Genotypic variability in physiological, biomass and yield response to drought stress in pigeonpea

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Abstract Three pigeonpea (*Cajanus cajan* L. Millsp.) genotypes- GT-1, AKP-1 and PRG-158 with varying crop duration, growth habit and flowering pattern were evaluated for variability in their response for drought stress. Drought stress was imposed at initiation of flowering and the observations on biomass and seed yield parameters were recorded at harvest. The magnitude of response of individual component to drought stress was found to be genotype specific. Drought stress significantly decreased photosynthetic rate (P_N), transpiration rate (Tr) and relative water content (RWC) in all the genotypes, however the magnitude of reduction differed with genotype. With drought stress, the reduction of P_N was highest in GT-1 while reduction in Tr was highest in PRG-158. The genotype AKP-1, accumulated significantly higher concentrations of osmotic solutes especially proline under water deficit stress, this facilitated it to maintain higher relative water content (RWC) and lower malondialdehyde (MDA) content as compared to other genotypes. Drought stress also impacted biomass production and their partitioning to vegetative and reproductive components at harvest. There was significant variability between the genotypes for seed yield under drought stress while it was non-significant under well-watered condition. Drought stress enhanced flower drop and decreased flower to pod conversion resulting in reduced pod number and seed number in PRG-158 and GT-1. The genotype AKP-1 recorded superior performance for seed yield under stress environment due to its ability in

maintaining pod and seed number as well as improved test weight (100 seed weight). Under drought stress, significant positive association of seed yield with proline, seed number, pod number and test weight clearly indicating their role in drought tolerance.

Keywords *Cajanus cajan* · Drought stress · WUE · Biomass partitioning · Proline

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major food legume crop of the tropics and sub-tropics and it is the second most important pulse crop after chickpea in India. It is a nutritious high protein crop with high digestible protein (68 %), low in fat and sodium with no cholesterol and has high dietary fibers. Interest in this crop is growing in many other countries because of its multiple uses as a source of food, feed, fuel, and fertilizer (Wilson et al. 2012).

Abiotic stresses like drought, salinity, high and low temperatures and water logging have adverse effects on crop productivity and causes severe production losses mainly in arid and semi arid tropical regions (Abdul et al. 2006; Rodriguez et al. 2005; Zhang et al. 2006). Drought is the major constraint which reduces the crop productivity worldwide especially in rainfed areas. When plants are exposed to abiotic stresses, organic solutes which includes total soluble carbohydrates, amino acids, proline and betaines tend to accumulate at higher concentrations (Hasegawa et al. 2000). It is well established that this will help in maintaining plant water relations, removal of free radicals and maintenance of ionic homeostasis as well as stabilization of macromolecules such as proteins, protein complexes and membranes (Gilbert et al. 1998). Accumulation of proline in plants is one of the known

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tolerance mechanism to drought stress which plays an important role in cellular osmotic adjustment, thereby protects and stabilizes essential cell components, photosynthetic apparatus and detoxifies reactive oxygen species (Ashraf and Foolad 2007). The osmotic adjustment reduces the cellular osmotic potential in drought stressed plants and contributes to the maintenance of cell turgor, thereby reducing the ill effects of drought stress on stomatal opening, photosynthesis and cell expansion (Serraj and Sinclair 2002).

Drought stress lowers the growth and yield as plants tend to reduce stomatal opening under moisture deficit stress in order to conserve water, consequently decreasing the assimilation rate (Kawamitsu et al. 2000). Moisture deficit reduces the fresh and dry biomass production of crop plants (Farooq et al. 2009) and plant productivity under drought stress is strongly related to the processes of temporal biomass distribution and partitioning (Kage et al. 2004). Angra et al. (2010) reported that water deficit during seed development considerably limited crop yield in soybean genotypes. It is known that pigeonpea thrives well under drought prone condition, however there is great genotypic variability for yield performances. Adopting suitable agronomic practices along with drought tolerant genotypes is necessary to improve the productivity of pigeonpea from rainfed areas in order to meet the demand of growing population. The present assessment of pigeonpea genotypes will help to identify the physiological and biomass parameters contributing to the drought tolerance.

