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Physiological efficiencies in mini-core peanut germplasm accessions during summer season

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Abstract

In the present study, the physiological efficiencies of 181 mini-core peanut accessions (genotypes) were evaluated according to variability in their physiological performance in the field during summer (2012). Genotypes were categorized into groups of high, medium, and low physiological activity. Thirty-four genotypes showed high net photosynthetic rate (P_N > 33 μmol m^{-2} s^{-1}), 28 genotypes exhibited high stomatal conductance (g_s > 0.54 mmol m^{-2} s^{-1}), 33 genotypes manifested high transpiration rate (E > 11.8 mmol m^{-2} s^{-1}), 30 genotypes performed with high water-use efficiency (WUE > 3.8), 30 genotypes reached high chlorophyll SPAD values (SCMR > 40), and 35 genotypes showed high maximum quantum yield of PSII (F_v/F_m > 0.86). In addition, few genotypes showed high values for multiple physiological traits. A total of 54 genotypes exhibited higher values in two, 20 genotypes showed a high value in three, and in eight genotypes, high values occurred in four different physiological traits. Interestingly, only two genotypes, NRCG 14493 and 14507, showed high values for five different traits. Positive correlation was observed between g_s and P_N, E, and g_s, and between P_N and F_v/F_m, while WUE and E showed a negative correlation. The genotypes with high P_N, g_s, and WUE coupled with high SCMR and F_v/F_m could be used in peanut crop improvement programme for yield enhancement as well as stress tolerance.

Additional key words: chlorophyll fluorescence; core collection; crop productivity; gene bank.

Introduction

The peanut (*Arachis hypogaea* L.) is a leguminous oilseed crop, spread worldwide in around 120 countries, grown on about 24 million ha with overall production of 38 million tons of pods, with an average productivity of 1,580 kg ha^{-1} (FAO 2012). India has an area of 6.5 million ha on which peanut is grown as a crop, but the average productivity fluctuates between 1,000–1,450 kg ha^{-1} (below the world average productivity of peanut) due to adverse climatic conditions. As a part of crop improvement programme for enhanced production and productivity of peanut, Directorate of Groundnut Research (DGR) and its coordinated centres in India and International Crop Research Institute for Semi-Arid Tropics (ICRISAT), India, have succeeded in identifying trait-specific genotypes for developing cultivars with variations in a yield and physiological traits (Singh 2011). But most peanut cultivars have a very narrow genetic base (Upadhyaya *et al.* 2002, Nigam *et al.* 2005). This calls for utilization of germplasm resources in breeding programmes to enhance the diversity of cultivars; however, the large collection of peanut germplasm (> 15,000 genotypes) has been characterized for only a limited number of traits because it is difficult to assess the physiological performance of all the genotypes at a time.

Plant breeding approaches require large amount of variability within species in order to get contrasting parents with divergent characteristics for different traits. However, such genotypic variations are present in the nature in the form of huge germplasm collections. Until now, unavailability of low cost tools to identify similarities or differences among accessions led our gene banks to hold such huge collections of germplasm (Upadhyaya *et al*. 2002). A core collection represents the genetic diversity of a crop species and its wild relatives with a minimum repetitiveness, containing approximately 10% of the entire collection, and comprising of roughly 2,000–3,000 genotypes, to provide the starting material for breeders

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Abbreviations: Chl – chlorophyll; E – transpiration rate; F_v/F_m – maximum photochemical efficiency of PSII; g_s – stomatal conductance; P_N – net photosynthetic rate; SCMR – soil-plant-analytical-development chlorophyll meter reading; WUE – water-use efficiency.
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for crop improvement programme (Frankel and Brown 1984). The peanut core collection has been suggested as a way to enhance use of genetic resources in crop improvement (Upadhyaya and Ortiz 2001). But still the peanut core collection contains more than 1,700 genotypes, which is again too large for assessing physiological traits. Upadhyaya *et al.* (2002) developed further a mini-core subset, at ICRISAT, India, which contains about 1% of total genotypes, but captures most of the useful variations of the crop to enhance genetic exploitation. But until now, characterization of this mini-core peanut germplasm for physiological efficiencies has not been done. Thus, we utterly need to investigate some of the basic physiological processes, such as photosynthesis, transpiration, and chlorophyll (Chl) fluorescence parameters, in the mini-core subset, namely those directly associated with dry matter production and yield of peanut.

