Phenotypic variation for agronomic characteristics in a groundnut core collection for Asia

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Abstract

The groundnut (*Arachis hypogaea* L.) core collection for Asia consists of 504 accessions of which 274 belong to subsp. *fastigiata* (var. *fastigiata* and *vulgaris*) and 230 to subsp. *hypogaea* (var. *hypogaea*). This core collection was evaluated for 20 agronomic characteristics in the 2000 rainy season and for 21 characteristics in the 2000/2001 post-rainy season at two locations, Raichur and Kawadimatti, India, to estimate phenotypic diversity and determine the importance of different descriptor traits. All traits, except leaflet length and width, pod length and width, and seed length and width showed genotype × location interactions. All traits except leaflet width, number of primary branches, nodes on main stem, nodes on cotyledonary branches, total and mature pods, and length of primary and cotyledonary branches, pod length and width, and seed length and width showed genotype × season interaction. The *fastigiata* and *hypogaea* groups differed significantly for all traits except one trait each in the rainy season at Raichur and post-rainy season at Kawadimatti and five traits in the post-rainy season at Raichur. The *hypogaea* group took longer to flower, had more primary branches, longer primary and cotyledonary branches, more nodes on cotyledonary branches, more total pods, mature pods and pegs per plant, longer and wider pods and heavier seeds than the *fastigiata* group. The range for most traits was different in the two groups. There were significant phenotypic correlations among the various characteristics. Three of these, between number of total pods and mature pods, number of total pods and pegs, and number of mature pods and pegs had values greater than 0.707 ($r^2 = 50\%$) in both the *fastigiata* and *hypogaea* groups and in the entire regional collection. Principal component analysis showed that 20 agronomic traits were important in explaining multivariate polymorphism. Pod yield per plant did not significantly account for variation in the first five principal components of *fastigiata* and *hypogaea* types as well as for the entire regional collection in either season or location, indicating its relatively low importance as a descriptor. Average phenotypic diversity index was similar in both groups. The Shannon–Weaver diversity index varied among traits between the two groups, and the diversity within a group depended on location, season, and traits recorded.
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1. Introduction

Groundnut is an important oilseed crop cultivated in 107 countries. Annual production in 2001 was 35.09 Mt from 25.54 million ha (FAO, 2001). In Asia, the crop is cultivated in 27 countries, accounting for 67% of global production and 58% of global area. India with 8.2 million ha (55.9% of Asia) and China with 4.6 million ha (31.6% of Asia) are the two major producers in Asia. Other important countries are Indonesia (0.65 million ha), Myanmar (0.6 million ha), and Vietnam (0.25 million ha). Average productivity in Asia (1.6 t ha^{-1}) is higher than the world average (1.37 t ha^{-1}), largely due to large productivity increases in China in last two decades: by 47.2% from the 1970s (1.2 t ha^{-1}) to the 1980s (1.8 t ha^{-1}) and by another 42.7% from 1980s to 1990s (2.5 t ha^{-1}). In comparison, the global productivity increase during this period was 16.1% from 1970s to 1980s and 19.4% from 1980 to 1990s.

Crop improvement has played a significant role in yield increases in Asia, as elsewhere. However, only a small amount of the genetic variability contained in the germplasm accessions has been utilized to date. For example, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) holds in trust over 14,000 accessions of cultivated groundnut (peanut) but very few have been used in the breeding programs (Upadhyaya et al., 2002). This suggests that most cultivars developed by ICRISAT have a narrow genetic base. In a review of utilization of peanut genetic resources in China, Jiang and Duan (1998) concluded that introduced foreign germplasm and wild relatives had seldom been utilized in cultivar development. In the USA, the cultivar Dixie Giant is the major germplasm source in all pedigrees of runner market-type groundnut while Small White Spanish-1 cultivar was in 90% or more of pedigrees. These two lines contributed nearly 50% of the germplasm of runner cultivars (Knauft and Gorbet, 1989).

Emphasis on conserving crop germplasm has led to collection and subsequent maintenance of very large germplasm collections. Frankel and Bennett (1970) proposed that the representativeness of collections could be achieved through large collections; however, the accessibility and usefulness of a collection may be inversely related to its size (Frankel and Soulé, 1981). Of the 14,310 germplasm accessions in the ICRISAT Genebank, 4738 are from 21 Asian countries. These accessions were acquired mainly by donations from different countries, supplemented by collection missions (1256 accessions, 26.5%). A total of 30 collection missions were undertaken in India, Indonesia, Malaysia, Myanmar, the Philippines, Nepal, and Vietnam. India accounted for 3663 accessions (77.3%) of which 1000 accessions (27.3%) were collected through 22 collecting missions. China contributed 213 accessions (4.5%) through donation.

Development of a core collection is one way to enhance the use of genetic resources in crop improvement (Frankel, 1984). A core collection is a subset of accessions from the entire collection that captures most of the available genetic diversity of the species (Brown, 1989). Upadhyaya et al. (2001) developed a core collection for Asia, consisting of 504 entries from 4738 accessions from 21 countries, using taxonomical, geographical, and morphological descriptors to enhance the use of genetic resources in improvement programs in the region. The accessions were first stratified by botanical varieties, and then by country of origin. The accessions from small countries and those with similar agro-climatic conditions were grouped together. Data on 15 morphological descriptors, growth habit, branching pattern, stem color, stem hairs, leaf color, leaf shape, leaf hairs, flower color, streak color, peg color, pod beak, pod constriction, pod reticulation, seeds per pod, and seed color were used to separate accessions into clusters using Ward's method. From each cluster about 10% accessions were randomly selected to constitute the Asia core. In the USA, Holbrook et al. (1993) developed a groundnut core collection of 831 accessions on the basis of six morphological variables (plant type, pod type, seed size, testa color, seeds per pod, and seed weight). This core collection has been evaluated for various traits to identify useful parents (Isleib et al., 1995; Holbrook and Anderson, 1995; Anderson et al., 1996; Hammond et al., 1997; Holbrook et al., 1997, 1998, 2000; Franke et al., 1999).

The main objectives of this study were to assess phenotypic diversity of various agronomic traits in the rainy and post-rainy seasons at two locations in India, determine the importance of different descriptor traits, and evaluate associations among descriptors in the regional core subset and the most diverse genotypes, in order to facilitate the identification of useful

parents for future improvement in Asia, and possibly elsewhere.

