



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(7): 1267-1272
Received: 02-05-2026
Accepted: 08-06-2026

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Photosynthetic efficiency regulates phenotypic variation under moisture stress in finger millet (*Eleusine coracana* L.)

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DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i7p.6096>

Abstract

Drought is one of the major abiotic stresses limiting finger millet (*Eleusine coracana* L.) productivity, particularly during the reproductive stage. The present study was undertaken to evaluate constitutive and acquired drought tolerance traits in nine finger millet genotypes (GPU67, GE1537, GE4597, GPU28, GE2811, GE5166, GE1286, GE1829 and PR202) under three soil moisture regimes corresponding to 100% (well-watered control), 65% (moderate stress) and 45% field capacity (severe stress). Moisture stress was imposed for 25 days using the gravimetric method. Physiological responses were assessed by measuring photosynthetic rate and stomatal conductance, while biochemical responses were evaluated through proline and malondialdehyde (MDA) contents. Root length, root volume, root weight and total biomass were recorded to determine the influence of drought on plant growth. Increasing moisture stress significantly reduced photosynthetic rate, stomatal conductance, root growth and biomass accumulation, whereas proline and MDA contents increased progressively, indicating activation of osmotic adjustment and oxidative stress responses. Considerable genotypic variability was observed for all physiological, biochemical and biometric traits. Among the evaluated genotypes, GE1537 consistently maintained the highest photosynthetic rate under moderate and severe drought stress, while GE1829 and GE5166 exhibited comparatively higher stomatal conductance under stress. Genotypes GE2811, GE1286, GPU28 and PR202 maintained superior root traits and biomass under moisture-limited conditions, indicating better water acquisition and growth. Although PR202 and GE4597 accumulated higher proline levels under drought, the simultaneous increase in MDA suggested greater oxidative damage in some genotypes. The study demonstrated that drought tolerance in finger millet is governed by the combined effects of physiological efficiency, biochemical defence mechanisms and root system architecture. Overall, GE1537, GE1829, GE2811, GE5166 and GPU28 emerged as promising drought-tolerant genotypes and can serve as valuable genetic resources for breeding climate-resilient finger millet cultivars adapted to water-limited environments.

Keywords: Nanourea, conventional urea, growth, lai, yield and wheat

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the most important small millets cultivated in the semi-arid and tropical regions of Asia and Africa. It is valued for its exceptional nutritional quality, being rich in calcium, dietary fibre, essential amino acids, iron, and other micronutrients. The crop is highly adaptable to marginal lands and is commonly grown under rainfed conditions where other cereals often fail. Owing to its resilience and nutritional significance, finger millet has gained considerable attention as a climate-smart crop capable of contributing to food and nutritional security under changing climatic conditions. Although finger millet is a C₄ species with relatively high photosynthetic efficiency and better water-use efficiency than many C₃ cereals, it is not completely tolerant to drought. Moisture stress occurring during germination, vegetative growth, flowering, or grain filling adversely affects plant growth, physiological processes, and ultimately grain yield. Since the crop is predominantly cultivated in rainfed ecosystems, erratic rainfall and prolonged dry spells frequently expose plants to water deficit, resulting in significant yield losses. The increasing frequency and intensity of drought due to climate change further emphasize the need to develop drought-resilient finger millet cultivars.

Drought tolerance is a complex trait governed by the interaction of morphological, physiological, biochemical, and molecular mechanisms. Superior performance under water-limited conditions depends on the presence of constitutive and acquired adaptive traits such as efficient root systems for water mining, higher water-use efficiency, improved carboxylation efficiency with reduced transpiration, enhanced canopy cover, better light interception, osmotic adjustment, maintenance of cellular membrane stability, and effective antioxidant defence mechanisms. The extent of expression of these traits varies among genotypes, indicating the existence of valuable genetic variability that can be exploited in breeding programmes.

