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GENETIC VARIABILITY AND MORPHO-PHYSIOLOGICAL RESPONSE OF COWPEA (*VIGNA UNGUICULATA* (L.) WALP) GENOTYPES UNDER MOISTURE STRESS

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ABSTRACT

Cowpea (*Vigna unguiculata* (L.) Walp) is a nutritionally rich and agronomically valuable legume cultivated widely across tropical and subtropical regions. The present investigation was carried out to evaluate the response of thirty-five cowpea genotypes under control and moisture stress conditions with respect to morphological, physiological, biochemical, and genetic parameters associated with drought tolerance. Four seeds of each accession were grown in pots. Water stress was imposed by withholding irrigation until the relative water content reached 70% and a control set consisting of all genotypes was maintained under well-irrigated conditions. Under control conditions, all genotypes recorded higher values for growth-related traits compared to moisture stress conditions. Significant variation was observed among genotypes under drought stress for root length, shoot length, root dry weight, shoot dry weight, proline content, chlorophyll content, and superoxide dismutase (SOD) activity. Genetic parameter analysis revealed high phenotypic and genotypic coefficients of variation for root dry weight, proline content, root length, shoot length, shoot dry weight, and chlorophyll content. High heritability coupled with high genetic advance was recorded for most traits, suggesting the predominance of additive gene action and the scope for effective selection under drought stress. Superoxide dismutase showed moderate heritability and genetic advance. Correlation analysis indicated strong positive associations between root length and root dry weight at both phenotypic and genotypic levels. Chlorophyll content showed a negative correlation with proline content, while proline content was positively correlated with SOD activity. Based on higher proline accumulation under moisture stress, the genotypes CP-6, CP-8, Vamban-3, DC-15, IC-201079 and CP-12 were identified as drought-tolerant. These genotypes may be utilized in future cowpea breeding programmes aimed at improving drought tolerance.

***Keywords* :** Cowpea, drought stress, proline, chlorophyll, super oxide dismutase.

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp) is an important grain legume crop with immense nutritional, agronomic and economic value. It belongs to the family Fabaceae, has a diploid chromosome number of 2n=22 and is widely cultivated as a crop of global importance (Duraipandian *et al.*, 2022). The crop is also known by several other names, including southern pea, black-eyed pea, and crowder pea (Aghora *et al.*, 2024). Cowpea is one of the most ancient crops known to humanity and has been grown across tropical and subtropical regions (Patel *et al.*, 2022). It constitutes a major portion of the daily diet for many populations in Asia, Africa, Central and South America (Osiptan *et al.*, 2021). Cowpea is grown worldwide, covering an extensive area of 15.19 Mha, yielding approximately 9.77 Mt annually, with an impressive yield of 6.4 t/ha (FAOSTAT, 2024).

The important components that contribute to improving cowpea yield potential include the number of pods per plant, pod length, seeds per pod and seed size (Patil *et al.*, 2015). Key traits such as the number of seeds and pods per plant, plant height, seed size and grain yield can be used as selection indices to guide future yield improvement programs for cowpea (Thapa *et al*., 2021).

A major constraint in cowpea production is the occurrence of drought in semi-arid tropics primarily due to erratic rainfall in the beginning and towards the end of the rainy season. Cowpea is often exposed to drought stress during both the early and late growth stages leading to substantial reduction in grain yield as well as biomass production (Nkomo *et al.*, 2021). Research suggests that the cowpea possesses a relatively high level of drought tolerance compared to other crops, enabling it to withstand dry environmental conditions to some extent (Santos *et al*., 2020). To develop superior cowpea varieties, breeders must have a thorough understanding of genetic variability, heritability, and genetic advance to make informed selections (Senthilkumar *et al*., 2024). In this context, the assessment of genetic parameters such as phenotypic and genotypic variability, heritability, genetic advance, and correlation among traits assumes critical importance. Therefore, a systematic evaluation of cowpea genotypes under drought stress conditions is necessary to identify resilient and high-yielding genotypes.

Materials and Methods

The experimental material comprised of thirty-five grain cowpea accessions collected from the AICRP on Pulses, Regional Agricultural Research Station, Pattambi, Kerala Agricultural University. The particulars of the accessions evaluated in the present study are illustrated in Table 1. The experiments were conducted at College of Agriculture, Vellayani located 8.5° N, longitude of 76.9°E and an altitude of 96 m above mean sea level.