2. Materials and methods

The materials for this study comprised 504 accessions from the Asia groundnut core collection, consisting of 274 accessions belonging to subsp. *fastigiata* (var. *vulgaris* and *fastigiata*) and 230 to subsp. *hypogaea* (var. *hypogaea*). These 504 accessions and four control cultivars, Gangapuri (*fastigiata*), ICGS 44 (*vulgaris*), ICGS 76 (*hypogaea*) and S 230 (*hypogaea*) were evaluated in an augmented design in the 2000 rainy and 2000/2001 post-rainy seasons at Regional Research Station, Raichur and Agricultural Research Station, Kawadimatti, Karnataka, India. The accessions were sown by hand. Each treatment consisted of a 4 m row on a ridge. Spacing was 60 cm between rows and 15 cm between plants. The four control cultivars were repeated after every nine entries. Care was taken to ensure uniform depth of planting. Seeds of accessions belonging to var. *hypogaea* were treated with ethrel (2-chloroethylphosphonic acid) before sowing to overcome the possible effects of post-harvest seed dormancy.

The experiments received 25 kg N ha^{-1}, 75 kg P$_2$O$_5$ ha^{-1}, 500 kg gypsum ha^{-1}, full irrigation (three irrigations in the rainy and five irrigations in the post-rainy seasons, each irrigation with 5 cm water) and protection against diseases, insect pests and weeds. In each accession, five representative plants were selected to record leaflet length and width at 60 days after planting (DAP) in the rainy season and 75 DAP in the post-rainy season, plant height, length and number of primary branches and cotyledonary branches, nodes on main stem, length of nodes on cotyledonary branches (cm), number of total pods, mature pods, and pegs per plant, and yield per plant at harvest. Data on days to first flower (days from sowing to appearance of first flower), cessation of flowering (days from sowing to the cessation of flowering), pod length and width, shelling percentage, seed length and width, and 100-seed weight were recorded on a plot basis. The entire plot was harvested and pods were stripped, dried and weighed. A 200 g sample of mature pods was used to estimate shelling percentage. Pod length and width were recorded on 10 mature pods and seed length and width on 10 mature seeds, while 100 mature seeds were used to record weight. Oil content was measured in the 2000/2001 post-rainy season at both locations with a commercial nuclear magnetic resonance spectrometer following the procedure described by Jambunathan et al. (1985). All the readings were taken on oven-dried (110 °C, 16 h) samples and values were expressed on a uniform 50 g kg^{-1} seed moisture.

The data were analyzed using ASREML (residual maximum likelihood). Variance components and associated standard errors due to genotypes, seasons, locations, and genotypes × location, genotype × season were estimated. Significance of the variance components was determined using Z-test.

Means of the two subspecies *fastigiata* and *hypogaea* were compared using the Newman–Keuls procedure (Newman, 1939; Keuls, 1952) for all traits in the rainy and post-rainy seasons at both locations. The homogeneity of variances of these groups was tested using Levene's (1960) test. Phenotypic correlations were calculated among all traits in the core collection and in the two subspecies in both the seasons and locations. Principal component analysis (PCA) of data was performed to investigate the importance of different traits in explaining multivariate polymorphism. The mean observations of agronomic traits for each accession were standardized by subtracting from each observation the mean value of the character and then dividing by its respective standard deviation. This resulted in standardized values for each trait with average 0 and standard deviation of 1 or less. The standardized values were used to perform PCA using Genstat 5 Release 4.1.

A phenotypic distance matrix was created by calculating the differences between each pair of entries for each characteristic. The diversity index was calculated by averaging all the differences in the phenotypic values for each trait divided by the respective range (Johns et al., 1997). The diversity index (H') (Shannon and Weaver, 1949) was calculated and used as a measure of phenotypic diversity of each trait. The index was estimated for each character across all entries in the two groups.

3. Results and discussion

The estimate of variance component due to genotypes was significant for days to first flower and

cessation of flowering, plant height, leaflet length and width, length of primary branches, number of nodes on main stem, length of cotyledonary branches, number of nodes on cotyledonary branches, total pods, mature pods, and pegs, pod length and width, shelling percentage, seed length and width, 100-seed weight, and oil content (data not shown). Location variance was significant for days to first flower and cessation of flowering, leaflet length, length of primary branches, number of nodes on main stem, shelling percentage, 100-seed weight, pod yield, and oil content (data not shown). All traits except leaflet length and width, pod length and width, and seed length and width showed genotype × location interactions. Nine traits including days to first flower and cessation of flowering, plant height, leaflet length, pegs per plant, shelling percentage, 100-seed weight, yield per plant, and oil content showed significant genotype × season interactions (data not shown). These results indicated that the genotypes included in the Asia core subset

have significant variability for most traits and the two locations and seasons were different. The significant interactions of genotypes with location for 15 traits and with seasons for nine traits indicated that the selection for a trait is location and season specific.

The differences between mean values for 19 traits in the rainy season at Raichur, 20 traits in both seasons at Kawadimatti, and 16 traits in post-rainy season at Raichur were significantly different in the *fastigiata* and *hypogaea* groups (Table 1). For the 15 traits—days to first flower and cessation of flowering, plant height, leaflet length and width, number of primary branches, length of primary branches and cotyledonary branches, nodes on cotyledonary branches, number of total pods, mature pods, and pegs per plant, pod length and width, and 100-seed weight—the differences between the *fastigiata* and *hypogaea* groups were significant in both seasons and locations (Table 1). Values in the *fastigiata* group were significantly greater

Table 1
Mean of 21 agronomic characters for two subspecies of an Asia region groundnut core collection in the 2000 rainy and 2000/2001 post-rainy seasons, Raichur and Kawadimatti, India[a]