Identification of drought-tolerant genotypes through the evaluation of constitutive and acquired adaptive traits is therefore essential for crop improvement. Characterizing the available genetic variability enables breeders to identify superior parental lines and understand the physiological basis of drought tolerance. In this context, the present investigation was undertaken to assess the variability in constitutive and acquired drought tolerance traits among selected finger millet genotypes under moisture stress conditions. The outcomes of this study will provide valuable information for the development of high-yielding, drought-resilient finger millet varieties suited to rainfed agro-ecosystems.

Materials and Methods

The present investigation was carried out using nine finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes exhibiting variability in drought response. The genotypes included GPU67, GE1537,

GE4597, GPU28, GE2811, GE166, GE1286, GE1829 and PR202 (Table 1). Healthy and uniform seeds were obtained from the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Raichur.

Table 1: List of Genotypes used in the present study

Sl. No.	Genotypes
1	GPU67
2	GE1537
3	GE4597
4	GPU28
5	GE2811
6	GE166
7	GE1286
8	GE1829
9	PR202

Experimental Site

The experiment was conducted under controlled pot culture conditions at the Department of Crop Physiology, College of Agriculture, University of Agricultural Sciences (UAS), Raichur, Karnataka, India. The crop was raised under recommended agronomic practices until the initiation of drought stress.

Experimental Design and Treatments: The experiment was laid out in a Factorial Completely Randomized Design (FCRD) with three replications. The treatments consisted of nine finger millet genotypes and three moisture regimes.

Table 2: Factors used in the study (G vs M)

Factor 1: Genotypes (G)	Factor II: Moisture Regimes (M)
G1 – GPU67	M1 – 100% Field Capacity (Well-watered control)
G2 – GE1537	M2 – 65% Field Capacity (Moderate drought)
G3 – GE4597	M3 – 45% Field Capacity (Severe drought)
G4 – GPU28	
G5 – GE2811	
G6 – GE166	
G7 – GE1286	
G8 – GE1829	
G9 – PR202	

Imposition of Moisture Stress

Drought stress was imposed during the reproductive stage, which is the most sensitive stage for yield determination in finger millet. Soil moisture levels corresponding to 100%, 65% and 45% field capacity were maintained for 25 days using the gravimetric method. The field capacity of the potting mixture was determined before stress imposition. Each pot was weighed daily, and the quantity of water lost through evapotranspiration was replenished to maintain the desired moisture level throughout the experimental period.

Recording of Gas Exchange Parameters

Gas exchange parameters were recorded 10 days after the imposition of drought stress using a Portable Photosynthesis System (LI-6400XT, LI-COR Biosciences, Lincoln, USA). Observations were recorded on the youngest fully expanded leaf between 9:00 AM and 11:00 AM under natural light conditions. The following parameters were measured: Net photosynthetic rate (Pn; $\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$), Stomatal conductance (gs; $\text{mol H}_2\text{O m}^{-2} \text{ s}^{-1}$), Transpiration rate (E; $\text{mmol H}_2\text{O m}^{-2} \text{ s}^{-1}$), Intercellular CO_2 concentration (Ci; $\mu\text{mol mol}^{-1}$) and Water use efficiency (WUE).

Estimation of Proline Content

Proline content was estimated following the method (Bates *et al.*, 1973) [2]. Fresh leaf tissue (0.5 g) was homogenized with 3% sulfosalicylic acid and filtered. Two millilitres of filtrate were mixed with acid ninhydrin and glacial acetic acid, heated at 100°C for one hour and cooled rapidly. The chromophore was extracted with toluene, and absorbance was measured at 520 nm using a UV-Visible spectrophotometer. The proline content was expressed as $\mu\text{mol g}^{-1}$ fresh weight.