Table 1 : List of grain cowpea genotypes used in the study

Genotypes	**Name of genotype**	**Genotypes**	**Name of genotype**
T1	Pant lobia-3	T23	Kanakamoni
T2	DC-15	T24	T_4(AVT)
T3	Vamban-3	T25	CP$_{15}$(IVT)
T4	CHESCP-17	T26	CP-6
T5	PGCP-6	T27	CP-7
T6	IC-201079	T28	CP-12
T7	CP-15	T29	CP-8
T8	CP-14	T30	CP-10
T9	PCP	T31	CP$_9$(IVT)
T10	T_7(AVT)	T32	TC-901
T11	T_6(AVT)	T33	CP-3
T12	T_1(AVT)	T34	CP-11
T13	T_2(AVT)	T35	CP-1
T14	T_8(AVT)		
T15	T_5(AVT)		
T16	T_3(AVT)		
T17	CPP-119		
T18	KBC-4		
T19	PGCP-63		
T20	KBC-9		
T21	CP$_4$(IVT)		
T22	CP-13		

The pot experiment was carried out from March to June 2025 using a Completely Randomized Design, comprising thirty-five grain cowpea accessions with three replications. Four seeds of each accession were grown in pots. Water stress was imposed by withholding irrigation until the relative water content reached 70% as given by Hayatu *et al.* (2014). A control set consisting of all genotypes was maintained under well-irrigated conditions. Observations were recorded on three randomly selected plants from each genotype for various morpho-physiological observations, including root length at drought stress, shoot length at drought stress, root dry weight at drought stress, shoot dry weight at drought stress, proline content, chlorophyll content and super oxide dismutase.

The data were analyzed using analysis of variance (ANOVA) following the procedure described by Fisher (1935) for testing the significance of genotypic differences. PCV and GCV were calculated as suggested by Burton and DeVane (1953), whereas broad-sense heritability and genetic advance as percentage of mean were estimated using the formulas of Allard (1960) and Johnson *et al.* (1955), respectively. Correlation analysis among traits was carried out following the method described by Falconer (1964). Statistical analyses for the estimation of genetic parameters and correlation among traits were carried out using KAURAISINS software.

Results

Mean performance of thirty-five cowpea genotypes for root length, shoot length, root dry weight, shoot dry weight, proline content, chlorophyll content, and superoxide dismutase (SOD) activity under moisture stress is presented in Table 2. Significant variation was observed among genotypes for all traits studied.

Table 2 : Variation among grain cowpea genotypes for morpho-physiological and biochemical traits under drought stress condition in pot experiment

