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Research article

Evaluation of Polyethylene Glycol (PEG-6000) Induced Drought Stress Tolerant Mungbean Genotypes by using Correlation, Principal Component, Hierarchical Clustering and Multi-Trait Genotype-Ideotypes Distance Index Analysis

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Abstract

Determining a plant's ultimate population under water stress requires seedling establishment and germination. The current study was aimed at identifying mungbean genotypes that were tolerant to drought stress. The treatments were: Factor A: polyethylene glycol 6000 (PEG-6000) inducing different levels of water potential (i.e., 0.0 (distilled water as a control), -0.7, -1, -2, and -4 bar) and Factor B: Thirty-three mungbean genotypes, collected from various national and international organizations. Each genotype's seeds were planted in a petri dish (9 cm diameter) containing sand bed and were moistened with appropriate amounts of water potential and left to develop into seedlings of all genotypes for up to 10 days. The findings showed that when PEG-6000 concentration was raised, germination, shoot and root length, and the associated fresh and dry weights decreased significantly. Among these tested genotypes, BMX-08010-2, BMX-08009-7, BMX-01015, BARI Mung-8, BARI Mung-2, and BU Mung-2 were found to be tolerant against drought stress based on their % germination and germination indices, as well as their seedling traits. Principal component analysis, multi-trait genotype-ideotype

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distance index (MGIDI), two-dimensional heat map, and hierarchical clustering analysis also revealed the same genotypes to be stable and capable of withstanding water deficiency stress. In response to water stress, the genotypes BARI Mung-1, BARI Mung-3, BU Mung-4, and BMX-05001 showed poor germination indices along with relatively poor seedling characteristics. The results of the present research provide criteria for the selection of drought-tolerant mungbean genotypes in future breeding programs.

Keywords: water deficit stress; PEG-6000; germination; seedling growth; mungbean

1. Introduction

Plants experience various environmental stresses including drought, salinity, heat, cold and waterlogging, which can negatively impact crop productivity. Of these factors, drought is one of the main issues and accounts for 26% of all plant stresses (Mirzaei et al., 2014), and drought alone is responsible for 70% of agricultural yield losses globally (Boyer, 1982). Water shortage restricts plant survival and early seedling enlargement through delayed establishment or decreased ultimate germinability (Gamze et al., 2005). The most important stages for seed establishment that determine effective crop output are early seed germination and seedling development (Swathi et al., 2017). Globally, mungbean (*Vigna radiate* L. Wilczek) is a significant short-duration pulse with the capacity to fix nitrogen, inhibit soil erosion, and improve soil. The plant needs few inputs, has broad adaptability, and flourishes in drought-prone environments. It is a valuable source of vitamins, calcium, phosphorus, and protein. However, there is a lot of variation in the mungbean genotype capacity to withstand drought. Its complete reliance on the rainy season for moisture, together with the rapidly decreasing rainfall, prevents it from going through normal physiological activities related to growth and development (Kumar, 2003). Water deficiency with a variable level affects several physiological and metabolic processes in crops during development, including germination, photosynthesis, growth, respiration, and nutrient metabolism. This may result in low yield and poor growth (Durga et al., 2003). Thus, there is a huge need for drought-tolerant cultivars that can tolerate limited soil moisture stress while producing larger yields. When choosing novel kinds, it might be challenging to select complicated mechanisms of resistance due to the broad variation of plant stress responses and the overlap in functions among their component components (Rajwinder et al., 2017). Nevertheless, the present crop of mungbean do not produce high-yields and the existing cultivars do not have a sufficient degree of drought resistance.

It is possible to manage drought stress by identify genotypes that are capable of withstanding drought stress. However, drought tolerance is a complicated nature that requires several strategies and techniques to overcome. Selection of greater drought resilience may make it easier to create new genotypes. In arid climates, having a variety of parents that can withstand drought is essential (Ashraf et al., 1992; Tuberosa & Salvi, 2006). The variation of the elements and their relationship to water scarcity tolerance in crop field environments has led to efforts to assess the degree of tolerance through a sole parameter that has limited utility (Dutta & Bera, 2008). Research on water potential has enabled the identification of genotypes capable of thriving under water stress. Some genotypes, known to germinate in environments with lower water potentia,l often successfully do so and progress into vigorous seedlings (Michel & Kaufmann,1973). However, PEG-6000 is a component of drought that creates osmotic shock, and changes in water potential might result from adding PEG-6000 solution to the growth medium for

seed germination. This makes it possible to identify genotypes that are desirable for growing under conditions of water deficit stress. This study was aimed to identify drought-tolerant genotypes based on germination and relative performance of seedling traits by screening 33 mungbean genotypes for their water deficit stress tolerance under various water potentials (0 bar, -0.7 bar, -1 bar, -2 bar, and -4 bar) induced by PEG 6000 in a laboratory setting. To boost the production of summer mungbean, it is vital to screen these cultivars for drought tolerance and comprehend the processes that underlie the tolerance. The selection of genotypes suited to various geographic locations may result from the seedling tests conducted under varying levels of osmotic stress. Therefore, an effort was made to pinpoint the genotypes of mungbean that were tolerant to drought throughout the germination and seedling development phases when cultivated under various stress circumstances.

2. Materials and Methods

2.1 Experimental location and condition

The experiment was performed under laboratory conditions at the Department of Agronomy, Hajee Mohammad Danesh Science and Technology University (HSTU), Dinajpur. The experiment was carried out at ambient laboratory room temperature (25±0.3°C) under natural light conditions (8-10 h) and relative humidity of 74±1%. The average photosynthetic photon flux density was 200-210 $cm^{-2}s^{-1}$, as measured by a digital Lux meter (model LX-101, made in Portugal).

2.2 Materials to be used in this study

The study aimed to screen out water deficit stress tolerant mungbean genotypes through the evaluation of germination indices and relative seedling growth under conditins of water stress induced by PEG-6000. PEG-6000 induced levels of water potential (i.e., control (0), -0.7, -0.1, -2, and -4 bar) were used as treatments. Thirty-three mungbean genotypes were obtained from the following national agricultural research organizations: BARI (Bangladesh Agricultural Research Institute), BINA (Bangladesh Institute of Nuclear Agriculture), and BSMRAU (Bangabandhu Sheikh Mujibur Rahman Agricultural University) in Bangladesh. Table 1 shows a list of the mungbean genotypes that includes popular released varieties as well as improved breeding lines.

