Variability for Drought Resistance Related Traits in the Mini Core Collection of Peanut

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ABSTRACT

Peanut (*Arachis hypogaea* L.) productivity is low in the semiarid tropics mainly because of drought caused by low and erratic rainfall. Identification of genotypes that have a greater ability to use limited available water is important to enhance productivity of the crop. Water-use efficiency (WUE) is correlated with specific leaf area (SLA) and soil plant analysis development (SPAD) chlorophyll meter reading (SCMR) and both have been suggested as surrogate traits for selecting for WUE in peanut. The present study was conducted to: (i) identify genotypes with high WUE using SLA or SCMR and (ii) evaluate relationship between and relative stability of SCMR and SLA in these genotypes. The 184 mini core entries, consisting of 37 *fastigiata*, 58 *vulgaris*, 85 *hypogaea*, two *peruviana*, and one each of *aequitoriana* and *hirsuta* and four control cultivars, M 13, Gangapuri, ICGS 44 and ICGS 76 were evaluated for SLA, SCMR, and 19 vegetative, reproductive, and quality traits in the 2001 rainy and 2001–2002 postrainy seasons at ICRISAT Center. Data were analyzed by REML analysis. Seasons were significant for all traits. Variances due to genotypes were significant for SCMR and SLA at 60 and 80 d after sowing (DAS) and other traits except pods per plant, yield per plant, haulm yield per plot, and protein and oil contents. The genotype × season interactions were significant for both SCMR and SLA at 80 DAS only and for all other quantitative traits except number of primary branches, and pod width. The SCMR values at different stages and seasons were more positively correlated with each other than the correlation of SLA values together. SCMR and SLA were negatively correlated. SCMR values were more strongly correlated with pod yield and other economic traits such as 100-seed weight at both 60 and 80 DAS than SLA. On the basis of higher heritability and lower proportion of genotype × season interaction variance to phenotypic variance, SCMR appeared to be more stable than SLA. On the basis of SLA and SCMR values compared with the control cultivar, five *vulgaris* and 13 *hypogaea* accessions were selected. These accessions and control cultivars were grouped by scores of the first 15 principal components (PCs). The clustering by UPGMA method indicated that the selected accessions were diverse from the control cultivars and can be used in the peanut improvement programs to develop cultivars with a broad genetic base.

P EANUT, an annual legume, is grown primarily for high quality edible oil and easily digestible protein in its seeds. It is cultivated in over 100 countries in tropical, subtropical, and warm temperate regions of the world. The crop is grown on about 24.7 million hectares world wide with an estimated total production of 34.1 million megagrams in shell and an average productivity of 1.38 Mg ha^{-1} (FAO, 2002). Over two-thirds of the global production occurs in seasonally rainfed regions

where drought is a potential constraint for crop production (Smartt, 1994), and productivity ranges from 0.7 to 0.8 Mg ha^{-1}. However, even under a commercial system where peanut productivity ranges 2.0 to 4.0 Mg ha^{-1}, water may also be a limiting factor. For both situations, cultivars that are efficient in water utilization are required.

In a biological model (Passioura, 1986), seed yield is a function of water transpired (T), WUE, and harvest index (HI). The WUE, defined as total biomass production per unit of water transpired (g kg^{-1}), is not an easy trait to measure. It is virtually impossible to include such a trait in screening. However, several researchers (Farquhar et al., 1982; Hubick et al., 1986; Wright et al., 1988, 1994) have found WUE to be negatively correlated with leaf carbon isotopic composition (Δ) in a range of crop species including peanut, raising the possibility of its use in screening and selection for high water-use efficient genotypes. But the facilities for Δ analysis are not available everywhere, and it is expensive to analyze large numbers of germplasm and segregating populations, particularly in developing countries. Studies by Wright et al. (1994) and Nageswara Rao and Wright (1994) reported positive correlations between specific leaf area SLA (cm^{2}g^{-1}), which is negatively related to leaf thickness, and Δ and hence WUE, over a wide range of cultivars and environments in peanut. Significant and high correlations between SLA and specific leaf nitrogen (SLN) (Nageswara Rao and Wright, 1994) and SLA and ribulose 1-5 bisphosphate carboxylase (Rubisco) (Nageswara Rao et al., 1995) in independent studies suggested that photosynthetic capacity per unit leaf area is the major factor contributing to variation in WUE in peanut. Although SLA can be measured easily and cost effectively, and can be used as a surrogate for WUE, it is significantly influenced by factors such as time of sampling and leaf age (Wright and Hammer, 1994; Nageswara Rao et al., 1995). The strength of the correlation between SLA and Δ varied from 0.71 to 0.94 for a range of peanut genotypes and environments (Wright et al., 1996), suggesting the need for further studies on the factors influencing SLA in peanut (Nageswara Rao et al., 2001). The SPAD chlorophyll meter has been proposed to determine leaf nitrogen content nondestructively in a number of crops including maize (*Zea mays* L., Chapman and Barreto, 1997), barley (*Hordeum vulgare* L., Araus et al., 1997), tobacco (*Nicotiana tabacum* L., Mackown and Sutton, 1998), and peanut (Nageswara Rao et al., 2001). Nageswara Rao et al. (2001) reported significant and high interrelationship among SLA, SLN, and SPAD chlorophyll meter reading (SCMR). Bindu Madhava et al. (2003) reported a strong positive relationship between SCMR and WUE in peanut. Nageswara Rao et al. (2001) and Bindu Madhava et al. (2003) suggested that SCMR could be used as a

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reliable and rapid measure to identify genotypes with low SLA or high SLN (and hence high WUE) in peanut.