Estimation of Malondialdehyde (MDA)

Lipid peroxidation was estimated by determining malondialdehyde (MDA) content using the thiobarbituric acid (TBA) method given by Heath, R. L., & Packer, L. (1968) [10]. Fresh leaf tissue (0.5 g) was homogenized in 0.1% trichloroacetic acid (TCA), centrifuged and the supernatant reacted with TBA reagent. The reaction mixture was heated at 95°C for 30 minutes, cooled rapidly and absorbance was recorded at 532 and 600 nm. MDA content was calculated using an extinction coefficient of $155 \text{ mM}^{-1} \text{ cm}^{-1}$ and expressed as nmol g^{-1} fresh weight.

Measurement of Root Traits

Plants were harvested at physiological maturity and roots were carefully washed to remove adhering soil particles.

Root Length (RL)

Root length was measured from the base of the stem to the tip of the longest root using a measuring scale and expressed in centimetres (cm).

Root Volume (RV)

Root volume was determined by the water displacement method using a graduated measuring cylinder and expressed in cubic centimetres (cm³).

Root Weight (RW)

Fresh root weight was recorded immediately after washing using a digital electronic balance and expressed in grams (g).

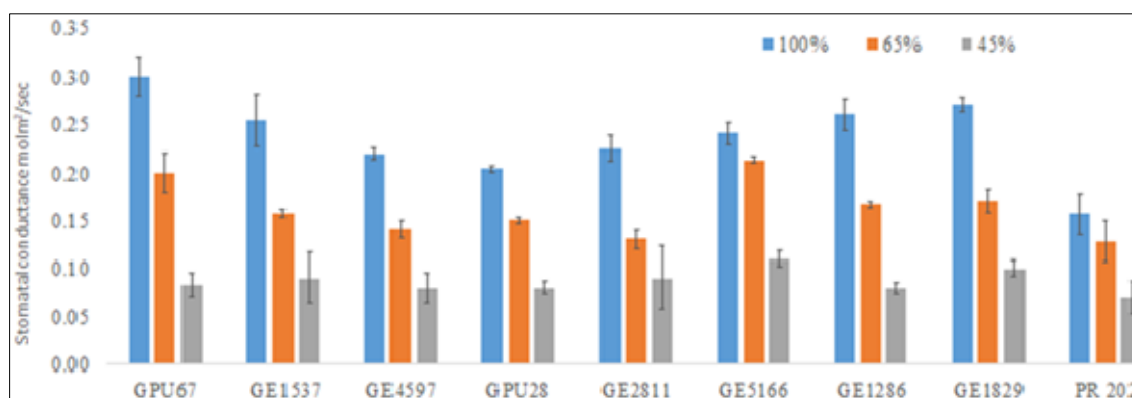
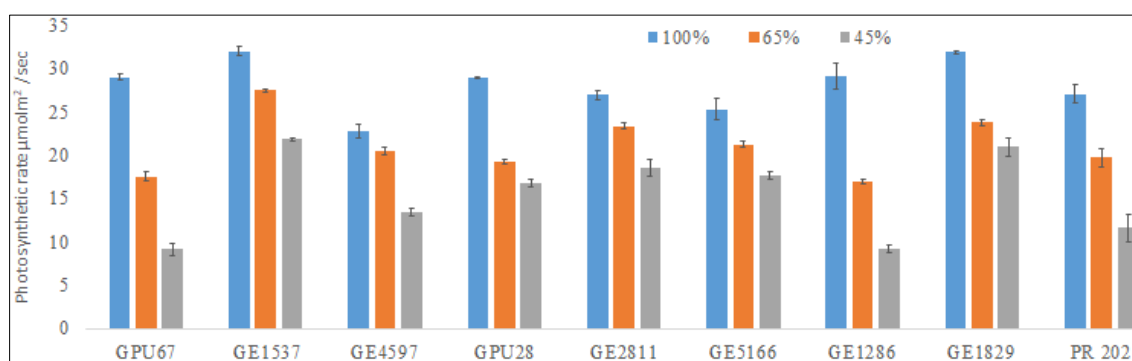
Total Biomass (TBM)

The harvested plants were separated into shoots and roots and dried in a hot-air oven at 70 ± 2 °C until constant weight was obtained. The total dry weight of the plant was recorded and expressed as g plant⁻¹.