2.3 Design and treatment

The experiment was carried out in two factor completely randomized design (CRD) with three replications. Stress levels (different levels of water potential) were divided in Factor A while genotypes were partitioned in Factor B. The levels of PEG 6000 induced water potential (0.0, -0.7, -1, -2, and -4 bars) were developed by dissolving the calculated amount of PEG-6000 in distilled water. Distilled water was used as a control (0.0 bar). According to Michel and Kaufmann's equation (Michel & Kaufmann,1973), the level of various concentrations of PEG 6000 was computed as follows:

$$\text{Water potential (bar index)} = (-1.18\times10^{-2}) \times C - (1.18\times10^{-4}) \times C + (2.67 \times 10^{-4}) \times C \times T + (8.39 \times 10^{-7}) \times C^2T$$

Where, C=PEG-6000 concentration and T=temperature (centigrade).

Table 1. Pedigrees of the mungbean genotypes tested in the current experiment

Sl. No.	Genotypes	Code	Pedigree/Parents	Remark	Releasing Year
1.	BARI Mung-1 (Mubarik)	G1	Advance line of Mung 7706 (India)	V	1982
2.	BARI Mung-2 (Kanti)	G2	VC 2768A × VC 6141-36 (7715)	V	1987
3.	BARI Mung-3	G3	Sonamung(Local) × BARI Mung- 2 (BMX-842243)	V	1996
4.	BARI Mung-4	G4	Sonamung(Local) × BARI Mung- 2 (BMX-841121)	V	1996
5.	BARI Mung-5	G5	VC- 2768B × VC-6141-36 (NM-92) (AVRDC)	V	1997
6.	BARI Mung-6	G6	NM-36 × VC- 2768A (NM-94) (AVRDC)	V	2003
7.	BARI Mung-7	G7	VC-3960A-88 × VC-6173C (BMX-97024-13)	V	2015
8.	BARI Mung-8	G8	Local Selection (LM-101)	V	2015
9.	BINA Mung-6	G9	VC-6173-10 collected from AVRDC	V	2005
10.	BINA Mung-7	G10	BINA Mung-2 applying EMS mutagen	V	2005
11.	BINA Mung-8	G11	MB-149 (Irradiated with 400 Gy dose of gamma-ray)	V	2010
12.	BU Mung-2	G12	VC 2768A x VC 6141-36 {AVRDC ID- VC-6370 (30-65)}	V	2001
13.	BU Mung-4	G13	GK7 (AVRDC, Taiwan)	V	2006
14.	BMX-01019-1	G14	128001 × NM-94	AL	2001
15.	BMX-01007	G15	BARI Mung-3 × BARI Mung-5	AL	2001
16.	BMX-01015	G16	NM-94 × BARI Mung-3	AL	2001
17.	BMX-030011-6	G17	BMX-97004-1 × BARI Mung- 5	AL	2003
18.	BMX-04005-3	G18	BMX-97004-1 × BMX-97014-3	AL	2004
19.	BMX-05001	G19	BARI Mung- 5 × BARI Mung- 6	AL	2005
20.	BMX-05004	G20	BARI Mung- 6 × BARI Mung- 5	AL	2005
21.	BMX-05009	G21	BMX-94002-2 × BARI Mung- 6	AL	2005
22.	BMX-050012-6	G22	BMX-99002-2 × BARI Mung- 5	AL	2005
23.	BMX-06001	G23	BARI Mung- 5 × VC-6469-12-1-4A	AL	2006
24.	BMX-06007	G24	BARI Mung- 5 × BMX-97024-8	AL	2006
25.	BMX-07007-4	G25	BMX-00014 × Nilphamari local	AL	2007
26.	BMX-07009-10	G26	BARI Mung- 6 × BMX-00016	AL	2007
27.	BMX-08009-7	G27	BARI Mung- 6 × BAU Mung-2	AL	2008
28.	BMX-08011-8	G28	BARI Mung- 2 × BMX-9902-2	AL	2008
29.	BMX-08010-2	G29	BARI Mung-6 × BMX-9902-2	AL	2008
30.	BMX-08011-2	G30	BARI Mung- 2 × BMX-9902-2	AL	2008
31.	BMX-09009-6	G31	Nilphamari local × BMX-9902-2	AL	2009
32.	BMX-97024-13	G32	VC-3960A-88 × VC-6173C	AL	1997
33.	VC-2764B	G33	An advanced line of Mung (AVRDC)	AL	-

Note: 1-33 = serial number of the genotypes (G1-G33), V= Variety, AL= Advance line

2.4 Seed preparation and management

Mungbean seeds of each genotype were surface sterilized by immersing them in a solution of 0.1% mercuric chloride ($HgCl_2$) for 2 min while occasionally shaking. The seeds were then thoroughly rinsed in distilled water (Dutta & Bera, 2008; Saminathan, 2013; Swathi et al., 2017). Then, petri dishes containing sand bed were moistened with respective prepared PEG solutions. Thereafter, for each replication, a total of 70 randomly chosen surface-sterilized seeds of each mungbean genotype were placed in a sterilized petri dish and then kept at room temperature (25°C). Respective PEG solutions at concentrations of -0.7 bar, -1 bar, -2 bar, and -4 bar were added (5 ml) daily to each petri dish. The control was also moistened daily with uniform amounts of distilled water. The seedlings were allowed to grow up to 10 days after placement of seeds for germination.