A peanut mini core collection, (184 accessions) has been developed (Upadhyaya et al., 2002). To select this mini core collection, the 1704 core collection (Upadhyaya et al., 2003) entries were evaluated for 13 morphological and 16 agronomic traits in the 1999 rainy season and for 18 agronomic and quality traits in the 1999–2000 postrainy season at Patancheru, Andhra Pradesh, India. A phenotypic distance matrix was created by calculating differences between each pair of accessions for each of the 47 traits. The diversity index was calculated by averaging all the differences in the phenotypic values for each trait divided by the respective range. The distance matrix was subjected to the hierarchical cluster algorithm of Ward (1963) at an R^2 (squared multiple correlation value) of 0.75 by SAS 8.2. The proportional sampling strategy was used, and from each cluster, approximately 10% of the accessions were randomly selected for the mini core subset. At least one accession was included from each cluster even if they had 10 accessions or less. The mini core collection represented core collection, which represented the entire collection.

The primary objective of this study was to identify genotypes with low SLA or high SLN among 184 mini core entries (Upadhyaya et al., 2002) with a SPAD chlorophyll meter and evaluate the relationship between and relative stability of SCMR and SLA in these genotypes.

MATERIALS AND METHODS

The peanut mini core collection consisting of 184 entries (Upadhyaya et al., 2002) was selected from 1704 entries of the core collection of peanut representing 14 310 accessions available in the ICRISAT genebank (Upadhyaya et al., 2003). The experimental materials for this study consisted of 184 mini core entries: 37 *fastigiata*, 58 *vulgaris*, 85 *hypogaea*, two *peruviana*, and one each of *aequitoriana*, and *hirsuta* and four control cultivars, M 13 (*hypogaea*), Gangapuri (*fastigiata*), ICGS 44 (*vulgaris*), and ICGS 76 (*hypogaea*). M 13 (Reddy, 1988) and Gangapuri (Isleib et al., 1994) are Indian cultivars. ICGS 44 (ICGV 87128, PI 537112) (Nigam et al., 1990) and ICGS 76 (ICGV 87141, PI546372) (Nigam et al., 1991) are ICRISAT-bred high-yielding cultivars released for cultivation in India. The 188 entries were evaluated in α design (four blocks each of 47 plots) with three replications in the 2001 rainy and 2001–2002 postrainy seasons at Patancheru, Andhra Pradesh, India, in the alfisol-Patancheru Soil Series (Udic Rhodustolf) fields. Each plot consisted of a single 4-m row on ridge in a ridge-furrow system. The distance between rows was 60 cm and between plants 10 cm. Care was taken to ensure uniform depth of planting. Seeds of *hypogaea* and *hirsuta* entries were treated with ethrel (2-chloroethylphosphonic acid) before sowing to overcome the possible effects of postharvest seed dormancy.

The experiments received 60 kg P_2O_5, 400 kg gypsum ha^{-1}, full irrigation (12 irrigations in the postrainy and six in the rainy season, with each irrigation totaling 5 cm of water) and protection against diseases and insect pests and weeds. In each plot, five representative plants were selected randomly to record SPAD readings and specific leaf area. The SPAD Chlorophyll meter (SPAD-502, Minolta Corp., Ramsey, NJ, USA) readings (SCMR) were made on 60 and 80 d after sowing (DAS) in the 2001 rainy season and on equivalent

cumulative thermal time (CTT, measured in degree days, °Cd, 10°C as base temperature) (Rao et al., 1992), 1000 °Cd and 1270 °Cd, respectively in the 2001-2002 postrainy season. The CTT was measured by the following formula:

$$ \text{CTT (°Cd)} = \sum_{P}^{H} \left(\frac{T_{max} + T_{min}}{2} \right) - T_{base} $$

where T_{max} = daily maximum temperature, T_{min} = daily minimum temperature, T_{base} = mean base temperature for peanut, P = planting date, and H = harvest date.

Two SCMRs were recorded on each of the four leaflets of the tetrafoliate leaf. Only one fully expanded second or third leaf from the apex of the main axis of all five sampled plants was used to record SCMR (Nageswara Rao et al., 2001). In recording the SCMR, care was taken to ensure that the SPAD meter sensor fully covered the leaf lamina and that the interference from veins and midribs was avoided. After recording SCMR, the leaves were processed (soaking in water for 2 h to bring to full turgor) for SLA measurement. The leaf area of the four leaflets was measured with a leaf area meter (LI-COR Area Meter Model 3000, LI-COR Inc., Lincoln, NE) after which the leaves were oven dried at 80°C for at least 48 h to determine the leaf dry weight. Data were recorded on leaflet length and width (mm) and plant height (cm) at 80 DAS in the rainy season and corresponding 1270°Cd in the postrainy season and the number of primary branches per plant, pods per plant, and yield per plant (g) at harvest. Data were recorded on a plot basis for days to emergence (days from sowing to emergence), 50% flowering (days from emergence to the stage when 50% of the plants had begun flowering), pod length and width, seed length and width, plot pod yield (kg ha^{-1}) and plot haulm yield (kg ha^{-1}), shelling percentage, and 100-seed weight (g). The entire plot was harvested and pods were removed, air-dried, and weighed. Weight of dry haulms after 1 wk of air-drying was recorded. The yield of five plants was added to determine total plot yield. Pod weight was multiplied with a correction factor of 1.65 (Duncan et al., 1978) to adjust for the differences in the energy requirement for producing pod dry matter compared with vegetative parts for calculating HI. The HI was determined as a ratio of adjusted pod weight to biomass, where adjusted pod weight = pod weight × 1.65 and biomass = adjusted pod weight + vegetative weight. A 200-g mature pod sample was used to estimate shelling percentage. The seeds and shells were separated and shelling percentage was calculated as follows:

Shelling percentage = (weight of seeds × 100)/

(weight of seeds + weight of shells).