Sl. No.	Genotypes	Root length (cm)		Shoot length (cm)		Root dry weight (g)		Shoot dry weight (g)	
		Stress	Control	Stress	Control	Stress	Control	Stress	Control
1.	Pant lobia-3	20.18	11.09	57.68	72.77	0.23	0.16	2.35	1.77
2.	DC-15	12.74	12.04	73.96	91.77	0.16	0.83	1.80	3.86
3.	Vamban-3	29.57	24.05	57.33	72.91	0.45	0.35	2.16	5.56
4.	CHESCP-17	34.00	12.97	82.10	126.18	1.05	0.30	2.45	4.72
5.	PGCP-6	20.45	17.67	69.06	101.61	0.27	0.95	2.36	4.58
6.	IC-201079	14.69	11.97	99.21	108.64	0.19	0.54	2.38	3.97
7.	CP-15	12.58	12.27	53.52	99.50	0.41	1.15	2.96	5.51
8.	CP-14	15.55	28.77	52.82	79.07	0.17	1.13	3.87	7.29
9.	PCP	16.82	15.30	32.20	37.28	0.18	0.17	0.98	5.96
10.	T_7(AVT)	25.58	12.90	118.17	129.85	0.17	0.49	1.71	2.89
11.	T_6(AVT)	9.88	9.55	118.07	151.71	0.23	0.26	2.92	4.97
12.	T_1(AVT)	16.71	13.14	70.31	136.60	0.42	0.52	2.49	5.80
13.	T_2(AVT)	41.25	30.71	71.83	93.41	0.59	1.23	2.90	6.16
14.	T_8(AVT)	23.66	13.94	65.80	73.57	0.42	1.08	3.03	5.46
15.	T_5(AVT)	23.56	10.82	62.31	88.41	0.20	0.78	2.37	8.29
16.	T_3(AVT)	15.20	13.52	68.65	121.28	0.16	0.21	2.31	6.70
17.	CPP-119	36.08	28.94	52.80	89.57	0.47	0.99	2.26	4.35
18.	KBC-4	13.66	12.15	80.22	124.22	0.13	0.58	2.37	7.03
19.	PGCP-63	18.74	12.25	89.29	171.18	0.34	0.49	2.63	4.54
20.	KBC-9	31.02	23.76	61.10	76.38	1.06	1.22	2.73	3.64
21.	CP_4(IVT)	20.62	18.38	101.43	132.31	0.66	1.14	2.86	4.03
22.	CP-13	21.46	17.73	92.56	124.38	0.26	0.60	2.23	4.00
23.	Kanakamoni	11.03	9.53	97.31	136.95	0.23	0.86	2.65	5.92
24.	T_4(AVT)	18.86	8.38	40.84	74.18	0.17	0.51	2.36	3.24
25.	CP_{15}(IVT)	22.95	12.01	88.35	135.34	0.18	0.41	2.16	4.83
26.	CP-6	26.47	12.14	95.88	125.72	0.64	0.28	3.24	2.82
27.	CP-7	18.93	14.59	51.08	95.94	0.33	0.50	3.47	2.36
28.	CP-12	28.87	23.05	60.01	92.37	0.70	1.00	3.05	5.65
29.	CP-8	14.93	21.72	59.90	169.71	0.25	0.20	2.70	4.02
30.	CP-10	19.74	16.29	52.13	86.03	0.19	0.81	3.35	5.55
31.	CP_9(IVT)	16.95	11.76	71.01	116.91	0.17	0.52	3.26	4.90
32.	TC-901	20.26	12.46	86.67	101.67	0.35	1.33	2.16	3.62
33.	CP-3	23.88	16.89	50.77	72.01	0.69	1.01	2.76	5.44
34.	CP-11	18.55	17.23	72.39	82.72	0.33	0.55	1.84	3.68
35.	CP-1	18.58	20.43	54.33	85.65	0.31	0.15	0.25	1.72
	Mean	20.97	16.01	71.74	105.07	0.36	0.665	2.49	4.708
	SE(d)	0.72		3.05		0.06		0.09	
	C.D	1.43		6.08		0.12		0.17	
	C.V	4.19		5.2		20.16		4.24	

Sl. No.	Genotypes	Proline content (μmolg^{-1})		Chlorophyll content (μmolm^{-2})		Super oxide dismutase (mg protein)	
		Stress	Control	Stress	Control	Stress	Control
1.	Pant lobia-3	3.97	1.14	1.15	1.58	1.82	1.56
2.	DC-15	8.54	2.84	1.05	1.33	1.56	1.08
3.	Vamban-3	8.65	3.23	0.83	1.24	1.99	1.86
4.	CHESCP-17	1.71	1.41	1.50	1.71	2.11	1.73
5.	PGCP-6	2.83	1.86	1.52	1.85	1.60	1.34
6.	IC-201079	8.36	1.49	0.84	0.97	2.14	1.76
7.	CP-15	3.05	1.04	0.77	0.89	1.34	1.02
8.	CP-14	3.65	2.12	0.97	1.36	1.67	1.13
9.	PCP	3.01	2.17	1.07	1.54	1.57	1.44
10.	T_7(AVT)	4.19	1.59	1.25	1.63	1.46	0.96
11.	T_6(AVT)	7.40	1.98	1.16	1.44	1.37	0.92
12.	T_1(AVT)	6.81	1.96	0.92	1.36	1.47	1.01

