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Unveiling drought-tolerant mungbean genotypes through integrated multi-trait selection

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Mungbean (*Vigna radiata* (L.) R. Wilczek var. radiata) is a highly nutritious legume grown in diverse cropping systems. However, its productivity is often hindered by abiotic stresses, particularly drought, which significantly impacts yield during critical growth stages such as flowering and pod filling. With climate change projected to increase drought frequency, leguminous crops are expected to be more vulnerable, exacerbating food security concerns. This study aimed to identify drought-tolerant mungbean genotypes by evaluating 122 genotypes (116 minicore accessions and six check varieties) under well-watered (WW) and drought-stressed (DS) conditions in a semi-controlled pot culture setup. Drought tolerance was assessed using multiple stress indices (e.g., STI, GMP), principal component analysis (PCA), and the multi-trait genotype-ideotype distance index (MGIDI). Significant genetic variability was observed across both WW and DS conditions, with drought stress leading to reductions in grain yield (21.1%), leaf area (35.4%), canopy greenness (32.1%), and photosynthetic rate (51.8%). Traits such as plant height, number of branches, pods per plant, seeds per pod, transpiration rate, and grain yield showed high heritability and genetic advance, indicating strong breeding potential. PCA analysis identified major traits contributing to drought tolerance, including yield-related traits and physiological responses, such as transpiration rate, stomatal conductance, and photosynthetic efficiency. MGIDI effectively identified 18 genotypes based on multi-trait performance. Among them, genotypes VI003685AG, VI002051BG, VI000852AG, VI002402BG, and VI003957AG consistently ranked as top performers across both traditional indices and MGIDI, demonstrating preliminary drought tolerance. The integration of stress indices, PCA, and MGIDI provided a comprehensive approach to genotype selection, offering potentially valuable genetic resources for future mungbean breeding programs targeting drought-prone environments. However, these findings are preliminary and require multi-location field validation before breeding use.

Keywords Drought tolerance, Stress indices, Multi-trait, MGIDI index, Mung, Drought stress

Mungbean (*Vigna radiata* (L.) R. Wilczek var. radiata) is a vital pulse crop cultivated across India, Asia, Africa, South America, and Australia. It is valued not only for its high protein content (20–25%) and essential nutrients but also for its role in improving soil fertility through biological nitrogen fixation[1,2]. In India, mungbean ranks as the third most important legume crop after chickpea and pigeonpea, occupying nearly 5.51 million hectares and producing around 4 million tonnes annually, with an average yield of 570 kg/ha[3]. Being largely rainfed, mungbean is particularly vulnerable to drought, which is the most severe constraint limiting productivity, especially during flowering and pod-filling stages. Drought-induced yield losses can range from 51 to 85%, depending on genotype, stress intensity, and environmental conditions[4–6]. Climate change is expected to exacerbate these challenges by increasing the frequency and severity of drought events, threatening global food security and the achievement of Sustainable Development Goal 2: Zero Hunger[7,8].

Although agronomic interventions such as mulching, conservation tillage, and plant growth-promoting rhizobacteria (PGPR) can mitigate drought effects, their impact is often limited, site-specific, and economically constrained[9]. Developing genetically drought-resilient cultivars offers a more sustainable and cost-effective

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solution. However, drought tolerance is a complex, polygenic trait influenced by genotype × environment interactions, stress intensity, and timing. Physiological and biochemical traits, such as canopy temperature, relative water content (RWC), stomatal conductance, and net CO_2 assimilation, are commonly used to characterise genotypic responses under water-limited conditions[6].

Further, several stress indices, including Tolerance Index (TOL), Stress Tolerance Index (STI), Yield Index (YI), Yield Stability Index (YSI), Stress Susceptibility Index (SSI), Mean Productivity (MP), and Geometric Mean Productivity (GMP), have been widely applied to evaluate drought effects on yield[10–12]. However, most studies focus on single traits or stress indices in isolation, which may fail to capture the complex, integrated responses of genotypes to drought and often yield inconsistent selection outcomes[13,14]. Multivariate approaches, such as principal component analysis (PCA) and the Multi-trait Genotype-Ideotype Distance Index (MGIDI), allow simultaneous evaluation of multiple traits, account for trait correlations, and improve selection accuracy[15,16]. Despite their potential, these approaches remain underutilised in mungbean breeding programs, and limited studies have explored the integration of physiological, yield, and stress indices to identify drought-resilient genotypes.

Against this background, we hypothesise that integrating morphophysiological traits with drought stress indices using multivariate approaches (PCA and MGIDI) can effectively identify mungbean genotypes with superior, balanced drought tolerance under controlled water-limited conditions, providing insights for targeted breeding. Accordingly, the present study had two broad objectives: (i) to evaluate the performance and drought resilience of diverse mungbean genotypes under well-watered and drought-stressed conditions by integrating morpho-physiological traits and stress indices, and (ii) to explore genetic variability and trait associations using multivariate analyses to identify promising genotypes for future breeding programs. By combining physiological measurements, drought indices, and advanced multivariate approaches, this study provides a comprehensive framework for assessing drought tolerance. However, it is important to note that these findings are preliminary and require multi-location field validation before breeding use. This approach addresses a critical knowledge gap in multi-trait selection in mungbean.

Materials and methods

Site description

The experiment was conducted in 2024 at a controlled-environment greenhouse facility (Allice Biotechnology®) of the ICAR–National Institute of Abiotic Stress Management (NIASM), Baramati, Maharashtra, India (18°09′30.62″ N, 74°30′03.08″ E). The semi-automated greenhouse maintained average daily conditions of 26 ± 2.5 °C temperature, 68.2 ± 10.8% relative humidity, and photosynthetically active radiation (PAR) ranging between 450 and 750 $\mu mol\ m^{-2}\ s^{-1}$.

Plant materials

The plant materials used in this study consisted of a mungbean minicore collection developed by the World Vegetable Centre[17] and six local and national check varieties (IPM-205-7, Vaibhav, NM-94, PAU-911, PDM-139, and EC-0398949). Among these, EC-0398949 was registered explicitly with NBPGR, India, for drought-adaptive traits. The original minicore collection comprised 296 genetically diverse genotypes representing broad agroecological and geographical origins. However, due to poor germination and susceptibility to powdery mildew, only 116 genotypes were deemed viable for drought screening. Including the six check varieties, a total of 122 accessions were selected for experimental trials and subsequent data analysis. Detailed information on the selected genotypes and check varieties is provided in Supplementary Table 1.

Preparation of pots, fertiliser application, and seed sowing

Mungbean genotypes were cultivated in plastic pots, each measuring 15 cm in height and 12 cm in diameter, with three drainage holes at the base to ensure adequate water percolation. Prior to potting, the soil was sterilised to eliminate soilborne pathogens and ensure uniform microbial conditions. Each pot was filled with 8 kg of a homogenised mixture of black soil and farmyard manure (FYM) at a volumetric ratio of 50:1 (V/V). Macronutrients, viz., nitrogen (N), phosphorus (P), and potassium (K), were applied at the recommended agronomic dose of 10:45:10 kg ha^{-1}, respectively. The required NPK quantities were calculated based on the total soil weight per pot and uniformly incorporated into the soil matrix. After mixing, each pot was adjusted to precisely 8 kg to standardise soil volume and initial moisture content across all treatments. Each genotype was represented by six pots: three allocated to well-watered (WW) conditions and three to drought-stress (DS) treatment. Three healthy seeds were manually sown per pot at a depth of 15–18 mm. Following germination, thinning was performed to retain one vigorous seedling per pot, thereby minimising intra-specific competition. The experiment was laid out using a completely randomised block design (CRBD) with three biological replicates per treatment to ensure statistical robustness.