Material and methods

Plant material and experimental conditions

Three pigeonpea (*Cajanus cajan* L. Millsp.) genotypes—GT-1, AKP-1 and PRG-158 with varying crop duration, growth habit and flowering pattern were selected to assess their response to drought stress in terms of biomass production, partitioning and yield. GT-1 is short duration genotype with spreading plant habit and determinate flowering pattern, while AKP-1 is short medium genotype with spreading plant habit and semi-determinate flowering pattern and the seeds of these two genotypes were obtained from Indian Institute of Pulse Research, Kanpur. PRG-158 is medium duration genotype with semi-spreading plant habit and semi-determinate flowering pattern and the seeds of this genotype were procured from Regional Agricultural Research Station, Palem. A field experiment was conducted during Kharif 2014 at Central Research Institute for Dryland Agriculture (CRIDA), located between 17.20°N latitude and 78.30°E longitude, Hyderabad, Telangana (India). The seeds were treated with Thiram and inoculated with Rhizobium. For raising a good pigeonpea crop, entire quantity of recommended dose of

fertilizer (25:50::N: P₂O₅ kg ha⁻¹) was applied as basal dose at the time of sowing and regular weeding and plant protection measures were taken care. Complete randomized block design was adopted with spacing of 0.30 m within row and 0.90 m between rows with 3 replications of each genotype for each moisture level.

Two moisture levels were maintained, one as well-watered (WW) control with regular irrigations and the other as water deficit (WD) treatment. A rainless period of 20 days from 95 to 115 days after sowing corresponded with flowering and pod setting stage of water deficit (WD) treatment was utilized to create moisture deficit stress and once wilting symptoms appeared stress was released by irrigating the WD plots. Soil moisture was determined by gravimetric method (Reynolds 1970) before providing irrigation in water deficit plots. The soil moisture reduced from field capacity of 16 % to 5.6 %.

Physiological observations were recorded during stress and one week after stress relief in both well-watered control and water deficit treatments. The photosynthetic measurements, relative water content (RWC), malondialdehyde (MDA) and proline contents were recorded from the third leaf of all the genotypes in both WW and WD treatments during and after relieving of moisture stress. During the crop growth period, the average minimum and maximum temperatures were 17 °C and 33 °C respectively and crop received 223 mm rainfall in 12 rainy days with >2.5 mm. The crop was harvested at its physiological maturity and biomass and yield parameters of each genotype were recorded on randomly selected three plants from both moisture levels.

The main objective of the present study was to quantify the variability in response of the selected pigeonpea genotypes to drought stress in terms of phenological, physiological, biomass and yield parameters and to identify the traits imparting tolerance.

Phenological observations

The phenological observations of days to 50 % flowering and 50 % podding of individual genotype were recorded for both moisture levels.

Physiological parameters

Net photosynthetic rate (P_N), stomatal conductance (g_s) and transpiration rate (Tr) were measured at flowering stage with a portable photosynthesis system (LI-6400, LI-COR, Nebraska, USA). The observations were made between 10:00 and 12:00 h on fully expanded young leaves of three randomly selected plants for each genotype at well-watered and water deficit conditions with irradiance set at 1200 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$. Water use efficiency (WUE) was calculated as the ratio of P_N and Tr using the formula $\text{WUE} = P_N/Tr$.

Relative water content (RWC)

Fully expanded third leaf from the top of the main stem of three plants from each well-watered and water deficit treatment were selected to measure the relative water content (RWC). Initial fresh weight of leaves was recorded and then they were soaked in distilled water for 8 h and blotted for surface drying and water saturated leaf turgid weight was determined. The samples were oven-dried at 60 °C until constant weights were attained and leaf dry weight could be determined. RWC was calculated based on the formula suggested by Gonzalez and Gonzalez-Vilar (2001) as follows.

$$\text{RWC}(\%) = (\text{FW} - \text{DW}) / (\text{TW} - \text{DW}) \times 100$$

Where, FW is the sample fresh weight, TW is turgid weight and DW is dry weight.