13.	T$_2$(AVT)	4.43	3.20	2.07	2.15	1.75	1.38
14.	T$_8$(AVT)	4.15	2.23	1.23	1.55	1.45	1.13
15.	T$_5$(AVT)	3.87	2.04	0.72	1.10	1.54	1.15
16.	T$_3$(AVT)	7.96	1.07	1.06	1.27	1.49	0.14
17.	CPP-119	2.93	1.12	0.68	1.24	1.53	1.35
18.	KBC-4	5.06	2.08	0.85	1.18	1.89	1.73
19.	PGCP-63	1.68	2.30	1.16	1.32	1.56	1.36
20.	KBC-9	4.27	1.98	0.69	0.77	1.33	0.98
21.	CP$_4$(IVT)	2.84	1.26	1.17	1.48	1.58	0.83
22.	CP-13	1.59	1.36	1.32	1.47	1.83	1.22
23.	Kanakamoni	1.89	1.23	1.25	1.52	1.28	0.85
24.	T$_4$(AVT)	2.89	2.11	1.82	1.96	1.56	0.94
25.	CP$_{15}$(IVT)	2.16	1.88	0.93	1.22	1.84	1.46
26.	CP-6	9.18	1.37	0.83	1.04	2.06	1.76
27.	CP-7	8.17	1.54	1.11	1.29	1.67	1.36
28.	CP-12	7.64	1.53	1.35	1.58	1.44	1.28
29.	CP-8	8.82	4.93	0.64	0.95	1.58	1.36
30.	CP-10	4.11	2.76	0.94	1.18	1.44	1.24
31.	CP$_9$(IVT)	3.01	1.94	0.88	1.26	1.54	1.29
32.	TC-901	2.23	1.30	0.83	1.19	1.74	1.30
33.	CP-3	1.51	1.25	0.83	1.24	1.51	1.03
34.	CP-11	7.07	1.77	0.65	1.36	1.70	1.26
35.	CP-1	2.08	1.65	0.67	0.99	1.78	1.51
	Mean	4.62	1.906	1.04	1.34	1.63	1.24
	SE(d)	0.19		0.07		0.2	
	C.D	0.38		0.13		0.4	
	C.V	5.1		7.85		14.94	

Under moisture stress, root length varied significantly from 9.88 to 41.25 cm. The highest root length was recorded in T$_2$(AVT), which was significantly superior to all other genotypes, while the lowest was observed in T$_6$(AVT), which was statistically similar to Kanakamoni. Twenty-two genotypes recorded root length values below the overall mean (20.97 cm). Shoot length ranged from 32.20 to 118.17 cm under drought stress. The longest shoot was recorded for T$_7$(AVT), which was statistically similar to T$_6$(AVT). PCP recorded the shortest shoot length. All genotypes recorded higher shoot length under control conditions than under stress, and twenty genotypes had shoot length below the mean (71.74 cm) under moisture stress. Root dry weight under moisture stress ranged from 0.13 g to 1.06 g, with KBC-9 recording the highest value, which was statistically similar to CHESCP-17. KBC-4 recorded the lowest root dry weight, similar to several other genotypes (Pant Lobia-3, DC-15, IC-201079, CP-14, PCP, T$_7$(AVT), T$_6$(AVT), T$_5$(AVT), T$_3$(AVT), Kanakamoni, T$_4$(AVT), CP$_{15}$(IVT), CP-10, CP$_9$(IVT)). Under stress, twenty-three genotypes had root dry weight below the mean (0.36 g). Shoot dry weight varied significantly from 0.25 g to 3.87 g under moisture stress. CP-14 recorded the highest shoot dry weight, whereas CP-1 had the lowest. Nineteen genotypes exhibited shoot dry weight below the mean (2.49 g) under moisture stress. Proline content ranged from 1.51 to 9.18 µmol g^{-1}, with CP-6 recording the highest, being statistically similar to CP-8**.** CP-3 had the lowest proline content and was similar to CHESCP-17, PGCP-63, CP-13, Kanakamoni.

Analysis of variance (ANOVA) revealed significant differences among genotypes for all the traits studied (Table 3). Estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), and genetic advance are presented in Table 4.

Table 3 : ANOVA of morpho-physiological and biochemical parameters under drought stress

Sl. No.	Characters	MSS of source	MSS of error	F
1.	Root length (cm)	154.99**	30.79	3.31**
2.	Shoot length (cm)	1293.56**	6.84	394.86**
3.	Root dry weight (g)	0.17**	0.00	194.15**
4.	Shoot dry weight (g)	1.38**	0.04	173.58**
5.	Proline content (µmolg^{-1})	19.41**	0.01	336.58**
6.	Chlorophyll content (µmolm^{-2})	0.32**	0.01	51.04**
7.	Super oxide dismutase (mg protein)	0.15**	0.01	46.97**

*Since the P-value in ANOVA table is <0.05, there is significant difference between atleast a pair of treatments.