2.5 Experimental measurement

After the end of the 10th day, germination percentage (Kinfemichael & Gezahagn, 2008), speed of germination (SG) (Maguire, 1962), co-efficient of germination (CEG) (Copeland, 1976), mean germination time (MGT) (Moradi et al., 2008), vigor index (VI) (Baki & Anderson, 1973), shoot length (SL), root length (RL), shoot fresh weight (SFW), shoot dry weight (SDW), root fresh weight (RFW), and root dry weight (RDW) were recorded. Lengths of shoot and root of individual seedlings were measured manually in cm from the seed to the tip of the leaf blade using a measuring scale. The fresh weight of the shoot and root corresponding to their dry weight was measured in milligrams (mg) using a sensitive electric balance (Model- AND EK- 300 i). The formulae for germination indices as well as the vigor index are as follows:

i. Germination percentage (GP) = $\frac{\text{Total number of seeds germinated at final count}}{\text{Total number of seeds placed for germination}} \times 100$

ii. Speed of germination (SG) $= \frac{n_1}{d_1} + \frac{n_2}{d_2} \ldots\ldots\ldots + \frac{n_{10}}{d_{10}}$

Where n_1, n_2… n_{10} are the number of emerged seedlings at times d_1, d_2… d_{10} (in days).

iii. $\text{Co - efficient of germination (CEG)} = \frac{100\,(A_1 + A_2 + \ldots\ldots\ldots A_n)}{A_1T_1 + A_2T_2 + \ldots\ldots\ldots A_nT_n}$

A **=** Number of seeds germinated; T**=**Time **(**days**)** corresponding to A; n**=** No**.** of days to the final count

iv. Mean germination time (MGT) $= \frac{\sum(D \times n)}{\sum n}$

where, n is the number of seeds germinated on day D, and D is the number of days counted from the beginning of germination. Cotyledons were not included in fresh and dry weight.

V. vigor index (VI) = Germination (%) × [(shoot length (cm) + root length (cm)]

The relative performance of study traits of mungbean genotypes was calculated using the following formulae:

vi. Relative performance = $\frac{\text{Values of a plant character under stress condition}}{\text{Values of that character under control condition}}$

2.6 Statistical analysis

Using a computer and the R-stat software application (R Core Team, 2019), the recorded values of different traits were examined by dividing the total variance in accordance with Gomez and Gomez's fundamental methodology (Gomez & Gomez, 1984). When significant result was found with F value, the means isolations were carried out using a least significant difference (LSD) test at 0.05 probability level to ascertain the statistical variations between means. For PCA and associated findings, the programs "ggplot2," "factoextra," and "FactoMineR" (Lê et al., 2008; Wickham, 2016) were used. We used the Complex Heatmap program to display two-dimensional heatmaps (Gu, 2022). A method for identifying superior genotypes that are better and more stable with numerous features within stress levels is the multi trait genotype ideotype distance index (MGIDI) (Olivoto & Nardino, 2020). All attributes were subject to a selection difference with a threshold of less than 20%. The 'metan' package in the R program was used to perform the index computation (Olivoto et al., 2021). By using this technique, the genotype that was closest to the ideotypes had the lowest MGIDI and was associated with lower contributions from variables, meaning that all examined features within each stress level had reached their intended levels.

3. Results and Discussion

3.1 Effects of PEG 6000 induced water deficit stress on the germination indices of mungbean genotypes

3.1.1 Germination percentages

Table 2 shows the germination percentage (GP) of every mungbean genotype under various osmotic potential treatments and the control. The GP decreased with decreasing osmotic potential, i.e. with increasing PEG-6000 concentration. Among the studied genotypes, the GP significantly reduced and showed diversified results with increasing PEG-6000 concentration. Moreover, depending on the genotype in each treatment, there were different levels of germination decrease. GP in the range of 85-93.33, 71.67-86.67, 61.67-80, 40-68.33, and 0-61.67% were seen for water potentials of control, -0.7, -1, -2, and -4 bar, respectively. It was clear that increased moisture deficit stress (-4.0 bars) led to a significant reduction in GP. However, the highest germination capacities (56.67-61.67%) at higher stress level (-4.0 bars) were obtained for the G29, G8, G16 and G27 genotypes, showing physiological means of tolerance to dryness. Mungbean genotypes at higher stress levels showed higher germination percentages, which notified a physiological way of resistance to moisture stress (Rajwinder et al., 2017). The lowest germination was found in G1, G3, G13 and G19 at the highest level of stress (-4.0 bars). However, absolute inhibition (100%) of germination was found in BARI Mung-1 at -4 bar. This complete inhibition (100%) of germination was observed by Gupta et al. (1993) and Safarnejad (2008) at >-4.0 bars of water stress. There were reports of a decline in germination percentage in soybean (Kosturkova et al., 2008), pea (Okcu et al., 2005), and mungbean (Dutta & Bera, 2008) as moisture shortage stress increased. Legumes'

Table 2. Effects of genotypes and stress level (PEG 6000) on germination percentage of mungbean genotypes induced by PEG 6000

Genotypes	Control	-0.7 bar	-1 bar	-2 bar	-4 bar
G1	86.67	71.67	61.67	40.00	0.00
G2	90.00	83.33	75.00	63.33	53.33
G3	86.67	73.33	65.00	45.00	28.33
G4	88.33	80.00	71.67	53.33	35.00
G5	86.67	78.33	70.00	46.67	35.00
G6	88.33	80.00	71.67	55.00	45.00
G7	90.00	81.67	75.00	61.67	46.67
G8	93.33	81.67	78.33	66.67	56.67
G9	86.67	78.33	73.33	55.00	41.67
G10	90.00	81.67	73.33	55.00	51.67
G11	86.67	78.33	70.00	58.33	38.33
G12	88.33	83.33	75.00	61.67	51.67
G13	86.67	73.33	63.33	43.33	28.33
G14	90.00	81.67	73.33	61.67	43.33
G15	91.67	83.33	75.00	63.33	53.33
G16	93.33	85.00	78.33	66.67	56.67
G17	91.67	83.33	75.00	60.00	46.67
G18	86.67	78.33	70.00	58.33	48.33
G19	85.00	75.00	63.33	46.67	30.00
G20	88.33	78.33	70.00	58.33	41.67
G21	86.67	78.33	70.00	58.33	48.33
G22	85.00	75.00	68.33	56.67	46.67
G23	90.00	81.67	73.33	61.67	45.00
G24	90.00	83.33	75.00	63.33	51.67
G25	86.67	76.67	68.33	56.67	46.67
G26	88.33	80.00	71.67	60.00	50.00
G27	91.67	86.67	78.33	66.67	56.67
G28	91.67	83.33	75.00	63.33	51.67
G29	93.33	85.00	80.00	68.33	61.67
G30	88.33	76.67	68.33	56.67	46.67
G31	86.67	78.33	70.00	58.33	45.00
G32	90.00	78.33	71.67	61.67	48.33
G33	85.00	78.33	66.67	51.67	36.67
Mean			68.34		
CV (%)			7.22		
LSD (0.05)			7.95		
MSerror			24.46		
LS			**		