Determination of osmotic potential

The unused leaflets of the same trifoliate leaf used for RWC measurements were excised and dipped in liquid nitrogen and subsequently stored at –80 °C until analysis of leaf osmotic potential. Frozen tissue samples were thawed and cell sap was squeezed out from leaves, which was subsequently analyzed for osmotic potential (Scholander et al., 1966) using a vapor pressure osmometer (Wescor- 5500 Wescor Inc., USA)

Determination of proline content

Proline was extracted from 0.5 g of fresh leaf material in 3 % (w/v) aqueous sulphosalicylic acid and estimated using ninhydrin reagent (Bates et al. 1973). The absorbance of fraction with toluene aspirated from liquid phase was measured spectrophotometrically at 520 nm. Proline concentration was determined using a calibration curve and expressed as µg/g F.Wt.

Malondialdehyde (MDA) content

The lipid peroxidation (LP) level was measured in terms of malondialdehyde (MDA) content as per Heath and Packer (1968). The absorbance of MDA content was recorded at 532 nm and the non-specific absorption at 600 nm was subtracted. The MDA content was calculated using its absorption coefficient of 155 mM/cm and expressed as mg/g F. Wt.

Biomass and yield parameters

At harvest, three plants of each genotype from irrigated and drought stress treatment were uprooted carefully and separated into different plant components. The roots were washed carefully to made free from adhered soil particles and used

for its biomass estimation. The biomass of leaves, stem and roots was measured after drying them at 60 °C in hot air oven till constant weights were attained. The data on per plant yield parameters such as pod number, pod weight, seed number, seed yield and test weight (100 seed weight) were recorded. Total biomass, vegetative biomass, reproductive biomass and HI were calculated from the recorded data sets.

The analysis of variance (ANOVA) was carried out to assess the significance of genotypes, moisture levels and their interaction.

Results and discussion

The moisture levels significantly influenced the response of physiological, biomass and yield parameters (Tables 1 and 2) in selected pigeonpea genotypes.

Effect of drought stress on phenology of flowering and podding

Drought stress influenced the phenology of flowering and podding in the selected pigeonpea genotypes. With drought stress, 50 % flowering was early by 3 days in both short and short medium genotypes- GT-1 and AKP-1 while it was early by 2 days in medium duration genotype PRG-158. Similarly, the earliness in 50 % podding was by one day in GT-1 and AKP-1 and no change in PRG-158 as compared with their well-watered (WW) controls.

Effect of drought stress on physiological parameters

The ANOVA results revealed that the genotypes differed significantly ($P < 0.05$) for stomatal conductance, while the effect of moisture levels was highly significant ($P < 0.01$) for photosynthetic rate, stomatal conductance, transpiration rate and WUE (Table 1). The interaction of genotypes and moisture levels was highly significant ($P < 0.01$) for stomatal conductance, WUE and significant ($P < 0.05$) for transpiration rate.

The WD condition significantly reduced the photosynthetic rate of selected three genotypes. The mean P_N values were 28.2, and 18.9 µmol CO₂ m⁻² s⁻¹ with PRG-158, 30.8 and 19.5 µmol CO₂ m⁻² s⁻¹ with AKP-1 while 31.5 and 17.7 µmol CO₂ m⁻² s⁻¹ with GT-1 under WW and WD conditions respectively. However, when moisture stress was relieved, the recovery of P_N was complete with genotypes PRG-158 and GT-1 while only 80 % recovery was observed with genotype AKP-1. Though the impact of WD on P_N was highest with GT-1 (43.3 %), it is interesting to observe that this genotype recovered to normal level once stress was relieved. While the decrease in P_N of the PRG-158 (33 %) and AKP-1 (37 %) was moderate with WD, only PRG-158

