3.5 and 1.6 to 3.1, respectively in four different growing seasons. However, the mean number of branches was about 7.4 and 6.0 for the Subsp. *hypogaea* and Subsp. *fastigiata* for present investigation, respectively (Table 4). Results showed that our collection had high variation for number of branches. The trait also contributed positively to PC1 and correlated with days to the first flowering in concordance with Swamy *et al*. (2003) and Canavar and Kaynak (2010).

The genotypes having higher number of pods per plant offers an opportunity for improving seed yield in groundnut (Nath and Alam 2002; Awal and Ikeda 2003; Luz *et al*. 2011). In the present investigation, number of pods per plant indicated positive correlation with seed yield and thousand seed weight (Table 6). Similar relationship was observed in

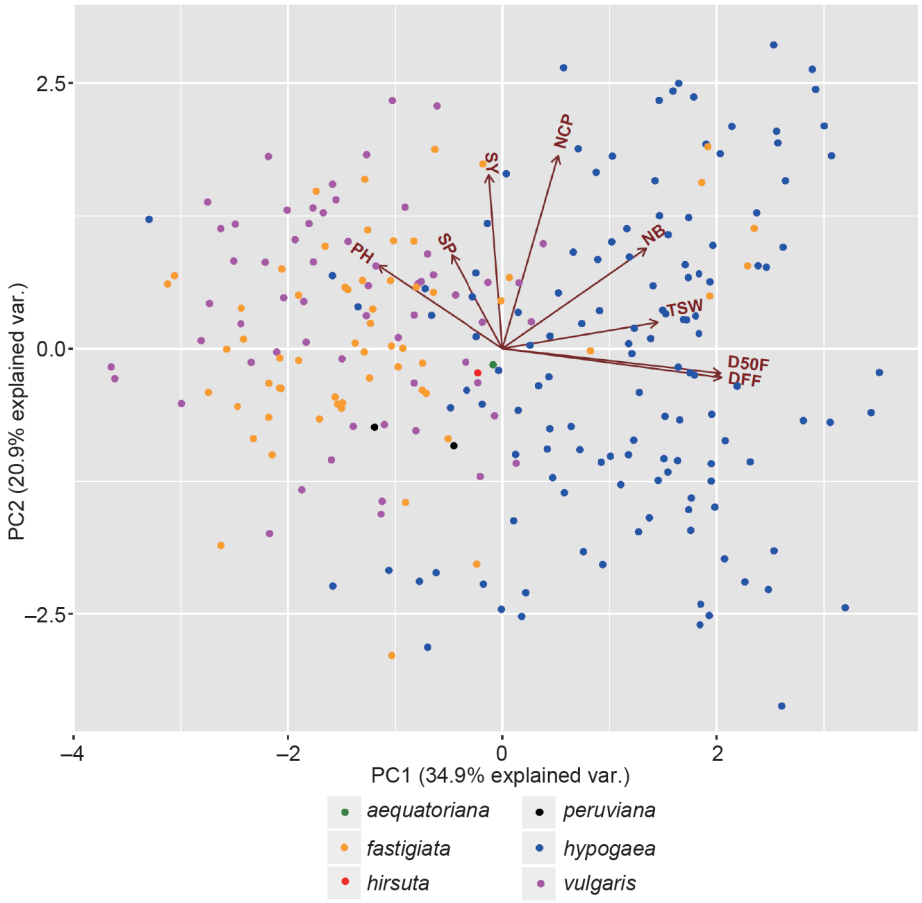


Fig. 5 Associations among 256 *Arachis hypogaea* L. genotypes according to botanical varieties using the first two principal coordinates (the 1st principal component (PC1), and the 2nd principal component (PC2)) obtained from a principal component (PC) analysis. PH, plant height; SP, shelling percentage; SY, seed yield; NCP, number of pods per plant; NB, number of branches; TSW, thousand seed weight; D50F, days to 50% flowering; DFF, days to the first flowering.

Table 6 Correlation coefficients for different traits of groundnut genotypes evaluated in Mediterranean type environment

Traits	Days to the first flowering	Days to 50% flowering	Number of branches	Plant height	Number of pods per plant	Shelling percentage	Thousand seed weight
Days to 50% flowering	0.982**						
Number of branches	0.376**	0.378**					
Plant height	–0.381**	–0.363**	–0.165**				
Number of pods per plant	0.124*	0.137*	0.428**	–0.136*			
Shelling percentage	–0.112**	–0.103	–0.071	–0.108	0.131*		
Thousand seed weight	0.405**	0.410***	0.305**	–0.281**	0.244**	–0.168**	
Seed yield	–0.128*	–0.110	0.152*	–0.077	0.303**	0.109	0.133*

* and ** are statistically significant at 0.05 and 0.01, respectively.