Character	Raichur rainy		Raichur post-rainy		Kawadimatti rainy		Kawadimatti post-rainy	
	fastigiata	*hypogaea*	*fastigiata*	*hypogaea*	*fastigiata*	*hypogaea*	*fastigiata*	*hypogaea*
Days to first flower (no.)	28.06 b	31.22 a	31.55 b	32.6 a	26.93 b	31.69 a	31.42 b	33.26 a
Days to cessation of flowering (no.)	108.92 a	83.28 b	94.96 a	77.43 b	110.77 a	84.73 b	95.76 a	75.39 b
Plant height (cm)	30.35 a	27.53 b	30.64 a	26.58 b	22.97 a	21.53 b	29.51 a	26.34 b
Leaflet length (cm)	6.043 a	5.068 b	5.973 a	5.025 b	5.882 a	4.792 b	5.981 a	5.019 b
Leaflet width (cm)	2.404 a	2.146 b	2.455 a	2.102 b	2.631 a	2.147 b	2.698 a	2.141 b
Primary branches (no.)	1.641 b	2.855 a	3.102 b	3.551 a	1.614 b	2.457 a	2.285 b	3.296 a
Length of primary branches (cm)	5.648 b	11.499 a	7.581 a	7.805 b	8.002 b	10.134 a	5.159 b	7.699 a
Nodes on main stem (no.)	15.72 a	15.37 a	16.47 a	15.67 a	14.55 a	13.74 b	16.37 a	15.74 b
Length of cotyledonary branches (cm)	33.21 b	38.45 a	34.39 b	37.37 a	27.1 b	31.74 a	31.81 b	34.01 a
Nodes on cotyledonary branches (no.)	25.74 b	31.85 a	27.4 b	30.31 a	21.2 b	27.34 a	26.13 b	29.21 a
Pods per plant (no.)	15.79 b	20.62 a	19.51 b	23 a	11.95 b	16.73 a	18.64 b	21.14 a
Mature pods per plant (no.)	11.96 b	15.9 a	13.92 b	16.85 a	9 b	11.85 a	13.03 b	15.21 a
Pegs per plant (no.)	19.96 b	25.5 a	25.66 b	29.2 a	15.18 b	21.41 a	24.09 b	26.9 a
Pod length (cm)	2.507 b	2.873 a	2.415 b	2.7 a	2.567 b	2.866 a	2.557 b	2.804 a
Pod width (cm)	1.119 b	1.258 a	1.092 b	1.221 a	1.115 b	1.199 a	1.178 b	1.23 a
Shelling percentage	66.18 a	64.44 b	65.15 a	63.9 a	62.16 b	67.46 a	64.62 a	63.62 a
Seed length (cm)	1.159 b	1.47 a	1.204 a	1.363 a	1.191 b	1.478 a	1.184 b	1.395 a
Seed width (cm)	0.7558 b	0.8094 a	0.7555 a	0.753 a	0.7469 b	0.7964 a	0.7446 b	0.8607 a
100-Seed weight (g)	33.79 b	38.12 a	34.76 b	38.54 a	35.54 b	40.14 a	33.43 b	37.68 a
Yield per plant (g)	8.764 b	11.492 a	6.996 a	6.675 a	4.692 b	9.618 a	5.998 b	8.882 a
Oil content (%)			46.27 a	45.69 b			46.17 a	45.51 b

[a] Differences between means of *fastigiata* and *hypogaea* types in a season tested by the Newman–Keuls test. Means followed by different letters indicate significant differences at $P = 0.05$.

than in *hypogaea* for five traits in both seasons at Raichur, five in the rainy season at Kawadimatti, and six traits in the post-rainy season at Kawadimatti. Values in the *hypogaea* group were significantly greater for 14 traits in the rainy and 11 traits in the post-rainy seasons at Raichur, 15 traits in the rainy season and 14 in the post-rainy season at Kawadimatti (Table 1). The *hypogaea* group took longer to first flower, had more primary branches, longer primary and cotyledonary branches, more nodes on cotyledonary branches, more total pods, mature pods and pegs per plant, larger and wider and heavier seeds than the *fastigiata* group. The range for most traits was different in the two types in both seasons and locations. The *fastigiata* group represented 100% of the range variation of the entire regional core collection for two traits (nodes on main stem and shelling percentage) in the rainy season and three traits (days to first flower, length of primary branches, yield per plant) in the post-rainy season at Raichur, five traits (days to first flower, plant height, number and length of primary branches, length of cotyledonary branches) in the rainy season and two traits (days to first flower, plant height) in the post-rainy season at Kawadimatti (data not shown). The *hypogaea* group represented 100% range of the entire regional core collection for more traits than *fastigiata*. The *hypogaea* represented 100% range variation for days to first flower, number of primary branches, length of cotyledonary branches, number of nodes on cotyledonary branches in the rainy season at Raichur; and days to cessation of flowering, leaflet length, number of primary branches and nodes on cotyledonary branches, pods per plant, pegs per plant, seed length and 100-seed weight in the post-rainy season at Raichur; days to first flower, leaflet length and width, number of nodes on main stem, pegs per plant, pod length, shelling percentage, and 100-seed weight in the rainy season at Kawadimatti; and days to cessation of flowering, length of primary branches, length of cotyledonary branches, number of nodes on cotyledonary branches, pod length, shelling percentage, and oil content in the post-rainy season at Kawadimatti (data not shown). This indicated that for the traits at these locations the accessions in *hypogaea* group displayed more extreme values than the accessions in the *fastigiata* group. Overall, the *fastigiata* group captured 81.1% (range 77.1% at Raichur rainy

to 86.1 at Raichur post-rainy) range variation of the entire regional core collection as compared with 92.0% (range 89.9 at Kawadimatti rainy to 93.1% at Raichur rainy) by the *hypogaea* group. The variances between *fastigiata* and *hypogaea* were homogeneous for seven traits in the rainy and 13 traits in post-rainy season at Raichur, and two traits each in the rainy and the post-rainy seasons at Kawadimatti (data not shown). For leaflet length, length of cotyledonary branches, and pod width, variances were homogeneous in both seasons and locations indicating the similar within group variability in the *fastigiata* and *hypogaea* groups.