Plant growth is often influenced by the Chl content, and by physiological processes, such as photosynthesis and transpiration. During the pod filling stage in peanut, Nautiyal *et al.* (1999) showed the plant exhibited high leaf-level P_N. The Chl content measured in terms of SPAD (soil plant analytical development) Chl meter reading (SCMR) showed high positive correlation with spectrophotometric measurements of leaf Chl content in peanut. Hence, SCMR values can be used as a rapid and portable method for Chl evaluation, especially when handling a large number of genotypes (Samdur *et al*. 2000). WUE or *E* are the traits that can contribute directly to productivity under a moisture limited environment (Wright *et al*. 1994), because the reduction in CO_2 assimilation under water deficit conditions is mostly due to stomatal closure (Arnau *et al.* 1997). Hence the genotypes with higher WUE have higher g_s to water and CO_2 which increases the relative diffusion of CO_2 into the leaf and finally its incorporation into biomass. Thus, WUE emerged as a key factor determining plant productivity under limited water supply (Saranga *et al*. 1999) and it is mentioned as a strategy to improve crop performance under water limited conditions (Araus *et al*. 2002). Studies on WUE and relevant physiological traits demonstrated close relationship between SCMR and WUE in peanut. The objective of the present study was to characterize the mini-core subset of peanut genotypes for different physiological parameters, *i.e*., P_N, g_s, *E*, SCMR, and Chl fluorescence parameters. We aimed to generate a complete set of information that would be of immense help for future researchers in selecting useful genotypes in peanut crop improvement programme.

Materials and methods

Plant material and growing conditions: This research was conducted during the summer of 2012 at the research farm of the Directorate of Groundnut Research, Junagadh (70.36ºE and 21.31ºN). The climate at this site is characterized as semiarid, and soils are classified as black calcareous Ustochrept soil (Singh *et al*. 2000) with an average pH of 7.5 and medium fertility with 15% $CaCO_3$, clayey (35% sand and 44% clay) soil containing 0.75% of organic C, 710 mg kg^{-1} of total N, 6.5 mg kg^{-1} of available P (Olsen P), 11 mg kg^{-1} of heat soluble S (available S), 3.02, 4.9, 0.71, and 0.50 mg kg^{-1} of diethylene triamine pentaacetic acid (DTPA) extractable Fe, Mn, Zn, and Cu, respectively. The field was prepared by ploughing and levelling and divided into small plots of 50 m^2 (10 m × 5 m) by raising bunds. N (40 kg ha^{-1}) and P (20 kg ha^{-1}) as diammonium phosphate, 30 kg(P) ha^{-1} as single superphosphate, and 50 kg(K) ha^{-1} as muriate of potash as basal and 1,000 kg ha^{-1} of gypsum were added uniformly 40 d after emergence (DAE) during flowering in all the plots with a prior application of farm-yard manure (5 t ha^{-1}). Before sowing, seeds of 181 mini-core germplasm were treated with *Bavistin* (Carbendazim, 50% WP, *BASF India Ltd.*, India), 2 g per 100 g of seeds, and they were sown in 5 m row in randomized block design with three replications at 45 × 10 cm spacing in the furrows (3–5 cm deep) and covered with soil after sowing. The crop was grown according to recommended practices, and a proper care was taken to protect it from weeds, insects, pests, and diseases during the entire cropping season (Singh and Basu 2005).

Observations were recorded at 60–65 d after sowing (DAS) corresponding to stages of a pod formation to onset of pod filling, *i.e*., R4–R5 stage in peanut (Boote 1982).

Weather condition during crop growth period: The crop growth period coincided with 5th–24th meteorological standard week. The mean temperature at the time of sowing was 21ºC and ranged between 20–25ºC during the early vegetative stage and 30–32ºC during the pod development stage (Fig. 1*A*). The relative humidity varied between 37 and 85% during the entire growing season. The total, bright sunshine hours (BSS) were 181 with the highest BSS in the 19th standard week. The evaporation per day ranged from 5.7–10.7 mm with an average of 8.5 mm (Fig. 1*B*).

Leaf-level gas exchange: All gas-exchange measurements were recorded using a portable photosynthesis system (*Model LI-6400*, *LI-COR*, USA) between 08:00–11:30 h in the third leaf from the main axis. Leaf temperature was set at ambient values and giving a stable reading. PAR was set at 1,650 µmol(photon) m^{-2} s^{-1} inside the cuvette, and CO_2 concentration was set at ambient value (390 µmol m^{-2} s^{-1}).