Table 1 Performance of physiological and biochemical parameters of pigeonpea genotypes under well-watered, water deficit and stress release conditions

Genotypes	PRG-158				AKP-1				GT-1				Mean sum of square			
	WW	WD	Stress release		WW	WD	Stress release		WW	WD	Stress release		G df(2)	ML df(2)	G*ML df(4)	Error df(16)
P_N [$\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$]	28.2	18.9	29.2	30.8	30.8	19.5	24.9	31.5	31.5	17.7	29.9	4.169	332.689**	14.450	5.902	
g_s [$\text{mol m}^{-2} \text{ s}^{-1}$]	0.300	0.075	0.111	0.292	0.292	0.122	0.175	0.236	0.236	0.109	0.161	0.003*	0.073**	0.003**	0.001	
Tr [$\text{mmol H}_2\text{O m}^{-2} \text{ s}^{-1}$]	6.05	2.77	6.13	6.04	6.04	3.92	4.63	6.84	6.84	3.60	5.49	0.354	18.745**	1.162*	0.295	
WUE [$\mu\text{moles CO}_2 \mu\text{mol H}_2\text{O}^{-1}$]	4.81	7.03	4.90	5.56	5.56	4.98	5.41	4.65	4.65	4.97	5.47	0.536	1.651*	2.192**	0.410	
RWC (%)	87.12	70.69	88.83	90.59	90.59	75.37	90.36	87.17	87.17	70.09	87.92	36.360**	830.696**	2.497	1.475	
Osmotic potential (MPa)	-1.113	-1.803	-1.513	-0.956	-0.956	-2.631	-1.488	-0.927	-0.927	-1.616	-1.431	0.306**	2.335**	0.302**	0.000	
Proline ($\mu\text{g g}^{-1} \text{ F.wt}$)	59.75	179.75	56.75	59.75	59.75	241.92	55.75	66.42	66.42	180.67	58.33	1089.01**	59,967.70**	1384.00**	3.179	
MDA ($\text{mg g}^{-1} \text{ F.wt}$)	13.31	22.65	15.72	14.48	14.48	20.99	17.63	13.87	13.87	21.08	17.97	0.603*	133.953**	3.724**	0.106	

*Significant at 0.05 % and **significant at 0.01 %; WW = Well-Water, WD = Water Deficit, ML = Moisture levels, G = genotypes, df = degrees of freedom. P_N = photosynthetic rate, g_s = stomatal conductance, Tr = transpiration rate, WUE = water use efficiency, OP = osmotic potential, RWC = relative water content, MDA = malondialdehyde content

recovered to normal level once stress was relieved. Kalariya et al. (2013) reported that the reduction and recovery in photosynthetic rate differed significantly among the groundnut cultivars at water deficit and stress relief conditions.

Drought stress reduced stomatal conductance significantly and it ranged from 54 % (GT-1) to 75 % (PRG-158). When moisture stress was relieved, recovery of stomatal conductance was still lower by 63 % in PRG-158, 40 % in AKP-1 and 32 % in GT-1. Lisha et al. (2015) reported that drought stress reduced the photosynthetic rate and stomatal conductance in four *Hevea* clones. Canopy photosynthesis is reduced by moisture stress mainly due to reduction in stomatal conductance in order to reduce transpiration and as a consequence, the entry of carbon dioxide is also reduced (Singh 2011). Among the selected three genotypes, the highest reduction (55 %) in transpiration rate with drought stress was recorded by PRG-158, however with stress release it recovered completely. While the reduction in transpiration rate of AKP-1 (35 % and 23 %) and GT-1 (48 % and 20 %) was moderate but their recovery was incomplete. Highest WUE at drought stress was recorded by PRG-158 as the reduction of Tr was much higher than reduction in P_N . Gilbert et al. (2011) concluded that when soybean genotypes exposed to drought stress, WUE increased due to variation in photosynthetic capacity and stomatal conductance. In the present investigation also, the genotype PRG-158 lowered its stomatal conductance and transpiration rate to maximum extent with less impact on photosynthetic rate and recovered to the normal status on stress release revealing its adaptive nature to the drought stress.