Chinese groundnut mini‐core collection (Jiang *et al*. 2014) and Asian groundnut core collection (Swamy *et al*. 2003) showing number of pods per plant is one of the selection criteria to obtain higher seed yield in groundnut breeding. The trait also had significant differences among genotypes in the collection in accordance with Swamy *et al*. (2003) and Upadhyaya *et al*. (2006). The highest number of pods per plant were observed in genotypes belonging to Subsp. *hypogaea* however there was no statistically significant difference between Subsp. *hypogaea* and *fastigiata* unlike the previous result reported by Upadhyaya (2003). ACG 221, ACG 202 and ACG 7 produced the highest number of pods per plant and therefore, could be integrated as a genetic resource for potential higher seed yield genotypes in the Mediterranean areas and possibly elsewhere. Sastry *et al*. (1985) proposed that early flowering genotypes produce

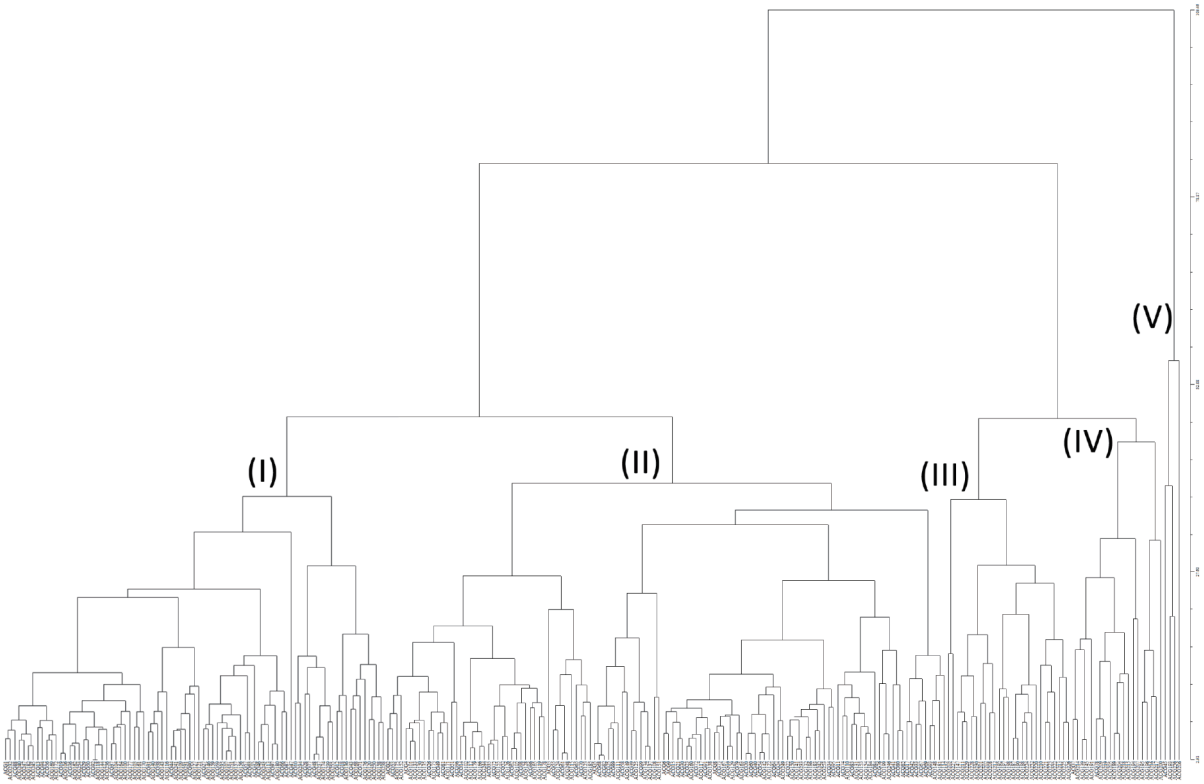


Fig. 6 Dendrogram of 256 genotypes of *Arachis hypogaea* L. based on three years field evaluation data in Antalya, Turkey.

greater numbers of pods in groundnut. However, the genotypes which had higher number of pods per plant showed later flowering in our collection. This phenomenon might be related with number of flowers because groundnut produces about 600–1000 flowers and only those of 15–20% result in pods that contribute to yield (Smith 1954), reductions in flower numbers might influence pod production. It also might be attributed to genotypic differences and their response to different environmental effects.