The first five principal components (PCs) explained 65.4% variation in the regional core collection in the rainy season and 53.6% in the post-rainy season at Raichur, 66.3% in the rainy season and 53.6% in the post-rainy season at Kawadimatti (data not shown). This analysis reduced the original 20 characters in the rainy season to 13 each at Raichur and Kawadimatti, and 21 characters in the post-rainy season to 12 at Raichur and 11 at Kawadimatti. The first five PCs explained more variation (except at Kawadimatti in the rainy season) in the *fastigiata* group than in the *hypogaea* group (data not shown). PC 1, which is the most important component, accounted for more variation in the rainy season than in the post-rainy season at both locations: 29.5% variation in the rainy season, 18.3% in the post-rainy season at Raichur, and 31.9% in the rainy season and 19.4% in the post-rainy season at Kawadimatti (data not shown). Similarly, PC 1 explained 19.6% in the rainy season, 17.5% in the post-rainy season at Raichur, 18.8% in the rainy, and 16.5% in the post-rainy at Kawadimatti in *fastigiata* and 18.6% in rainy season vs. 15.4% in the post-rainy season at Raichur and 20.7% in the rainy vs. 15.5% in the post-rainy season at Kawadimatti in the *hypogaea* group (data not shown). The eigen values of PC 1 were 5.89 in the rainy season and 3.83 in the post-rainy season at Raichur and 6.38 in the rainy season and 4.07 in the post-rainy season at Kawadimatti in the total regional core collection indicating that more traits differentiated the accessions in this core in the rainy season than in the post-rainy season (data not shown). The eigen values were 3.91, 3.68, 3.76, and 3.47 in *fastigiata* subset and 3.72, 3.24, 4.13, and 3.26 in *hypogaea* subset, respectively, in the four evaluations (data not shown).

The PC 1 separates accessions on six traits (days to cessation of flowering, leaflet length, length of primary branches, nodes on cotyledonary branches, pod width, seed length) in rainy and four traits (leaflet width, total pods, mature pods, pegs per plant) in post-rainy seasons at Raichur and six traits (days to first flower and cessation of flowering, leaflet length and width, nodes on cotyledonary branches, seed length, in rainy and four traits (total pods, mature pods, pegs per plant, seed length) in post-rainy seasons at Kawadimatti (data not shown) in the entire regional core collection. In the *fastigiata* group, four traits each in both seasons and locations, except the post-rainy season at Kawadimatti, separated accessions. Thus number of total pods, mature pods and pegs per plant and pod width in rainy and nodes on cotyledonary branches, total pods, mature pods and pegs per plant in the post-rainy at Raichur, days to cessation of flowering, pod length and width, and seed length in rainy at Kawadimatti separated the accessions in *fastigiata* (data not shown). In the *hypogaea*, four traits in the rainy season each at Raichur (number of nodes on cotyledonary branches, total pods, mature pods, and pegs) and Kawadimatti (length of cotyledonary branches, total pods, mature pods, and pegs) and three traits in the post-rainy season each at Raichur (number of total pods, mature pods, and pegs per plant) and Kawadimatti (number of total pods, mature pods, and pegs per plant) were important (data not shown). Interestingly, seed length which had positive loadings in the *fastigiata* and *hypogaea* types showed negative loadings in the entire core collection in the rainy season at Raichur. Considering the analyses of *fastigiata* and *hypogaea* groups and the regional core subset over both locations and seasons, all together, 20 agronomic traits had high loadings and occurred at least once out of 12 in the first five PCs, indicating their importance as descriptors. The agronomic traits are days to first flower and cessation of flowering, plant height, leaflet length and width, number of primary branches, length of primary branches, nodes on main stem, length of cotyledonary branches, nodes on cotyledonary branches, total pods, mature pods, pegs, pod length and width, shelling percentage, seed length and width, 100-seed weight, and oil content. Yield per plant in both seasons and both locations made no contribution in explaining variation in the first five PCs of *fastigiata* and *hypogaea* groups and

entire regional core collection, indicating its low importance as a groundnut descriptor.

Phenotypic correlations were conducted between all the traits in the entire core subset, *fastigiata* and *hypogaea* groups and in both seasons and locations independently. Within a group the correlations were tested for significance (Snedecor and Cochran, 1980). Correlation between 20 traits in the rainy and 21 traits in post-rainy seasons at both locations, and the probability of their significance in the entire regional core collection, are presented in Table 2. Any correlation coefficient with more than $500°$ of freedom (e.g. for the entire regional core collection) with an absolute value greater than 0.088 will be significant at $P = 0.05$ and 0.115 at $P = 0.01$. In the entire regional core collection, there were 63 correlations out of total 190 in rainy, 41 in post-rainy seasons at Raichur, 99 in rainy and 45 in post-rainy seasons at Kawadimatti, which were significant at $P = 0.01$ (Table 2). The number of such correlations was 46, 40, 58, and 32 in *fastigiata* and 39, 27, 66, and 34 in *hypogaea*, respectively (data not shown). The correlations which were significant at $P = 0.01$ in both the seasons and locations were 29 in the entire regional core (Table 2), 20 in the *fastigiata* subset, and only 15 in the *hypogaea* subset. However, the correlation coefficients greater than 0.707 or smaller than -0.707 have been suggested to be biologically meaningful (Skinner et al., 1999), as more than 50% of the variation in one trait is predicted by the other (Snedecor and Cochran, 1980). In this study, we found five such meaningful relationships of which three occurred in the entire regional core collection and in the *fastigiata* and *hypogaea* subsets in both seasons and locations (Table 3). The correlations across seasons were highly significant within each subset ($P \leq 0.0001$) (Table 3). These results suggested that in future germplasm evaluations, either of these traits can be evaluated in either of seasons or locations.

