Developing a Core Collection of Peanut Specific to Valencia Market Type

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ABSTRACT

Crop improvement and the dissection of complex genetic traits require germplasm diversity. A core collection is a gateway for the use of diverse accessions with beneficial traits in applied breeding programs. Valencia germplasm consisting of 630 peanut (*Arachis hypogaea* L. ssp. *fastigiata var. fastigiata*) accessions from the USDA collection and a check cultivar, New Mexico Valencia C, were evaluated for 26 descriptors in an augmented design for two seasons. The accessions were stratified by country of origin, and data on morphological and agronomic descriptors were used for clustering following Ward's method. About 10% or a minimum of one accession from each cluster and region were selected to develop core subset of 77 accessions. Comparison of means between the core subset and the entire collection indicated that the genetic variation available for these traits in the entire collection has been preserved in the core subset. The similarity in correlation coefficients in the entire collection and core subset suggests that this core subset has preserved most of the coadapted gene complexes controlling these associations. Peanut breeders engaged in improving the genetic potential of Valencia peanuts will find this core subset useful in cultivar development.

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Abbreviations: DAS, days after sowing; IBPGR, International Board for Plant Genetic Resources; SLA, specific leaf area; SPAD, Soil–Plant Analyses Development.

Valencia peanuts (*Arachis hypogaea* L. ssp. *fastigiata* var. *fastigiata*) for the in-shell market are predominantly grown in eastern New Mexico and west Texas. Average yield in this region is about 3750 kg ha^{-1}, with an annual production of 39,200 Mg ha^{-1} and an estimated value of US$37 million in income to growers. The area under peanut, however, has declined in recent years. Higher yield, drought tolerance, and reduced diseases would improve the competitiveness of peanut vs. corn production, especially since corn requires significantly more water than peanut. Furthermore, to maintain the monopoly of this region for the production of specialty peanuts (Valencia market type), growers need to have peanut cultivars that mature early, produce more with less water (high water use efficiency), resist fungal infection, and maintain good seed quality.

Understanding the range of diversity and the genetic structure of gene pools is critical for the effective management and use of germplasm resources. Continuous progress in plant breeding depends on the discovery of new sources of genetic variation, accurate identification of lines with beneficial traits, and their judicious

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use in such a way that a combination of alleles when brought together produces progenies with superior performance. Many of the agronomic and seed quality traits show considerable genotype × environment interaction, necessitating replicated multilocation evaluation to identify germplasm with beneficial traits for use in crop improvement programs. However, replicated multilocation evaluation of such a large collection of germplasm for a range of traits is impossible because of the resource limitations and would be of little value due to low precision. A core collection, which is a subset of accessions representing at least 70% of the genetic variation present in the entire collection of the species (Brown, 1989), is a gateway for the utilization of diverse germplasm with beneficial traits in crop breeding programs. Core or mini-core (10% of core or 1% of entire collection) (Upadhyaya and Ortiz, 2001) collections are reported in peanut (Holbrook et al., 1993; Upadhyaya et al., 2002, 2003; Holbrook and Dong, 2005). These subsets, however, are composed of accessions from all six subspecies (*hypogaea*, *vulgaris*, *fastigiata*, *aequitorania*, *hirsuta*, and *peruviana*) and four market (Virginia bunch, Virginia runner, Spanish bunch, and Valencia bunch) types; thus sampling limited genetic variation from each group. Moreover, crosses involving Valencia and Virginia types have not been successful in selecting the Valencia type peanuts with desired characteristics because of a predominance of Virginia traits in segregating populations. There is therefore an urgent need to develop core collections for major market types in peanut to allow breeders to use a greater range of diverse germplasm within the botanical and market type in crossing and selection. For example, peanut breeders working on enhancing the genetic potential of Valencia peanuts will find a core collection specific to Valencia peanuts more useful in a breeding program.