Pod length and width was 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 with a commercial nuclear magnetic resonance spectrometer following the procedure described by Jambunathan et al. (1985). All the readings for oil and protein contents were taken on oven-dried (110°C, 16 h) samples, and values were expressed on a uniform 50 g kg^{-1} seed moisture. Protein content was estimated with a Technicon Autoanalyser (Pulse Instrumentation Ltd., Saskatoon, SK) (Singh and Jambunathan, 1980). Oil and protein contents were measured on a plot basis in the 2001 rainy season and on an entry basis in the 2001–2002 postrainy season. Mean values were used for statistical analysis.

Data were analyzed for α design following REML (residual maximum likelihood) analysis with seasons as fixed and entries as random on GENSTAT 5.1. The correlations were calculated separately in both seasons with best linear unbiased predictors (BLUPs) for SCMR and SLA at 60 and 80 DAS

and other traits. The component of phenotypic variance (δ_p^2) due to genotype (δ_g^2), genotype $\times$ environment (δ_{ge}^2), the residual, and their standard errors were calculated. The proportion of δ_p^2 due to δ_{ge}^2 was calculated for both SCMR and SLA and the one having lowest proportion being considered as more stable. Heritability in broad sense was estimated as proportion of δ_g^2 to the δ_p^2 assuming the following model:

$$\delta_p^2 = \delta_g^2 + \delta_{ge/ne}^2 + \delta_{e/ne \times nr}^2$$

where δ_e^2 is error (residual) variance, ne is the number of environments (seasons) and nr is the number of replications.

The mean SCMR and SLA values of entries in the mini core collection were compared with the best control cultivar out of four used and the entries, which showed mean significantly superior ($P = 0.05$) for a trait in each season were determined. If none of the entries was superior to the best control cultivar, the entries were grouped into different classes on the basis of the standard deviation (SD). The entries which have mean SCMR value up to class maximum –1 SD and SLA value up to minimum +1 SD were selected. This was done to select entries which showed values in the desirable direction for both SCMR (high) and SLA (low). Principal component analysis (PCA) of data on all traits of selected entries and control cultivars was performed. The mean observations for each trait were standardized by subtracting from each observation the mean value of the character and subsequently dividing by its respective standard deviation. This resulted in standardized values for each trait with average 0 and standard deviation of 1. The standardized values were used to perform principal component analysis (PCA) using Genstat 5.1. Cluster analysis using the unweighted pair group method of arithmetic means (UPGMA) (Sneath and Sokal, 1973) was performed with scores of the first 15 PCs.

RESULTS

The REML analysis of data for individual seasons separately revealed that genotypic variance was significant for both SLA and SCMR at 60 and 80 DAS and for 19 other traits in both seasons (Table 1), indicating that the entries included in the mini core displayed high variation among genotypes. In the combined REML analysis across seasons, there was a significant season effect for SCMR and SLA between 60 and 80 DAS and for all other quantitative traits. The components of variance due to genotypes were significant for SCMR and SLA at 60 and 80 DAS and other traits except pods per plant, yield per plant, haulm yield per plot, and protein and oil contents (Table 1), indicating genotypic differences. The genotypes $\times$ season interactions were significant for both SCMR and SLA at 80 DAS only and for all other quantitative traits except number of primary branches and pod width (Table 1). The magnitude of genotype variance vis-à-vis that due to the genotype $\times$ season (environment) interactions was greater for SCMR than for the SLA indicating greater importance of genotypes and low importance of g $\times$ e interactions for SCMR than for the SLA. This was clear when the percentage contribution of δ_{ge}^2 to δ_p^2 was calculated. The contribution of δ_{ge}^2 to δ_p^2 was 4.70% for SCMR compared to 8.42% for SLA at 60 DAS and 18.96% for SCMR versus 28.09% for SLA at 80 DAS. The heritability estimates in broad sense were higher for SCMR than for SLA at both stages (Table 1).

Mean SCMR values in the 2001–2002 postrainy season (41.31 $\pm$ 0.180 at 60 DAS, 42.85 $\pm$ 0.270 at 80 DAS)

Table 1. Estimates of variance components and heritability in broad sense for 19 vegetative, reproductive and quality traits, and specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) values at 60 and 80 d after sowing (DAS) in the peanut mini core collection, 2001 rainy (R) and 2001–2002 postrainy (PR) seasons and combined (C) analyses, ICRISAT Center, Patancheru, India.

Random term	Days to emergence (no.) Variance	s.e.	Days to 50% flowering (no.) Variance	s.e.	Primary branches (no.) Variance	s.e.	Plant height (cm) Variance	s.e.	Leaflet length (mm) Variance	s.e.	Leaflet width (mm) Variance	s.e.	Pod length (mm) Variance	s.e.	Pod width (mm) Variance	s.e.
Genotype (R)	0.52	0.08	9.53	1.04	0.35	0.05	46.11	5.01	48.74	5.36	8.21	0.93	31.63	3.44	1.42	0.16
Genotype (PR)	0.63	0.10	4.06	0.83	0.57	0.08	8.94	1.12	25.77	3.22	3.25	0.46	22.16	2.83	1.45	0.19
Genotype (C)	0.30	0.07	4.37	0.72	0.40	0.05	16.25	2.47	32.60	3.84	4.78	0.60	26.05	2.93	1.40	0.16
Genotype $\times$ season	0.26	0.06	2.32	0.46	0.04	0.02	10.85	1.36	4.31	0.87	0.88	0.19	1.02	0.48	0.05	0.03
Residual	0.74	0.04	5.95	0.34	0.51	0.03	6.44	0.37	11.31	0.64	2.64	0.15	9.73	0.51	0.71	0.04
Heritability (%)	54.0		67.0		79.1		71.4		89.0		84.5		92.4		90.7	