Table 4 : Estimates of genetic variability parameters of various characters in grain cowpea genotypes

Sl. No.	Characters	Mean	PCV (%)	GCV (%)	H^2(%)	GA (%)
1.	Root length (cm)	20.97	34.444	34.188	98.5	69.904
2.	Shoot length (cm)	71.74	29.252	28.786	96.8	58.354
3.	Root dry weight (g)	0.36	67.389	64.536	91.7	127.316
4.	Shoot dry weight (g)	2.49	27.369	27.045	97.6	55.053
5.	Proline content (µmolg^{-1})	4.62	55.209	54.971	99.1	112.751
6.	Chlorophyll content (µmolm^{-2})	1.04	32.07	31.061	93.8	61.972
7.	Super oxide dismutase (mg protein)	1.63	18.221	10.361	32.3	12.136

The PCV values ranged from 18.221 to 67.389, while GCV values varied from 10.361 to 64.536. High PCV and GCV were recorded for root length (34.444, 34.188), shoot length (29.252, 28.786), root dry weight (67.389, 64.536), shoot dry weight (27.369, 27.045), proline content (55.209, 54.971), and chlorophyll content (32.070, 31.061), indicating substantial genetic variability for these traits. Superoxide dismutase exhibited moderate PCV and GCV values (18.221, 10.361), suggesting comparatively lower genetic variability.

Heritability estimates ranged from 32.3 to 99.1%. High heritability was observed for proline content (99.1%), root length (98.5%), shoot dry weight (97.6%), shoot length (96.8%), chlorophyll content (93.8%), and root dry weight (91.7%). Superoxide dismutase recorded moderate heritability (32.3%). Genetic advance varied from 12.136 to 127.316. High genetic advance was recorded for root dry weight (127.316), proline content (112.751), root length (69.904), chlorophyll content (61.972), shoot length (58.354), and shoot dry weight (55.053), indicating the predominance of additive gene action for these traits. Superoxide dismutase exhibited moderate genetic advance (12.136).

Phenotypic and genotypic correlation coefficients among the studied traits were estimated, and the results are presented in Tables 5 and 6, respectively. Significant positive and negative correlations were observed at 1% and 5% levels of significance. Root length showed a high positive phenotypic correlation with root dry weight (0.637), followed by chlorophyll content (0.271) and superoxide dismutase (0.172). Root dry weight exhibited a significant positive correlation with shoot dry weight (0.186). Shoot dry weight showed a positive phenotypic association with root dry weight (0.186). Superoxide dismutase was positively correlated with root length (0.172). Chlorophyll content showed a significant positive correlation with root length (0.271) but a negative correlation with proline content (-0.199). Proline content was negatively correlated with chlorophyll content (-0.199). Genotypic correlation coefficients revealed stronger associations compared to phenotypic correlations. Root length exhibited a high positive genotypic correlation with root dry weight (0.670), superoxide dismutase (0.318), and chlorophyll content (0.279). Shoot length showed a positive genotypic correlation with superoxide dismutase (0.191). Root dry weight was positively correlated with shoot dry weight (0.199). Shoot dry weight exhibited a negative genotypic correlation with superoxide dismutase (-0.224). Superoxide dismutase showed positive correlations with root length (0.318), shoot length, and proline content (0.191), while a negative correlation was observed with shoot dry weight (-0.224). Chlorophyll content exhibited a significant positive correlation with root length (0.279) and a negative correlation with superoxide dismutase and proline content (-0.209). Proline content showed a positive genotypic correlation with superoxide dismutase (0.191) and a negative correlation with chlorophyll content (-0.209).

Table 5 : Phenotypic correlation of drought related traits in grain cowpea

	RL	SL	RDW	SDW	SOD	TC	PRO
RL	1						
SL	-0.112	1					
RDW	0.637**	-0.018	1				
SDW	0.038	0.038	0.186*	1			
SOD	0.172*	0.114	0.034	-0.12	1		
TC	0.271*	0.107	0.065	0.13	0.011	1	
PRO	0.138	0.057	-0.079	0.159	0.115	-0.199*	1

*****Significance at 5% level **Significance at 10% level

RL- Root length (cm)
RWC- Relative water content (%)
PRO- Proline content (µmolg^{-1})
SL- Shoot length (cm)
TC- Chlorophyll content (µmolm^{-2})
SOD- Super oxide dismutase (mg protein)
RDW- Root dry weight (g)
SDW- Shoot dry weight (g)