Core or mini-core collections have been developed for many crops, and when further evaluated, new sources of genetic variation have been reported for agronomic traits, including resistance to biotic and abiotic stresses. In peanut, for example, such traits include early maturity (Upadhyaya et al., 2006); high yield, greater shelling percentage, and seed weight (Upadhyaya et al., 2005); tolerance to drought and low temperature (Upadhyaya et al., 2001; Upadhyaya, 2005); and resistance to root-knot nematode [caused by *Meloidogyne arenaria* (Neal)], early leaf spot [caused by *Cercospora arachidicola* (Hori)], pepper spot [caused by *Leptosphaerulina crassiasca* (Sechet)], tomato spotted wilt virus, and many soil-borne fungal diseases, including preharvest aflatoxin contamination (Isleib et al., 1995; Anderson et al., 1996; Holbrook et al., 1998, 2000; Franke et al., 1999; Damicone et al., 2003). These new accessions have trait-specific characteristics similar or agronomically superior to the best control but diverse from the previously identified sources. The use of these diverse sources would help bring in much needed diversity and broaden the genetic base of peanut cultivars. In the present study, we report the development of a core collection specific to Valencia peanut that will be directly relevant to peanut breeders engaged in improving the genetic potential of Valencia peanut market type.

MATERIALS AND METHODS

Six hundred and thirty accessions belonging to *A. hypogaea* L. subsp. *fastigiata* var. *fastigiata* (Valencia peanut market type) from the USDA peanut germplasm collection were evaluated in this study using augmented designs. A locally grown cultivar, New Mexico Valencia C, was used as a repetitive control after every five test entries. The experiment was conducted on raised beds, 1.5-m-long ridge, in a ridge-furrow system at South Research Facility, south of Clovis, New Mexico, in 2004 and also on a grower field in 2006. The soil is classified as Amarillo fine sand (fine-loamy, mixed, superactive, thermic, Aridic Paleustalf). A basal dose of 62 kg ha^{-1} of nitrogen and 56 kg ha^{-1} of phosphorus was incorporated into the soil during the land preparation. Another 56 kg ha^{-1} of nitrogen was top dressed at 60 d after sowing (DAS). The seeds were treated with Captan {cis-N [(trichloromehtyl) thio]-4cyclohexene-1,2-dicarboximide} to prevent soil-borne fungal diseases. A spacing of 90 cm between ridges and 10 cm between seeds within ridge was used. Each plot consisted of 15 seeds per plot. A pre-emergence herbicide flumioxazin at 0.09 kg ha^{-1} was applied immediately after peanuts were sown and irrigated with a center pivot to field capacity. Chlorothalonil (Bravo Ultrex, Syngenta Crop Protection, Greensboro, NC) at 1.26 kg a.i. ha^{-1} was sprayed seven times at 14-d intervals. The crop received 813 mm of water in 2004, of which 318 mm was rainfall, and 656 mm of water in 2006, of which 123 mm was rainfall. Observations on five competitive plants were recorded on 12 morphological and 14 agronomic descriptors. The morphological descriptors, including growth habit, branching pattern, stem hair, stem pigmentation, peg pigmentation, leaf color and leaf shape, seeds per pod, pod beak, pod constriction, pod reticulation, and seed color, were recorded using International Board of Plant Genetic Resources and International Crops Research Institute for the Semi-Arid Tropics (1992) descriptors. The agronomic descriptors included plant height (cm), plant width (cm), number of primary branches, leaf length (mm), leaf width (mm), SPAD (Soil-Plant Analyses Development Unit, Minolta Corp., Ramsey, NJ) chlorophyll meter reading, specific leaf area (SLA), pod length (mm), pod width (mm), seed length (mm), seed width (mm), 100 seed weight (g), shelling percentage, and pod yield (g) per plant. The SPAD chlorophyll meter readings were recorded between 85 and 95 DAS. The second fully expanded tetrafoliate leaves from the main axis were excised between 0900 to 1200 h to record chlorophyll content directly after removal from the plant. The SPAD chlorophyll meter measures absorbance by plant tissues of wavelengths in the visible spectrum and serves as a measure of the relative internal concentration of chlorophyll a and b. Each reading was recorded on each of the four leaflets, care being taken to avoid the midrib, and averaged to correct for possible nonhomogeneous distribution of chlorophyll throughout the leaf (Sheshshayee et al.,

2006). Tetrafoliate leaves were then placed on ice and taken to the laboratory for measuring leaf area. Leaflets were removed from each petiole, and the leaf area of the four leaflets was measured with an LI-3000A leaf area meter (LICOR, Inc., Lincoln, NE) and summed to give total leaf area. The same leaves were used for measuring the leaflet length and width. Leaves were then oven dried at 80°C for 48 h and weighed. The SLA was calculated as the ratio of leaf area to leaf dry weight. A bulk sample of 200 g of mature pods was used to estimate shelling percentage. Pod length and width were recorded on 20 mature pods, and seed length and width were recorded on 20 mature seeds. One hundred mature seeds were randomly picked to record seed weight.