**= 1% level of significance; LS, Level of significance

reduced ability to germinate seeds was a result of PEG-induced drought stress (Murillo-Amador et al., 2002). As soon as a seed breaks its dormancy, water intake causes the metabolic processes to begin (Katembe et al., 1998). It is possible that the high PEG content hindered seeds' ability to absorb water, which in turn prevented seeds from germinating (Afzali et al., 2006). According to another claim, a decrease in the osmotic

potential gradient between seeds and the medium they are in has a negative impact on seed germination because of the restricted water absorption by the seeds and the (resultant) events that follow in the growth and development of the seedlings (Shitole & Dhumal, 2012).

3.1.2 Mean germination time (MGT)

Water stress caused the MGT to rise in response to a reduction in the osmotic potential in the PEG solution (water deficit stress levels) and the results differed markedly across the genotypes of mungbeans. The MGT ranged from 4.39 to 5.05, 4.44-5.31, 4.56-5.41, 4.74 5.99 and 5.20-6.30 for the control, -0.7 bar, -1 bar, -2 bar and -4 bar levels, respectively (Table 3).

The G2, G29, G27, G8 and G16 genotypes showed the lowest % increases of MGT of 17.72, 18.51, 19.35, 20.05 and 20.25% corresponding with MGT of 5.69, 5.20, 5.35, 5.33 and 5.29 days, respectively, followed by G15 (20.39% with 5.90 days) at -4.0 bars stress. In contrast, the G13, G19, G3 genotypes provided the highest increases in MGT (26.40, 24.76, and 24.59% corresponding to 6.30, 6.13 and 6.25 days, respectively) and can thus be considered to be sensitive to this stress level. In general, the effect on MGT was most apparent at higher PEG concentrations. Moreover, the delay in germination was notable in insensitive and intermediate genotypes compared to the tolerant genotypes (Sadeghi et al., 2011). The current investigation supports the findings of Kaydan & Yagmur (2008), who found that PEG-induced water deficiency stress reduced seed germination and prolonged the time it took for germination to occur. However, our study showed that PEG 6000 induced stress delayed MGT to varying degrees among the studied genotypes. In this work, elevated MGT in several mungbean genotypes may have resulted from osmotic stress-induced general germination process delay or from the direct harmful effects of PEG 6000. According to Murillo-Amador et al. (2002), MGT increased in cowpeas as PEG levels rose. Similarly, as the osmotic potential of the PEG solution decreased, so did the mean germination time (MGT) in maize (Zahra et al., 2012). This observation was in agreement with the findings of Alebrahim et al. (2008). Furthermore, PEG may influence MGT by producing an external osmotic potential that prevents the intake of water (Zahra et al., 2012). According to Dezfuli et al. (2008), osmoprimed seeds treated with PEG-6000 solution showed increased MGT.

3.1.3 Coefficient of germination (CEG)

The distinct variation of CEG in different mungbean genotypes was observed under normal and stressed conditions (Table 4). The highest CEG belonged to the control and increasing water deficit stress levels gradually reduced the CEG in all genotypes. The CEGs varied between 19.99 to 22.85, 19.12 to 22.53, 18.55 to 22.04, 16.77 to 21.12, and 0 to 19.37, respectively, for the control, -0.7 bar, -1 bar, -2 bar and -4 bar levels. The % reduction varied from 1.41 to 5.26%, 2.19 to 8.87%, 6.63 to 16.09% and 15.22 to 100%, respectively, at the -0.7 bar, -1 bar, -2 bar and -4 bar levels compared to control (0 bar). The data showed that at higher stress level (-4 bar), the G29, G27, G16, G8 and G2 produced the lowest reduction (15.22 to 16.91%) with maximum CEG values (19.37 to 17.41) while the maximum reduction was observed in the G3, G19, G13 and G1 genotypes (20.24 to 100%). Genotype G29 produced the maximum CEG value (19.37) among all tested mungbean genotypes along with the lowest reduction (15.22%), while