Shelling percentage is an index of the percentage of grains or seeds (Dapaah *et al*. 2014) and is one of the important selection criteria in groundnut breeding (Anothai *et al*. 2008). In the present study, this trait positively contributed to PC3 and showed wide variation among genotypes and subspecies. The *fastigiata* group had significantly greater mean than *hypogaea* group, in accordance with previously reported result by Swamy *et al*. (2003) who evaluated Asia groundnut core collection in rainy and rainy-post seasons. However, a different result was observed in same climatic conditions in ICRISAT groundnut core collection (Upadhyaya 2003) indicating shelling percentage is highly influenced by genotypic x environment interactions (Minimol *et al*. 2001). On the other hand, our collection had higher grand mean compared to Asian groundnut core collection (Swamy *et al*. 2003), ICRISAT groundnut core collection (Upadhyaya 2003) and Chinese groundnut mini-core collection (Jiang *et al*. 2014) for shelling percentage.. Individually, the genotypes ACG 224, ACG 204, ACG 205 and ACG 192 from subsp. *hypogaea* showed the highest shelling percentage followed by ACG 235 from subsp. *fastigiata*. Additionally, ACG 192 had higher number of pods per plant and this genotype should be evaluated for combining yield traits in breeding studies for Mediterranean areas.

There are four market types of groundnuts: virginia, runner, spanish, and valencia. Virginia and runner types are in the Subsp. *hypogaea*, while spanish and valencia are in the Subsp. *fastigiata*. Generally, virgina and runner market types have higher 1 000 seed weight than valencia and spanish types because of larger seed size. Plants with thousand seed weight between 500 and 700 g are considered runner market type; seed weight higher than 700 g is considered Jumbo type, a specific market for snacks (Suassuna *et al*. 2015). Five genotypes (ACG 200, ACG 217, ACG 216, ACG 196 and ACG 195) from Subsp. *hypogaea* had higher than 700 g thousand seed weight and they are good sources for breeding studies for large seed size and also for direct market usage. In the evaluted collection, the genotypes of ACG 19, ACG 147, ACG 175 had 436.9, 643.7 and 387.6 g thousand seed weight in means of three years however they had values of 380, 563 and 557 g for Indian

environment (Upadhyaya *et al*. 2014) indicating seed size and weight may differ due to production environment and cultivation practices. The trait therefore should be evaluated for each specific region in groundnut breeding. Thousand seed weight had significant and positive correlations with important yield attributed traits in this study (Table 6). Similarly it indicated positive correlations with number of pods per plant (Nath and Alam 2002; Dapaah *et al*. 2014), number of branches (Jiang *et al*. 2014) and early flowering time (Upadhyaya 2003) in different studies. This common associations obtained from different studies have implications in reducing number of traits in characterization by using easily measurable correlated traits in groundnut.

Obtaining higher seed yield for different environmental conditions is one of the most important challenges in plant breeding. In the present study seed yield showed wide variation among genotypes in the collection. However there was no significant difference between the two subspecies for seed yield. This situation might be sourced of differences of each yield components between subspecies. The traits of thousand seed weight and number of branches had significant higher values for Subsp. *hypogaea*. On the other hand, the traits of plant height and shelling percentage significantly higher in Subsp. *fastigiata* might cause to balance for seed yield between Subps. *hypogaea* and Subsp. *fastigiata*. PC analysis demonstrated that seed yield and number of pods per plant had high and positive values in PC2. Similar positive contribution to PC was obtained by Kumar *et al*. (2010) in estimation of genetic diversity of advanced breeding lines. Early flowering trait should also be integrated to understand the relationship between seed yield and number of pods per plant to develop genotypes suitable for second crop farming. Since immature and economically unacceptable pods waste a great amount of seed yield (Caliskan *et al*. 2008a), cultivars with early flowering and higher number of mature pods are well adapted to the Mediterranean climate conditions. However, the genotypes with high yield and number of pods per plant in the collection tend to be late flowering. These genotypes, therefore, should be used as parents in crossing programs to obtain superior recombinant genotypes which have early maturity and higher seed yield characteristics. Selection in different taxanomic groups for seed yield trait is important for groundnut improvement programs because certain market groups are preferred for particular characteristics, such as differences in seed weight, seed size, shell type, seed color, taste, flavor, and oil characteristics. ACG 206 from subps. *hypogaea* var. *hypogaea* and ACG 45 from Subsp. *fastigiata* var. *vulgaris* indicated highest seed yield in the collection. ACG 206 had also desirable thousand seed weight (about 670 g) for direct commercial usage in virginia market group which is highly demanded because of large pod/seed size for processing industry particularly for salting, confections, and roasting in the shells. ACG 45 is suitable for spanish market group generally used in candy, peanut butter and oil production. This genotype had also early flowering trait which provides on the post-wheat second crop production. ACG 45 and ACG 206 were also clustered together with ACG 193 and ACG 256 in the dendogram while showing considerable difference from remaining genotypes in the collection implying that they had distinct agronomical properties. Although these genotypes were from different subspecies and botanical varieties, they were agronomically superior and provide better opportunities for developing high seed yielding cultivars.