To develop this core collection, we first stratified the accessions on the basis of country of origin and then used Ward's method to form clusters using distance matrix based on 12 morphological and 14 agronomic traits on 630 accessions, similar to Upadhyaya et al. (2003) and Holbrook et al. (1993). The data on 14 agronomic traits were analyzed separately for each of the two seasons and also combined to determine the importance of various components of variance following residual maximum likelihood analysis considering genotype as random and season fixed using Genstat 9.1 (Payne et al., 2006). The use of a control cultivar repeatedly grown after five test entries provided error variance, and the mean (balanced linear unbiased predictor [BLUP]) was calculated for each entry and trait in both seasons and in the combined analysis. The significance of variance components due to genotype in each season as well as combined over seasons and genotype × season interactions were tested against their respective standard errors using *t* tests. The significance of the seasons was tested using Wald statistic. The seasons were nonsignificant for all the traits, and genotype × season interaction was nonsignificant for five traits (primary branches, SPAD, leaf width, SLA, and pod yield per plant). Because of this, the mean obtained from combined analysis was used for further analysis. The mean value based on combined analysis was used to create a distance matrix. The distance matrix was calculated using 12 morphological and 14 quantitative descriptors. The distance between two accessions was calculated as the difference in trait values divided by the overall range for that trait. To form the distance matrix, the individual trait distance of each pair of accessions was summed and divided by the number of traits (Johns et al., 1997). A hierarchical algorithm of Ward (1963) at an R^2 (squared multiple correlations) value of 0.70 was used for clustering, using SAS (SAS Institute, 2006). A total of 48 clusters were obtained. About 10%, or a minimum of one accession from each cluster and region, were selected to develop the core subset.

Means of the entire collection and the core subset were compared using the Newman–Keuls (Newman, 1939; Keuls, 1952) test for the 14 agronomic descriptors. The homogeneity of variances of the entire collection and the core subset was tested with Levene's test (Levene, 1960). The distribution homogeneity for each of the 14 descriptors among the entire collection and the core subset was analyzed using the χ^2 test. The diversity index (H′) of Shannon and Weaver (1949) was estimated and used as a measure of phenotypic diversity in the entire collection and core collection for each trait. The phenotypic correlations among different traits in the entire collection and the core subset were estimated independently to determine whether these associations, which may be under genetic control, were conserved in the core subset.

RESULTS AND DISCUSSION

Residual maximum likelihood analysis indicated that the variance due to genotypes was significant for all the traits except shelling percentage, number of primary branches, SPAD reading, SLA, leaflet width, plant height, plant width, and yield per plant in the 2004 season. In the 2006 season, the genotypic variance was significant for all traits except seed width, SLA, and pod yield per plant. In the pooled analysis, the season effect was nonsignificant, while genotype effect was significant for all the traits except SLA and plant yield. The genotype × season interaction was significant for all the traits except for primary branches, SPAD, leaf width, SLA, and pod yield per plant.

A core subset of 77 accessions was selected from 630 accessions belonging to subsp. *fastigiata* var. *fastigiata* (Valencia peanut market type). These 77 accessions were selected from 48 distinct clusters following method of selection, 10% or a minimum of 1 accession from each cluster. The core subset represented ≈12% of the 630 Valencia germplasm accessions evaluated (Table 1). Sixty-one accessions from South America grouped into 41 clusters showing diversity from the region, while only 3 to 4 accessions were included from Africa and North America since these regions in this study were represented by few accessions. Despite the high number of accessions from South America in the core subset, nonsignificant χ^2 across regions revealed homogeneous distribution of accessions among the entire collection and core subset (Table 2). This core subset predominantly consists of peanut cultivars and landraces from South America that are adapted to extreme variation in environmental conditions in the region and therefore represent a good source to identify new genetic variation for adaptation to stress conditions for use in breeding programs. Landrace is defined as an autochthonous (primitive) variety with a high capacity to tolerate biotic and abiotic stresses, resulting in high yield stability and an intermediate yield level under a low-input agricultural system (Zeven, 1998).