Chl fluorescence and SCMR measurements: Chl fluorescence parameters, *i.e*., maximum fluorescence of the dark-adapted leaf (F_m), variable fluorescence (F_v), and the

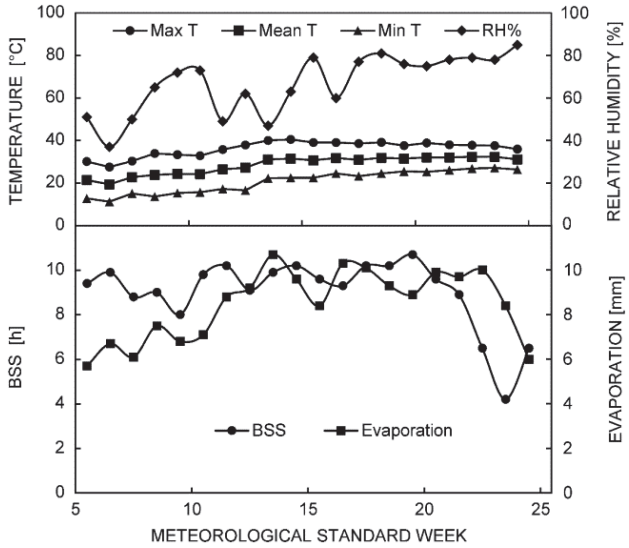

Fig. 1. Variation in different weather parameters based on standard meteorological weeks during the crop growing season. Max T – maximum temperature; Mean T – mean temperature; Min T – minimum temperature; RH – relative humidity; BSS – bright sunshine.

maximum photochemical efficiency of PSII (F_v/F_m) were recorded using a *Handy Plant Efficiency Analyzer (PEA*, *Hansatech*, USA) according to the method described by Havaux (1993). The selected leaves were dark adapted for a period of 30 min using leaf clips. A saturating flash light of 3,000 μmol(photon) m^{-2} s^{-1} was applied to achieve the maximum fluorescence. The SPAD Chl meter readings (SCMR) were recorded using *SPAD-502 Plus* (*Konica Minolta*, Japan) on the third leaf from the main axis uniformly for all the genotypes (Nageswara Rao *et al*. 2001).

Statistical analyses: All data recorded were the mean values of at least three independent observations with three replications each. The data were analyzed by analysis of variance (*ANOVA*) appropriate to the experimental design using *DSAASTAT* (Onfri 2007). The regression and correlation for various parameters was worked out and data were tested for their significance. Different relationships among various parameters associated with physiological efficiencies were obtained. The peanut genotypes were categorized according to various parameters and sorted based on deviation in their values from average. The genotypes showing higher values for P_N, g_s, E, WUE, SCMR, and F_v/F_m were identified and categorized into 'high' group when $X_i - sd_i > X_p + sd_p$, whereas genotypes with lower values were identified and categorized into the 'low' group when $X_i + sd_i > X_p - sd_p$, where X_i is the mean of the individual genotype; X_p is the population mean; sd_i is the standard deviation of the individual genotype; and sd_p is the standard deviation of population. The genotypes with values between those two were categorized into the 'medium' group. Associations of traits were made and germplasms having the highest values were checked with association of traits and then they were separated accordingly.

Results

The analysis of variance showed significant difference between the germplasm genotypes with highly significant mean squares for all the physiological characters (Table 1).

Gas-exchange measurements: The P_N in 181 mini-core genotypes varied from 14.5–40.8 μmol(CO_2) m^{-2} s^{-1}, with a mean value of 28.5 μmol m^{-2} s^{-1} (Table 1S). Among all the genotypes, 34 genotypes showed the $P_N > 33$ μmol m^{-2} s^{-1} and they were assigned to the high P_N group as photosynthetically more efficient. From those, four genotypes (NRCG 14475, 14506, 14507, and 14505) showed a P_N greater than 36.7 μmol m^{-2} s^{-1} (Table 2). On the other hand, 124 genotypes showed the P_N between 24–33 μmol m^{-2} s^{-1} and they were classified as a medium category. Twenty three genotypes showed the P_N lower than 24 μmol m^{-2} s^{-1} and they were categorized as low

Table 1. Mean square values showing genotypic variations for different physiological traits in mini-core peanut germplasm. P_N – photosynthetic rate [μmol m^{-2} s^{-1}]; E – transpiration rate [mmol m^{-2} s^{-1}]; g_s – stomatal conductance [mmol m^{-2} s^{-1}]; WUE – water-use efficiency; SCMR – SPAD chlorophyll meter reading; F_v/F_m – maximum photochemical efficiency of PSII; ** – statistically significant values at 1% level of significance; DF –degrees of freedom; LSD – least significant difference; CV – coefficient of variation; SEM – standard error of mean.

	DF	P_N	g_s	E	WUE	SCMR	F_v/F_m
Block	1	6.931	0.020	3.440	0.957	3631.745	0.000
Genotype	180	39.938**	0.026**	10.031**	1.202**	12.265**	0.000**
Residual	180	9.519	0.008	2.155	0.457	7.386	0.000
Total	361	24.679	0.017	6.086	0.829	19.858	0.000
CV [%]		10.820	20.530	15.300	21.560	7.190	1.170
SEM (±)		2.180	6.260	1.040	0.480	1.920	7.030
$LSD_{0.05}$		6.090	0.170	2.900	1.330	5.360	1.960
$LSD_{0.01}$		8.030	0.230	3.820	1.760	7.080	2.590

Table 2. Categorization of mini-core peanut germplasm based on different physiological traits. P_N – photosynthetic rate [μmol m^{-2} s^{-1}]; E – transpiration rate [mmol m^{-2} s^{-1}]; g_s – stomatal conductance [mmol m^{-2} s^{-1}]; WUE – water-use efficiency; SCMR – SPAD chlorophyll meter reading; F_v/F_m – maximum photochemical efficiency of PSII.