Soil moisture assessment and stress imposition

Soil field capacity (FC) and wilting point (WP) were determined gravimetrically, with the soil exhibiting an FC of 30–35%, a WP of 12–14%, and an available water range of 16–23%. To determine FC, finely ground, oven-dried soil was placed in perforated pots, saturated overnight by capillary action, drained to remove excess water, and weighed to calculate moisture content relative to dry weight. During the experiment, soil moisture in each pot was monitored daily using a precision digital balance, and the exact amount of water lost was restored to maintain the target moisture range for each treatment. Under well-watered (WW) conditions, moisture was kept at 28–31% (near FC), while drought-stress (DS) pots were maintained at 14–18% by supplying only the water required to keep moisture within this narrow range from bud initiation to physiological maturity. This gravimetric approach ensured consistent stress levels across replicates and minimised variation caused by differential evapotranspiration. Although pot experiments ensure uniform stress imposition, they inherently restrict root volume, which may lead to pot-bound stress that could interact with drought responses. While we used appropriately sized pots and ensured uniform seedling establishment to minimise these effects, this limitation remains when extrapolating the results to field conditions.

Trait measurement
Growth, morphological, and yield-related traits were assessed for all plants under WW and DS conditions in each replication. The measured traits included: Plant height (PH; cm), number of primary branches per plant (NPB), number of secondary branches per plant (NSB), number of pods per plant (PP), pod length (PL; cm), number of seeds per pod (NSP), test weight (TW; g) and grain yield per plant (GY; g),

Physiological parameters
Physiological parameters were assessed during peak stress periods to evaluate plant responses under well-watered and drought-stress conditions.

Leaf area (LA; cm^2 per leaf) was measured non-destructively using a handheld leaf area meter (LI-3000C®, LI-COR, USA). Canopy greenness was quantified using the Normalised Difference Vegetation Index (NDVI), recorded with a GreenSeeker® handheld sensor (Trimble, USA) positioned 1.0 m above the plant canopy, following the method of[18]. NDVI was calculated as:

$$NDVI = (NIR - IR)/(NIR + IR)$$

where NIR is near-infrared reflectance, and IR is infrared reflectance. Chlorophyll fluorescence (Qmax = Fv/Fm) was determined using a real-time chlorophyll fluorescence imaging system (FluorCam FC 1000-H®, Photon Systems Instruments) according to the protocol described by[19], where Fv = Fm-F0. Additionally, gas exchange parameters including leaf temperature (Tleaf; °C), vapor pressure deficit (VPD; Pa/kPa), stomatal conductance (GH_2O; mmol m^{-2} s^{-1}), transpiration rate (E; mmol m^{-2} s^{-1}), and net CO_2 assimilation rate (A; µmol m^{-2} s^{-1}) were measured using a portable gas exchange system (GFS-3000®, WALZ, Germany) between 09:00 and 11:30 AM, following the method described by[20].

Data analysis
Descriptive statistical analyses were performed for all measured morpho-physiological traits under both well-watered (WW) and drought-stressed (DS) conditions to evaluate phenotypic variability among genotypes. Parameters such as mean, minimum, and maximum values were computed using R software (version 4.5.1). To visualise the distribution, symmetry, and spread of trait data under the two water regimes, violin plots were generated using PAST software version 4.03[21].

Analysis of variance
The data collected on growth, yield, and physiological traits were first subjected to the Shapiro–Wilk test to assess normality and Levene's test to evaluate homogeneity of variances. As the data met the assumptions of normal distribution and equal variance, no transformation was applied. A two-way analysis of variance (ANOVA) was conducted separately for each trait to determine the effects of genotype (G), water regime (W), and their interaction (G × W). The following linear model was used**:**

$$Yijk = \mu + Gi + Wj + (G \times W)ij + \varepsilon ijk$$

where Yijk is the observed value of the trait for the k-th replicate of the i-th genotype under the j-th water regime. µ: overall mean, Gi is the effect of the i-th genotype, Wj is the effect of the j-th water regime, $(G \times W)ij$ is the interaction effect between genotype and water regime, εijk is the random error term, $\varepsilon ijk \sim N(0, \sigma^2)$.

The significance of main and interaction effects was tested using F-tests. Where significant differences were observed, mean comparisons were performed using Tukey's Honest Significant Difference (HSD) test at a 5% significance level. All statistical analyses were conducted in R (version 4.5.1) using the packages metan, lme4, and agricolae.

Genetic parameters, including the genotypic coefficient of variation (GCV; %), phenotypic coefficient of variation (PCV; %), heritability in the broad sense (h^2bs; %), genetic advance (GA), and genetic advance as a percentage of the mean (GAM), were calculated following the methodology outlined by[22].

Correlation studies: Pearson's correlation coefficients were calculated for all morphophysiological traits under both WW and DS conditions to assess the strength and direction of trait associations. Correlation analysis was performed using R software version 4.5.1[23], and the resulting correlation matrices were visualised using a correlogram.

Principal Component Analysis (PCA): Principal Component Analysis (PCA) was performed to examine the multivariate structure of the trait data and identify key traits contributing to genotypic variation under each water regime. PCA was conducted on standardised trait values, and biplots were generated to visualise the relationships between genotypes and traits in the reduced dimensions of the first two principal components (PC1 and PC2).

Multi-trait Genotype–Ideotype Distance Index (MGIDI): To identify drought-tolerant genotypes based on multiple traits, the Multi-trait Genotype–Ideotype Distance Index (MGIDI) was computed following the method of[24]. This index integrates multiple traits by calculating the Euclidean distance between each genotype and an ideotype (ideal genotype). Traits were grouped based on their contributions to the principal components, and factor analysis was used to address multicollinearity. The ideotype was defined to reflect breeding goals:

Indices	Abbreviation used	Formula	References
Tolerance Index	TOL	Yp-Ys	[25]
Mean Productivity	MP	(Ys + Yp)/2	[25]
Geometric Mean Productivity	GMP	(YpxYs)0.5	[26]
Stress Susceptibility Index	SSI	(1 – Ys/Yp)/(1 – Ms/Mp)	[27]
Stress Tolerance Index	STI	$YpYs/(Mp)^2$	[26]
Yield Index	YI	Ys/Ms	[28]
Yield Stability Index	YSI	Ys/Yp	[29]
Relative Stress Index	RSI	(Ys/Yp)/(Ms/Mp)	[30]
Rank Sum	RS	Rank means + Standard Deviation of rank	[30]

Table 1. Different indices used to identify drought-tolerant mungbean genotypes. Yp: Grain yield of genotype under well-watered(WW) conditions; Ys: Grain yield of genotype under drought stress conditions; Mp: Mean yield of all genotypes under WW conditions; Ms: Mean yield of all genotypes under DS conditions.

Source of variation	D.F	Mean sum of squares							
		PH	NPB	NSB	PP	SPP	PL	TW	GY
Factor A—Conditions	1	30,380.44**	781.66**	1199.23**	132.51**	10.62**	29.73**	0.012**	2.75**
Factor B—Genotypes	121	125.42**	6.21**	12.89**	262.49**	15.93**	11.48**	5.30**	4.85**
Interaction effect (A × B)	121	70.34**	3.11**	6.39**	0.71**	0.06**	0.042**	0.01**	0.006**
Error	243	0.51	0.13	0.25	1.50	0.14	0.046	0.02	0.015

Table 2. Analysis of variance for morphometric and yield related traits of mungbean genotypes under well-watered and drought stress conditions. DF; Degrees of freedom, WW: Well-watered, DS: Drought stress, S.V: Source of Variations, D.F: Degrees of Freedom, PH: Plant Height (cm), NPB: No. of Primary branches per plant, NSB: No. Secondary branches per plant, PP: Pods per plant NSP No. of Seeds per pod, TW: Test weight (g), GY: Grain yield per plant (g), PL: Pod Length (cm), LA: Leaf Area (cm^2 per leaf), NDVI: Normalized Difference Vegetation Index, Qmax: Quantum efficiency of PSII, Tleaf: Leaf Temperature (^{O}C), GH$_2$O: Stomatal Conductance (mmol/m^{2}s), A: Net CO$_2$ Assimilation rate (μmol/m^{2}s), E: Transpiration rate (mmol/m^{2}s), VPD: Vapour Pressure deficit. *: significant at $p < 0.05$, **: significant at $p < 0.01$.

higher values were desirable for PH, NPB, NSB, PP, NSP, PL, TW, GY, A, E, GH$_2$O, NDVI, LA, and Qmax, while lower values were preferred for VPD and Tleaf. All traits were standardised and direction-adjusted so that lower MGIDI scores indicated closer similarity to the ideotype and thus greater desirability. Analyses were conducted in R using the metan package. Selection differentials and contributions of individual traits to the MGIDI were also evaluated to determine key drivers of genotype performance under drought.