The differences between means and the variances of the core subset and the entire collection were not significant for any of the 14 agronomic descriptors (Table 3). The variances for each of the 14 agronomic traits in the core subset and entire collection were homogenous (Table 3). The core subset represented 76 to 100% of the variation for most of the agronomic descriptors except for pod yield per plant, for which only 48% variation of the entire collection was recovered (Table 3). On average, the core subset represented 86.7% variation of entire collection. Except for branching pattern ($P = 0.012$) among

Table 1. Geographic origin and biological status of the 77 accessions included in 48 clusters forming a core subset of Valencia peanut.

Cluster	Germplasm identity	Geographic region	Country	Biological status
1	PI 259601	Australia	Australia	Traditional cultivar, landrace
	PI 493536	South America	Argentina	Developed
2	PI 259580	Caribbean	Jamaica	Traditional cultivar, landrace
	PI 493501	South America	Argentina	Developed
	PI 497447	South America	Bolivia	Traditional cultivar, landrace
	PI 602494	South America	Argentina	Traditional cultivar, landrace
3	PI 493630	South America	Argentina	Developed
4	PI 493518	South America	Argentina	Developed
	PI 576604	South America	Bolivia	Unknown
	PI 493446	South America	Argentina	Developed
5	PI 365564	South America	Bolivia	Traditional cultivar, landrace
	PI 406718	Central America	Costa Rica	Traditional cultivar, landrace
	PI 429430	Africa	Zimbabwe	Traditional cultivar, landrace
	PI 475913	South America	Bolivia	Traditional cultivar, landrace
	PI 476078	South America	Brazil	Traditional cultivar, landrace
6	PI 429427	Africa	Zimbabwe	Traditional cultivar, landrace
	PI 493344	South America	Argentina	Developed
	PI 493688	South America	Argentina	Developed
7	PI 476089	South America	Brazil	Traditional cultivar, landrace
	PI 493339	South America	Argentina	Developed
	PI 493458	South America	Argentina	Developed
8	PI 493507	South America	Argentina	Developed
	PI 476079	South America	Brazil	Traditional cultivar, landrace
9	PI 476074	South America	Brazil	Traditional cultivar, landrace
	PI 493562	South America	Argentina	Developed
	PI 497459	South America	Bolivia	Traditional cultivar, landrace
10	PI 493405	South America	Argentina	Developed
	PI 493461	South America	Argentina	Developed
	PI 493865	South America	Argentina	Developed
11	PI 493415	South America	Argentina	Developed
	PI 493470	South America	Unknown	Developed
12	PI 315612	Africa	South Africa	Developed
	PI 493325	South America	Argentina	Developed
	PI 493340	South America	Argentina	Developed
13	PI 493624	South America	Argentina	Developed
14	PI 493810	South America	Argentina	Developed
15	PI 501985	South America	Peru	Traditional cultivar, landrace
16	PI 338337	South America	Venezuela	Advanced, improved cultivar
17	Breeding line	North America	USA	New breeding line
	PI 493382	South America	Argentina	Developed
18	PI 493360	South America	Argentina	Developed
	PI 493523	South America	Argentina	Developed
19	PI 475925	South America	Bolivia	Traditional cultivar, landrace
20	PI 494019	South America	Argentina	Developed
21	PI 493565	South America	Argentina	Developed
22	PI 493584	South America	Argentina	Developed
	PI 536300	South America	Uruguay	Traditional cultivar, landrace
23	PI 493660	South America	Argentina	Developed
	PI 536307	South America	Uruguay	Traditional cultivar, landrace
24	PI 493373	South America	Argentina	Developed
25	PI 497642	South America	Ecuador	Traditional cultivar, landrace

Table 1. Continued.