Physiological traits	P_N	g_s	E	WUE	SCMR	F_v/F_m
Qualifying value for efficient genotype (mean + SD)	33 μmol m^{-2} s^{-1}	0.54 mmol m^{-2} s^{-1}	11.8 mmol m^{-2} s^{-1}	3.8	40	0.860
Qualified genotypes in efficient category (having values more than the qualifying value)	14475, 14506, 14507, 14505, 14459, 14407, 14474, 14414, 14384, 14405, 14424, 14381, 14478, 14348, 14380, 14413, 14360, 14472, 14408, 14464, 14482, 14477, 14501, 14473, 14483, 14435, 14373, 14386, 14379, 14493, 14491, 14485, 14484, 14354	14506, 14347, 14343, 14345, 14379, 14472, 14425, 14489, 14348, 14424, 14500, 14386, 14333, 14485, 14466, 14337, 14463, 14491, 14505, 14478, 14493, 14464, 14441, 14435, 14344, 14507, 14340, 14467	14452, 14451, 14459, 14343, 14456, 14347, 14345, 14507, 14454, 14365, 14360, 14448, 14341, 14337, 14342, 14447, 14333, 14407, 14435, 14413, 14458, 14457, 14408, 14405, 14506, 14344, 14453, 14460, 14450, 14424, 14439, 14430, 14461	14477, 14484, 14496, 14482, 14499, 14497, 14473, 14377, 14395, 14397,14463, 14493, 14400, 14462, 14486, 14501, 14324, 14417, 14474, 14464, 14476, 14354, 14356, 14475, 14487	14479, 14488, 14412, 14370, 14390, 14489, 14397, 14338, 14331, 14409, 14505, 14502, 14466, 14504, 14507, 14402, 14418, 14421, 14386, 14410, 14442, 14463, 14382, 14493, 14467, 14464, 14491, 14357, 14351, 14422, 14324, 14482, 14474, 14375, 14438, 14406	14497, 14469, 14467, 14483, 14479, 14412, 14429, 14462, 14501, 14373, 14456, 14474, 14477, 14489, 14493, 14426, 14368, 14389, 14505, 14352, 14457, 14459, 14357, 14461, 14472, 14409, 14478, 14487, 14494, 14500, 14507, 14422, 14452, 14463, 14481
Number of genotypes in efficient category	34	28	33	25	36	35