The relative water content of pigeonpea genotypes varied from 85 % to 90 % under well-watered condition and decreased with imposition of drought stress. Among the selected genotypes, highest decrease (25 %) of RWC was recorded with GT-1 followed by PRG-158 (23 %) and AKP-1 (20 %) as compared to the respective well-water controls. However, all three pigeonpea genotypes recovered completely when stress was relieved. Drought stress decreased RWC of groundnut leaves as compared with irrigated controls (Kalariya et al. 2013).

Effect of drought stress on osmotic potential

Accumulation of compatible solutes is known to impart drought stress tolerance through active reduction in osmotic potential. Among three pigeonpea genotypes, accumulation of compatible solutes was higher with AKP-1 (175 %) followed by GT-1 (75 %) and PRG-158 (62 %) and it resulted in reduction in osmotic potential. However, with stress relief it reduced to the original level of well-water control. Farouk et al. (2013) reported that higher accumulation of osmolytes in cowpea crop under drought stress reduced the osmotic potential.

Table 2 Performance of biomass and yield parameters of pigeonpea genotypes under well-watered and water deficit conditions

Genotypes	PRG-158		AKP-1		GT-1		Mean sum of square			
	WW	WD	WW	WD	WW	WD	G df(2)	ML df(1)	G*ML df(2)	Error df(10)
Biomass/pl										
Leaf dry weight (g)	13.70	8.46	16.40	14.57	18.41	15.83	58.594**	45.761**	4.904	3.271
Stem dry weight (g)	54.47	41.50	45.93	45.70	76.92	59.36	910.167**	473.294**	120.936**	10.258
Root dry weight (g)	11.14	7.72	12.78	9.63	16.50	12.97	43.755**	51.342**	0.037	1.643
Vegetative biomass (g)	79.30	57.70	75.10	69.90	111.80	88.20	1762.534**	1278.494**	154.384*	23.825
Reproductive biomass(g)	69.26	36.27	64.50	58.41	70.19	44.67	113.780**	2084.427**	288.482**	9.714
Total Biomass (g)	148.57	93.94	139.61	128.31	182.02	132.83	2020.002**	6624.005**	835.387**	26.596
Yield parameters/pl										
Pod number	151.0	85.4	146.4	118.6	104.4	86.6	2084.802**	6197.556**	950.569**	34.813
Number of seed	446.0	243.0	360.0	322.0	400.0	250.0	631.891*	76,550.019**	10,607.102**	101.051
Pod weight (g)	69.26	36.27	64.50	58.41	70.19	44.67	113.780**	2084.427**	288.482**	9.714
100 seed weight (g)	10.57	10.25	12.31	14.43	11.87	11.60	12.942*	1.227	2.802	2.402
Seed yield (g)	46.42	23.14	45.30	40.23	46.70	28.14	99.308	1100.430**	134.162*	27.835
Harvest Index (%)	31.24	24.67	32.42	31.33	25.73	21.15	106.942**	74.868*	11.558	11.930

* Significant at 0.05 % and **significant at 0.01 %; WW = Well-Water, WD = Water Deficit, ML = Moisture levels, G = genotypes, df = degrees of freedom

Effect of drought stress on proline content

Drought stress induced higher accumulation of proline was observed in all genotypes. Higher accumulation of proline was recorded in AKP-1 (313 %) followed by GT-1 (217 %) and PRG-158 (203 %), however, it decreased to normal level with stress release in all three genotypes. Baroowa and Gogoi (2012) also reported that drought induced accumulation of proline in leaves of blackgram and greengram. Priyanka et al. (2010) isolated a hybrid-proline-rich protein gene (*CcHyPRP*) from pigeonpea plants subjected to drought stress and validated its function in *Arabidopsis*. Srinath et al. (2014) reported that abiotic stress tolerance through increased levels of antioxidant enzymes, proline, and reducing sugars in transgenic *Arabidopsis* with gene (*CcCDR*) isolated from drought stressed pigeonpea.