Stress tolerance indices and ranking of genotypes

Various stress tolerance indices were calculated based on yield performance under both WW and DS conditions, as detailed in Table 1. These indices were used to rank genotypes according to their relative tolerance to drought stress.

Ranking of genotypes

To identify the most drought-tolerant genotypes, the rank sum (RS) was calculated across all stress indices. Genotypes were ranked from 1 to 122 based on their grain yield under both non-stress (Yp) and stress (Ys) conditions, with the highest-yielding genotypes receiving rank 1. Stress tolerance indices, including the Stress Tolerance Index (STI), Yield Stability Index (YSI), Geometric Mean Productivity (GMP), Mean Productivity (MP), and Yield Index (YI), which are positively correlated with drought tolerance, were ranked in descending order. Conversely, stress-sensitivity indices, such as Tolerance (TOL) and Stress Susceptibility Index (SSI), were ranked in ascending order, with lower values indicating greater tolerance. The RS for each genotype was obtained by summing the ranks from all indices. Genotypes with the lowest RS were considered the most drought-tolerant and received the highest final ranking, and vice versa[12].

Results

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) revealed highly significant effects ($p < 0.01$) for treatment, genotype, and the genotype × treatment (G × E) interaction across all evaluated traits (Tables 2 and 3). The significant G × E interaction indicated that genotypes responded differently to water stress. Genotypes VI003685AG, VI001408BG, and VI001435AG exhibited stable performance across both WW and DS conditions for yield and physiological traits, indicating robustness. In contrast, genotypes like VI001514AG and VI000938AG demonstrated greater sensitivity, showing significant declines in performance under drought conditions. These findings underscore

Source of variation	D.F	Mean sum of squares							
		LA	NDVI	Tleaf	VPD	E	GH_2O	A	Qmax
Factor A—Conditions	1	15,020.41	6.71**	523.73**	2244.16**	371.35**	1,810,855.5**	9238.87**	1.27**
Factor B—Genotypes	121	162.69	0.02*	1.89*	11.78**	2.71*	7340.51**	16.30**	0.02*
Interaction effect (A × B)	121	52.15	0.015*	0.73*	4.51**	1.55*	5097.06**	12.03**	0.02*
Error	243	0.14	0.002	0.03	0.008	0.001	3.46	0.06	0.005

Table 3. Analysis of variance for physiological traits of mungbean genotypes under well-watered and drought stress conditions. DF; Degrees of freedom, WW: Well-watered, DS: Drought stress, S.V: Source of Variations, D.F: Degrees of Freedom, PH: Plant Height (cm), NPB: No. of Primary branches per plant, NSB: No. Secondary branches per plant, PP: Pods per plant NSP No. of Seeds per pod, TW: Test weight (g), GY: Grain yield per plant (g), PL: Pod Length (cm), LA: Leaf Area (cm^2 per leaf), NDVI: Normalized Difference Vegetation Index, Qmax: Quantum efficiency of PSII, Tleaf: Leaf Temperature (^{O}C), GH_2O: Stomatal Conductance ($mmol/m^2s$), A: Net CO_2 Assimilation rate ($\mu mol/m^2s$), E: Transpiration rate ($mmol/m^2s$), VPD: Vapour Pressure deficit. *: significant at $p < 0.05$, **: significant at $p < 0.01$.

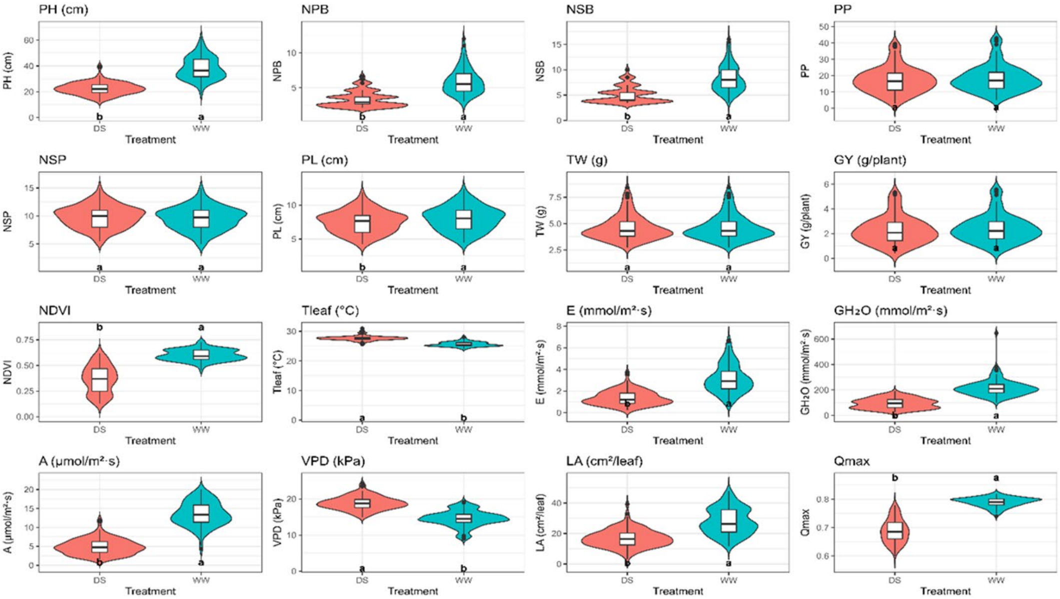

Fig. 1. Violin plot illustrating the genotypic variability in morpho-physiological traits of mungbean under well-watered (WW) and drought-stressed (DS) conditions. The plot visualizes the distribution, density, and spread of trait values across different genotypes, highlighting the effects of drought stress on trait expression. Significance was tested at P < 0.05%. *Note*: PH: Plant height, NDVI: Normalised Difference Vegetation Index, Qmax: Photosystem II efficiency, VPD: Vapour Pressure Deficit, GH2O: Stomatal Conductance.

the potential to identify genotypes with consistent performance across environments to develop drought-resilient cultivars.

Growth, morphological, physiological, and yield attributes of mungbean genotypes

Mungbean genotypes exhibited substantial variation under both well-watered (WW) and drought-stressed (DS) conditions. Violin plots (Fig. 1) revealed distinct shifts in trait distributions, with most traits showing significant declines under drought stress. Plant height (PH), primary branches (NPB), secondary branches (NSB), pods per plant (PP), seeds per pod (SPP), pod length (PL), test weight (TW), grain yield (GY), and leaf area (LA) all decreased significantly under drought stress, indicating the negative impact of water limitation on growth, reproduction, and photosynthetic potential.

Physiological traits showed the most drastic changes. Net CO_2 assimilation (A), stomatal conductance (GH_2O), and transpiration rate (E) dropped significantly (− 51.8%, − 49.3%, and − 48.8%, respectively) under drought stress. Conversely, leaf temperature (Tleaf) and vapour pressure deficit (VPD) increased by 8.1% and 27.5%, respectively, reflecting a greater evaporative demand. Chlorophyll fluorescence (Qmax) declined slightly by 12%, indicating a relative stability of PSII under drought conditions.