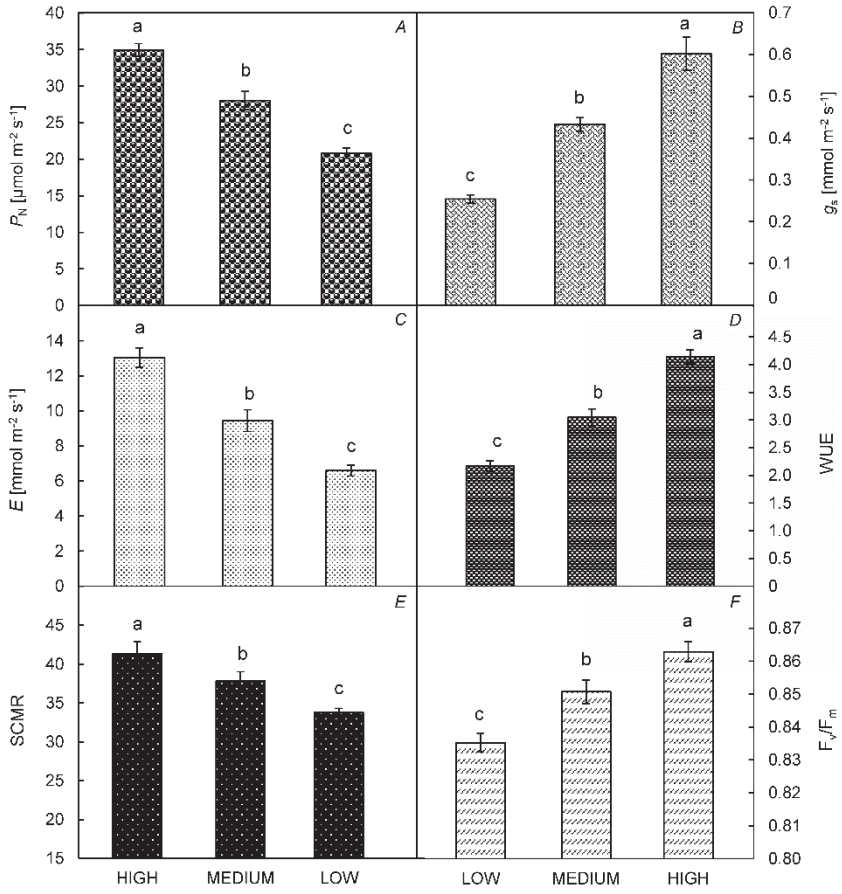

Fig. 2. Variation in (*A*) net photosynthesis rate (P_N); (*B*) stomatal conductance (g_s); (*C*) transpiration rate; (*D*) water-use efficiency (WUE); SPAD chlorophyll meter reading (SCMR) value (*E*); and (*F*) maximum efficiency of PSII (F_v/F_m) in 'high', 'medium', and 'low' category of 181 mini-core peanut genotypes. The individual values in each category are means ± SE. Means sharing *the same letter* for a particular trait are not significantly different ($P \leq 0.05$) according to *Duncan*'s multiple range test.

and photosynthetically inefficient (Fig. 2*A*). The genotypes NRCG 14388, 14366, 14327, and 14391, showed P_N value below 18.8 μmol m^{-2} s^{-1}.

The g_s in 181 mini-core germplasm genotypes ranged from 0.128–0.702 mmol m^{-2} s^{-1} with a mean value of 0.431 mmol m^{-2} s^{-1}. Among all genotypes, 28 showed the g_s > 0.54 mmol m^{-2} s^{-1} and were categorized as the high conductance genotypes (Table 2). In addition, 29 genotypes with g_s < 0.32 mmol m^{-2} s^{-1} were categorized as the low conductance genotypes. There were 124 genotypes with the g_s value between 0.32–0.54 mmol m^{-2} s^{-1}, and these were categorized as the medium conductance genotypes (Table 2S). The high conductance genotypes (*i.e.*, NRCG 14343, 14345, 14347, and 14506) showed the g_s > 0.66 mmol m^{-2} s^{-1}. On the other hand, four genotypes showed the g_s < 0.31 mmol m^{-2} s^{-1} (*i.e.*, NRCG 14366, 14367, 14368, 14371) (Fig. 2*B*).

The *E* of 181 genotypes ranged from 4.0–14.8 mmol m^{-2} s^{-1} with the mean value of 9.6. Thirty three genotypes showed high *E* > 11.9 mmol m^{-2} s^{-1} (Table 2), and 116 genotypes showed *E* between 7.4–11.8 μmol m^{-2} s^{-1}; they were classified as the medium transpiration genotypes. Thirty two genotypes showed the *E* < 7.4 mmol m^{-2} s^{-1} and were classified as the low transpiring genotypes (Table 3S). Among the highly transpiring, 7 genotypes (NRCG 14452, 14451, 14459, 14343, 14456, 14347, and 14345) showed the *E* > 14.0 mmol m^{-2} s^{-1}. Among genotypes classified as the low transpiring (NRCG 14388, 14496, 14395, and 14397), *E* was below 5.8 mmol m^{-2} s^{-1}. The genotypes with the highest and lowest *E* were NRCG 14345 and 14388, with their respective values of 14.84 and 4.00 mmol m^{-2} s^{-1} (Fig. 2*C*).

Water-use efficiency: The WUE based on P_N/E in germplasm ranged across 1.70–5.16 with a mean value of 3.09. Genotype NRCG 14482 showed the highest WUE, while genotype NRCG 14453 showed the lowest value (Table 4S). Twenty five genotypes showed the WUE greater than 3.8 (Table 2). Four genotypes (NRCG 14477, 14484, 14496, and 14482) showed the WUE above 4.84. Twenty seven germplasms had the low WUE (< 2.4) and of these genotypes, NRCG 14453, 14456, 14450, and 14451, showed the WUE below 1.84 (Fig. 2*D*).

SCMR: Among the 181 mini-core germplasm, the range of SCMR was 30–43 with an average of 38. The minimum value was found for genotype NRCG 14367, and the maximum value was observed in NRCG 14397. Thirty six genotypes showed the SCMR greater than 40 and these were grouped in the category of high SCMR (Table 2), while 24 showing the SCMR < 35 were assigned to the low SCMR and 121 were medium SCMR (Table 5S). NRCG 14479, 14488, 14412, 14370, 14390, 14489, and 14397 showed SCMR > 42, while the genotypes NRCG 14367, 14332, and 14425 showed the SCMR below 30 (Fig. 2*E*).