Table 3. Mean germination time of mungbean genotypes as induced by PEG 6000

Genotypes	Control	-0.7 bar	% R	-1 bar	% R	-2 bar	% R	-4 bar	% R
G1	5.05	5.31	5.00	5.41	6.97	5.99	18.43	-	-
G2	4.83	4.94	2.16	5.14	6.36	5.16	6.83	5.69	17.72
G3	5.02	5.25	4.53	5.43	8.30	5.71	13.78	6.25	24.59
G4	4.85	5.09	4.90	5.30	9.26	5.48	13.05	5.86	20.72
G5	4.80	4.95	3.11	5.07	5.57	5.37	11.94	5.96	24.15
G6	4.73	4.88	3.01	5.00	5.70	5.26	11.18	5.81	22.66
G7	4.74	4.87	2.56	5.03	6.12	5.34	12.47	5.88	24.02
G8	4.44	4.53	2.03	4.56	2.54	4.79	7.87	5.33	20.05
G9	4.96	5.12	3.10	5.29	6.66	5.69	14.65	6.12	23.36
G10	4.91	5.07	3.32	5.18	5.51	5.49	11.96	6.10	24.36
G11	4.84	4.99	3.13	5.16	6.60	5.46	12.75	6.03	24.53
G12	4.70	4.83	2.67	4.98	6.05	5.21	10.81	5.75	22.26
G13	4.98	5.21	4.70	5.40	8.44	5.73	14.98	6.30	26.40
G14	4.87	4.99	2.51	5.15	5.80	5.41	11.09	6.01	23.38
G15	4.90	5.00	2.08	5.13	4.70	5.45	11.27	5.90	20.39
G16	4.40	4.47	1.67	4.57	3.88	4.79	8.78	5.29	20.25
G17	4.83	4.91	1.78	5.07	4.96	5.36	11.05	5.91	22.47
G18	4.90	5.05	2.96	5.20	6.04	5.46	11.45	5.98	22.01
G19	4.91	5.19	5.54	5.38	9.43	5.75	17.06	6.13	24.76
G20	4.91	5.06	3.08	5.24	6.70	5.63	14.63	5.96	21.38
G21	4.61	4.75	3.03	4.83	4.68	5.34	15.82	5.69	23.25
G22	4.63	4.74	2.42	4.83	4.34	5.25	13.48	5.79	25.10
G23	4.82	4.94	2.41	5.05	4.70	5.33	10.50	5.85	21.35
G24	4.78	4.89	2.20	5.11	6.89	5.43	13.44	5.93	24.07
G25	4.92	5.03	2.18	5.18	5.11	5.49	11.48	6.12	24.19
G26	4.77	4.91	3.05	5.07	6.38	5.33	11.78	5.77	20.97
G27	4.48	4.55	1.47	4.67	4.28	4.83	7.79	5.35	19.35
G28	4.89	5.00	2.35	5.20	6.27	5.43	11.09	6.09	24.53
G29	4.39	4.44	1.22	4.57	4.01	4.74	8.04	5.20	18.51
G30	4.85	5.04	3.98	5.12	5.54	5.48	12.97	5.86	20.87
G31	4.97	5.08	2.30	5.33	7.16	5.46	9.89	5.96	19.85
G32	4.86	5.01	3.07	5.28	8.65	5.53	13.75	5.92	21.79
G33	4.87	4.99	2.45	5.17	6.14	5.42	11.27	5.97	22.55
Mean					5.21				
CV (%)					4.44				
LSD (0.05)					0.05				
MSerror					0.0011				
LS					**				

**= 1% level of significance; % R= Percent reduction; LS, Level of significance

Table 4. Coefficient of germination (CEG) of mungbean genotypes as induced by PEG 6000

Genotypes	Control	-0.7 bar	% R	-1 bar	% R	-2 bar	% R	-4 bar	% R
G1	19.99	19.20	3.93	18.55	7.18	16.77	16.09	00.00	-
G2	20.76	20.26	2.40	19.52	5.96	19.38	6.63	17.41	16.13
G3	20.14	19.12	5.04	18.58	7.73	17.55	12.83	16.06	20.24
G4	20.96	19.90	5.08	19.17	8.55	18.35	12.45	16.74	20.16
G5	20.94	20.36	2.80	19.80	5.45	18.73	10.58	16.78	19.86
G6	21.15	20.68	2.21	20.05	5.19	19.06	9.87	17.31	18.17
G7	21.28	20.62	3.10	19.90	6.49	19.12	10.18	17.01	20.09
G8	22.53	22.18	1.57	22.04	2.19	20.98	6.89	18.78	16.64
G9	20.18	19.69	2.43	18.96	6.03	17.69	12.32	16.34	19.01
G10	20.42	19.74	3.31	19.36	5.19	18.24	10.65	16.39	19.74
G11	20.72	20.08	3.07	19.47	6.00	18.37	11.35	16.61	19.83
G12	21.29	20.78	2.40	20.14	5.39	19.20	9.79	17.41	18.21
G13	20.10	19.30	3.97	18.66	7.18	17.52	12.85	15.89	20.96
G14	20.61	20.12	2.39	19.49	5.42	18.72	9.19	16.67	19.11
G15	20.53	20.09	2.13	19.59	4.58	18.62	9.30	16.95	17.42
G16	22.81	22.41	1.77	21.93	3.87	21.03	7.80	18.95	16.91
G17	20.89	20.43	2.23	19.78	5.31	18.78	10.11	16.92	19.03
G18	20.42	19.92	2.44	19.34	5.26	18.41	9.84	16.74	17.99
G19	20.49	19.41	5.26	18.67	8.87	17.48	14.71	16.32	20.37
G20	20.57	19.91	3.19	19.19	6.71	17.93	12.82	16.78	18.42
G21	21.69	21.08	2.83	20.75	4.33	18.71	13.72	17.60	18.85
G22	21.64	21.21	1.99	20.71	4.27	19.05	11.98	17.28	20.16
G23	20.88	20.25	3.00	19.98	4.27	18.77	10.11	17.11	18.02
G24	20.93	20.55	1.81	19.76	5.61	18.44	11.90	17.03	18.64
G25	20.44	19.97	2.31	19.42	4.99	18.45	9.76	16.35	20.00
G26	21.06	20.58	2.31	19.86	5.73	18.80	10.76	17.35	17.62
G27	22.51	22.20	1.41	21.60	4.08	20.80	7.60	18.74	16.77
G28	20.51	20.11	1.94	19.50	4.93	18.56	9.50	16.43	19.90
G29	22.85	22.53	1.41	21.96	3.90	21.12	7.59	19.37	15.22
G30	20.73	20.27	2.24	19.62	5.39	18.57	10.42	17.07	17.65
G31	20.31	19.77	2.66	19.20	5.47	18.38	9.50	16.80	17.25
G32	20.61	20.05	2.69	19.58	4.99	18.14	11.97	16.90	17.97
G33	20.56	20.19	1.80	19.43	5.50	18.50	10.01	16.76	18.49
Mean				19.29					
CV (%)				2.76					
LSD (0.05)				0.06					
MSerror				0.0013					
LS				**					

**= 1% level of significance; % R= Percent reduction; LS, Level of Significance

the minimum CEG value (0) with absolute reduction (100%) was observed in the G1 at the same treatment. This result might be due to the effect of osmotic potentiality being greatly hindered by PEG-6000 stress. The germination time and the CEG have an inverse connection according to Scott et al. (1984), who reported that the higher the drought stress levels, the lower the CEG, and the longer the germination period. According to a study of Mohammadi & Mojaddam (2014), as drought stress rises, germination takes longer and the velocity of germination coefficient falls.