The magnitude of drought-induced reductions varied across traits (Table 4). For example, PH decreased by 28.5%, NPB by 33.2%, and NSB by 24.9%, while PP showed a moderate decline of 7%, and PL remained stable. Grain yield demonstrated considerable genotypic variation, with VI003685AG achieving the highest yield under

Traits	Mean		Min		Max		% Reduction
	WW	DS	WW	DS	WW	DS	
Plant height (cm)	36.74	26.28	18.70	12.11	57.56	46.51	28.5
No. of primary branches per plant	5.66	3.78	3.00	2.00	10.00	8.15	33.2
No. of secondary branches	7.42	5.57	3.00	2.00	13.50	10.00	24.9
No. of pods per plant	19.64	18.19	6.01	4.00	41.00	38.01	7.4
No. of seeds per Pod	10.45	10.14	5.00	5.00	15.00	14.00	3.0
Pod length (cm)	8.44	7.84	4.50	4.26	14.25	12.36	7.1
Test weight (g)	4.57	4.35	2.76	2.53	8.43	8.23	4.8
Normalized Difference Vegetation Index	0.61	0.41	0.45	0.13	0.74	0.69	32.1
Leaf temperature (^{O}C)	25.65	27.73	24.03	25.12	28.07	30.95	+8.1
Transpiration rate (mmol/m^{2}s)	3.28	1.68	0.89	0.25	6.69	4.72	48.8
Stomatal conductance (mmol/m^{2}s)	212.11	107.59	63.78	27.74	647.00	265.03	49.3
Net CO_2 Assimilation rate (μmol/m^{2}s)	13.50	6.51	5.04	1.39	19.96	17.86	51.8
Vapor pressure deficit (Pa/kPa)	14.53	18.53	8.95	12.84	19.21	24.29	+27.5
Leaf area (cm^2 per Leaf)	27.11	17.50	11.62	3.18	48.02	39.29	35.4
Qmax (Fv/Fm)	0.79	0.70	0.74	0.60	0.82	0.81	12.0
Grain yield per plant (g)	2.60	2.05	0.58	0.43	5.52	5.27	21.1

Table 4. Descriptive statistics for morpho-physiological and yield-related traits under well-watered and drought stress conditions mungbean genotypes. WW: Well-watered, DS: Drought stress, Min: Minimum, Max: Maximum.

both WW (5.52 g) and DS (5.27 g) conditions, whereas VI001514AG produced the lowest yields (0.58 g WW; 0.43 g DS).

Genotypic variability was observed in both morphological and physiological traits. For instance, PH ranged from 18.7 to 62.3 cm under WW and 12.11 to 46.51 cm under DS. NPB ranged from 3 to 10 (WW) and 2 to 8.15 (DS), while NSB varied from 3 to 13.5 (WW) and 2 to 10 (DS). PP ranged from 6.01 to 41 (WW) and 4 to 38.01 (DS), while PL remained stable at 4.26 to 12.36 cm across both conditions. TW showed a slight decrease of 4.8%, and LA ranged from 11.62 to 48.02 cm^2 under WW and 3.18 to 39.29 cm^2 under DS. NDVI was highest in Vaibhav (0.74) under WW and VI003685AG (0.74) under DS. The photosynthetic rate (A) peaked in VI003685AG under both conditions, while VI002739AG had the lowest rate under DS. Stomatal conductance and transpiration varied significantly, with VI003685AG consistently performing best.

Overall, the data show that drought stress adversely affected most traits, but the extent of reduction varied widely among genotypes. Genotype VI003685AG exhibited superior performance across morphological, physiological, and yield parameters, indicating its strong potential for drought tolerance.

Assessment of genetic variability in mungbean genotypes under WW and DS conditions

Genetic variability parameters, including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2bs), and genetic advance as a percentage of the mean (GAM), are summarised in Table 5. For most traits, PCV values were only slightly higher than their corresponding GCV values. Traits such as PH, PB, NSB, PP, NSP, TW, GY, and key physiological parameters (A, E, and gH_2O) showed high GCV and PCV values (>20%) under both WW and DS conditions. In contrast, Qmax, NDVI, and VPD displayed low to moderate variability, suggesting that these traits are more stable across genotypes.

Heritability estimates were high for most traits (>0.60), indicating that the traits are predominantly under genetic control and thus responsive to selection. High GAM values, especially for yield-related and physiological traits, further underscore the potential for significant genetic improvement through breeding.

Trait associations between grain yield and morpho-physiological traits

Pearson's correlation analysis revealed significant positive associations between grain yield (GY) and several morphological and physiological traits under both WW and DS conditions (Figs. 2 and 3). Under WW conditions, GY was positively correlated with PH (r = 0.35), NPB (r = 0.45), NSB (r = 0.51), PP (r = 0.55), NSP (r = 0.50), PL (r = 0.42), NDVI (r = 0.31), E (r = 0.30), GH_2O (r = 0.19), LA (r = 0.40), and A (r = 0.27). TW and Qmax also showed positive, though non-significant, associations.

Under DS conditions, these relationships were strengthened. GY exhibited strong positive correlations with PH (r = 0.67), NPB (r = 0.58), NSB (r = 0.62), PP (r = 0.53), NSP (r = 0.51), PL (r = 0.38), TW (r = 0.18), NDVI (r = 0.52), E (r = 0.57), gH_2O (r = 0.38), LA (r = 0.60), Qmax (r = 0.41), and A (r = 0.63). These strong correlations highlight the importance of canopy development, reproductive efficiency, and photosynthetic performance in maintaining productivity under drought. Conversely, Tleaf (r = − 0.18) and VPD (r = − 0.30) were negatively correlated with GY under DS, indicating that increased heat load and evaporative demand contribute to yield penalties.

Characters	GCV %		PCV %		h^2_{bs}		GA		GAM %	
	WW	DS	WW	DS	WW	DS	WW	DS	WW	DS
Plant height (cm)	22.57	21.25	22.69	21.26	0.78	0.7	17.71	9.84	46.28	43.75
No. of primary branches per plant	30.87	33.41	31.39	34.73	0.85	0.85	3.68	2.22	62.54	66.22
No. of secondary branches	31.80	31.36	32.32	33.06	0.97	0.9	5.30	3.12	64.46	61.30
No. of pods per plant	44.84	45.56	45.08	46.14	0.85	0.86	16.89	16.08	91.87	92.69
No. of seeds per Pod	21.11	20.01	21.43	20.05	0.79	0.8	4.09	4.05	42.83	41.14
Pod length (cm)	21.92	21.67	22.10	21.67	0.91	0.9	3.59	3.36	44.79	44.64
Test weight (g)	25.26	25.31	25.26	25.31	0.89	0.87	2.39	2.39	52.03	52.15
Normalised Difference Vegetation Index	8.02	35.91	10.18	37.96	0.62	0.89	0.08	0.25	13.04	69.99
Leaf temperature (^{O}C)	3.09	2.99	3.09	2.99	0.65	0.75	1.63	1.71	6.37	6.17
Transpiration rate (mmol/m^{2}s)	41.74	49.30	41.74	49.32	0.74	0.65	2.67	1.38	85.97	86.44
Stomatal conductance (mmol/m^{2}s)	31.40	43.25	31.42	43.26	0.67	0.61	18.02	19.46	64.65	89.07
Net CO_2 Assimilation rate (μmol/m^{2}s)	23.25	42.20	23.25	42.26	0.65	0.62	6.50	4.22	47.89	86.83
Vapour pressure deficit (Pa/kPa)	15.01	9.74	15.02	9.75	0.74	0.71	4.50	3.78	30.91	20.04
Leaf Area (cm^2 per Leaf)	30.78	34.50	30.80	34.62	0.79	0.78	17.68	11.90	63.39	70.83
Qmax (Fv/Fm)	1.27	5.65	2.84	6.36	0.2	0.79	0.01	0.07	1.17	10.34
Grain yield per plant (g)	45.91	48.59	46.01	48.89	0.75	0.63	2.27	2.24	74.35	79.48

Table 5. Genetic variability parameters for morpho-physiological and yield-related traits under well-watered and drought stress conditions of mungbean genotypes. GCV: Genotypic Coefficient of Variance, PCV: Phenotypic Coefficient of Variance,h^2_{bs}: Heritability (Broad Sense), GA: Genetic Advance, GAM: Genetic Advance as percentage of Mean.

Stress tolerance indices and genotype ranking

Yield-based drought tolerance indices (Table 6) provided additional insights into genotype performance across WW and DS environments. VI003685AG maintained the highest grain yield in both conditions, while VI001514AG consistently produced the lowest. Tolerance index (TOL) values varied widely, with VI001435AG (0.001) and VI001974BG (0.005) showing minimal yield reductions under DS, indicating superior stability. In contrast, the check variety PDM-139 recorded the highest TOL (0.54), reflecting high sensitivity. At the same time, mean productivity (MP) and geometric mean productivity (GMP) identified VI001191BG as the top performer, whereas VI001514AG ranked lowest. The stress susceptibility index (SSI) further highlighted VI001435AG (0.001) as the most tolerant, while VI000938AG (0.48) was the most susceptible. The stress tolerance index (STI) placed VI001191BG highest (4.21), and the yield index (YI) and yield stability index (YSI) favoured VI003957AG and V001435AG, respectively.