Chl fluorescence: The F_v/F_m value in mini-core germplasms ranged across 0.814–0.871 and the genotypes having F_v/F_m > 0.86 were categorized as high (Table 2). F_v/F_m < 0.84 were categorized as low and F_v/F_m values between 0.84–0.86 as medium (Table 6S). Furthermore, the F_v/F_m was the highest in NRCG 14412, while it was the lowest in NRCG 14329. The average value of F_v/F_m was 0.851 indicating that most of the plants were physiologically active without stress. Thirty five genotypes exhibited F_v/F_m > 0.86 and were categorized high, of which six genotypes (NRCG 14497, 14469, 14467, 14483, 14479, and 14412) showed the F_v/F_m > 0.865. Five genotypes (NRCG 14329, 14496, 14410, 14328, and 14366) in the low category showed F_v/F_m < 0.830 (Fig. 2*F*).

Correlation studies: There was a positive correlation between P_N and g_s, P_N and *E*, P_N and WUE, P_N and Chl fluorescence ratio of F_v/F_m, SCMR and F_v/F_m. The *E* showed positive correlation with g_s, while it was negatively correlated with WUE (Table 3).

Combination of various parameters: The efficient genotypes showing high values for P_N, g_s, *E*, WUE, SCMR, and F_v/F_m, were cross-checked and the genotypes showing high values in 2–5 parameters are listed in Table 4. There were a total of 54 genotypes which exhibited higher values in two traits, of these, 20 genotypes showed high value in three traits, and 7 genotypes, *i.e.*, NRCG 14386, 14435, 14463, 14464, 14474, 14493, 14505, and 14507 showed high values at least in four traits from those of P_N, g_s, *E*, WUE, SCMR, and F_v/F_m. There were no genotypes showing high value both for *E* and WUE. Two genotypes, NRCG 14507 and 14493, were quite promising, showing high values in five physiological traits.

Table 3. Linear correlation among different physiological traits for mini-core peanut germplasm. ** – relations significant at *P*=0.01 level. P_N – photosynthetic rate [μmol m^{-2} s^{-1}]; *E* – transpiration rate [mmol m^{-2} s^{-1}]; g_s – stomatal conductance [mmol m^{-2} s^{-1}]; WUE – water-use efficiency; SCMR – SPAD chlorophyll meter reading; F_v/F_m – maximum photochemical efficiency of PSII.

	P_N	g_s	*E*	WUE	SCMR	F_v/F_m
P_N	-					
g_s	0.640**					
E	0.411**	0.453**				
WUE	0.257**	–0.032	–0.748**			
SCMR	0.025	0.093	–0.164	0.138		
F_v/F_m	0.223**	0.152	0.066	0.076	0.203**	-

Table 4. Highly efficient genotypes on the basis of physiological traits. P_N – photosynthetic rate [μmol m^{-2} s^{-1}]; E – transpiration rate [mmol m^{-2} s^{-1}]; g_s – stomatal conductance [mmol m^{-2} s^{-1}]; WUE – water-use efficiency; SCMR – SPAD chlorophyll meter reading; F_v/F_m – maximum photochemical efficiency of PSII.