Effect of drought stress on MDA content

Lipid peroxidation is used as an index of oxidative damages caused by various abiotic stresses in plants. Stress induced reactive oxygen species (ROS) reacts with lipids and leads to the formation of highly active peroxy radical, this in turn starts chain propagation reaction of lipid peroxidation. Therefore the resultant MDA content can be used as indicator of stress-induced damages at the cellular level. The highest increase (70 %) in MDA content with drought stress was recorded with PRG-158 followed by GT-1 (52 %) and AKP-1 (44 %), however it reduced to normal level in all the genotypes with stress release. Vijayalakshmi et al. (2012) reported that lower MDA content under drought stress in pearl millet

hybrid than its parents revealing its ability to maintain relatively better membrane stability under stressful environment.

Effect of drought stress on dry matter accumulation and partitioning

The dry matter accumulation and its partitioning in three pigeonpea genotypes was quantified both under well-watered and water deficit conditions. Genotypes and moisture levels are highly significant ($P < 0.01$) for all the biomass parameters. The interaction of genotypes and moisture levels were highly significant ($P < 0.01$) for stem biomass, reproductive biomass and total biomass while significant ($P < 0.05$) for vegetative biomass and non-significant for leaf and root biomass (Table 2).

Among the three genotypes, highest leaf (18.4 & 15.8 g/pl), stem (76.9 & 59.4 g/pl), root (16.5 & 13.0 g/pl), total biomass (182 & 133 g/pl) was registered with GT-1 under both irrigated and drought stress conditions. With the drought stress, the range of reduction in leaf biomass was from 12 % (AKP-1) to 38 % (PRG-158), stem biomass was 1 % (AKP-1) to 24 % (PRG-158), root biomass was 22 % (AKP-1) to 30 % (PRG-158) and total biomass was 8 % (AKP-1) to 37 % (PRG-158). Under irrigated conditions, GT-1 recorded the highest per se vegetative (112 g/pl) and reproductive biomass (70 g/pl) and it also maintained highest vegetative biomass (88 g/pl) under stress condition though moisture deficit reduced both vegetative and reproductive biomass. The impact of drought stress was less on AKP-1 as the reduction of vegetative and reproductive biomass was the lowest (7 % & 10 %) as compared

Table 3 Correlation analysis for physiological, biomass and yield parameters of pigeonpea genotypes under well-water condition

Variables	P _N	g _s	Tr	WUE	Proline	OP	RWC	MDA	LDW	SDW	RDW	VBM	RBM	TBM	Pod No.	Seed No	100 seed weight	Seed yield	HI
P _N	1.000	-0.743	0.652	0.152	0.667	-0.998**	0.322	0.726	0.981*	0.163	0.485	0.586	-0.169	0.151	-0.730	-0.769	0.899	-0.127	-0.535
g _s		1.000	-0.991**	0.546	-0.994**	0.701	0.393	-0.081	-0.857	-0.780	-0.945	-0.977*	-0.532	-0.773	0.999**	0.145	-0.377	-0.567	0.962*
Tr			1.000	-0.648	0.999**	-0.605	-0.506	-0.045	0.785	0.853	0.979*	0.996**	0.635	0.847	-0.994**	-0.018	0.257	0.667	-0.989**
WUE				1.000	-0.633	-0.213	0.984*	0.789	-0.038	-0.950*	-0.790	-0.711	-0.999**	-0.953*	0.562	-0.749	0.568	-0.999**	0.752
Proline					1.000	-0.620	-0.490	-0.026	0.797	0.843	0.974*	0.994**	0.620	0.837	-0.996**	-0.037	0.275	0.653	-0.986**
OP						1.000	-0.379	-0.767	-0.968*	-0.102	-0.430	-0.535	0.229	-0.090	0.687	0.806	-0.924	0.188	0.482
RWC							1.000	0.884	0.135	-0.881	-0.671	-0.578	-0.987*	-0.887	0.410	-0.852	0.702	-0.980*	0.627
MDA								1.000	0.582	-0.559	-0.248	-0.130	-0.800	-0.569	-0.062	-0.997**	0.953*	-0.774	0.191
LDW									1.000	0.348	0.642	0.729	0.021	0.336	-0.847	-0.633	0.800	0.063	-0.686
SDW										1.000	0.941	0.895	0.944	0.999**	-0.792	0.504	-0.283	0.957*	-0.920
RDW											1.000	0.992**	0.779	0.937	-0.951*	0.185	0.055	0.805	-0.998**
VBM												1.000	0.699	0.889	-0.981**	0.067	0.173	0.728	-0.998**
RBM													1.000	0.948	-0.548	0.760	-0.582	0.999**	-0.741
TBM														1.000	-0.785	0.515	-0.294	0.961*	-0.915
Pod No															1.000	0.126	-0.360	-0.583	0.967*
Seed no																1.000	-0.970*	0.731	-0.127
100 seed weight																	1.000	-0.547	-0.113
Seed yield																		1.000	-0.769
HI																			1.000