The Shannon–Weaver diversity index was calculated to compare phenotypic diversity index (H') among characters and groups across seasons and locations. A low H' indicates extremely unbalanced frequency classes for an individual trait and lack of genetic diversity. The estimates of H' were made for each trait and two groups for both seasons and locations and pooled across traits and location–season combinations for each group (Table 4). The diversity

Table 2

Correlation coefficients between 21 characters in the entire Asia region core collection of groundnut in 2000 rainy and 2000/2001 post-rainy seasons, Raichur, and Kawadimatti, India[a]

Character	Location[b]	DFF	DCF	PLHT	LLN	LWD	NPB	LPB	NNMS	LCB	NNCB	TNP	NMP	NPP	PLN	PWD	SH	SLN	SWD	SDWT	PYP
DCF	R-R	−0.053																			
	R-PR	−0.094																			
	K-R	−0.198																			
	K-PR	0.000																			
	P	0.016																			
PLHT	R-R	−0.069	−0.054																		
	R-PR	0.068	0.031																		
	K-R	−0.088	−0.028																		
	K-PR	0.000	−0.027																		
	P	0.021	0.577																		
LLN	R-R	−0.103	0.081	0.178																	
	R-PR	0.066	−0.034	0.174																	
	K-R	−0.152	0.166	0.207																	
	K-PR	0.000	0.186	0.149																	
	P	0.001	0.001	0.929																	
LWD	R-R	−0.060	0.058	0.094	0.522																
	R-PR	0.070	0.030	0.106	0.536																
	K-R	−0.212	0.167	0.170	0.650																
	K-PR	0.000	0.093	0.211	0.488																
	P	0.000	0.137	0.173	0.001																
NPB	R-R	0.140	−0.025	−0.012	0.013	0.020															
	R-PR	0.000	0.000	0.000	0.000	0.000															
	K-R	0.075	−0.122	0.047	−0.038	−0.073															
	K-PR	0.000	−0.005	−0.047	−0.019	−0.056															
	P	0.078	0.237	0.827	0.762	0.390															
LPB	R-R	−0.052	−0.077	0.044	0.025	−0.009	−0.091														
	R-PR	−0.034	−0.084	0.114	0.048	−0.028	0.000														
	K-R	0.096	−0.093	0.114	−0.003	−0.055	0.051														
	K-PR	0.000	−0.078	0.064	−0.101	−0.085	−0.013														
	P	0.140	0.377	0.072	0.109	0.575	0.583														
NNMS	R-R	−0.067	−0.099	0.525	0.112	0.099	0.038	0.042													
	R-PR	0.072	−0.067	0.472	0.055	0.045	0.000	0.096													
	K-R	0.037	−0.068	0.457	0.132	0.065	0.141	−0.057													
	K-PR	0.000	0.024	0.408	0.111	0.148	0.033	0.032													
	P	0.043	0.118	0.016	0.562	0.121	0.796	0.053													
LCB	R-R	0.025	−0.022	0.596	0.145	0.072	0.073	0.065	0.468												
	R-PR	0.016	0.019	0.476	0.086	0.056	0.000	0.051	0.259												
	K-R	0.031	−0.069	0.603	0.122	0.070	0.165	0.028	0.807												
	K-PR	0.000	−0.024	0.392	0.108	0.045	0.097	0.075	0.290												
	P	0.798	0.891	0.000	0.725	0.843	0.327	0.042	0.000												

Table 2 (*Continued*)

Character	Location[b]	DFF	DCF	PLHT	LLN	LWD	NPB	LPB	NNMS	LCB	NNCB	TNP	NMP	NPP	PLN	PWD	SH	SLN	SWD	SDWT	PYP
NNCB	R-R	0.033	−0.098	0.378	0.086	0.029	0.094	0.032	0.371	0.685											
	R-PR	0.033	0.031	0.339	0.056	0.038	0.000	0.027	0.256	0.654											
	K-R	0.038	−0.043	0.415	0.069	0.018	0.191	−0.026	0.880	0.853											
	K-PR	0.000	−0.069	0.245	0.094	0.024	0.083	0.093	0.239	0.711											
	P	0.551	0.043	0.121	0.232	0.996	0.076	0.077	0.060	0.022											
TNP	R-R	0.035	−0.101	−0.008	−0.006	−0.038	0.147	0.030	0.080	0.151	0.184										
	R-PR	−0.054	0.054	0.010	−0.021	−0.041	0.000	−0.005	0.105	0.130	0.164										
	K-R	0.072	0.081	0.133	−0.014	−0.020	0.164	0.097	0.151	0.245	0.209										
	K-PR	0.000	−0.050	0.022	0.026	−0.028	0.158	0.062	0.113	0.130	0.179										
	P	0.268	0.007	0.278	0.850	0.987	0.030	0.207	0.655	0.139	0.651										
NMP	R-R	0.036	−0.097	0.025	0.007	−0.040	0.142	0.017	0.092	0.186	0.218	0.947									
	R-PR	−0.049	0.020	0.044	−0.013	−0.014	0.000	0.027	0.130	0.163	0.199	0.935									
	K-R	0.068	0.081	0.148	0.016	0.000	0.122	0.095	0.175	0.282	0.230	0.891									
	K-PR	0.000	−0.050	0.013	0.004	−0.022	0.182	0.088	0.140	0.137	0.186	0.912									
	P	0.341	0.017	0.339	0.989	0.936	0.025	0.264	0.427	0.047	0.646	0.000									
NPP	R-R	0.044	−0.106	−0.015	−0.005	−0.037	0.142	0.047	0.077	0.145	0.189	0.964	0.926								
	R-PR	−0.072	0.055	−0.014	−0.025	−0.038	0.000	0.014	0.070	0.112	0.142	0.929	0.899								
	K-R	0.106	0.088	0.087	−0.057	−0.066	0.179	0.060	0.147	0.231	0.207	0.902	0.863								
	K-PR	0.000	−0.031	0.016	0.039	−0.016	0.170	0.060	0.125	0.154	0.190	0.951	0.893								
	P	0.047	0.006	0.647	0.393	0.884	0.019	0.595	0.688	0.309	0.619	0.000	0.000								
PLN	R-R	0.048	−0.128	−0.008	0.041	0.023	0.018	0.061	0.018	0.062	0.115	−0.125	−0.101	−0.134							
	R-PR	−0.001	−0.123	−0.020	−0.041	−0.066	0.000	−0.044	0.072	0.003	0.023	−0.079	−0.079	−0.086							
	K-R	−0.016	−0.158	0.097	−0.034	0.001	0.029	0.164	0.041	0.076	0.043	−0.140	−0.145	−0.116							
	K-PR	0.000	−0.088	0.064	−0.041	−0.006	0.081	−0.035	0.015	0.077	0.076	−0.072	−0.061	−0.062							
	P	0.753	0.742	0.196	0.480	0.536	0.608	0.002	0.697	0.519	0.508	0.606	0.529	0.651							
PWD	R-R	0.052	−0.036	0.070	−0.076	−0.036	0.010	−0.039	−0.003	0.065	0.048	−0.133	−0.131	−0.123	0.365						
	R-PR	0.005	−0.059	0.076	−0.014	−0.042	0.000	0.018	0.085	−0.019	−0.007	0.037	0.054	0.040	0.520						
	K-R	0.025	−0.139	0.078	0.065	0.034	0.104	0.099	0.012	0.033	0.018	−0.125	−0.103	−0.131	0.585						
	K-PR	0.000	−0.049	0.049	0.042	0.113	0.023	0.047	0.046	0.063	0.075	0.017	0.004	0.004	0.391						
	P	0.838	0.345	0.954	0.110	0.046	0.324	0.415	0.579	0.496	0.627	0.006	0.009	0.009	0.000						
SH	R-R	0.040	0.055	0.054	0.000	0.013	−0.028	−0.041	0.036	0.090	0.076	0.127	0.135	0.112	0.018	−0.045					
	R-PR	−0.025	−0.028	−0.012	−0.027	0.009	0.000	0.095	−0.091	0.011	−0.034	0.040	0.015	0.040	−0.073	0.031					
	K-R	0.017	−0.049	0.069	−0.112	−0.086	0.014	0.083	0.014	0.071	0.080	0.144	0.175	0.124	−0.011	0.061					
	K-PR	0.000	−0.012	0.006	−0.036	−0.003	0.069	0.112	0.021	0.024	0.002	0.031	0.043	0.044	0.061	0.041					
	P	0.770	0.384	0.508	0.316	0.349	0.475	0.289	0.141	0.358	0.013	0.158	0.032	0.390	0.190	0.355					
SLN	R-R	0.051	−0.068	−0.065	−0.016	−0.025	−0.021	0.022	0.024	0.007	−0.003	−0.069	−0.076	−0.089	0.295	0.285	−0.048				
	R-PR	0.031	−0.075	−0.032	−0.006	−0.079	0.000	−0.035	−0.013	0.004	−0.022	−0.063	−0.051	−0.074	0.336	0.339	0.085				
	K-R	0.049	−0.160	−0.013	−0.005	−0.024	0.042	0.082	−0.003	−0.016	−0.024	−0.122	−0.106	−0.101	0.535	0.502	−0.020				
	K-PR	0.000	−0.095	−0.025	−0.034	−0.004	0.008	0.035	−0.062	0.034	0.047	−0.015	−0.038	−0.017	0.373	0.270	−0.020				
	P	0.840	0.438	0.873	0.966	0.665	0.796	0.274	0.587	0.770	0.382	0.389	0.703	0.547	0.000	0.000	0.157				