Random term	Seed length (mm) Variance	s.e.	Seed width (mm) Variance	s.e.	Pods per plant (no.) Variance	s.e.	Haulm yield (kg ha^{-1}) Variance	s.e.	Pod yield per plant (g) Variance	s.e.	Pod yield per plot (kg ha^{-1}) Variance	s.e.	Harvest index (%) Variance	s.e.	Shelling percentage Variance	s.e.
Genotype (R)	5.37	0.58	0.28	0.04	12.56	1.56	1 036 250.00	159 919.00	3.80	0.58	37 064.00	5 130.00	39.17	5.63	18.23	2.55
Genotype (PR)	3.24	0.40	0.18	0.03	12.92	2.26	3 816 848.00	614 546.00	23.65	3.70	251 185.00	34 898.00	46.46	7.26	16.14	2.27
Genotype (C)	4.07	0.46	0.20	0.03	0.00	–†	157 925.00	285 072.00	0.63	1.50	68 108	15 344	21.94	4.82	15.05	2.04
Genotype $\times$ season	0.26	0.07	0.03	0.01	12.42	1.33	1 933 706.00	387 407.00	13.20	2.07	78 178	13 238	19.89	4.13	2.44	0.87
Residual	1.21	0.07	0.28	0.02	15.26	0.86	5 035 560.00	280 339.00	19.13	1.07	137 849	7 756	55.96	3.12	15.94	0.91
Heritability (%)	92.5		75.9		0.0		8.0		6.0		52.3		53.2		79.5	

Random term	100-seed weight (g) Variance	s.e.	SLA at 60 DAS Variance	s.e.	SLA at 80 DAS Variance	s.e.	SCMR at 60 DAS Variance	s.e.	SCMR at 80 DAS Variance	s.e.	Oil content (%) Variance	s.e.	Protein content (%) Variance	s.e.
Genotype (R)	45.40	5.51	47.60	10.60	54.27	9.40	7.29	0.86	7.68	1.03	4.63	0.64	1.03	0.20
Genotype (PR)	64.67	8.79	66.30	18.10	92.20	18.20	7.63	1.08	11.49	1.62	3.87	0.40	7.56	0.79
Genotype (C)	47.64	6.15	34.60	10.10	47.00	10.40	6.56	0.83	7.53	1.08	0.00	–†	0.47	0.28
Genotype $\times$ season	7.53	2.19	7.00	11.20	24.60	9.10	0.37	0.31	1.91	0.56	3.40	0.41	1.87	0.38
Residual	36.74	2.10	270.20	14.00	169.70	9.50	7.03	0.37	9.48	0.54	2.87	0.26	2.17	0.21
Heritability (%)	82.8		41.6		53.7		82.8		74.8		0.0		26.4	

† = Estimate of genotypic variance component zero.

Table 2. Mean (± standard error) and range of best linear unbiased predictors (BLUPs) for SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) values at 60 and 80 d after sowing (DAS) in the *fastigiata* and *hypogaea* subsets and the entire peanut mini core in the 2001 rainy and 2001–2002 postrainy seasons, ICRISAT Center, Patancheru, India.

Character	Season	Mean			Range		
		fastigiata	*hypogaea*	Entire mini core	*fastigiata*	*hypogaea*	Entire mini core
SCMR 60DAS	2001 rainy	34.34 ± 0.196	37.46 ± 0.203	35.80 ± 0.182	29.13–39.42	30.58–41.19	29.13–41.19
SCMR 60DAS	2001–2002 postrainy	39.98 ± 0.200	42.83 ± 0.216	41.31 ± 0.180	34.4–45.87	37.00–46.54	34.40–46.54
SCMR 80DAS	2001 rainy	34.45 ± 0.216	36.72 ± 0.204	35.51 ± 0.171	29.99–39.93	29.21–40.94	29.21–40.94
SCMR 80DAS	2001–2002 postrainy	40.48 ± 0.245	45.54 ± 0.310	42.85 ± 0.270	33.64–48.13	32.61–50.59	32.61–50.59
SLA 60DAS	2001 rainy	101.50 ± 0.447	96.99 ± 0.612	99.39 ± 0.407	92.09–113.34	86.65–120.9	86.65–120.90
SLA 60DAS	2001–2002 postrainy	168.05 ± 0.619	163.66 ± 0.681	166.00 ± 0.485	145.67–183.11	148.88–184.90	145.67–184.90
SLA 80DAS	2001 rainy	101.00 ± 0.547	94.20 ± 0.663	97.82 ± 0.493	83.30–115.15	80.92–115.18	80.92–115.18
SLA 80DAS	2001–2002 postrainy	169.75 ± 0.741	160.72 ± 0.899	165.53 ± 0.664	152.13–191.86	139.77–199.12	139.77–199.12

were greater than in the 2001 rainy season (35.80 ± 0.182 at 60 DAS, 35.51 ± 0.171 at 80 DAS) at both 60 and 80 DAS in the mini core. This pattern was followed in both the *fastigiata* and *hypogaea* groups (Table 2). The increase was maximum in the *hypogaea* group from 36.72 ± 0.204 to 45.54 ± 0.310 at 80 DAS. The SLA was also greater in the postrainy season (166.00 ± 0.485 at 60 DAS, 165.53 ± 0.664 at 80 DAS) than in the rainy season (99.39 ± 0.407 at 60 DAS, 97.82 ± 0.493 at 80 DAS). The increase in the *fastigiata* group was slightly higher than the *hypogaea* group at 80 DAS (Table 2). The range of SCMR and SLA values differed at 60 and 80 DAS in the rainy and postrainy seasons in the mini core collection. SCMR ranged from 29.13 (ICG 9418) to 41.19 (ICG 6766) in the 2001 rainy season and 34.40 (ICG 9418) to 46.54 (ICG 14475) in the 2001–2002 post-rainy season at 60 DAS (Table 2). At 80 DAS it ranged from 29.21 (ICG 15287) to 40.94 (ICG 6766) in the 2001 rainy season and increased to 32.61 (ICG 8083) to 50.59 (ICG 14475) in the 2001–2002 postrainy season. SLA ranged from 86.65 (ICG 5827) to 120.90 (ICG 8083) and increased to 145.67 in ICG 2106-184.90 in ICG 8083