3.1.4 Speed of germination (SG)

Speed of germination (SG) showed significant differences with osmotic potential and gradually decreased with the lowering of water potential among the genotypes. In the present study, all genotypes recorded lower SG under PEG-induced water deficit stress when compared to the control (Table 5). For the control, the SG ranged from 3.61 to 4.45 but under stress conditions, the SG varied from 2.86 to 4.01, 2.36 to 3.60, 1.37 to 2.98 and 0 to 2.47 under -0.7, -1.0, -2.0 and -4.0 bars, which corresponded to reduction from 20.68 to 7.80, 34.65 to 19.03, 62.02 to 33.08 and 100 to 44.55% compared to control. The present study indicated that as water deficit stress level increased from -0.7 bar to -4 bar, the mean SG was strongly reduced in all the studied mungbean genotypes. At higher levels of water deficit stress (-4 bar), the G29, G16, G27 and G8 genotypes performed the best, giving the highest SG values (2.47, 2.19, 2.18 and 2.18) with the lowest reduction (44.55, 50.73, 49.91 and 50.35%, respectively) compared to their respective control whereas the G1, G13, G3 and G19 gave the lowest SG values (0.0, 0.92, 0.93 and 1.0) with maximum reduction (100, 74.73, 74.68 and 72.49%, respectively).

In general, more energy is needed to complete the biological processes under stress conditions, so the SG was less under higher stress compared to the control. The current result is consistent with that of Mohammadi & Mojaddam (2014), who found that higher drought stress levels reduced SG and that tolerant cultivars seemed to exhibit higher SG under drought stress circumstances. There is a strong relationship between SG and water potential because as drought stress rises, so does the amount of time needed for sprouting and the coefficient of germination velocity. The results agreed with the findings of Hamidi (2005) on corn as well.

3.2 Effects of PEG-6000 induced drought stress on the seedling growth indices of mungbean genotypes

3.2.1 Relative shoot and root length

Tested genotypes showed considerable differences in the way they grew as seedlings with respect to shoot and root length, both under control management and under stressful circumstances, with respect to shoot and root length (Tables 6 & 7). Drought tolerance is defined as a genotype's performance relative to other genotypes under the same drought stress. The decreasing water potentials of -0.7 bar, -1 bar, -2 bar and -4 bar caused a reduction in the relative shoot and root length of individual genotypes compared with the control (Tables 6 &7). The shoot and root lengths of different mungbean genotypes were found to be significantly different from one another and negatively influenced by PEG. This ultimately affected the fresh and dry weights of the seedlings (Kaydan & Yagmur,

Table 5. Speed of germination of mungbean genotypes as induced by PEG 6000

Genotypes	Control	-0.7bar	% R	-1bar	% R	-2 bar	% R	-4 bar	% R
G1	3.61	2.86	20.68	2.36	34.65	1.37	62.02	0.00	100.00
G2	3.90	3.51	10.00	2.98	23.53	2.52	35.39	1.90	51.14
G3	3.66	2.90	20.97	2.48	32.38	1.62	55.87	0.93	74.68
G4	3.89	3.31	14.90	2.81	27.65	2.01	48.37	1.19	69.43
G5	3.78	3.32	12.21	2.85	24.62	1.78	52.86	1.19	68.52
G6	3.92	3.45	12.16	2.92	25.48	2.16	44.86	1.58	59.63
G7	4.04	3.52	13.03	3.07	24.14	2.41	40.39	1.60	60.31
G8	4.38	3.77	14.07	3.54	19.14	2.89	34.15	2.18	50.35
G9	3.66	3.17	13.38	2.85	21.99	1.99	45.59	1.38	62.26
G10	3.87	3.30	14.94	2.88	25.55	2.06	46.90	1.72	55.58
G11	3.74	3.28	12.41	2.82	24.77	2.19	41.46	1.29	65.56
G12	3.91	3.56	9.09	3.08	21.20	2.45	37.48	1.83	53.25
G13	3.64	2.93	19.36	2.43	33.08	1.58	56.49	0.92	74.73
G14	3.89	3.40	12.58	2.93	24.83	2.35	39.63	1.47	62.24
G15	3.92	3.48	11.27	3.02	23.08	2.40	38.88	1.83	53.35
G16	4.44	3.94	11.25	3.53	20.50	2.89	35.05	2.19	50.73
G17	3.98	3.56	10.61	3.05	23.32	2.30	42.15	1.65	58.55
G18	3.74	3.24	13.38	2.78	25.81	2.20	41.18	1.64	56.28
G19	3.64	3.00	17.45	2.42	33.50	1.66	54.24	1.00	72.49
G20	3.77	3.26	13.69	2.75	27.17	2.15	43.09	1.42	62.40
G21	3.91	3.46	11.51	2.98	23.70	2.23	42.88	1.72	56.01
G22	3.85	3.34	13.13	2.91	24.51	2.21	42.49	1.63	57.74
G23	3.97	3.45	13.24	2.99	24.75	2.37	40.34	1.56	60.81
G24	3.96	3.53	10.73	3.04	23.21	2.39	39.51	1.77	55.22
G25	3.71	3.20	13.79	2.73	26.41	2.16	41.78	1.54	58.43
G26	3.94	3.39	13.99	2.88	26.75	2.30	41.62	1.76	55.37
G27	4.34	4.01	7.80	3.48	20.00	2.84	34.64	2.18	49.91
G28	3.91	3.48	11.21	3.00	23.46	2.41	38.44	1.72	56.03
G29	4.45	3.96	11.11	3.60	19.03	2.98	33.08	2.47	44.55
G30	3.82	3.23	15.26	2.73	28.45	2.15	43.77	1.61	57.87
G31	3.70	3.20	13.50	2.73	26.25	2.19	40.78	1.53	58.59
G32	3.90	3.24	16.89	2.88	26.21	2.30	41.12	1.66	57.48
G33	3.66	3.28	10.47	2.65	27.61	1.95	46.79	1.25	65.80
Mean					2.79				
CV (%)					8.48				
LSD (0.05)					0.07				
MSerror					0.0018				
LS					**				