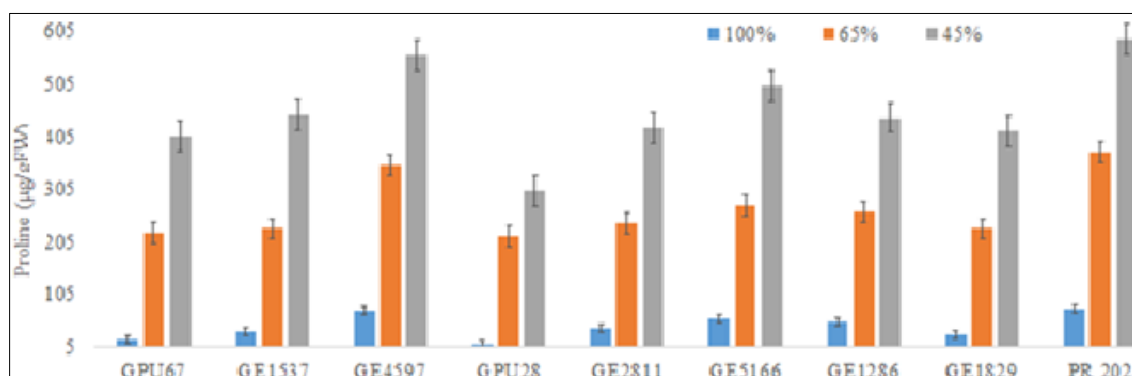
Statistical Analysis

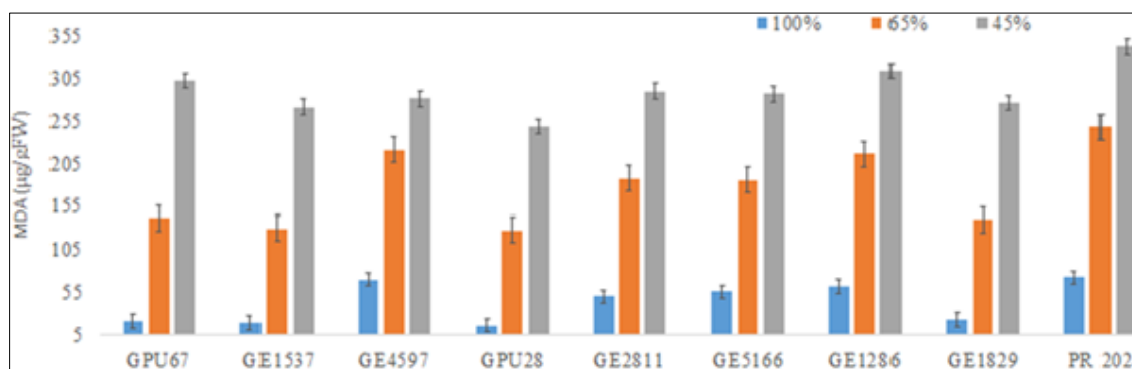
The experimental data generated for biometric traits, gas exchange parameters, biochemical traits, root characteristics, biomass, and yield were subjected to analysis of variance (ANOVA) appropriate for a Factorial Completely Randomized Design (FCRD), considering genotypes (G), moisture regimes (M), and their interaction (G × M) as sources of variation. The significance of treatment effects was tested at the 5% probability level ($p \leq 0.05$). Mean separation among genotypes and moisture regimes was carried out using the Critical Difference (CD) test whenever the F-test was significant. Statistical analyses were performed using R software (Version 4.3.3). The following traits were subjected to statistical analysis: Biometric traits: Plant height, root length (RL), root volume (RV), root weight (RW), total biomass (TBM), and grain yield. Gas exchange parameters: Net photosynthetic rate (Pn), stomatal conductance (gs), transpiration rate (E), intercellular CO₂ concentration (Ci), and water use efficiency (WUE). Biochemical traits: Proline content and malondialdehyde (MDA) content under well-watered (100% FC), moderate drought (65% FC), and severe drought (45% FC) conditions.