at 60 DAS and from 80.92 (ICG 6766)-115.18 (ICG 20016) to 139.77 (ICG 6766)-199.12 (ICG 8013) at 80 DAS in the postrainy season. The range (maximum–minimum) in the *fastigiata* and *hypogaea* groups was multiplied by 100, and the product was divided by the range of entire mini core to determine the percentage of range represented by the group. Accessions in the *fastigiata* group represented low range of the entire mini core for SCMR (86.28%) and SLA (79.35%) compared with the *hypogaea* group, which represented 91.64% range for SCMR and 98.0% range for SLA (Table 2). Overall, *hypogaea* group represented 94.80% range of mini core compared to 82.82% by the *fastigiata* group, indicating that for both SCMR and SLA *hypogaea* group accessions represented extreme values.

None of the entries in the mini core collection showed significantly greater SCMR values than the best control cultivar ICGS 76 at 60 DAS in the 2001 rainy and 2001–2002 postrainy seasons and 80 DAS in the 2001 rainy season. However, at 80 DAS in the 2001–2002 postrainy season, ICG 14475 showed significantly greater SCMR than ICGS 76 (Table 3). For SLA, none of the mini

Table 3. SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) at 60 and 80 d after sowing (DAS) in peanut mini core collection entries, 2001 rainy (*R*) and 2001–2002 postrainy (PR) seasons, ICRISAT Center, Patancheru, India.

Germplasm line	Origin	Botanical variety	SCMR at 60 DAS		SCMR at 80 DAS		SLA at 60 DAS		SLA at 80 DAS	
			2001 R	2001–2002 PR	2001 R	2001–2002 PR	2001 R	2001–2002 PR	2001 R	2001–2002 PR
ICG 118	India	*vulgaris*	39.42	40.36	39.93	45.27	105.0	168.27	102.0	162.48
ICG 532	Unknown	*hypogaea*	37.21	40.81	36.80	48.48	90.7	160.08	86.2	151.25
ICG 862	India	*hypogaea*	36.42	43.13	35.25	45.17	89.6	157.87	81.5	150.99
ICG 2106	India	*vulgaris*	35.18	41.06	35.68	42.41	92.1	145.67	98.2	162.58
ICG 2511	India	*hypogaea*	35.61	45.56	34.86	47.27	90.3	158.58	84.4	156.37
ICG 2773	Tanzania	*hypogaea*	39.67	44.57	38.34	45.16	91.9	159.27	87.0	151.99
ICG 4527	Uganda	*hypogaea*	40.51	44.63	38.37	46.14	97.6	165.71	93.3	160.57
ICG 5236	Chile	*vulgaris*	36.44	42.53	38.61	40.48	96.4	157.09	93.0	158.96
ICG 5827	USA	*hypogaea*	35.39	43.33	36.43	43.03	86.7	148.88	83.8	143.38
ICG 6654	Unknown	*vulgaris*	36.13	45.32	37.96	48.13	94.0	153.79	97.2	155.97
ICG 6766	USA	*hypogaea*	41.19	44.42	40.94	48.96	89.8	152.09	80.9	139.77
ICG 7243	USA	*hypogaea*	40.43	46.13	39.56	48.55	91.1	154.13	90.4	148.49
ICG 8285	USA	*hypogaea*	39.73	44.15	38.81	47.26	101.0	167.63	97.9	166.72
ICG 11219	Mexico	*hypogaea*	39.34	45.26	39.26	46.44	89.9	154.74	95.5	159.71
ICG 11855	Korea	*hypogaea*	39.56	44.66	39.06	48.07	98.2	166.62	95.6	163.73
ICG 14475	Nigeria	*hypogaea*	36.80	46.54	36.46	50.59	95.0	157.38	95.2	155.24
ICG 14523	Unknown	*hypogaea*	40.93	46.26	39.73	47.78	105.0	174.26	97.4	152.45
ICG 14985	Unknown	*vulgaris*	38.35	45.52	38.64	42.93	99.1	160.63	93.0	157.77
Control cultivars										
Gangapuri	India	*fastigiata*	37.06	40.71	35.50	40.61	101.0	169.06	92.7	163.78
ICGS 44	ICRISAT	*vulgaris*	38.29	41.89	38.78	44.66	99.1	168.18	93.2	162.75
ICGS 76	ICRISAT	*hypogaea*	39.46	45.13	39.88	45.59	99.6	160.15	105.0	161.81
M 13	India	*hypogaea*	38.03	44.93	36.96	50.10	90.9	155.7	86.6	148.81
Trial mean			35.85	41.34	35.56	42.89	99.4	165.97	97.8	165.42
SEM ±			0.93	1.51	1.35	1.588	5.85	5.997	5.83	1.516
LSD (5%)			2.59	4.19	3.73	4.41	16.2	18.04	16.2	18.86
CV (%)			4.5	6.5	7.6	5.8	10.3	10.2	8.3	8.9

core entries had significantly lower SLA than ICGS 76 at 60 DAS in the 2001 rainy season and 2001–2002 postrainy seasons. But at 80 DAS in the 2001 rainy season, six mini core entries, ICG 532, ICG 862, ICG 2511, ICG 2773, ICG 5827, and ICG 6766 and one entry, ICG 6766 in the 2001-2002 postrainy season showed significantly lower SLA than ICGS 76 (Table 3). These and other entries which had the mean SCMR values in the maximum –1 SD class or mean SLA values in the minimum +1 SD class were identified for selection. Considering both SCMR and SLA at 60 and 80 DAS in both seasons, the number of times an entry occurred in the desirable class (maximum SCMR – 1 SD or minimum SLA + 1 SD) was determined and used in the final selection of mini core entries. ICG 6766 was the only entry which occurred eight times in the desired classes. ICG 7243 occurred six and ICG 2511, ICG 2773, ICG 5827, ICG 8285, ICG 11219 (PI 355273), ICG 11855, and ICG 14523 occurred 4 out of eight times in the desired classes. We selected 18 entries, using criteria of significantly higher SCMR or lower SLA than ICGS 76 or occurrence in the desired classes.