Cluster	Germplasm identity	Geographic region	Country	Biological status
26	PI 493612	South America	Argentina	Developed
27	PI 493484	South America	Argentina	Developed
28	PI 493816	South America	Argentina	Developed
29	PI 493566	South America	Argentina	Developed
30	PI 493451	South America	Argentina	Developed
31	PI 501269	South America	Ecuador	Traditional cultivar, landrace
32	PI 536121	South America	Brazil	Breeding, research material
33	PI 493514	South America	Argentina	Developed
34	PI 468208	South America	Bolivia	Advanced, improved cultivar
	PI 493666	South America	Argentina	Developed
35	PI 493381	South America	Argentina	Unknown
36	PI 502023	South America	Peru	Unknown
37	PI 475921	South America	Bolivia	Traditional cultivar, landrace
38	PI 501293	South America	Peru	Breeding, research material
39	PI 306361	Asia	Israel	Developed
	PI 493629	South America	Argentina	Developed
40	PI 493442	South America	Argentina	Developed
41	PI 407451	South America	Ecuador	Unknown
42	PI 390432	South America	Ecuador	Traditional cultivar, landrace
43	PI 409037	Africa	Zimbabwe	Traditional cultivar, landrace
44	Grif 13802	South America	Ecuador	Unknown
45	PI 599612	North America	USA	Developed
46	PI 508278	North America	USA	Breeding, research material
47	PI 493521	South America	Argentina	Developed
48	PI 314980	Europe	Russia	Traditional cultivar, landrace
	PI 468225	North America	Bolivia	Traditional cultivar, landrace

morphological descriptors, analysis of the frequency distribution indicated homogeneity of distribution among the entire collection and core subset for all the morphological descriptors (Table 4).

The Shannon–Weaver diversity index (H′) is used in genetic studies as a measure of both allelic richness and allelic evenness. A low H′ indicates an extremely unbalanced frequency of classes for an individual trait and lack of genetic diversity. The H′ in the core subset was similar to that of the entire collection for all the morphological and agronomic descriptors (Table 5), indicating that the diversity of the entire collection was represented in the core subset. The average H′ in the core subset was 0.350 (0.335 for the entire collection) for morphological descriptors and 0.589 (0.609 for the entire collection) for agronomic descriptors, indicating that the diversity in both morphological and agronomic descriptors was adequately sampled in the core subset.

A proper and adequate sampling has been suggested for the conservation of phenotypic associations arising out of coadapted gene complexes in core collections (Ortiz et al., 1998). Phenotypic correlations were calculated between 14 agronomic descriptors both in the entire collection and in the core subset independently (Table 6). Fourteen correlation coefficients in the core subset (absolute value ≥ 0.293 at 75 df at $P = 0.01$) and 39 correlation coefficients in the entire collection (absolute value ≥ 0.092 at 628 df at $P = 0.01$) were significant. The proportion of variance in one trait that can be attributed to its relationship with the other trait is indicated by its coefficient of determination (Snedecor and Cochran, 1980). The correlation coefficients with an absolute value greater than 0.71 have been

Table 2. Comparison of frequency distribution of number of accessions included from different continents to form the core subset of Valencia peanut.

Continent	No. of entries in entire collection	No. of entries in core subset	df	χ^2	Probability
Africa	53	4	1	0.290	0.590
Asia	19	1	1	1.748	0.186
Australia	1	1	1	0.770	0.380
Central America	2	1	1	0.571	0.450
Caribbean	1	1	1	0.770	0.380
Europe	1	1	1	0.770	0.380
North America	11	4	1	0.215	0.643
South America	530	61	1	0.380	0.537
Other	12	3	1	0.142	0.706
Total	630	77	8	5.658	0.686

Table 3. Range of variation (%) captured in core subset, and mean and variance for the 14 agronomic descriptors, based on pooled data, in the entire collection and core subset of Valencia peanut.