Color of the seed coat or testa is also an important market trait whose intensity may vary depending on maturity, environment, genotype or the interaction between genotype and environment (Rao and Murty 1994). The groundnut collection offered a wide diversity of seed coat colors with desirable agronomic traits for commercial usage and breeding studies. Pink, red, tan and shades of these colors are generally selected for snack food and confectionary industries and many high yield genotypes had these seed coat colors in the collection. Transferring seed coat color by hybridization is possible in groundnut (Branch 2011) and therefore, the genotypes with desirable seed coat color but lower yield should be used as parent in breeding studies.

5 Conclusion

The present investigation provided comprehensive data on agro-morphological traits with potential for utilization in groundnut improvement programs. Several genotypes from different subspecies and botanical varieties in the collection had many desirable traits for commercial purposes. Especially, the genotypes with high pod yield and shelling percentage could be used directly and also integrated into hybridization programs indirectly to acquire superior genotypes. In order to promote nutritionally precious groundnut cultivars, this base material must be improved with respect to high oleic acid content.

Acknowledgements

This study was supported by the Ministry of Science, Industry and Technology of Turkey (SANTEZ- 01527-STZ-2012-2), and the Scientific Research Projects Coordination Unit of Akdeniz University, Turkey (FDK-2015-673), respectively. We are grateful to the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Gene bank, Hyderabad, India for supplying genetic material several times.

Appendix associated with this paper can be available on http://www.ChinaAgriSci.com/V2/En/appendix.htm

References

Anothai J, Patanothai A, Jogloy S, Pannangpetch K, Boote K J, Hoogenboom G. 2008. A sequential approach for determining the cultivar coefficients of peanut lines using end-of-season data of crop performance trials. *Field Crops Research*, **108**, 169–178.

Awal M A, Ikeda T. 2003. Controlling canopy formation, flowering, and yield in field-grown stands of peanut (*Arachis hypogaea* L.) with ambient and regulated soil temperature. *Field Crops Research*, **81**, 121–132.

Bishi S K, Lokesh K, Dagla M C, Mahatma M K, Rathnakumar A L, Lalwani H B, Misra J B. 2013. Characterization of Spanish peanut germplasm (*Arachis hypogaea* L.) for sugar profiling and oil quality. *Industrial Crops and Products*, **51**, 46–50.

Brach W D. 2011. First 100 years — Inheritance of testa color in peanut (*Arachis hypogaea* L.). *Crop Science*, **51**, 1–4.

Caliskan S, Caliskan M E, Arslan M. 2008a. Genotypic differences for reproductive growth, yield, and yield components in groundnut (*Arachis hypogaea* L.). *Turkish Journal of Agriculture and Forestry*, **32**, 415–424.

Caliskan S, Caliskan M E, Arslan M, Arioglu H. 2008b. Effects of sowing date and growth duration on growth and yield of groundnut in a Mediterranean-type environment in Turkey. *Field Crops Research*, **105**, 131–140.

Canavar O, Kaynak M A. 2010. Growing degree day and sunshine radiation effects on peanut pod yield and growth. *African Journal of Biotechnology*, **9**, 2234–2241.

Craufurd P Q, Wheeler T R, Ellis R H, Summerfield R J, Prasad V P V. 2000. Escape and tolerance to high temperature at flowering in groundnut (*Arachis hypogaea* L.). *Journal of Agricultural Science*, **135**, 371–378.

Dapaah H K, Mohammed I, Awuah R T. 2014. Growth and yield performance of groundnuts (*Arachis hypogaea* L.) in response to plant density. *International Journal of Plant & Soil Science*, **3**, 1069–1082.