**= 1% level of significance; % R= Percent reduction; LS, Level of Significance

Table 6. Relative shoot length (cm) of mungbean genotypes as induced by PEG 6000

Genotypes	-0.7 bar	% D	-1 bar	% D	-2 bar	% D	-4 bar	% D
G1	0.61	39.15	0.33	67.16	0.21	79.10	0.00	100.00
G2	0.80	20.45	0.57	43.26	0.49	51.26	0.28	72.15
G3	0.60	40.05	0.31	69.18	0.24	76.03	0.11	89.22
G4	0.69	31.08	0.45	55.21	0.34	65.90	0.19	80.70
G5	0.64	36.24	0.44	55.51	0.34	66.15	0.16	84.00
G6	0.64	36.16	0.40	60.18	0.29	71.40	0.17	83.00
G7	0.66	34.00	0.44	55.74	0.38	61.97	0.22	77.91
G8	0.81	19.30	0.58	42.21	0.52	47.63	0.34	65.53
G9	0.71	29.06	0.48	52.32	0.32	68.36	0.26	73.80
G10	0.72	27.79	0.42	57.82	0.34	65.58	0.25	75.00
G11	0.78	21.89	0.48	52.33	0.34	65.63	0.19	80.74
G12	0.80	19.72	0.58	41.66	0.43	57.33	0.32	67.67
G13	0.63	36.82	0.36	63.84	0.22	77.91	0.15	84.58
G14	0.72	28.27	0.47	52.59	0.34	65.53	0.23	77.42
G15	0.78	22.09	0.57	42.90	0.29	71.43	0.21	78.57
G16	0.81	18.51	0.61	39.44	0.50	50.02	0.38	61.56
G17	0.62	38.10	0.36	63.99	0.30	69.60	0.22	78.28
G18	0.62	37.95	0.33	66.60	0.23	76.81	0.18	82.30
G19	0.63	37.37	0.37	62.60	0.23	77.43	0.15	84.72
G20	0.78	21.99	0.46	54.07	0.34	65.82	0.25	74.85
G21	0.75	24.79	0.42	58.21	0.28	72.49	0.18	81.89
G22	0.69	31.32	0.44	55.77	0.37	63.42	0.22	77.78
G23	0.73	27.26	0.43	57.47	0.37	62.80	0.17	82.86
G24	0.79	20.53	0.48	51.77	0.31	69.38	0.20	80.00
G25	0.79	20.50	0.47	52.98	0.32	68.05	0.23	76.79
G26	0.77	23.21	0.48	52.15	0.33	66.87	0.23	76.92
G27	0.82	18.09	0.63	37.37	0.52	47.69	0.39	61.18
G28	0.66	34.28	0.45	54.74	0.34	65.99	0.19	81.02
G29	0.84	15.65	0.70	30.43	0.54	46.38	0.42	58.13
G30	0.80	20.09	0.48	52.38	0.34	66.31	0.26	74.12
G31	0.77	22.64	0.47	52.77	0.34	65.69	0.26	73.59
G32	0.79	20.64	0.47	52.56	0.31	69.23	0.23	76.86
G33	0.61	38.81	0.46	54.25	0.34	66.21	0.21	79.15
Mean				0.44				
CV (%)				7.66				
LSD (0.05)				0.08				
MSerror				0.0026				
LS				**				

**= 1% LS; % D= Percentage decrease; LS, Level of significance

Table 7. Relative root length (cm) of mungbean genotypes as induced by PEG 6000

Genotypes	-0.7bar	% D	-1 bar	% D	-2 bar	% D	-4 bar	% D
G1	0.69	30.95	0.57	42.93	0.37	62.79	0.09	91.00
G2	0.87	13.49	0.79	20.61	0.61	38.84	0.41	59.00
G3	0.75	25.18	0.55	44.97	0.44	56.26	0.30	70.02
G4	0.76	23.69	0.65	35.00	0.60	40.31	0.31	69.03
G5	0.76	24.05	0.62	37.54	0.57	43.34	0.37	63.02
G6	0.80	20.06	0.69	31.17	0.59	41.02	0.40	60.05
G7	0.80	20.04	0.68	31.57	0.58	41.64	0.39	60.57
G8	0.85	14.96	0.81	19.15	0.66	33.73	0.42	58.02
G9	0.79	20.55	0.71	29.13	0.51	48.60	0.36	64.33
G10	0.80	20.49	0.67	32.53	0.53	46.73	0.39	60.74
G11	0.76	24.29	0.60	40.02	0.45	55.28	0.34	65.93
G12	0.89	10.95	0.76	24.12	0.58	41.92	0.41	58.85
G13	0.66	33.79	0.53	46.74	0.36	64.50	0.28	72.15
G14	0.73	26.52	0.69	31.45	0.58	41.97	0.36	64.04
G15	0.79	20.57	0.70	29.95	0.60	39.69	0.41	59.04
G16	0.85	15.37	0.80	19.77	0.62	37.56	0.46	54.01
G17	0.74	26.24	0.69	30.62	0.62	37.86	0.38	62.26
G18	0.75	24.78	0.63	37.41	0.59	41.32	0.37	63.27
G19	0.62	37.83	0.58	41.50	0.32	67.93	0.25	75.00
G20	0.71	28.57	0.64	36.29	0.55	45.36	0.33	67.29
G21	0.73	26.50	0.64	35.99	0.57	43.13	0.38	62.35
G22	0.83	16.55	0.76	23.86	0.52	48.09	0.36	63.99
G23	0.83	17.40	0.79	20.97	0.53	47.06	0.40	60.00
G24	0.75	24.84	0.67	32.98	0.57	43.24	0.39	60.78
G25	0.75	24.97	0.71	29.25	0.60	40.26	0.32	68.11
G26	0.73	27.31	0.62	37.68	0.54	45.59	0.36	64.13
G27	0.88	12.49	0.82	17.60	0.63	36.79	0.47	53.02
G28	0.79	21.05	0.63	36.85	0.51	48.77	0.34	65.99
G29	0.88	11.99	0.83	16.63	0.64	35.76	0.48	51.98
G30	0.73	27.07	0.59	41.14	0.48	51.80	0.38	62.45
G31	0.70	29.83	0.62	37.93	0.55	45.12	0.36	63.83
G32	0.73	27.25	0.63	36.71	0.51	48.59	0.38	61.79
G33	0.75	25.08	0.61	38.91	0.54	45.73	0.35	64.96
Mean				0.59				
CV (%)				7.23				
LSD (0.05)(0.05)				0.09				
MSerror				0.0031				
LS				**				