Descriptor	Core collection (range of variation)	Mean		Variance	
		Entire collection	Core subset	Entire collection	Core subset
	%				
Plant height	99.1	36.3	36.3	5.36	6.38
Plant width	100.0	71.0	70.8	6.24	7.95
Primary branches	81.9	5.1	5.2	0.70	0.78
Leaf length	84.9	60.1	60.5	8.28	7.27
Leaf width	90.3	28.4	28.5	4.52	5.33
Pod length	100.0	33.8	33.7	9.08	12.92
Pod width	100.0	13.8	14.1	2.12	2.10
Seed length	94.5	13.5	13.6	1.28	1.31
Seed width	79.3	8.2	8.2	0.27	0.35
100-seed weight	86.5	46.8	47.3	19.14	19.11
Shelling percentage	80.3	61.4	60.9	15.72	19.01
SPAD†	91.8	38.6	38.6	0.40	0.56
Specific leaf area	76.8	137.5	137.5	1.81	1.68
Pod yield per plant	48.4	53.4	53.4	0.63	0.55
Mean ± SE	86.7 ± 3.7				

†SPAD, Soil-Plant Analyses Development chlorophyll meter reading.

Table 4. Comparison of frequency distribution for 12 morphological descriptors, based on pooled data, in the entire collection and core subset of Valencia peanut.

Descriptor	Number of classes	χ^2	Probability
Growth habit	4	1.392	0.846
Branching pattern	1	6.301	0.012
Stem pigmentation	1	0.049	0.825
Stem hair	4	2.196	0.700
Peg pigmentation	1	2.654	0.103
Leaf color	2	0.303	0.860
Leaf shape	11	5.195	0.921
Seeds per pod	3	7.107	0.069
Pod beak	3	0.183	0.980
Pod constriction	4	6.869	0.143
Pod reticulation	5	1.623	0.899
Seed color	5	5.912	0.315

suggested to be meaningful (Skinner et al., 1999), so that more than 50% of the variation in one trait is predicted by the other. The correlation (*r*) values in the present study, except for leaf length and leaf width ($r = 0.731$ in the core subset and 0.620 in the entire collection), were low, indicating that although significant, these correlations did not explain a large fraction of total variation. Other correlations with significant importance in this study include positive correlations between pod and seed characteristics, which should probably help breeders to identify germplasm with desired pod and seed characteristics for use in breeding programs.

Table 5. Shannon-Weaver diversity index for 12 morphological and 14 agronomic descriptors, based on pooled data, in the entire collection and core subset of Valencia peanut.

Descriptor	Entire collection	Core subset
Morphological descriptor		
Growth habit	0.219	0.196
Branching pattern	0.005	0.030
Stem pigmentation	0.301	0.300
Stem hair	0.330	0.345
Peg pigmentation	0.057	0.104
Leaf color	0.410	0.422
Leaf shape	0.434	0.435
Seeds per pod	0.416	0.489
Pod beak	0.521	0.525
Pod constriction	0.445	0.485
Pod reticulation	0.539	0.525
Seed color	0.339	0.345
Mean	0.335	0.350
SE ±	0.049	0.048
Agronomic descriptor		
Plant height	0.626	0.599
Plant width	0.612	0.581
Primary branches	0.583	0.520
Leaf length	0.619	0.619
Leaf width	0.622	0.626
Pod length	0.623	0.604
Pod width	0.604	0.581
Seed length	0.610	0.595
Seed width	0.595	0.552
100-seed weight	0.632	0.607
Shelling percentage	0.599	0.600
SPAD†	0.624	0.605
Specific leaf area	0.621	0.624
Pod yield per plant	0.562	0.532
Mean	0.609	0.589
SE ±	0.005	0.009
Mean (26 descriptors)	0.483	0.479
SE ±	0.035	0.032

†SPAD, Soil-Plant Analyses Development chlorophyll meter reading.

Genetic diversity is the basis for genetic improvement. Knowledge of the germplasm diversity can significantly impact the improvement of crop plants. The genetic base of Valencia peanut cultivars grown in New Mexico and west Texas is quite narrow. Until now, only five Valencia peanut cultivars have been released for cultivation in New Mexico (Isleib et al., 2001), and all, except New Mexico Valencia C, are selections from plant introductions. Of these, New Mexico Valencia C is the most commonly grown Valencia peanut cultivar in

Table 6. Correlation coefficients between 14 agronomic traits in the core subset (above diagonal)† and the entire collection (below diagonal)‡ of Valencia peanut.