Results and Discussion



Variability in gas exchange parameters among ragi genotypes in three water regimes (Fig.1 & 2)





Proline and MDA content in well water and water limited conditions (Fig.3 & 4)

Variability in biometric in selected genotypes of ragi at three water regimes (Table 3)

Treatment	RL (cm) 100%	65%	45%	RV (cm ³) 100%	65%	45%	RW (g) 100%	65%	45%	TBM (g) 100%	65%	45%
GPU67	76.25	72.4	70.2	125	86.25	81.5	72.5	19.6	38.8	177.5	138.2	120.8
GE1537	61.5	84.7	72.3	102	107.5	91.6	65.5	43	36.75	172.1	121.5	98.02
GE4597	63.2	67	66	100	180	43.3	57	68.5	17.8	159.3	126.2	107.8
GPU28	81.5	67.2	64.5	131.25	92.5	83.75	51.2	38.4	24.6	152.2	139.8	128.9
GE2811	72	64.2	70.4	27.5	90	142	20.5	44	48	149.1	128.9	103.5
GE5166	76.5	72.6	64	88.3	71.25	85	62	28	39.75	139.7	115.7	99.2
GE1286	95.6	59.5	69.5	170	61.6	100	74	44.5	39.6	157.3	116.7	138.1
GE1829	64.4	61	59	61.25	84	123.3	25	29	60.5	150.8	102.7	90.3
PR202	62.4	81.3	71.5	22.9	90	130	22.7	39	37	123.6	116.3	112

Note: RL (cm): Root Length; RV (cm³): Root Volume; RW (g): Root Weight; TBM (g): Total Biomass

Variability in gas exchange parameters among ragi genotypes in three water regimes

The photosynthetic rate and stomatal conductance of the nine finger millet genotypes decreased progressively with increasing moisture stress, indicating significant effects of drought on leaf gas exchange (Fig. 1 and Fig. 2). Under well-watered conditions (100% FC), the photosynthetic rate ranged from 22.7 to 32.0 $\mu\text{mol m}^{-2} \text{s}^{-1}$, with GE1537 (32.0 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and GE1829 (31.9 $\mu\text{mol m}^{-2} \text{s}^{-1}$) recording the highest values, followed by GE1286 (29.0 $\mu\text{mol m}^{-2} \text{s}^{-1}$), GPU67 (28.9 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and GPU28 (28.8 $\mu\text{mol m}^{-2} \text{s}^{-1}$). Similarly, stomatal conductance varied from 0.16 to 0.30 $\text{mol m}^{-2} \text{s}^{-1}$, with the highest value observed in GPU67 (0.30 $\text{mol m}^{-2} \text{s}^{-1}$), followed by GE1829 (0.27 $\text{mol m}^{-2} \text{s}^{-1}$) and GE1286 (0.26 $\text{mol m}^{-2} \text{s}^{-1}$), reflecting their superior gas exchange capacity under non-stress conditions.

Under moderate drought stress (65% FC), both photosynthetic rate and stomatal conductance declined in all genotypes, although the extent of reduction differed significantly. GE1537 maintained the highest photosynthetic rate (27.4 $\mu\text{mol m}^{-2} \text{s}^{-1}$), followed by GE1829 (23.8 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and GE2811 (23.2 $\mu\text{mol m}^{-2} \text{s}^{-1}$), whereas GPU67 and GE1286 exhibited comparatively larger reductions. A similar trend was observed for stomatal conductance, where GE5166 (0.215 $\text{mol m}^{-2} \text{s}^{-1}$) maintained the highest conductance followed by GPU67 (0.20 $\text{mol m}^{-2} \text{s}^{-1}$) and GE1829 (0.17 $\text{mol m}^{-2} \text{s}^{-1}$). The decline in these parameters under moderate water deficit indicates partial stomatal closure to minimize transpirational water loss while maintaining sufficient CO₂ uptake for photosynthesis. Genotypes capable of sustaining higher gas exchange under moderate stress are considered physiologically more efficient and better adapted to drought conditions (Farooq *et al.*, 2009; Flexas *et al.*, 2004) [6, 7].