FAO (Food and Agriculture Organization). 2013. FAOSTAT. [2016-08-26]. http://faostat.fao.org/site/567/default.aspx

Garba N M I, Bakasso Y, Zaman-Allah M, Atta S, Mamane M I, Adamou M, Hamidou F, Idi S S, Mahamane A, Saadou M. 2015. Evaluation of agro-morphological diversity of groundnut (*Arachis hypogaea* L.) in Niger. *African Journal of Agricultural Research*, **10**, 334–344.

Gregory, W C, Gregory M P. 1976. Groundnut. In: Simmonds N W, ed., *Evolution of Crop Plants*. Longman, London. pp. 151–154.

Gupta S K, Baek J, Carrasquilla-Garcia N, Penmetsa R V. 2015. Genome-wide polymorphism detection in peanut using next-generation restriction-site-associated DNA (RAD) sequencing. *Molecular Breeding*, **35**, 145.

Holbrook C C, Anderson W F, Pittman R N. 1993. Selection of a core collection from the U.S. germplasm collection of peanut. *Crop Science*, **33**, 859–861.

Holbrook C C, Dong W. 2005. Development and evaluation of a mini core collection for the U.S. peanut germplasm collection. *Crop Science*, **45**, 1540–1544.

Hwang J Y, Wang Y T, Shyu Y, Wu J S. 2008. Antimutagenic and antiproliferative effects of roasted and defatted peanut dregs on human leukemic U937 and HL-60 cells. *Phytotherapy Research*, **22**, 286–290.

International Board for Plant Genetic Resources (IBPGR), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 1992. Descriptors for groundnut. In: *International Board for Plant Genetic Resources, Rome*. International Crops Research Institute for the Semi-Arid Tropics, Patancheru. pp. 1–125.

Isik H, Gul A. 2004. Peanut production cost and problems in Turkey. *Pakistan Journal of Biological Sciences*, **7**, 472–477.

Jiang H, Huang L, Ren X, Chen Y, Zhou X, Xia Y, Huang J, Lei Y, Yan L, Wan L, Liao B. 2014. Diversity characterization and association analysis of agronomic traits in a Chinese peanut (*Arachis hypogaea* L.) mini-core collection. *Journal of Integrative Plant Biology*, **56**, 159–169.

Kassa M T, Yeboah S O, Bezabih M. 2009. Profiling peanut (*Arachis hypogea* L.) accessions and cultivars for oleic acid and yield in Botswana. *Euphytica*, **167**, 293–301.

Krapovickas A, Gregory W C. 1994. Taxonomia del genero *Arachis* (Leguminosae). *Bonplandia*, **8**, 1–186.

Kumar S I, Govindaraj M, Kumar V K. 2010. Estimation of genetic diversity of new advanced breeding lines of groundnut (*Arachis hypogaea* L.). *World Journal of Agricultural Science*, **6,** 547–554.

Luz L N, Santos R C, Filho P A M. 2011. Correlations and path analysis of peanut traits associated with the peg. *Crop Breeding and Applied Biotechnology*, **11**, 88–93.

Minimol J S, Datke S B, Deshmukh S N, Satpute G N. 2001. Genotype x environment interaction in groundnut (*Arachis hypogaen* Linn.). *Annals of Plant Physiology*, **14**, 74–79.

Mothilal A. 2012. Groundnut. In: Gupta S K, ed., *Technological Innovations in Major World Oil Crops*, *Volume 1* (breeding). Springer-Verlag, New York. pp. 323–395.

Mozingo R W, O'Keefe S P, Sanders T H, Hendrix K W. 2004. Improving shelf life of roasted and salted inshell peanuts using high oleic fatty acid chemistry. *Peanut Science*, **31**, 40–45.

Nath U K, Alam M S. 2002. Genetic variability, heritability and genetic advance of yield and related traits of groundnut (*Arachis hypogaea* L.). *Journal of Biological Sciences*, **2**, 762–764.

Nigam S N, Aruna R. 2008. Improving breeding efficiency for early maturity in peanut. *Plant Breeding Reviews*, **30**, 295–322.

Poehlman J M, Sleper D A. 1995. *Breeding Field Crops*. Iowa state University Press, Ames.

Rao V R, Murty U R. 1994. Botany — morphology and anatomy. In: Smart J, ed., *The Groundnut Crop*: *A Scientific Basis for Improvement*. Chapman & Hall, London. pp. 45–95.