Table 6 : Genotypic correlation of drought related traits in grain cowpea

	RL	**SL**	**RDW**	**SDW**	**SOD**	**TC**	**PRO**
RL	1						
SL	-0.111	1					
RDW	0.67**	-0.028	1				
SDW	0.038	0.044	0.199*	1			
SOD	0.318*	0.191*	0.115	-0.224*	1		
TC	0.279*	0.114	0.081	0.135	-0.209*	1	
PRO	-0.137	0.06	-0.078	0.162	0.191*	-0.209*	1

*****Significance at 5% level **Significance at 10% level

RL- Root length (cm) RWC- Relative water content (%) PRO- Proline content (µmolg^{-1})
SL- Shoot length (cm) TC- Chlorophyll content (µmolm^{-2}) SOD- Super oxide dismutase (mg protein)
RDW- Root dry weight (g) SDW- Shoot dry weight (g)

Based on biochemical parameters, particularly proline content, the genotypes CP-6, CP-8, Vamban-3, DC-15 and IC-201079 were identified as drought-tolerant under pot culture conditions.

Discussion

Significant genotypic variation for root length under moisture stress indicated differential adaptive responses among cowpea genotypes. Several genotypes exhibited increased root length under stress, suggesting a compensatory mechanism for improved water uptake under limited moisture availability. Similar drought-induced enhancement of root traits in cowpea has been reported earlier (Harshani and Fernando, 2021).

Shoot length and shoot dry weight decreased under moisture stress in all genotypes, though the extent of reduction varied. Reduced shoot growth under drought has been widely reported in cowpea and other legumes and may reflect adaptive reallocation of assimilates towards root development and water conservation (Ranawake *et al*., 2011; Okon, 2013; Sajitha *et al*., 2022). Genotypes maintaining higher shoot biomass under stress are considered relatively more tolerant.

Root dry weight showed marked genotypic variation under stress, with higher values indicating preferential biomass allocation to roots. Similar responses have been reported in cowpea under drought conditions (Santos *et al*., 2020), highlighting the importance of root biomass in drought tolerance.

Moisture stress induced a significant increase in proline content, with pronounced genotypic differences. Enhanced proline accumulation under drought has been consistently reported in cowpea and reflects its role in osmotic adjustment and stress tolerance (Zegaoui *et al*., 2017; Goufo *et al*., 2017; Sanusi *et al*., 2025).

Chlorophyll content declined under stress, although some genotypes retained relatively higher levels, indicating better maintenance of the photosynthetic apparatus. Similar drought-induced reductions in chlorophyll have been reported in cowpea and chickpea (Mafakheri *et al*., 2010; Tengey *et al*., 2023).

Superoxide dismutase activity exhibited significant genotypic variation under moisture stress, with increased activity in certain genotypes, reflecting activation of antioxidant defense mechanisms under drought. Comparable responses have been reported earlier in cowpea and chickpea (Melo *et al*., 2024; Keerthi *et al*., 2023).

Significant differences among genotypes for all traits under moisture stress indicated substantial genetic variability for drought-related characters, as reported earlier in cowpea (Mwale *et al*., 2017; Manneh *et al*., 2024).

Higher PCV than GCV for all traits suggested environmental influence on trait expression. High PCV and GCV were recorded for root and shoot traits, proline content, and chlorophyll content, indicating good scope for selection, while SOD activity exhibited moderate variability. Similar trends were reported by Olajide and Ilori (2017) in cowpea.

High heritability coupled with high genetic advance for root length, shoot length, root dry weight, shoot dry weight, proline content, and chlorophyll content indicated predominance of additive gene action and effectiveness of direct selection. These findings are in agreement with earlier reports in cowpea under drought stress (Mwale *et al*., 2017; Singini *et al*., 2024).

Genotypic correlations were generally higher than phenotypic correlations, indicating a strong genetic basis of trait associations. Root length showed positive correlations with root dry weight, chlorophyll content, and SOD activity, emphasizing the importance of root traits in drought tolerance. Shoot dry weight was positively associated with root dry weight, while proline content was negatively correlated with chlorophyll content. Similar associations have been reported earlier in cowpea under drought stress (Mwale *et al*., 2017; Poudel *et al*., 2025).

Overall, the positive association of root traits, chlorophyll content, and antioxidant activity with biomass under moisture stress suggests that these characters can be effectively used as selection criteria for improving drought tolerance in grain cowpea.

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