Severe drought stress (45% FC) caused a marked reduction in both traits across all genotypes. The photosynthetic rate declined to 9.1–21.8 $\mu\text{mol m}^{-2} \text{s}^{-1}$, with GE1537 (21.8 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and GE1829 (20.8 $\mu\text{mol m}^{-2} \text{s}^{-1}$) maintaining significantly higher values than the remaining genotypes, while GPU67 (9.2 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and GE1286 (9.1 $\mu\text{mol m}^{-2} \text{s}^{-1}$) recorded the lowest values.

Likewise, stomatal conductance decreased to 0.07–0.11 $\text{mol m}^{-2} \text{s}^{-1}$, with GE5166 (0.11 $\text{mol m}^{-2} \text{s}^{-1}$) and GE1829 (0.10 $\text{mol m}^{-2} \text{s}^{-1}$) exhibiting comparatively higher conductance under severe stress. The sharp reduction in gas exchange parameters under severe drought reflects restricted stomatal opening, reduced mesophyll conductance, and inhibition of photosynthetic metabolism resulting from dehydration and oxidative stress (Chaves *et al.*, 2009; Blum, 2011) [4, 3].

The consistent superiority of GE1537 and GE1829 in maintaining higher photosynthetic rates across all moisture regimes, together with the ability of GE5166 and GE1829 to sustain relatively higher stomatal conductance under stress, suggests that these genotypes possess efficient drought-adaptive mechanisms, including better stomatal regulation, maintenance of leaf water status, and protection of the photosynthetic apparatus. In contrast, the pronounced reduction observed in GPU67 and GE1286 indicates greater susceptibility to moisture stress. These findings demonstrate substantial genetic variability for gas exchange traits among finger millet genotypes and emphasize that maintenance of photosynthesis and stomatal conductance under water deficit can serve as reliable physiological indicators for selecting drought-tolerant genotypes in finger millet breeding programmes. Similar observations have been reported in finger millet and other cereal crops by Blum (2011) [3], Farooq *et al.* (2009) [6], Chaves *et al.* (2009) [4], and Gupta *et al.* (2017) [9].

Proline and MDA content in well water and water limited conditions

The accumulation of proline and malondialdehyde (MDA) increased significantly with increasing moisture stress in all nine finger millet genotypes, indicating activation of osmotic adjustment and oxidative stress responses under drought conditions (Fig. 3 and Fig. 4). Under well-watered conditions (100% FC), proline content remained relatively low, ranging from approximately 10 to 70 $\mu\text{g g}^{-1} \text{FW}$, whereas MDA content ranged between 15 and 70 $\mu\text{g g}^{-1} \text{FW}$, reflecting normal cellular metabolism in the absence of water stress. Among the genotypes,

GE4597 and PR202 exhibited comparatively higher constitutive levels of both proline and MDA, while GPU28, GPU67, and GE1829 maintained lower concentrations. The low accumulation of these metabolites under optimum moisture conditions suggests minimal osmotic and oxidative stress, consistent with previous reports that proline synthesis is induced primarily under stress conditions (Bates *et al.*, 1973; Szabados and Saviouré, 2010) [2, 13]. Exposure to moderate moisture stress (65% FC) resulted in a substantial increase in proline accumulation across all genotypes, with values ranging from approximately 210 to 380 $\mu\text{g g}^{-1}$ FW. The highest proline content was recorded in PR202, followed by GE4597 and GE5166, whereas GPU28 accumulated comparatively lower amounts. A similar trend was observed for MDA content, which increased to 120–250 $\mu\text{g g}^{-1}$ FW, indicating enhanced membrane lipid peroxidation due to drought-induced oxidative stress. The increased accumulation of proline under moderate stress reflects its role as a compatible osmolyte that stabilizes proteins and membranes, maintains cellular osmotic balance, and scavenges reactive oxygen species (ROS). Simultaneously, the increase in MDA content indicates the onset of oxidative damage caused by ROS production under water-deficit conditions (Farooq *et al.*, 2009; Ashraf and Foolad, 2007) [6, 1].