Additionally, to integrate performance across all indices, a cumulative ranking approach was used. Genotypes VI003685AG, VI002051BG, VI004811BG, and VI000852AG emerged as the most drought-tolerant and stable performers, whereas check varieties such as Vaibhav, PAU-911, NM-94, EC-0398949, and IPM-205-7 ranked substantially lower than those genotypes.

Principal component analysis (PCA) and multi-trait genotype-ideotype distance index (MGIDI)

Principal Component Analysis (PCA) was conducted to examine the multivariate structure of trait variation across the mungbean genotypes. The first two principal components (PC1 and PC2) explained 30.7% of the total variability (Fig. 4). PC1 (17.3%) was primarily associated with yield-related traits, including NSP, PL, NPB, NSB, and GY, suggesting that PC1 captures the genotypic variation in reproductive potential and branching capacity. Genotypes that loaded higher on PC1, such as VI003379BG and VI003744AG, exhibited superior performance in NSP and PL, indicating that these genotypes possess better yield components (i.e., more seeds per pod and longer pods). This highlights the importance of PC1 in determining genotypic performance related to reproduction and overall productivity under both well-watered and drought-stressed conditions.

In contrast, PC2 (13.4%) primarily represented the variation in physiological traits, including E, LA, VPD, and GH_2O, reflecting differences in canopy activity, water-use efficiency, and stomatal regulation under drought stress. Genotypes such as VI000316AG and VI001400AG, which had higher loadings on PC2, were positioned closer to the PC2 axis, suggesting these genotypes possess better vegetative architecture and enhanced physiological responses to water stress. These genotypes demonstrated efficient gas exchange and canopy development, which are critical for sustaining productivity under drought conditions by improving the plant's ability to capture and use water efficiently. The PCA biplot (Fig. 4) provides a visual representation of how the various traits contribute to genotype performance across water regimes. Traits such as GY, NSP, PL, and NPB are strongly associated with PC1, emphasising their importance in determining yield potential. This aligns with the fact that higher PC1 loadings correspond to superior yield components. Conversely, physiological traits such as E, GH_2O, and VPD are more strongly correlated with PC2, highlighting their roles in drought adaptation mechanisms, such as water-use efficiency and stomatal conductance.

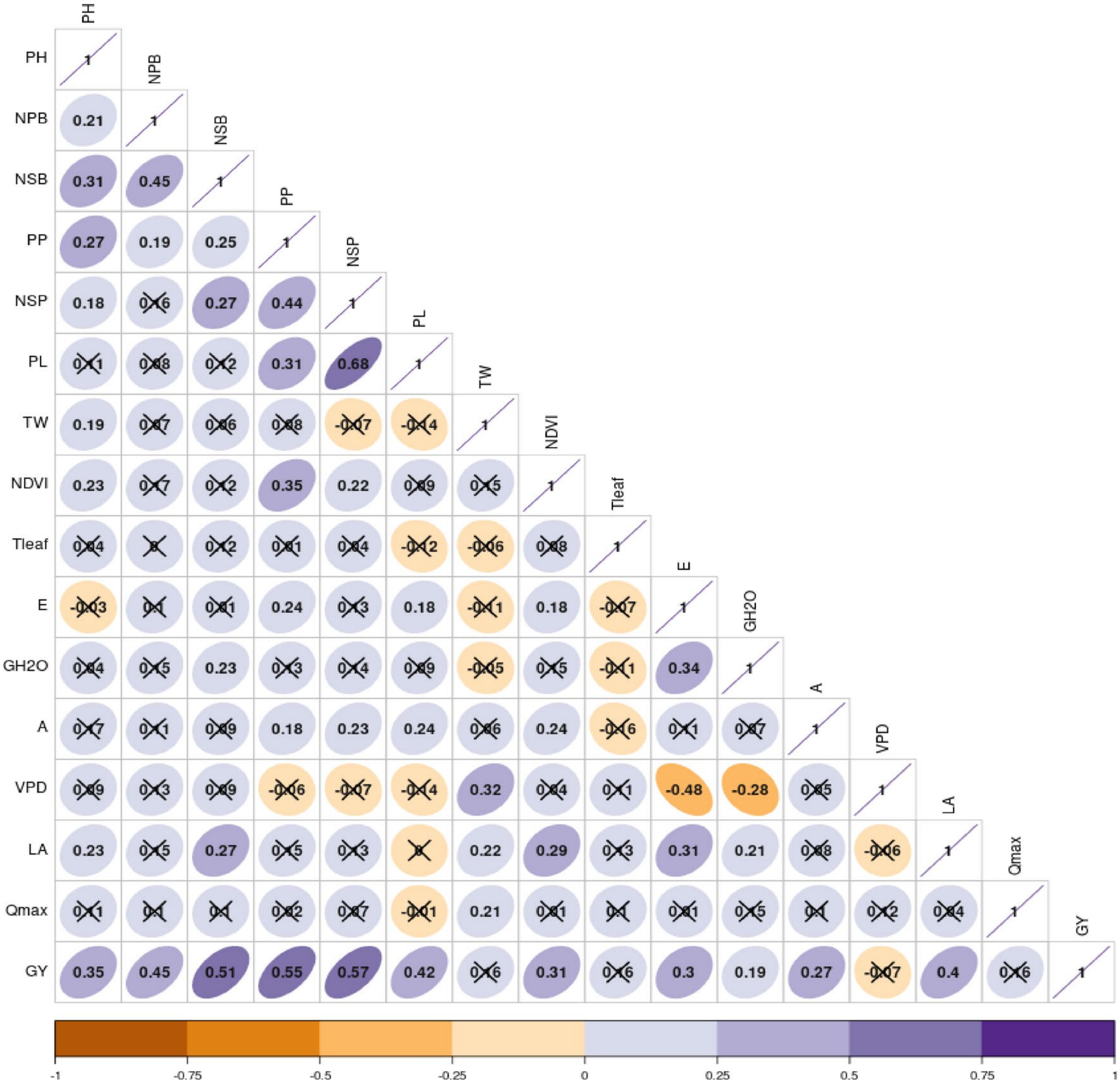

Fig. 2. Association of morpho-physiological traits with yield and yield-related attributes of mungbean genotypes under well-watered (WW) conditions. The figure illustrates the relationships between key physiological parameters and yield components, providing insights into trait contributions to productivity under WW conditions. WW: Well Watered, PH: Plant height, NPB: Number of Primary Branches, NSB: Number of Secondary Branches, PP: Pods per Plant, PL: Pod Length, TW: Test Weight, NDVI: Normalized Difference Vegetation Index, Tleaf: Leaf Temperature, E: Transpiration rate, A: Net CO2 Assimilation rate, VPD: Vapour Pressure Deficit, GH_2O: Stomatal Conductance, LA: Leaf area per leaf, GY: Grain yield per plant.

To integrate all the traits into a unified framework and identify genotypes with superior drought resilience, the Multi-trait Genotype-Ideotype Distance Index (MGIDI) was applied. The MGIDI ideotype was explicitly defined to align with breeding goals: higher values were considered desirable for PH, NPB, NSB, PP, NSP, PL, TW, GY, A, E, GH_2O, NDVI, LA, and Qmax, whereas lower values were preferred for Tleaf and VPD. The ideotype thus represents an ideal genotype with balanced traits that contribute to high productivity and physiological performance under drought stress. All traits were standardised and direction-adjusted, so that lower MGIDI values indicated genotypes closer to the ideotype and thus more desirable for breeding. Genotypes such as VI003685AG, VI002051BG, and VI003957AG were found to be closest to the ideotype, demonstrating a balanced combination of desirable morphological, yield, and physiological traits. These genotypes exhibited superior performance across a wide range of traits, including yield components, canopy development, and physiological performance under drought conditions, making them strong candidates for drought-tolerant breeding. MGIDI rankings further confirmed that these genotypes were among the best performers, combining productive plant architecture with enhanced drought-resilience mechanisms.