SWD	R-R	−0.010	−0.017	−0.027	−0.011	−0.026	−0.056	−0.063	−0.020	0.041	−0.003	−0.028	−0.015	−0.012	0.100	0.200	0.062	0.238			
	R-PR	−0.001	−0.016	0.025	−0.029	−0.047	0.000	0.013	0.015	−0.053	−0.038	−0.031	−0.031	−0.013	0.127	0.211	0.102	0.450			
	K-R	0.097	−0.119	0.073	−0.004	−0.062	0.007	0.018	0.080	0.102	0.106	−0.002	0.053	0.010	0.182	0.367	0.204	0.357			
	K-PR	0.000	−0.053	−0.028	−0.007	−0.037	0.037	0.028	−0.028	0.017	0.007	0.049	0.055	0.039	0.087	0.109	0.106	0.286			
	P	0.320	0.364	0.506	0.986	0.946	0.527	0.967	0.860	0.278	0.342	0.547	0.432	0.829	0.440	0.000	0.124	0.001			
SDWT	R-R	−0.011	−0.144	0.032	0.011	0.012	−0.013	−0.023	−0.034	−0.017	0.037	−0.018	−0.002	−0.015	0.254	0.162	0.160	0.187	0.249		
	R-PR	−0.031	−0.051	0.048	0.031	−0.046	0.000	0.019	−0.069	0.048	−0.023	0.041	0.022	0.046	0.112	0.114	0.114	0.194	0.170		
	K-R	0.066	−0.098	0.052	−0.031	−0.054	−0.016	0.157	−0.057	0.007	−0.022	0.032	0.043	0.030	0.224	0.247	0.268	0.172	0.303		
	K-PR	0.000	−0.044	0.005	0.062	0.057	−0.005	−0.015	−0.023	−0.041	−0.069	0.015	0.003	−0.010	0.137	0.170	0.139	0.190	0.181		
	P	0.394	0.325	0.692	0.584	0.256	0.998	0.034	0.277	0.101	0.059	0.765	0.818	0.680	0.057	0.180	0.053	0.988	0.063		
PYP	R-R	0.038	−0.065	−0.019	−0.071	−0.051	0.038	0.032	0.038	0.072	0.101	0.200	0.191	0.172	0.128	0.033	0.163	0.085	0.101	0.127	
	R-PR	−0.023	0.002	0.006	−0.045	−0.013	0.000	0.064	0.012	0.025	0.018	0.153	0.161	0.137	0.014	0.043	0.014	0.052	0.197	0.079	
	K-R	0.101	−0.074	−0.002	−0.034	−0.043	0.060	0.050	−0.014	0.072	0.050	0.261	0.257	0.290	0.063	0.135	0.202	0.150	0.290	0.197	
	K-PR	0.000	0.025	−0.056	−0.014	−0.027	−0.071	0.030	0.069	0.075	−0.003	0.029	0.062	0.038	0.009	0.041	0.037	0.035	0.065	0.059	
	P	0.223	0.310	0.778	0.835	0.933	0.173	0.762	0.198	0.662	0.249	0.002	0.014	0.001	0.200	0.317	0.004	0.267	0.001	0.111	
OIL	R-PR	−0.009	0.010	−0.060	0.005	−0.029	0.000	0.045	−0.039	−0.093	−0.039	0.034	0.011	0.048	−0.045	−0.033	0.059	0.046	0.158	0.159	0.147
	K-PR	0.000	−0.003	−0.017	0.043	0.079	0.035	−0.011	−0.015	−0.062	−0.029	0.000	−0.029	0.003	−0.063	−0.032	0.063	−0.029	0.043	0.074	−0.056
	P	0.582	0.822	0.572	0.684	0.156	0.311	0.358	0.213	0.166	0.867	0.072	0.129	0.267	0.743	0.734	0.978	0.290	0.043	0.164	0.001

[a] DFF, days to initiation of flowering (no.); DCF, days to cessation of flowering (no.); PLHT, plant height (cm); LLN, leaflet length (mm); LWD, leaflet width; NPB, number of primary branches; LPB, length of primary branches; NNMS, nodes on main stem (no.); LCB, length of cotyledonary branches; NNCB, nodes on cotyledonary branches; TNP, total pods per plant (no.); NMP, mature pods per plant (no.); NPP, pegs per plant; PLN, pod length (cm); PWD, pod width (cm); SH, shelling percentage; SLN, seed length (cm); SWD, seed width (cm); SDWT, 100-seed weight (g); PYP, pod yield per plant (g); OIL, oil content (%).