Under severe moisture stress (45% FC), both proline and MDA contents increased further in all genotypes. Proline accumulation reached the highest levels in PR202 ($\approx 590 \mu\text{g g}^{-1}$ FW) and GE4597 ($\approx 560 \mu\text{g g}^{-1}$ FW), followed by GE5166, GE1286, and GE1537, while GPU28 maintained the lowest proline content. Likewise, MDA content increased markedly under severe stress, with PR202 ($\approx 340 \mu\text{g g}^{-1}$ FW) and GE1286 ($\approx 310 \mu\text{g g}^{-1}$ FW) recording the highest values, whereas GPU28 showed comparatively lower lipid peroxidation. The substantial rise in MDA content under severe drought reflects increased membrane damage resulting from excessive ROS generation and reduced antioxidant protection. Although proline accumulation is generally considered a protective response, excessive MDA accumulation indicates that oxidative damage exceeded the cellular detoxification capacity in susceptible genotypes (Mittler, 2002; Gill and Tuteja, 2010) [12, 8].

The contrasting responses among genotypes demonstrate significant variability in drought-induced biochemical adaptation in finger millet. Genotypes such as GE4597, GE5166, and PR202 exhibited greater proline accumulation, suggesting a stronger osmotic adjustment mechanism under water deficit. However, the simultaneous accumulation of high MDA levels in PR202 and GE1286 indicates that enhanced proline synthesis alone was insufficient to completely prevent membrane damage under severe drought. In contrast, genotypes exhibiting relatively moderate MDA accumulation despite increased proline content are likely to possess more efficient antioxidant defence systems and greater cellular protection against oxidative stress. Therefore, simultaneous assessment of proline and MDA provides a reliable biochemical basis for distinguishing drought-tolerant and drought-sensitive genotypes in finger millet. These observations are in agreement with earlier studies in finger millet and other cereals, which reported increased proline accumulation and lipid peroxidation under drought stress and emphasized their importance as biochemical markers of drought tolerance (Bates *et al.*, 1973; Ashraf and Foolad, 2007; Szabados and Saviouré, 2010; Gupta *et al.*, 2017) [2, 1, 13, 9].

Variability in biometric in selected genotypes of ragi at three water regimes

The root traits and total biomass of the nine finger millet

genotypes exhibited considerable variation under different soil moisture regimes (100%, 65%, and 45% field capacity), indicating differential responses to drought stress (Table 3). Root length (RL) generally declined with increasing moisture stress in most genotypes, although the magnitude of reduction varied considerably. Under well-watered conditions, GE1286 recorded the maximum root length (95.6 cm), followed by GPU28 (81.5 cm) and GPU67 and GE5166 (76.5 cm). Under severe stress (45% FC), relatively higher root lengths were maintained by GE1537 (72.3 cm), PR202 (71.5 cm), GE2811 (70.4 cm) and GPU67 (70.2 cm), whereas GE1829 (59.0 cm) showed the lowest value. Maintenance of deeper and longer root systems under drought enables plants to explore a larger soil volume for water extraction and is considered an important constitutive drought adaptation trait. Similar observations have been reported in finger millet and other cereals, where increased root length contributed to improved drought tolerance and water acquisition (Blum, 2011; Comas *et al.*, 2013) [3, 5].