Factor analysis grouped traits into seven latent factors representing plant architecture, reproductive attributes, physiological drought-response mechanisms, and grain-yield determinants (Table 7). Branching traits (NPB and NSB) showed strong loadings within FA1, NSP, and PL defined FA2, and key physiological traits (E, gH_2O, VPD) clustered within FA3, with high communalities indicating robust trait representation. The ideotype was

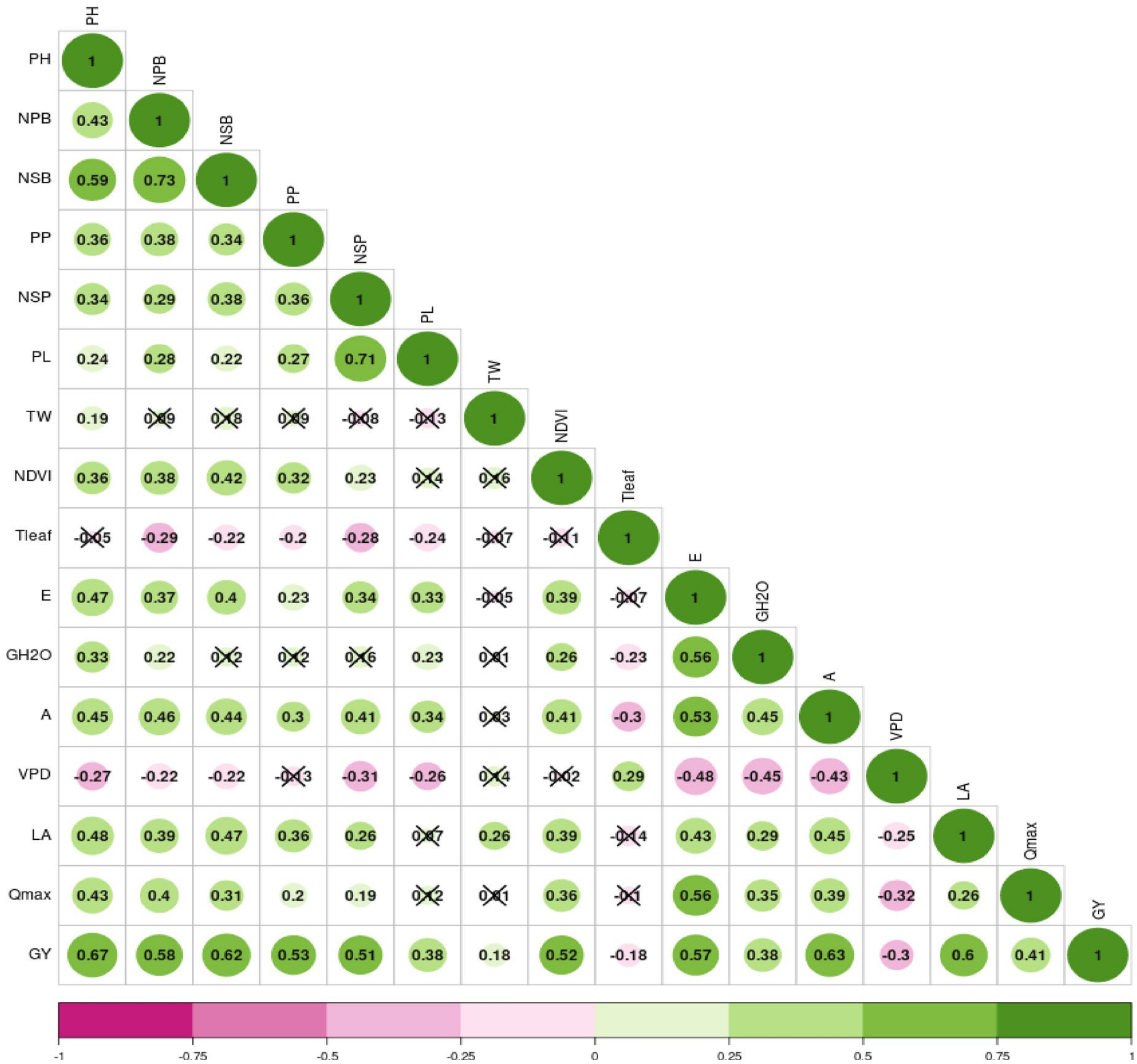

Fig. 3. Association of morpho-physiological traits with yield and yield-related attributes of mungbean genotypes under drought-stressed (DS) conditions. The figure highlights the relationships between key physiological traits and yield components, offering insights into trait contributions to productivity under drought stress conditions. DS: Drought Stress, PH: Plant height, NPB: Number of Primary Branches, NSB: Number of Secondary Branches, PP: Pods per Plant, PL: Pod Length, TW: Test Weight, NDVI: Normalized Difference Vegetation Index, Tleaf: Leaf Temperature, E: Transpiration rate, A: Net CO2 Assimilation rate, VPD: Vapour Pressure Deficit, GH_2O: Stomatal Conductance, LA: Leaf area per leaf, GY: Grain yield per plant.

explicitly defined to align with breeding goals: higher values were considered desirable for PH, NPB, NSB, PP, NSP, PL, TW, GY, A, E, gH_2O, NDVI, LA and Qmax, whereas lower values were desirable for VPD and Tleaf. All traits were standardised and direction-adjusted so that lower MGIDI values indicated greater similarity to the ideotype (Fig. 5).

Selection differentials demonstrated substantial improvement potential (Table 8). Grain yield exhibited the highest predicted gain (+ 23.0%), followed by strong gains for NSB (+ 20.2%), gH_2O (+ 19.2%) and NPB (+ 19.1%). Moderate positive gains in NDVI, LA and E further supported their contribution to drought adaptation. Based on MGIDI rankings, 18 genotypes were identified as closest to the ideotype, including VI002051BG, VI003685AG, VI001408BG, VI003957AG, VI002402BG, VI000316AG, VI001126BG, VI001435AG, VI003232AG, VI001448A-BLM, VI000852AG, VI001482BG, VI001284AG, VI004811BG, VI001419BG, VI000942AG, VI001400AG and VI004096AG. These genotypes demonstrated a balanced combination of productive plant architecture, favourable yield components and enhanced physiological performance under moisture stress. Overall, the application of the combined PCA–MGIDI approach provided a robust, multivariate framework for identifying genotypes that balance high productivity with physiological efficiency under water stress, offering valuable insights for targeted breeding programs aimed at developing drought-resilient mungbean cultivars.

Accessions	Yp	Ys	TOL	MP	GMP	SSI	STI	YI	YSI	RSI	RS	Final rank
VI003685AG	5.32	5.27	0.05	5.30	5.29	0.16	4.15	2.15	0.99	1.05	54	1
VI002051BG	5.18	5.13	0.04	5.15	5.15	0.15	3.93	2.09	0.99	1.05	74	2
VI004811BG	4.83	4.82	0.01	4.82	4.82	0.05	3.44	1.97	1.00	1.06	85	3
VI000852AG	5.21	5.14	0.07	5.17	5.17	0.24	3.96	2.10	0.99	1.05	94	4
VI001548AG	4.28	4.24	0.04	4.26	4.26	0.14	2.68	1.73	0.99	1.05	141	5
VI001435AG	3.56	3.56	0.00	3.56	3.56	0.00	1.88	1.45	1.00	1.06	148	6
VI001400AG	4.42	4.36	0.06	4.39	4.39	0.24	2.85	1.78	0.99	1.05	159	7
VI001448A-BLM	4.99	4.89	0.10	4.94	4.93	0.35	3.61	1.99	0.98	1.04	165	8
VI001408BG	4.34	4.28	0.06	4.31	4.31	0.26	2.75	1.75	0.99	1.04	175	9
VI000942AG	5.12	4.95	0.17	5.04	5.03	0.58	3.75	2.02	0.97	1.03	197	10
VI003720BG	4.52	4.40	0.12	4.46	4.46	0.46	2.95	1.80	0.97	1.03	213	11
VI003648BG	4.59	4.46	0.14	4.52	4.52	0.51	3.03	1.82	0.97	1.03	222	12
VI003379BG	4.49	4.36	0.13	4.42	4.42	0.51	2.89	1.78	0.97	1.03	230	13
VI000589B-BR	3.11	3.08	0.03	3.09	3.09	0.20	1.42	1.26	0.99	1.05	233	14
VI003678 BG	4.24	4.14	0.11	4.19	4.19	0.43	2.60	1.69	0.98	1.03	235	15
VI001191 BG	5.43	5.24	0.19	5.33	5.33	0.63	4.21	2.14	0.96	1.02	238	16
VI002402 BG	4.17	4.07	0.11	4.12	4.12	0.44	2.51	1.66	0.97	1.03	242	17
VI002926 AG	5.34	5.15	0.19	5.25	5.24	0.62	4.07	2.10	0.96	1.02	242	18
VI003212 B-BLM	3.01	2.99	0.02	3.00	3.00	0.15	1.33	1.22	0.99	1.05	245	19
VI004933 AG	3.35	3.29	0.06	3.32	3.32	0.34	1.63	1.34	0.98	1.04	245	20