In Table 3, the country of origin, SCMR, and SLA values of peanut mini core collection and control cultivars at 60 and 80 DAS in the 2001 rainy and 2001–2002 postrainy seasons is given. Of the 18 entries, five belong to subsp. *fastigiata* var. *vulgaris* and 13 to subsp. *hypogaea* var. *hypogaea*. They originated from India (4), Chile (1), USA (4), Mexico (1), Korea (1), Tanzania (1), Nigeria (1), and Uganda (1). Information on the origin of ICG 532, ICG 6654, ICG 14523, and ICG 14985 (PI 540500) is unknown (Table 3). Some of these lines have good pod yield (ICG 862, ICG 8285, ICG 11855), high

harvest index (ICG 2511, ICG 5827, ICG 11855), high shelling percentage (ICG 118, ICG 2106, ICG 5827), high 100-seed weight (ICG 11219, ICG 11855), high protein (ICG 5236, ICG 6654), and high oil (ICG 118, ICG 862, ICG 11219) contents (Table 4).

Correlations between SCMR and SLA values were calculated to know the relationship in the mini core collection between these two traits at 60 and 80 DAS in both seasons. All the correlations were highly significant. The SCMR values at different stages and seasons were more positively correlated with each other than the SLA values when correlated together (Table 5). The correlation coefficient between the SCMR at 60 DAS in the 2001 rainy and 2001–2002 postrainy seasons was 0.961 compared to 0.872 between the SLA values at 60 DAS both being highly significant (Table 5). SCMR and SLA were negatively correlated at all stages and within both seasons. Further, SCMR values were more strongly related with economic traits like pod yield and 100-seed weight at both 60 and 80 DAS than SLA. The correlations between pod yield and SCMR values were 0.320 ($r = 0.002$ between SLA and pod yield) in the 2001 rainy season and 0.477 ($r = -0.163$) in the 2001–2002 postrainy season at 60 DAS and 0.366 ($r = 0.101$) in the 2001 rainy season and 0.484 ($r = -0.265$) in the 2001–2002 postrainy season at 80 DAS (Table 5). The correlations between 100-seed weight and SCMR were 0.429 ($r = -0.184$ between SLA and 100-seed weight) in the 2001 rainy season and 0.389 ($r = -0.114$) in the 2001–2002 postrainy season at 60 DAS and 0.446 ($r = -0.073$) in the 2001 rainy season and 0.380 ($r = -0.244$) in the 2001–2002 postrainy season at 80 DAS. This indicated that the selection for SCMR, besides improv-

Table 4. Performance of peanut mini core entries, 2001 rainy (*R*) and 2001–2002 postrainy (PR) seasons, ICRISAT Center, Patancheru, India.

Germplasm lines	Pod yield		Harvest index		Shelling percentage		100-seed weight		Protein		Oil	
	2001 R	2001–2002 PR	2001 R	2001–2002 PR	2001 R	2001–2002 PR	2001 R	2001–2002 PR	2001 R	2001–2002 PR	2001 R	2001–2002 PR
	—— kg ha⁻¹ ——		—— % ——				—— g ——		—— % ——			
ICG 118	690.3	1796.1	37.80	51.7	71.9	70.8	42.6	56.6	18.6	25.5	51.5	51.3
ICG 532	591.0	1996.2	33.38	41.59	59.0	67.4	39.0	48.49	18.0	22.5	51.0	48.8
ICG 862	682.0	2503.4	32.89	48.04	66.0	67.9	36.0	45.88	19.0	22.3	52.0	51.7
ICG 2106	628.5	1693.0	27.00	46.10	66.9	71.7	30.3	44.6	18.6	25.6	50.9	47.2
ICG 2511	569.8	2057.5	34.70	54.90	65.3	68.3	41.0	56.1	18.5	20.4	49.7	50.1
ICG 2773	756.0	2211.5	30.60	43.00	59.7	68.1	37.0	51.8	18.0	21.7	48.9	48.4
ICG 4527	570.0	2056.6	27.92	43.16	64.0	66.3	37.0	46.38	19.0	21.1	48.0	47.5
ICG 5236	648.7	1727.2	32.10	46.30	66.0	68.1	29.4	49.5	18.0	26.5	52.5	47.8
ICG 5827	675.6	2294.3	29.80	54.30	61.6	71.4	42.8	47.3	20.9	25.5	48.9	47.7
ICG 6654	443.0	1075.1	28.20	48.27	64.0	70.7	31.0	48.92	18.0	27.1	51.0	46.1
ICG 6766	596.9	2202.3	25.70	48.20	61.7	62.7	48.4	65.8	19.6	24.3	45.1	45.2
ICG 7243	481.5	1758.6	20.70	48.80	62.0	69.7	32.9	54.9	18.8	23.7	49.4	48.9
ICG 8285	590.8	3034.0	27.40	51.60	58.0	65.9	39.4	56.1	19.5	25.1	47.1	47.8
ICG 11219	890.2	2368.7	32.90	48.20	58.7	68.7	46.8	73.2	19.0	23.3	50.1	51.5
ICG 11855	849.1	2548.6	36.00	56.30	58.2	67.6	45.5	63.8	18.3	24.3	49.1	49.1
ICG 14475	506.0	1772.9	19.85	39.51	64.0	67.8	41.0	64.39	19.0	26.1	51.0	47.7
ICG 14523	381.3	1251.3	17.80	31.60	62.5	62.7	38.5	46.2	18.3	22.3	47.3	44.5
ICG 14985	632.0	2066.9	36.14	56.17	63.0	70.9	38.0	57.85	20.0	26.8	48.0	46.2
					Control cultivars							
Gangapuri	543.7	1529.1	25.00	50.40	62.4	72.2	31.6	51.3	18.0	27.6	50.7	45.1
ICGS 44	953.5	1988.6	43.40	54.70	68.9	71.6	39.0	50.3	18.7	26.0	50.1	47.9
ICGS 76	1109.4	2664.6	40.50	51.90	68.2	72.0	47.5	57.4	18.8	22.8	49.1	47.9
M 13	756.5	2018.3	31.10	47.70	64.8	63.2	53.8	50.6	17.9	23.0	48.9	47.4
Trial mean	556.2	1711.34	26.91	45.79	61.26	67.75	34.43	49.28	18.95		49.64	
SEM ±	133.19	269.629	3.234	4.426	2.994	2.45	3.399	5.442	0.794		1.401	
LSD (5%)	370.0	748.9	9.0	12.3	8.3	6.8	9.4	15.1	2.2		3.9	
CV (%)	31.1	27.9	23.3	17.1	6.4	6.5	12.9	14.3	6.9		3.4	