Traits with high values	Germplasm with high efficiencies	Total
P_N, g_s	14348, 14485, 14506, 14379, 14472, 14424, 14386, 14491, 14478, 14464, 1443, 14507, 14493, 14489, 14505, 14474	16
P_N, E	14360, 14405, 14407, 14408, 14413, 14424, 14506, 14435, 14459, 14507	10
P_N, WUE	14354, 14473, 14475, 14484, 14464, 14474, 14493, 14477, 14501, 14482, 14507	11
P_N, F_v/F_m	14373, 14459, 14472, 14478, 14483, 14477, 14501, 14505, 14507, 14474, 14493, 14435, 14489	13
P_N, SCMR	14491, 14386, 14464, 14507, 14493, 14505, 14474, 14489, 14482	9
g_s, E	14347, 14343, 14345, 14344, 14506, 14424, 14435, 14507, 14333, 14337	10
g_s, WUE	14463, 14493, 14507, 14464	4
g_s, SCMR	14489, 14386, 14466, 14463, 14491, 14505, 14493, 14464, 14507, 14505, 14467	11
g_s, F_v/F_m	14472, 14500, 14463, 14505, 14478, 14493, 14507, 14489, 14435, 14467	10
E, WUE		
E, SCMR	14507	1
E, F_v/F_m	14452, 14456, 14457, 14461, 14459, 14507, 14435	7
WUE, SCMR	14493, 14482, 14397, 14463, 14324, 14464, 14474, 14507, 14410	9
WUE, F_v/F_m	14462, 14487, 14497, 14410, 14463, 14477, 14501, 14474, 14493, 14507	10
SCMR, F_v/F_m	14357, 14409, 14412, 14422, 14467, 14410, 14463, 14505, 14507, 14474, 14493, 14479, 14489	13
P_N, g_s, E	14506, 14424, 14435, 14507	4
P_N, g_s, WUE	14493, 14464, 14507	3
P_N, g_s, SCMR	14386, 14491, 14505, 14493, 14464, 14507, 14489	7
P_N, g_s, F_v/F_m	14472, 14505, 14507, 14478, 14493, 14435	6
P_N, E, SCMR	14507	1
P_N, E, F_v/F_m	14459, 14507, 14435	3
P_N, WUE, SCMR	14464, 14474, 14493, 14482	4
P_N, WUE, F_v/F_m	14477, 14501, 14474, 14493, 14507	5
P_N, SCMR, F_v/F_m	14505, 14474, 14493, 14507, 14489	5
g_s, E, SCMR	14507	1
g_s, E, F_v/F_m	14435, 14507	2
g_s, SCMR, F_v/F_m	14489, 14463, 14505, 14493, 14507, 14467	6
WUE, SCMR, F_v/F_m	14410, 14463, 14474, 14493, 14507	5
WUE, SCMR, g_s	14464, 14463, 14507, 14493	4
WUE, g_s, F_v/F_m	14463, 14493, 14507	3
P_N, g_s, E, SCMR	14507	1
P_N, g_s, E, F_v/F_m	14507, 14435	2
P_N, g_s, WUE, F_v/F_m	14507, 14493	2
P_N, g_s, WUE, SCMR	14464, 14493, 14507	3
P_N, g_s, SCMR, F_v/F_m	14505, 14493, 14507	3
P_N, E, SCMR, F_v/F_m	14507	1
P_N, WUE, SCMR, F_v/F_m	14474, 14493	2
g_s, E, SCMR, F_v/F_m	14507	1
g_s, WUE, SCMR, F_v/F_m	14463, 14493, 14507	3
P_N, g_s, E, SCMR, F_v/F_m	14507	1
P_N, g_s, WUE, SCMR, F_v/F_m	14493	1

Discussion

A core collection is a subset of genotypes from the entire germplasm collection showing most of the available genetic diversity of the species (Brown 1989). The genus *Arachis* exhibits a considerable amount of morphological diversity consisting of 30 to 50 species (Gregory *et al*. 1973). Characterization of 504 Asian core peanut genotypes for morphological and phenological traits indicated high physiological diversity among these genotypes (Mallikarjunaswamy *et al*. 2006). In the present study, the mini-core peanut germplasm was studied for different physiological parameters and categorized in the high, medium, and low groups according to their physiological efficiencies.

The peanut shows maximum growth 7–13 weeks after emergence and it is the period for high, leaf-level gas exchange (Singh and Joshi 1993). Nautiyal *et al.* (1999)

reported that due to diurnal variations in photosynthesis and stomatal conductance, it is ideal to measure these parameters between 08:00–13:00 h in peanut leaves. The peanut leaves become less photosynthetically efficient after two weeks from their full expansion, hence, in this study, the measurement was made during the pod development stage (60–65 DAS) in the third fully matured leaf from the top.

In the present study, the P_N in mini-core genotypes showed the wide range of variation and 34 genotypes out of the total set were identified as photosynthetically efficient. The P_N value observed in the mini-core germplasm was relatively higher in this study than that observed earlier by Nautiyal *et al.* (1999) mainly due to a summer season crop with high PAR and sunny days without interruption of clouds. The average P_N of peanut and its wild relatives has been reported to be varied from 15.14–25.87 μmol(CO_2) m^{-2} s^{-1} in USA (Bhagsari and Brown 1976) and 12.62–15.78 μmol(CO_2) m^{-2} s^{-1} in India (Nautiyal *et al*. 1999). However, photosynthetic rate as high as 48.58 μmol(CO_2) m^{-2} s^{-1} has been also reported (Trachtenberg and McCloud 1976). Earlier reports on released peanut cultivars in our laboratory showed the crop yield was usually limited due to lower photosynthetic efficiency of individual genotypes (Nautiyal *et al.* 2012). Liu *et al*. (2012) suggested P_N and P_N/C_i as effective selection indexes for the seed yield that can be used in future breeding programmes in soybean. Moreover, the studies under elevated CO_2 showing enhancement of both leaf P_N and yield, provide a very strong indication that a sustained increase in leaf photosynthesis leads to increased crop yield (Ainsworth and Long 2005).

Variation in g_s was recorded in peanut mini-core germplasm collection; the genotypes varied in their morphological characteristics and due to this the variation in g_s was obvious. Earlier studies reported that peanut productivity could be increased by enhancing g_s in the cultivars with high P_N, and by lowering the canopy-air temperature difference (Nautiyal *et al.* 2012).