Table 6. Stress tolerance indices and ranking of top 20 mungbean genotypes based on grain yield under well-watered (Yp) and drought stress conditions (Ys). Where, TOL = Drought Tolerance Index; MP = Mean Productivity; GMP = Geometric Mean Productivity; SSI = Ranking based on SSI values; STI = Stress Tolerance Index; YI = Yield Index; YSI = Yield Stability Index; RSI = Relative Stress Index; RS: Rank Sum.

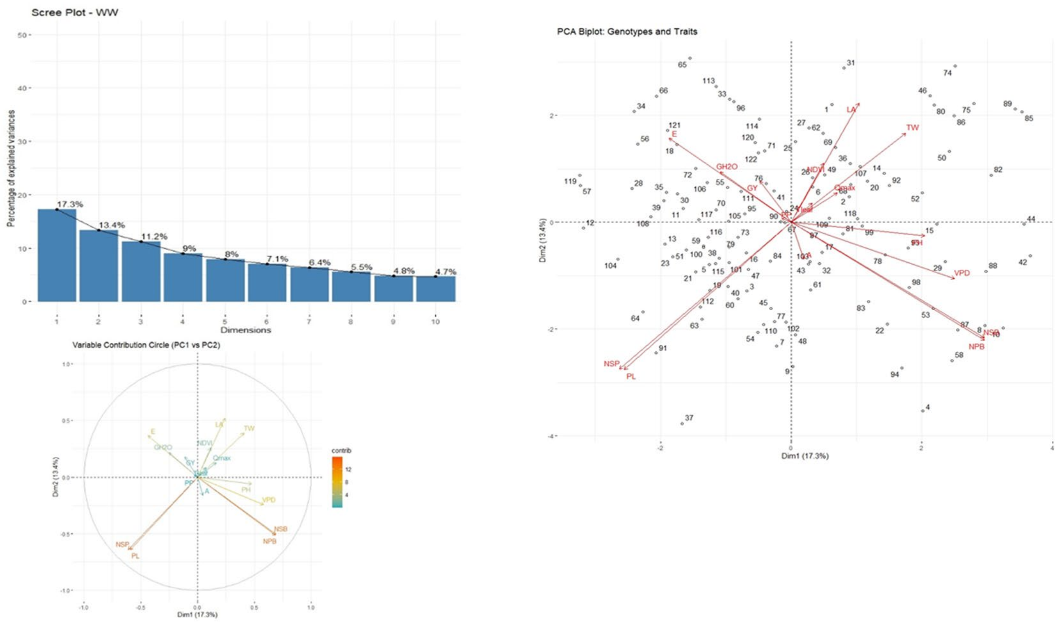

Fig. 4. Principal Component Analysis (PCA) biplot and scree plot illustrating the relationships among morpho-physiological traits, the distribution of 122 mungbean genotypes under drought stress, and the proportion of variance explained by each principal component. PC1 and PC2 together capture the majority of variation and effectively differentiate genotype responses.

Discussion

Drought stress represents a major limitation in rainfed mungbean production, particularly during the flowering and pod-filling stages, which are critical for yield determination[4,6]. In this study, 122 genetically diverse genotypes were evaluated under well-watered (WW) and drought-stressed (DS) conditions using a semi-controlled

Trait	FA1	FA2	FA3	FA4	FA5	FA6	FA7	Communality	Uniqueness
PH	− 0.42	− 0.01	− 0.14	0.38	0.33	0.12	− 0.25	0.52	0.48
NPB	− 0.96	0.07	− 0.12	− 0.04	− 0.02	0.03	0.1	0.96	0.04
NSB	− 0.96	0.08	− 0.11	− 0.02	− 0.05	0.02	0.09	0.96	0.04
PP	0.03	0.01	− 0.06	0.08	− 0.2	0.16	− 0.71	0.59	0.41
NSP	0.08	− 0.98	0.02	− 0.1	− 0.05	− 0.01	0.05	0.98	0.02
PL	0.06	− 0.98	0.01	− 0.07	− 0.06	− 0.02	0.03	0.98	0.02
TW	0.13	0.24	− 0.28	0.47	0.51	0.08	0.18	0.67	0.33
GY	0.1	− 0.17	0.04	0.24	0.1	− 0.75	− 0.07	0.67	0.33
NDVI	0.0	− 0.04	0.01	0.76	− 0.17	− 0.02	− 0.12	0.62	0.38
Tleaf	− 0.01	0.1	− 0.14	− 0.06	− 0.07	− 0.76	0.03	0.62	0.38
E	0.13	0.01	0.8	0.11	− 0.05	− 0.02	0.0	0.67	0.33
GH2O	− 0.04	0.0	0.71	0.05	0.13	0.15	0.24	0.61	0.39
A	− 0.11	− 0.07	0.02	0.1	− 0.2	0.23	0.73	0.65	0.35
VPD	− 0.21	0.03	− 0.76	0.15	0.18	− 0.01	0.1	0.68	0.32
LA	0.01	0.27	0.13	0.67	0.04	− 0.22	0.19	0.62	0.38
Qmax	0.0	0.04	0.0	− 0.15	0.87	− 0.05	− 0.01	0.78	0.22

Table 7. Factor loadings and communalities from factor analysis with rotation. FA, factor analysis.

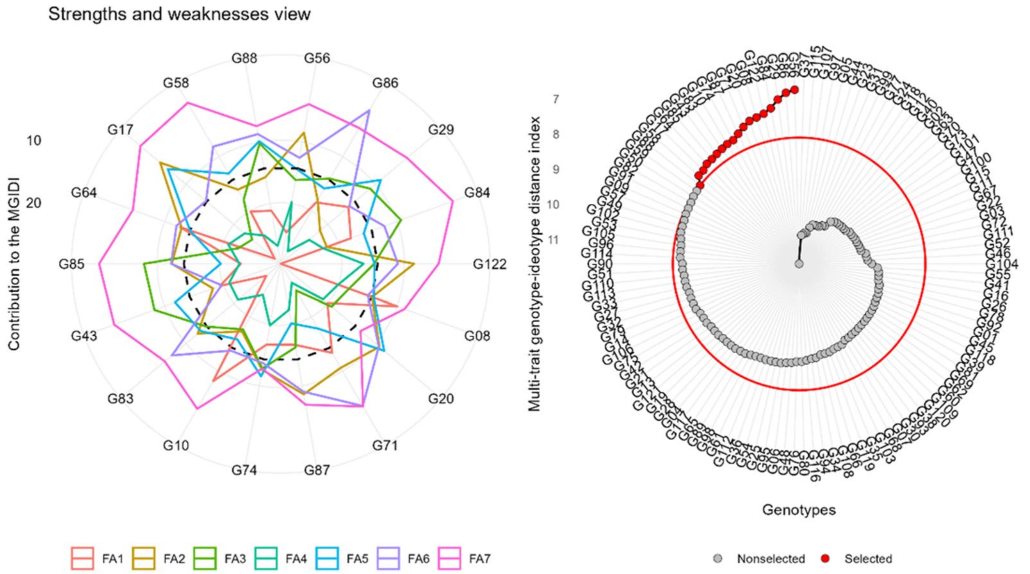

Fig. 5. MGIDI scores and factor contributions for 122 mungbean genotypes under drought stress. Genotypes with lower MGIDI values are closer to the ideotype and considered more drought-tolerant. Factor contributions indicate which trait groups most influenced each selected genotype's performance.

greenhouse setup. This approach allowed for precise stress imposition and phenotyping. However, the confined rooting volume in pots likely intensified drought stress compared with field conditions. Restricted root growth can limit water acquisition and exaggerate differences among genotypes, particularly for traits related to drought avoidance or deeper soil water extraction[31].