Table 5. Correlation between SPAD chlorophyll meter readings (SCMR) and specific leaf area (SLA) at 60 and 80 d after sowing (DAS), 100-seed weight, and pod yield per plot in the peanut mini core collection, 2001 rainy (R) and 2001–2002 postrainy (PR) seasons, ICRISAT Center, Patancheru, India.

Character	SCMR 60 DAS 2001R	SCMR 60 DAS 2001–2002PR	SCMR 80 DAS 2001R	SCMR 80 DAS 2001–2002PR	SLA 60 DAS 2001R	SLA 60 DAS 2001–2002PR	SLA 80 DAS 2001R	SLA 80 DAS 2001–2002PR	100-seed weight 2001 R (g)	100-seed weight 2001–2002 PR (g)	Pod yield per plot 2001 R (kg ha⁻¹)	Pod yield per plot 2001–2002 PR (kg ha⁻¹)
SCMR 60 DAS 2001R	1.000											
SCMR 60 DAS 2001–2002PR	0.961***	1.000										
SCMR 80 DAS 2001R	0.870***	0.804***	1.000									
SCMR 80 DAS 2001–2002PR	0.801***	0.786***	0.845***	1.000								
SLA 60 DAS 2001R	−0.431***	−0.448***	−0.444***	−0.519***	1.000							
SLA 60 DAS 2001–2002PR	−0.493***	−0.536***	−0.486***	−0.511***	0.872***	1.000						
SLA 80 DAS 2001R	−0.429***	−0.432***	−0.396***	−0.511***	0.665***	0.560***	1.000					
SLA 80 DAS 2001–2002PR	−0.534***	−0.532***	−0.563***	−0.683***	0.643***	0.646***	0.732***	1.000				
100-seed weight 2001 R (g)	0.429***	0.447***	0.446***	0.426***	−0.184*	−0.152*	−0.073	−0.270***	1.000			
100-seed weight 2001–2002 PR (g)	0.270***	0.389***	0.294***	0.380***	−0.145*	−0.114	−0.031	−0.244***	0.728***	1.000		
Pod yield per plot 2001 R (kg ha⁻¹)	0.320***	0.326***	0.366***	0.186*	0.002	−0.178*	0.101	−0.072	0.522***	0.210**	1.000	
Pod yield per plot 2001–0202 PR (kg ha⁻¹)	0.402***	0.477***	0.404***	0.484***	−0.189**	−0.163*	−0.131	−0.265***	0.536***	0.423***	0.529***	1.000

* Significant at $P = 0.05$.
** Significant at $P = 0.01$.
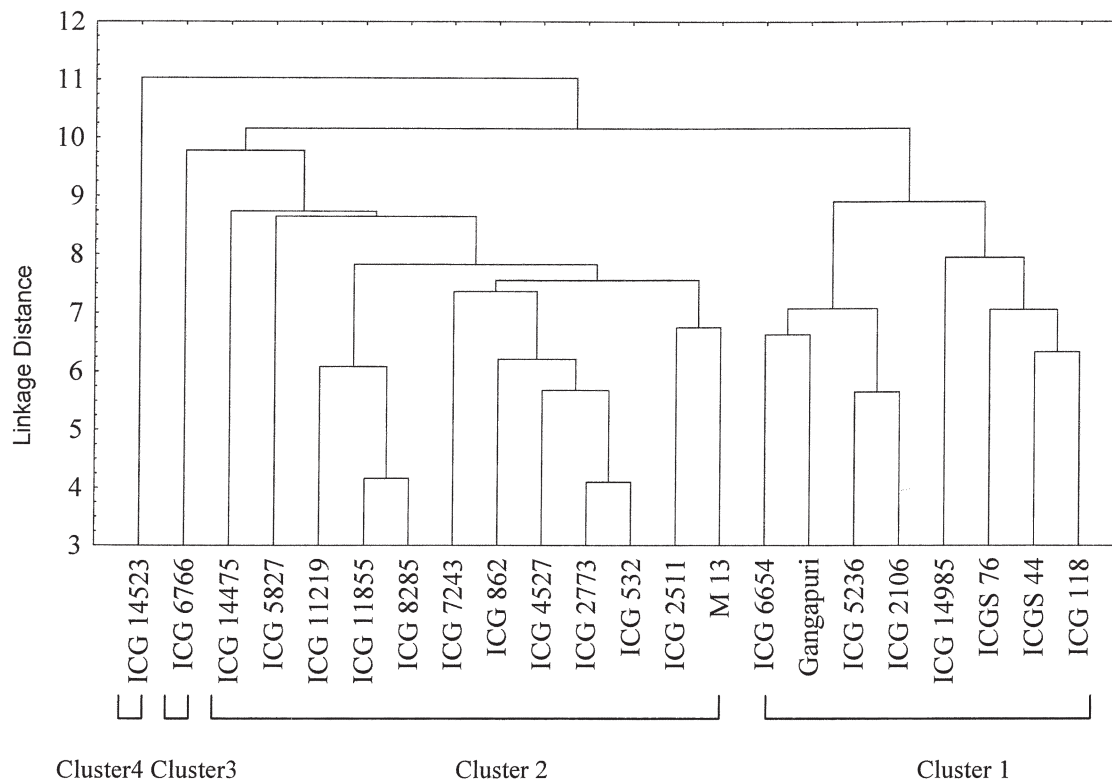*** Significant at $P = 0.001$.