[b] R-R, Raichur rainy season; R-PR, Raichur post-rainy season; KR, Kawadimatti rainy season; K-PR, Kawadimatti post-rainy season.

Table 3
Correlation coefficients with values more than 0.707 between agronomic traits in the entire and *fastigiata* and *hypogaea* subset of an Asia region core collection of groundnut in the 2000 rainy and 2000/2001 post-rainy seasons, Raichur and Kawadimatti, India

Relationship	Subset	Raichur rainy	Raichur post-rainy	Kawadimatti rainy	Kawadimatti post-rainy	χ^2-value	P
Number of total pods per plant–number of mature pods per plant	Entire	0.947	0.936	0.890	0.912	42.88	0.0001
	fastigiata	0.916	0.924	0.837	0.898	26.15	0.0001
	hypogaea	0.961	0.944	0.913	0.923	22.88	0.0001
Number of total pods per plant–number of pegs per plant	Entire	0.964	0.929	0.900	0.951	79.92	0.0001
	fastigiata	0.942	0.916	0.842	0.934	44.58	0.0001
	hypogaea	0.978	0.939	0.926	0.963	53.51	0.0001
Number of mature pods per plant–number of pegs per plant	Entire	0.926	0.899	0.861	0.893	27.54	0.0001
	fastigiata	0.863	0.919	0.827	0.869	22.91	0.0001
	hypogaea	0.962	0.882	0.875	0.911	54.89	0.0001

values were variable among traits and types. Thus, the diversity within a group depended upon the traits and seasons. Among the agronomic traits in the *fastigiata* group, leaflet length in rainy, pod width in post-rainy at Raichur, seed length in rainy and plant height in post-rainy at Kawadimatti, seed length in rainy, number of total pods in post-rainy at Raichur, number of primary branches in rainy and plant height in post-rainy at Kawadimatti had the highest H'. The average H' value across seasons and locations was highest for leaflet length in the *fastigiata* group and for seed length in the *hypogaea* group. The average H' across traits were similar between rainy and post-rainy seasons in both locations and groups (Table 4).

The grouping of similar genotypes depends on the level of dissimilarity among them, which can be determined by a phenotypic diversity index. The average diversity index was similar, except in the rainy season at Kawadimatti, in both the groups in both seasons and locations (Table 5). The range of phenotypic diversity was slightly higher in the *fastigiata* group than *hypogaea* at Raichur in both seasons. However, the diversity in the *hypogaea* group was greater than the *fastigiata* group in the rainy season and similar in the post-rainy season at Kawadimatti. The closest lines were ICG 5833 and ICG 7836 in the *fastigiata* group (total core subset also) and ICG 4324 and ICG 10717 in the *hypogaea* group in the rainy season at Raichur. The largest phenotypic diversity index was observed between ICG 9581 and ICG 9973 in the *fastigiata* group in the rainy season and between ICG 4906 and ICG 15126 in the *hypogaea* group in the

post-rainy season at Raichur (Table 5). It would be interesting to involve the lines showing highest phenotypic diversity index in the hybridization and selection program for various traits. However, it is important to consider the genetic background of the germplasm lines while selecting for inclusion in the breeding program, as it will be useful in predicting their behavior in hybrid combinations with the adapted lines. The less divergent the germplasm and adapted lines are, the more likely that the additive gene effects will play a primary role in the inheritance of quantitative traits (Isleib and Wynne, 1983). As the diversity between parents increases, the dominance and epistatic variations have significant roles in the inheritance of quantitative traits (Halward and Wynne, 1991). This would have implications in choosing an appropriate selection strategy in a self-pollinated crop like groundnut where epistasis has been detected for vegetative, reproductive (Upadhyaya and Nigam, 1998) and quality (Upadhyaya and Nigam, 1999) traits.

Groundnut is a native of South America. Krapovickas (1969) and Gregory and Gregory (1976) recognized the Chaco region between southern Bolivia and northwestern Argentina as the primary center of diversity, and other regions as secondary centers of diversity of cultivated groundnut. Recent evidence indicates a seventh secondary center of diversity in Ecuador (Simpson et al., 1992). Most authorities believe that the Portuguese carried two-seeded groundnut varieties from the east coast of South America (Brazil) to Africa, to the Malabar coast of

Table 4
Shannon–Weaver diversity index in the *fastigiata* and *hypogaea* groups of groundnut in the 2000 rainy and 2000/2001 post-rainy seasons, Raichur and Kawadimatti, India