P_N = photosynthetic rate, g_s = stomatal conductance, Tr = transpiration rate, WUE = water use efficiency, OP = osmotic potential, RWC = relative water content, MDA = malondialdehyde content, LDW = leaf dry weight, SDW = shoot dry weight, VBM = vegetative biomass, TBM = total biomass, HI-harvest index

*Significant at 0.05 % and **significant at 0.01 %

Table 4 Correlation analysis for physiological, biomass and yield parameters of pigeonpea genotypes under water deficit condition

Variables	P _N	g _s	Tr	WUE	Proline	OP	RWC	MDA	LDW	SDW	RDW	VBM	RBM	TBM	Pod No.	Seed No	100 seed weight	Seed yield	HI
P _N	1.000	0.088	0.103	0.177	0.756	0.865	0.827	0.129	-0.105	0.997**	0.234	-0.726	0.983*	0.903	0.743	0.708	0.550	0.550	0.938
g _s		1.000	0.999**	-0.964*	0.718	0.576	0.632	-0.976*	0.981*	0.015	0.989*	0.619	0.265	0.507	0.731	0.765	0.880	0.880	0.427
Tr			1.000	-0.960*	0.728	0.587	0.643	-0.972*	0.978*	0.029	0.991**	0.608	0.278	0.520	0.741	0.774	0.887	0.887	0.440
WUE				1.000	-0.508	-0.339	-0.405	0.998**	-0.997**	0.249	-0.914	-0.805	-0.001	-0.262	-0.525	-0.568	-0.723	-0.723	-0.173
Proline					1.000	0.982*	0.993**	-0.550	0.570	0.706	0.813	-0.100	0.861	0.964*	0.999**	0.997**	0.962*	0.962*	0.935
OP						1.000	0.997**	-0.385	0.407	0.825	0.690	-0.284	0.940	0.996**	0.978*	0.967*	0.894	0.894	0.985*
RWC							1.000	-0.449	0.470	0.784	0.739	-0.216	0.914	0.988*	0.990**	0.982*	0.924	0.924	0.970*
MDA								1.000	-0.999**	0.202	-0.933	-0.775	-0.049	-0.308	-0.566	-0.607	-0.756	-0.756	-0.220
LDW									1.000	-0.178	0.942	0.759	0.073	0.331	0.586	0.626	0.772	0.772	0.244
SDW										1.000	0.162	-0.775	0.968*	0.869	0.692	0.655	0.487	0.487	0.910
RDW											1.000	0.497	0.404	0.629	0.824	0.851	0.940	0.940	0.555
VBM												1.000	-0.592	-0.361	-0.081	-0.030	0.173	0.173	-0.444
RBM													1.000	0.965*	0.851	0.823	0.690	0.690	0.985*
TBM														1.000	0.958*	0.943	0.855	0.855	0.995**
Pod No															1.000	0.998**	0.957*	0.967*	0.928
Seed no																1.000	0.971*	0.978*	0.908
100 seed weight																	1.000	0.999**	0.804
Seed yield																		1.000	0.783
HI																			1.000