Root volume (RV) exhibited significant genotypic variation under moisture stress. Under control conditions, GE1286 (170 cm^3) and GPU28 (131.25 cm^3) possessed the highest root volume. Under moderate drought (65% FC), GE4597 (180 cm^3) maintained the highest root volume, followed by GE1537 (107.5 cm^3) and GPU28 (92.5 cm^3). Interestingly, under severe drought (45% FC), GE2811 (142 cm^3), PR202 (130 cm^3) and GE1829 (123.3 cm^3) exhibited larger root volumes than other genotypes, suggesting greater investment in root growth under water deficit. Such plasticity in root architecture enhances soil water exploration and is a characteristic feature of drought-adaptive genotypes. Previous studies have demonstrated that increased root volume and root proliferation under drought improve water uptake efficiency and enhance plant survival under moisture-limited conditions (Lynch, 2013; Uga *et al.*, 2013) [11, 14].

Root weight (RW) also varied significantly among genotypes across moisture regimes. Under well-watered conditions, GE1286 (74.0 g), GPU67 (72.5 g) and GE1537 (65.5 g) recorded the highest root biomass. Under moderate stress, GE4597 (68.5 g) exhibited the maximum root weight, whereas under severe drought GE1829 (60.5 g) and GE2811 (48.0 g) maintained greater root biomass than the remaining genotypes. Total biomass (TBM) declined progressively with increasing drought stress in almost all genotypes. The highest biomass under control conditions was recorded in GPU67 (177.5 g), followed by GE1537 (172.1 g) and GE4597 (159.3 g). Under severe drought, GE1286 (138.1 g), GPU28 (128.9 g), GPU67 (120.8 g) and PR202 (112.0 g) retained comparatively higher biomass, whereas GE1829 (90.3 g) exhibited the greatest reduction. The decline in biomass under drought is mainly attributed to reduced photosynthetic activity, restricted cell expansion and limited assimilate production resulting from water deficit (Farooq *et al.*, 2009) [6]. Overall, the substantial variability observed for root traits and total biomass indicates the existence of diverse constitutive and acquired drought tolerance mechanisms among the finger millet genotypes. Genotypes such as GE1537, GE2811, GE1286, GPU28, and PR202 maintained superior root growth and biomass under moisture stress, suggesting their ability to sustain water uptake and growth under drought conditions. In contrast, genotypes showing greater reductions in root development and biomass are likely to be more susceptible to water deficit. The maintenance of an extensive root system together with higher biomass under drought is an important adaptive strategy that enhances water extraction, supports continued physiological activity and ultimately contributes to improved grain yield. These findings agree with earlier reports that root architecture and biomass

accumulation are reliable selection criteria for improving drought tolerance in finger millet and other cereal crops (Blum, 2011; Comas *et al.*, 2013; Lynch, 2013; Gupta *et al.*, 2017) ^[3, 5, 11, 9].

Conclusion

The present study revealed significant variability in constitutive and acquired drought tolerance traits among the nine finger millet (*Eleusine coracana* L.) genotypes evaluated under three soil moisture regimes (100%, 65%, and 45% field capacity). Increasing moisture stress significantly reduced photosynthetic rate, stomatal conductance, root growth, biomass accumulation, and overall plant performance, while proline and malondialdehyde (MDA) contents increased progressively, reflecting osmotic adjustment and oxidative stress responses. The observed differences among genotypes confirmed that drought tolerance is governed by the interaction of physiological efficiency, biochemical defence mechanisms, and root system architecture. Among the evaluated genotypes, GE1537 exhibited superior drought tolerance by maintaining higher photosynthetic activity across all moisture regimes, while GE1829 and GE5166 sustained better stomatal conductance under stress. Genotypes GE2811, GE1286, GPU28, and PR202 maintained comparatively better root traits and biomass under drought conditions, indicating improved water acquisition and growth. Although PR202 and GE4597 accumulated higher proline levels, the accompanying increase in MDA under severe stress suggested greater oxidative damage in some genotypes. Overall, GE1537, GE1829, GE2811, GE5166, and GPU28 emerged as promising drought-tolerant genotypes and can be effectively utilized as donor parents in breeding programmes for developing climate-resilient finger millet cultivars adapted to water-limited environments.

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