Trait§	PLHT	PLWD	PRBR	LLN	LWD	PDL	PWD	SDL	SWD	SDWT	SHP	SPAD	SLA	PYPP
PLHT	–	0.532	0.016	0.085	−0.072	−0.045	−0.220	−0.070	−0.156	−0.178	0.150	−0.157	0.045	−0.022
PLWD	0.620	–	−0.138	−0.053	−0.183	−0.302	−0.173	−0.197	−0.137	0.084	0.132	−0.365	0.086	0.104
PRBR	−0.063	−0.034	–	−0.078	−0.126	−0.150	−0.096	−0.078	−0.104	−0.099	−0.137	0.352	−0.111	0.200
LLN	0.171	0.107	−0.090	–	0.731	−0.005	0.091	−0.061	−0.069	−0.272	−0.073	−0.105	−0.197	−0.214
LWD	0.102	−0.019	−0.036	0.672	–	−0.039	−0.035	−0.119	−0.018	−0.241	−0.004	0.095	−0.065	−0.279
PDL	0.120	−0.013	−0.106	0.146	0.029	–	0.411	0.556	0.318	0.262	0.217	0.024	0.092	0.107
PWD	−0.005	0.002	−0.045	0.086	−0.039	0.392	–	0.477	0.405	0.209	−0.173	−0.135	0.052	0.086
SDL	0.116	0.047	−0.081	0.112	0.050	0.495	0.521	–	0.540	0.349	0.072	−0.054	0.171	0.115
SWD	−0.030	−0.012	−0.012	−0.010	−0.038	0.219	0.390	0.499	–	0.222	0.045	0.005	0.231	0.060
SDWT	0.094	0.134	−0.061	0.093	−0.012	0.375	0.353	0.415	0.307	–	−0.019	−0.249	0.208	0.457
SHP	0.142	0.161	−0.028	−0.218	−0.257	−0.003	−0.056	−0.024	0.058	0.023	–	−0.057	0.127	0.252
SPAD	−0.068	−0.099	0.014	0.153	0.230	−0.046	0.003	−0.038	0.015	−0.058	−0.100	–	−0.329	−0.067
SLA	0.048	0.024	−0.053	−0.217	−0.162	0.085	−0.047	0.090	0.025	0.010	0.163	−0.351	–	0.045
PYPP	0.027	0.119	0.092	−0.061	−0.077	0.151	0.036	0.064	0.073	0.216	0.226	−0.034	0.051	–

†A correlation of ≥0.293 significant at $P = 0.01$ at 75 df for the core collection (above diagonal).

‡A correlation of ≥0.092 significant at $P = 0.01$ at 628 df for the entire collection (below diagonal).

§PLHT , plant height; PLWD, plant width; PRBR, primary branches; LLN, leaf length; LWD, leaf width; PDL, pod length; PWD, pod width; SDL, seed length; SDW, seed width; SDWT, seed weight, SHP, shelling percentage; SPAD, Soil-Plant Analyses Development chlorophyll meter reading; SLA, specific leaf area; PYPP, pod yield per plant.

eastern New Mexico and west Texas. It originated from an irradiated population of Colorado Manfredi, a pure line selection from Colorado de Córdoba (Hsi, 1980). In the past, no systematic efforts have been undertaken to enhance the genetic potential of this cultivar group, mainly because information on the genetic variability in Valencia germplasm possessing beneficial traits was lacking. The identification of this core subset thus provides an opportunity to look for new sources of genetic variation for agronomic traits and resistance to biotic and abiotic stresses within the subsps. *fastigiata* var. *fastigiata* (Valencia market type). Moreover, this core subset consists of Valencia accessions that are not represented, except for PI 407451, 497459, 476089, and 508278 (Holbrook et al., 1993), in peanut core subsets reported earlier (Holbrook et al., 1993; Upadhyaya et al., 2003).

The accessions included in this Valencia core collection represent elite source materials for the U.S. peanut breeders to identify new sources of genetic variation in Valencia-type peanut for the development of cultivars adapted to eastern New Mexico and west Texas. Furthermore, molecular characterization of this core subset should point to allelic variation associated with beneficial traits for use in genomics and in applied plant breeding.

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