P_N = photosynthetic rate, g_s = stomatal conductance, Tr = transpiration rate, WUE = water use efficiency, OP = osmotic potential, RWC = relative water content, MDA = malondialdehyde content, LDW = leaf dry weight, SDW = shoot dry weight, VBM = vegetative biomass, TBM = total biomass, HI = harvest index.

* significant at 0.05 % and **significant at 0.01 %

with well-watered control and it could able to maintain highest per se reproductive biomass (58 g/pl) even under stress condition. Rajababu et al. (2011) reported that with moisture deficit conditions dry matter production and root to shoot ratio were highly effected in groundnut while decreased biomass of almost all genotypes of sunflower (Tahir and Mehid 2001). In Bambara groundnuts, Vurayai et al. (2011) observed that shoot: root ratio was significantly reduced by water stress imposed at vegetative, flowering and pod filling stages.

Effect of drought stress on seed yield

Genotypes are highly significant ($P < 0.01$) for number of pods, number of seeds, pod weight and test weight while non-significant for seed yield. Moisture levels are highly significant ($P < 0.01$) for seed yield, number of pods, number of seeds and pod weight. The interaction of genotypes and moisture levels are highly significant for number of pods, number of seeds, pod weight and significant for seed yield (Table 2).

The seed yield of three genotypes was similar under irrigated condition whereas the reduction in seed yield varied with genotypes when drought stress was imposed. Drought stress reduced the seed yield from 46.4 g/pl to 23.14 g/pl of PRG-158, 45.3 g/pl to 40.23 g/pl of AKP-1 and 46.7 g/pl to 28.14 g/pl of GT-1. The reduction in seed yield due to drought stress was highest with GT-1 (40 %) and least with AKP-1 (11 %). It was observed that reduced seed yield of these pigeonpea genotypes with drought stress were due to reduced pod number or seed number. Among the genotypes, AKP-1 demonstrated lowest reduction in seed yield with drought stress due to better pod number and seed number as well as improved test weight, clearly indicating its ability in partitioning of biomass to economic components even under stressful environments. The proportioning of biomass to reproductive components of pigeonpea was also affected by drought stress and highest impact was observed with PRG-158 with a 21 % reduction in HI while AKP-1 able to maintain it. The reduced seed yield in soybean under water stress condition was due to fewer pods and seeds per unit area (Specht et al. 2001). Hence, the exposure of crop to dry spells during flowering stage appears more critical on the yield aspects of pigeonpea crop, however genotypic variability exists. Jongrunklang et al. (2008) observed that drought stress had reduced total dry matter, pod yield and leaf area in peanut genotypes. Mafakheri et al. (2010) also reported that highest seed yield under drought stress was obtained in drought tolerant chickpea cultivars and lowest in drought sensitive ones.

Simple correlation coefficient analysis revealed that various biomass, physiological and biochemical parameters association with seed yield varied with moisture levels. Seed yield had significantly positive association with stem biomass, pod weight, reproductive biomass and total biomass under well-

water conditions while significantly negative association with WUE and RWC (Table 3). The association of seed yield was significantly positive with proline content, seed number, pod number and test weight under water deficit condition indicating that such relationships can be positively attributed to drought tolerance in pigeonpea genotypes (Table 4).

From the above observations it can be concluded that the genotype AKP-1 a short-medium duration genotype with spreading growth habit and semi-determinate flowering pattern performed better even under drought stress condition as it able to maintain better pod and seed number with lowest reduction of yield contributing characters and improved 100 seed weight. This pigeonpea genotype accumulated highest proline content during stress there by able to maintain RWC and lower levels of MDA which enabled it to maintain reproductive vigour even under moisture deficit condition.

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