R Development Core Team. 2016. R: A language and environment for statistical computing. [2016-08-26]. www.r-project.org

Rehman A U, Wells R, Isleib T G. 2001. Reproductive allocation

on branches of virginia-type peanut cultivars bred for yield in North Carolina. *Crop Science*, **41**, 72–77.

Rohlf F J. 2000. NTSYS-pc: Numerical taxonomy and multivariate analysis system, version 2.1. Exeter Software. New York.

Sastry K S K, Chari M, Prasad T G, Udayakumar M, Sashidhar V R. 1985. Flowering pattern and pod development in bunch types of groundnut: Is there a relationship between synchrony in flowering and pod development? *Indian Journal of Plant Physiology*, **28**, 64–71.

Savage G P, Keenan J J. 1994. The composition and nutritive value of groundnut kernels. In: Smartt J, ed., *The Groundnut Crop*: *A Scientific Basis for Improvement*. Chapman & Hall, London. pp. 173–213.

Sekhon K S, Ahuja K L, Sandhu R S, Bhatia I S. 1972. Variability in fatty acid composition in peanut 1. Bunch group. *Journal of the Science of Food and Agriculture*, **23**, 919–924.

Shilman F, Brand Y, Brand A, Hedvat I, Hovav R. 2011. Identification and molecular characterization of homeologous Δ9-stearoyl acyl carrier protein desaturase 3 genes from the allotetraploid peanut (*Arachis hypogaea*). *Plant Molecular Biology Reporter*, **29**, 232–241.

Smartt J. 1994. The future of the groundnut crop. In: Smartt J, ed., *The Groundnut Crop: A Scientific Basis for Improvement*. Chapman & Hall, London. pp. 700–720.

Smith B W. 1954. *Arachis hypogaea*, reproductive efficiency. *American Journal of Botany*, **41**, 607–616.

Suassuna T M F, Suassuna N D, Moretzsohn M C, Bertioli S C M L, Bertioli D J, Medeiros E P. 2015. Yield, market quality, and leaf spots partial resistance of interspecific peanut progenies. *Crop Breeding and Applied Biotechnology*, **15**, 175–180.

Suchoszek-Lukaniuk K, Jaromin A, Korycinska M, Kozubek A. 2011. Health benefits of peanut (*Arachis hypogaea* L.) seeds and peanut oil consumption. In: Preedy V R, Watson R R, Patel V B, eds., *Nuts and Seeds in Health and Disease Prevention*. Elsevier, London. pp. 873–880.

Swamy B P M, Upadhyaya H D, Goudar P V K, Kullaiswamy B Y, Singh S. 2003. Phenotypic variation for agronomic characteristics in a groundnut core collection for Asia. *Field Crops Research*, **84**, 359–371.

Upadhyaya H D. 2003. Phenotypic diversity in groundnut (*Arachis hypogaea* L.) core collection assessed by morphological and agronomic evaluations. *Genetic Resources and Crop Evolution*, **50**, 539–550.

Upadhyaya H D, Bramel P J, Ortiz R, Singh S. 2002. Developing a mini core of peanut for utilization of genetic resources. *Crop Science*, **42**, 2150–2156.

Upadhyaya H D, Dwivedi S L, Vadez V, Hamidou F, Singh S, Varshney R K, Liao B. 2014. Multiple resistance and nutritionally dense germplasm identified from mini core collection in groundnut. *Crop Science*, **54**, 679–693.

Upadhyaya H D, Nigam S N. 1994. Inheritance of two components of early maturity in groundnut (*Arachis hypogaea* L.) *Euphytica*, **78**, 59–67.

Upadhyaya H D, Ortiz R, Bramel P J, Singh S. 2003. Development of a groundnut core collection using taxonomical, geographical and morphological descriptors. *Genetic Resources and Crop Evolution*, **50**, 139–148.

Upadhyaya H D, Reddy L J, Gowda C L L, Singh S. 2006. Identification of diverse groundnut germplasm: Sources of early-maturity in a core collection. *Field Crops Research*, **97**, 261–267.

Upadhyaya H D, Swamy B P M, Goudar P V K, Kullaiswamy B Y, Singh S. 2005. Identification of diverse groundnut germplasm through multienvironment evaluation of a core collection for Asia. *Field Crops Research*, **93**, 293–299.

Young C T, Waller G K. 1972. Rapid oleic/linoleic microanalytical procedure for peanuts. *Journal of Agricultural and Food Chemistry*, **20**, 1116–1118.

(Managing editor SHI Hong-liang)