P_N and E are affected by boundary layer resistance in stomata and this determines the rate at which gases diffuse through it. In the present study, E of mini-core germplasm genotypes showed a wide variation and among the genotypes studied, 33 showed high E, and 32 showed low E. Increased transpiration efficiency, *i.e.*, the ratio of mass accumulation to transpiration, is often suggested as a critical factor which could be intervened for genetic improvement to increase crop yields in water-limited environments. However, component traits, *i.e.*, P_N, g_s, and biomass accumulation, contributing to transpiration efficiency, are more effective in using available water throughout the growing season to maximize ultimately growth and yield of the crop (Sinclair 2012). From this study, some of the genotypes with high E and P_N could be used in yield maximization.

The WUE showed high variability within the mini-core germplasm and 30 highly efficient genotypes with WUE > 3.8 were identified; it could be useful for limited water supply conditions. Belko *et al.* (2012) reported that in cowpea, water-saving traits are critical for reproduction and terminal drought tolerance. The genotypes, which are able to use limited water resources through a lower canopy conductance and E, grew better under water stress. The SCMR values indicate the Chl status of the genotypes and are positively correlated with Chl content (Samdur *et al*. 2000). Present study showed the wide variation in SCMR values in the 181 mini-core peanut genotypes. Our earlier work (Singh *et al*. 2003) also showed that the genotypes with SCMR value higher than 40 were highly tolerant to chlorosis and contained high Chl concentration which resulted in higher P_N.

The Chl fluorescence is considered a signature of photosynthesis (Schreiber 2004). It is a highly useful parameter both for laboratory and field studies without much flaws and misinterpretation (Roháček *et al*. 2008). Also, the F_v/F_m ratio is one of the important tools in determining damage to photosynthetic apparatus under drought stress (Rahbarian *et al*. 2011). In the present study, the F_v/F_m value in the mini-core germplasm genotypes ranged 0.81–0.87. The genotypes having F_v/F_m higher than 0.86 were categorized as high, while having F_v/F_m < 0.84 were marked as low Chl fluorescence genotypes. Cao and Isoda (2008) reported that the P_N and F_v/F_m were high in some of the peanut genotypes, which showed higher seed yields due to high radiation use efficiency later in the growing season. Under water stress, Shahenshah and Isoda (2010) found increase in leaf temperature and decrease in the Chl content and F_v/F_m, indicating the damage and down regulation of PSII in peanut.

The correlation of various physiological parameters showed a positive correlation between P_N and g_s, P_N and E, P_N and WUE, and P_N and F_v/F_m in the present study. The E showed positive correlation with g_s while it was negatively correlated with WUE. The traits, such as P_N and E, help in empirical peanut selection (Nigam *et al*. 2005). The transpiration efficiency, an important source of yield variation under drought, is directly correlated with SCMR (Krishnamurthy *et al.* 2007). It was also supported here by a strong relationship between SCMR and E. In peanut, WUE is correlated with SCMR and SLA (Songsri *et al*. 2009) and the association of SCMR with SLA and WUE can be a useful selection trait to screen peanut genotypes under water limited conditions. The SCMR value also showed a positive correlation with F_v/F_m in the present study. In cereals, some of researchers reported the correlation between Chl content and Chl fluorescence parameters that might influence the growth of the crops, because these parameters are closely related to the rate of carbon exchange in the leaf, especially under environmental stress (Araus *et al*. 1998, Guo and Li 2000, Fracheboud *et al*. 2004).

Wright *et al*. (1994) found a positive correlation between WUE and SCMR in peanut under drought. The SCMR is highly useful parameter, directly associated

with WUE, and it can be used as surrogate parameter for selection of WUE germplasms. Strong positive correlation in peanut was also shown by Bindu Madhva *et al*. (2003) between WUE and SCMR. The WUE is correlated with SCMR and SLA (Upadhyaya *et al.* 2011). Nigam and Aruna (2008) advocated that SCMR and SLA, which is surrogate of WUE, can be recorded after 60 d of crop growth and it helps breeders to evaluate large populations. However, it is better if it is done between 60–80 DAS (Upadhyaya *et al.* 2012). Genotype selection based on SCMR has also practical advantage over other parameters (Upadhyaya 2005).

A critical evaluation of the physiological parameters responsible for growth and biomass production in mini-core subset of the peanut genotypes revealed significant variation within the group and their subsequent identification of genotypes for high, medium, and low P_N, g_s, E, WUE, SCMR and F_v/F_m shall be of immense use in future breeding programme. The genotypes with high P_N and WUE, high P_N and SCMR, and high P_N and F_v/F_m can help in increasing productivity. Two genotypes, NRCG 14463 and NRCG 14493, found as superior for multiple traits, *i.e.*, WUE, P_N, g_s, and Chl content in the leaf, especially at the later stages of growth, could be useful for developing peanut varieties with a good yield potential under water limited conditions.

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