Additionally, the study imposed only a single terminal drought, while mungbean often encounters intermittent or early-season drought in the field. Genotypes performing well under terminal stress may not exhibit the same resilience under fluctuating stress patterns. Similarly, grain yield per plant in pots does not fully reflect yield per unit area in the field, where factors like competition, plant architecture, and lodging susceptibility influence overall productivity. These factors underscore the importance of field validation of top-performing genotypes to ensure greenhouse results are representative of field performance.

Despite these limitations, substantial genotypic variation was observed for both morphological and physiological traits under WW and DS conditions. Yield-contributing traits, including plant height (PH), branching (NPB, NSB), pod number (PP), and leaf area (LA), exhibited strong positive correlations with grain yield (GY). In contrast, Tleaf and VPD were negatively associated with GY under DS, underscoring the

Traits	Factor	Xo	Xs	SD	SD%	h^2	SG	SG%	Objective	Goal
PH	FA1	38.3	43.2	4.94	12.9	0.95	4.92	12.8	Increase	100
NPB	FA1	5.89	7.04	1.15	19.5	0.93	1.13	19.1	Increase	100
NSB	FA1	8.23	9.92	1.69	20.6	0.94	1.66	20.2	Increase	100
NSP	FA2	9.54	10.7	1.16	12.2	0.95	1.15	12	Increase	100
PL	FA2	8.01	9.08	1.07	13.4	0.92	1.06	13.3	Increase	100
E	FA3	3.11	3.56	0.457	14.7	0.89	0.457	14.7	Increase	100
GH2O	FA3	215	257	41.4	19.2	0.91	41.3	19.2	Increase	100
VPD	FA3	14.6	14.6	0.0347	0.238	0.87	0.0346	0.238	Decrease	0
NDVI	FA4	0.598	0.611	0.0135	2.26	0.76	0.0104	1.73	Increase	100
LA	FA4	27.9	31.1	3.24	11.6	0.87	3.24	11.6	Increase	100
TW	FA5	4.74	5.25	0.514	10.8	0.81	0.514	10.8	Increase	100
Qmax	FA5	0.788	0.791	0.003	0.381	0.35	0.00107	0.135	INCREASE	100
GY	FA6	2.41	2.96	0.555	23.1	0.78	0.554	23	Increase	100
Tleaf	FA6	25.6	25.4	−0.174	−0.68	0.7	−0.174	−0.68	Decrease	0
PP	FA7	18.4	18.5	0.114	0.622	0.79	0.114	0.619	Increase	100
A	FA7	13.6	13.6	0.0575	0.424	0.69	0.0575	0.424	Increase	100

Table 8. Interrelations among correlated traits, selection differential, heritability, and indicators. FA, factor analysis; X0 , mean of the nonselected genotypes; XS , mean of the selected genotypes; SD, selection differential; h2b, heritability; SG, genetic gain owingto selection.

importance of canopy development and efficient water-use regulation for drought resilience[32,33]. Physiological traits such as net photosynthesis (A), stomatal conductance (gH_2O), and transpiration rate (E) retained moderate values in high-performing genotypes, suggesting partial maintenance of photosynthetic activity despite water limitation[34–37]. High heritability and genetic advance for these traits further suggest that direct selection for yield and key physiological parameters can be effective for improving drought adaptation[38–41].

To integrate multivariate trait responses, Principal Component Analysis (PCA) and the Multi-trait Genotype-Ideotype Distance Index (MGIDI) were employed. PCA revealed six principal components accounting for over 87% of the total variation, with the first component representing yield-related and architectural traits and the second capturing physiological attributes. This approach allowed the identification of genotypes with complementary adaptation strategies. For example, G91 (VI003379BG) and G104 (VI003744AG) were associated with reproductive yield components, while G8 (VI000316AG) and G98 (VI003648BG) were associated with vegetative branching, indicating distinct approaches to stress tolerance. The MGIDI further refined selection by integrating trait desirability, highlighting genotypes such as VI003685AG, VI002051BG, and VI004811BG, which combined high yield, stable branching, and favourable physiological traits, with predicted selection gains of + 23% for grain yield and + 20.2% for secondary branching[42]. This multivariate framework emphasises stable, integrated performance rather than focusing on single-trait extremes, partially mitigating the limitations inherent in pot-based screening.

However, the physiological mechanisms underlying tolerance in the top-ranked genotypes remain largely theoretical. The absence of root system data, water relations measurements, and biochemical assessments (e.g., osmolytes, antioxidants) limits our ability to interpret these mechanisms fully. High-performing genotypes likely combine efficient stomatal regulation, sustained photosynthesis, and canopy cooling to maintain productivity under drought stress, but these processes require validation through targeted physiological and molecular analyses[34–37]. Therefore, while the study provides valuable insights into genotype performance and trait associations, the findings must be regarded as preliminary until confirmed under field conditions, where natural variation in drought timing and intensity is present.

Overall, this study identifies genotypes with promising drought resilience and demonstrates the utility of integrating PCA and MGIDI to capture multidimensional trait performance. The combined evaluation of morphological, physiological, and yield traits provides a robust framework for preliminary selection, laying the foundation for breeding programs targeting drought-adaptive mungbean varieties. However, multi-environment field trials, along with complementary analyses of root traits, water-use efficiency, and biochemical responses, will be crucial to confirm the durability and mechanistic basis of the observed tolerance and to ensure that high-performing genotypes identified under controlled conditions perform well in real-world cultivation scenarios.

These findings are preliminary and require multi-location field validation before being utilised for breeding purposes. Although the greenhouse-based screening provided valuable insights into genotype performance under controlled drought stress, these results may not fully capture the complexity of field conditions. Therefore, further evaluation across diverse agro-ecological zones is essential to confirm the stability and reliability of the identified drought-resilient genotypes under real-world conditions.

Conclusion

This study identified drought-tolerant mungbean genotypes through an integrated approach combining phenotypic evaluation, physiological screening, stress indices, PCA and the MGIDI. Significant genetic variability was observed among the genotypes, highlighting strong potential for preliminary selection and improvement. Stress indices, such as the STI and GMP, efficiently identified genotypes with stable yield across environments, while PCA pinpointed key traits like grain yield, stomatal conductance, and transpiration rate as critical to drought adaptation. The MGIDI index provided a refined selection tool, identifying genotypes such as VI003685AG, VI002051BG, and VI003957AG as the most preliminarily identified drought-resilient genotypes. These genotypes exhibited superior performance in both morphological and physiological traits, demonstrating the value of a multifaceted selection approach. While pot-based screening was effective for controlled drought stress, further multi-location field validation is needed to confirm the stability and reliability of these genotypes under real-field conditions. The greenhouse conditions may not fully reflect the complexities of field environments, where factors such as competition, soil conditions, and environmental stress patterns influence genotype performance. Therefore, further evaluation across diverse agro-ecological zones is essential to confirm the stability and reliability of these drought-resilient genotypes. Overall, this study provides valuable insights and promising genetic material for breeding potential drought-tolerant mungbean cultivars, contributing to food security in the face of climate change.

Data availability

The manuscript presents all the data generated in this research. Additional data is provided in the supplementary material file.

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Source of seeds

Seeds were procured from World Vegetable Center - South and Central Asia, IN, Hyderabad- 502324, India.

Author contributions

BPS: Conception, writing and editing; RB, IVG, AG, SS, SG; data collection: JR, BKM, HCB, HMH, and SRK Manuscript editing; DS: editing and formal data analysis RN: Seed Supply and Editing manuscript. All the authors read the manuscript and approved it for submission.

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Declarations

Competing interests

The authors declare no competing interests.

Additional information

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