Fig. 1. Dendrogram of 18 selected germplasm lines and four control cultivars constructed on the basis of the scores of the first 15 principal components.

ing drought resistance, may result in greater correlated gains for other economic traits than the selection for SLA.

The PCA was used to provide a reduced dimension model that would indicate measured differences among 18 selected entries and four control cultivars. PC 1, which is the first and most important component, accounted for 29.83% and the second PC accounted for 12.61% of total variation. The last PC considered for clustering, PC 15, contributed 1.16% of the total variation. A hierarchical cluster analysis was conducted on the first 15 PC scores (total variation accounted 97.47%) and resulted in four clusters (Fig. 1). The five *vulgaris* entries, ICG 118, ICG 14985, ICG 2106, ICG 5236, and ICG 6654 and three control cultivars, Gangapuri (*fastigiata*), ICGS 44 (*vulgaris*), and ICGS 76 (*hypogaea*) grouped together in Cluster 1. The 11 *hypogaea* entries and control cultivar M 13 (*hypogaea*) grouped in Cluster 2 with ICG 6766 and ICG 14523 forming two separate clusters, indicating that they were diverse from the control cultivars.

DISCUSSION

The results of this evaluation of the peanut mini core collection revealed a large variation for SCMR and SLA. Mean SCMR and SLA values were higher in the postrainy season than in the rainy season (Table 2). This may be due to higher radiation and lower temperature in the postrainy season. Bell et al. (1992) have clearly demonstrated the influence of radiation and temperature on the production and utilization of photosynthates in peanut leaves. Eighteen diverse accessions, which were superior or similar to the best control cultivar for SCMR and SLA have been selected. The selected accessions also have good pod yield (ICG 862, ICG 8285, ICG 11855), shelling percentage (ICG 118, ICG 2106, ICG 5827), 100-seed weight (ICG 11219, ICG 11855), protein (ICG 5236, ICG 6654), and oil (ICG 118, ICG 862, ICG 11219) contents. The 18 accessions consisted of 5 *vulgaris* and 13 *hypogaea* types and originated from eight countries.

Our results and identification of the diverse accessions with high SCMR and low SLA may be useful in breeding for resistance to drought. Since these accessions have reasonably good agronomic value, they can be used in breeding programs without adversely affecting the speed of improvement program resulting from epistatic effects. While selecting exotic germplasm lines for inclusion in the breeding programs, it is important to consider the genetic background and agronomic performance of the lines as this will be useful in predicting its behavior in hybrid combinations with adapted genotypes. The less divergent the germplasm line and adapted lines are, the more likely it will be that the additive gene effects will play a primary role in inheritance of quantitative traits (Isleib and Wynne, 1983). As the diversity between parents increases, dominance effects and epistatic variations have significant roles in the inheritance of quantitative traits (Halward and Wynne, 1991). In a self-pollinated crop such as peanut, this would have implications in choosing an appropriate selection strategy.

SCMR and SLA were negatively correlated. The association between SCMR values between season or at different stages within a season is stronger than the relationship between SLA values. This may due to the less influence of environment (season) on genes controlling SCMR than those controlling SLA. SCMR also had a stronger association than SLA with economic traits like pod yield and 100-seed weight. This will have implications in breeding programs, as the selection for SCMR would result in greater correlated response to yield and other economic traits than the selection for SLA. Further, SCMR showed less genotype × season interaction (Table 1), lower contribution of δ^2_{ge} to δ^2_p, and higher heritability and was more stable than SLA.

Genetic resources will be the main contributing factor to much of the future progress in developing new cultivars. The size of germplasm collections is large and still increasing, which in turn increases the difficulty in using them in improvement programs through evaluations for traits of interest. Development of core collections, which make up about 10% of entire collection, has been proposed as a way to enhance efficiency of evaluation of germplasm collections to identify useful parents (Frankel, 1984; Frankel and Brown, 1984). However, in crops where the number of accessions in collections are very large, core collection (10% of entire collection) will be unwieldy for the examination of useful traits, which show high genotype × environment interactions and require replicated multilocational evaluations. For such situations, Upadhyaya and Ortiz (2001) suggested a two-stage strategy for constructing mini core collections that consist of only 1% of the entire collection but are representative of the diversity of the collections. The mini core collection, because of its drastically reduced size, can be evaluated extensively to select useful parents. Results of our study and those of Anderson et al. (1996), Hammond et al. (1997), Franke et al. (1999), Holbrook and Anderson (1995), Holbrook et al. (1997, 1998, 2000), Isleib et al. (1995), and Upadhyaya et al. (2001) demonstrate that a core or mini core can be used effectively to identify valuable genes in germplasm collections.

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