Character	*fastigiata*					*hypogaea*				
	Raichur rainy	Raichur post-rainy	Kawadimatti rainy	Kawadimatti post-rainy	Mean ± S.E.	Raichur rainy	Raichur post-rainy	Kawadimatti rainy	Kawadimatti post-rainy	Mean ± S.E.
Days to first flower (no.)	0.589	0.618	0.554	0.573	0.583 ± 0.012	0.564	0.607	0.602	0.595	0.592 ± 0.008
Days to cessation of flowering (no.)	0.323	0.456	0.495	0.503	0.444 ± 0.036	0.518	0.508	0.503	0.491	0.505 ± 0.005
Plant height (cm)	0.587	0.613	0.588	0.652	0.610 ± 0.013	0.581	0.609	0.623	0.622	0.609 ± 0.009
Leaflet length (cm)	0.631	0.623	0.607	0.623	0.621 ± 0.004	0.612	0.608	0.616	0.615	0.613 ± 0.002
Leaflet width (cm)	0.613	0.630	0.615	0.021	0.470 ± 0.130	0.581	0.622	0.527	0.577	0.577 ± 0.017
Primary branches (no.)	0.375	0.575	0.230	0.520	0.425 ± 0.067	0.575	0.565	0.634	0.584	0.589 ± 0.013
Length of primary branches (cm)	0.534	0.556	0.546	0.575	0.553 ± 0.007	0.575	0.558	0.599	0.572	0.576 ± 0.007
Nodes on main stem (no.)	0.599	0.600	0.622	0.632	0.613 ± 0.007	0.612	0.523	0.565	0.605	0.577 ± 0.018
Length of cotyledonary branches (cm)	0.615	0.591	0.107	0.540	0.463 ± 0.104	0.620	0.609	0.616	0.550	0.599 ± 0.014
Nodes on cotyledonary branches (no.)	0.611	0.613	0.623	0.605	0.613 ± 0.003	0.597	0.612	0.619	0.584	0.603 ± 0.007
Pods per plant (no.)	0.624	0.618	0.621	0.613	0.619 ± 0.002	0.580	0.630	0.600	0.553	0.590 ± 0.014
Mature pods per plant (no.)	0.611	0.620	0.617	0.632	0.620 ± 0.004	0.575	0.617	0.607	0.618	0.604 ± 0.009
Pegs per plant (no.)	0.606	0.615	0.613	0.610	0.611 ± 0.002	0.578	0.620	0.620	0.583	0.600 ± 0.01
Pod length (cm)	0.597	0.618	0.588	0.601	0.601 ± 0.006	0.624	0.621	0.598	0.611	0.613 ± 0.005
Pod width (cm)	0.591	0.631	0.603	0.633	0.614 ± 0.009	0.592	0.050	0.012	0.607	0.315 ± 0.142
Shelling percentage	0.555	0.588	0.558	0.584	0.571 ± 0.007	0.588	0.575	0.578	0.574	0.579 ± 0.003
Seed length (cm)	0.593	0.61	0.626	0.638	0.617 ± 0.008	0.627	0.614	0.615	0.604	0.615 ± 0.004
Seed width (cm)	0.623	0.559	0.597	0.626	0.601 ± 0.013	0.012	0.620	0.012	0.024	0.167 ± 0.131
100-Seed weight (g)	0.601	0.613	0.601	0.612	0.607 ± 0.003	0.595	0.614	0.616	0.585	0.603 ± 0.006
Yield per plant (g)	0.612	0.555	0.493	0.524	0.546 ± 0.022	0.572	0.568	0.555	0.565	0.565 ± 0.003
Oil content (%)		0.543		0.568	0.556 ± 0.009		0.589		0.557	0.573 ± 0.011
Mean ± S.E.	0.574 ± 0.018	0.593 ± 0.009	0.545 ± 0.03	0.566 ± 0.029	0.569 ± 0.009	0.559 ± 0.006	0.568 ± 0.006	0.536 ± 0.005	0.556 ± 0.002	0.555 ± 0.006

Table 5
Phenotypic diversity index in the *fastigiata* and *hypogaea* groups and in the entire Asia region core subset of groundnut

Locations	Mean phenotypic diversity index	Minimum phenotypic diversity index	Between accessions	Maximum phenotypic diversity index	Between accessions
Raichur rainy					
Entire	0.188	0.036	ICG 5833 and ICG 7836	0.433	ICG 8352 and ICG 9973
fastigiata	0.193	0.047	ICG 5833 and ICG 7836	0.463	ICG 9581 and ICG 9973
hypogaea	0.187	0.051	ICG 4324 and ICG 10717	0.437	ICG 7973 and ICG 10171
Raichur post-rainy					
Entire	0.181	0.045	ICG 8351 and ICG 8657	0.413	ICG 3145 and ICG 12341
fastigiata	0.189	0.058	ICG 12695 and ICG 14807	0.382	ICG 57 and ICG 5779
hypogaea	0.184	0.056	ICG 12873 and ICG 13130	0.446	ICG 4906 and ICG 15126
Kawadimatti rainy					
Entire	0.181	0.037	ICG 5490 and ICG 12684	0.438	ICG 521 and ICG 7262
fastigiata	0.172	0.048	ICG 5490 and ICG 12684	0.430	ICG 6957 and ICG 12883
hypogaea	0.197	0.053	ICG 5351 and ICG 5880	0.440	ICG 521 and ICG 10171
Kawadimatti post-rainy					
Entire	0.173	0.039	ICG 8682 and ICG 14807	0.386	ICG 7713 and ICG 14378
fastigiata	0.189	0.050	ICG 8682 and ICG 14807	0.407	ICG 8831 and ICG 12877
hypogaea	0.189	0.058	ICG 11428 and ICG 11436	0.396	ICG 3145 and ICG 4798

south-eastern India and possibly to the far east in the late 15th century. The Spaniards took three-seeded Peruvian types (including *hirsuta*) to Indonesia and China up to Madagascar from the west coast of South America via the western Pacific in the early 16th century. Groundnut made its way to North America from Africa as well as from the Caribbean islands, Central America, and Mexico, and was distributed worldwide by the middle of the 16th century. It became an important crop in West Africa, India, China, and USA, by the 19th century. In Asia, India, and China have long history of cultivation and landraces are considered other important centers of diversity.

4. Conclusions

The results of this study indicate that there is significant variation for agronomic traits in this Asian groundnut core collection. The phenotypic correlations depended upon subspecies group, season, and location. The mean number of days to first flower, number of primary branches, length of primary and cotyledonary branches, nodes on cotyledonary branches, total pods, mature pods, pegs per plant, pod length, pod width and 100-seed weight was higher

in the *hypogaea* group than in the *fastigiata* group in both seasons, while the opposite was true for plant height and leaflet length in both seasons and locations. The information presented in this study could be used to reduce the size of this regional core further to develop a mini core subset (Upadhyaya and Ortiz, 2001). This would be of value to plant breeders to evaluate more extensively to facilitate greater use of these genetic resources in groundnut improvement programs in Asia and globally.

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