**= 1% level of significance; % D= Percent decrease; LS, Level of significance

2008: Pratap & Sharma, 2010). The variation of relative shoot length (RSL) among the genotypes ranged from 0.61 to 0.84, 0.33 to 0.70, 0.21 to 0.54 and 0 to 0.42 under water potential levels of -0.7, -1.0, -2.0, and -4.0 bar, respectively. At -4 bar stress, RSL was reduced by 58.13 to 100% corresponding to RSL values of 0.42- to 0.00 compared to their respective controls (0 bar). Genotypes G29 (0.42), G27 (0.39), and G16 (0.38) showed the highest RSL values, followed by G8 (0.34). The lowest RSL values (with the highest reduction) were recorded for the G1, G3, G13 and G19 genotypes under both -2.0 and -4.0 bars stress which might be due to lower growth and development of seedlings by the effect of PEG. The reduction of shoot length could be due to the noxious effects of the PEG and unstable water uptake by seedlings. The results are consistent with those of Kaydan & Yagmur (2008), who suggested that a decrease in shoot length may be brought on by a reduction in the external osmotic potential created by PEG and decreased water absorption.

A species' or variety's root length is a crucial characteristic in determining its resistance to drought stress; a variation with longer root development is more drought-resistant (Leishman & Westoby, 1994). Encouraging root development can contribute significantly to the endurance of water deficiency stress. Table 7 shows that there were notable variations in the relative root length (RRL) across the genotypes, treatments, and also in their interactions. The root length reduced gradually with the increment of stress level. The RRL values were 0.62-0.89, 0.53-0.83, 0.32-0.66 and 0.09-0.48 at -0.7, -1.0, -2.0 and -4 bar stress levels, respectively (Table 7). The genotypes G29, G27 and G16 showed relatively higher root lengths (0.48, 0.47 and 0.46) at the maximum level of stress (-4 bar water potential) with the lowest reductions of 51.98, 53.02 and 54.01%, respectively, followed by G8 (0.42 and 58.02%) and G2 (0.41 and 59.00**%**), and can be considered to be tolerant against the water stress. For the same osmotic potential, the lowest RRL was recorded in G1 (0.09), G19 (0.25), G13 (0.28) and G3 (0.30) with the highest reductions of 91, 75, 72.15 and 70.02%, respectively. The present study is in line with Haq et al. (2010), who reported that shoot and root length reduced with increasing PEG concentration. The lessening in root lengths may be due to decreased physiological activities resulting from induced water deficit stress (Muscolo et al., 2014). The present study indicated that the RRL gradually decreased in all mungbean genotypes with increasing PEG concentration, but the effects of the treatments varied among the genotypes. The present result furthermore showed that the shoot and root lengths were affected severely by increasing PEG 6000 concentration, and the reduction of shoot length was comparatively higher than the root length under -1.0 to -4.0 bar. Moreover, the root length increased with declining water potential (-1 bar to -4 bar) demonstrated it as one of the morphological adaptations to drought. This was also an adaptive reaction that involved an increase in root length to access deeper water in the soil (Radhouane, 2007). These findings were consistent with previous findings in mungbean (Rajwinder et al., 2011; Sunil *et al.* (2011). Sunil *et al.* (2016) reported that the seedlings of tolerant genotypes maintained longer root lengths as compared to the susceptible genotypes under water deficit conditions. It could be also seen from the results that under 0.7 bar, all mungbean genotypes showed higher shoot length compared to root length. However, the further reduction of water potential to -1.0 bar, -2.0 bar and -4.0 bars in all the tested mungbean genotypes showed less shoot length compared to root length. Ranu et al. (2005) noted the same findings in black gram and mungbean. PEG may have detrimental effects on shoot and root length because it causes osmotic stress, which disrupts physiology, impairs metabolism, and ultimately stops plants from growing (Abdul, 2009; Khayatnezhad et al., 2010).

3.2.2 Relative shoot and root fresh weight

All the mungbean genotypes responded differently to water deficit stress concerning relative shoot fresh weight. Increased PEG concentration drastically reduced the fresh weights of the shoots and roots of the tested genotypes (Tables 8 & 9). The relative shoot fresh weight (RSFW) under -0.7 bar conditions ranged between 0.59 (G1) to 0.84 (G8). Further lowering of water potential to -1 bar, -2 bar and -4 bar led to a marked reduction in shoot fresh weight among the genotypes which ranged between 0.25 to 0.61 in -1 bar, 0.19 to 0.50 in -2 bar, and 0.00 to 0.31 in -4 bar. However, under the maximum stress (-4 bar) condition, the genotypes G29, G8 and G27 achieved the highest RSFW values of 0.31, 0.28 and 0.27 with 69.00, 72.27 and 72.73% reduction over control, followed by G16 (0.26 with 73.69%), whereas the genotypes G1, G13, G3 and G19 achieved much lower RSFW values of 100, 87, 86.16 and 85.61% reduction over control, respectively (Table 8). The result exposed that RSFW decreased with increasing PEG concentration. However, the reduction of RSFW varied with genotype and water potential level. This outcome was in line with Sunil *et al.* (2016). The reduction in RSFW might be the result of the seedlings' reduced ability to absorb water at varying PEG 6000 concentrations. PEG 6000 caused seedlings to experience water deficiency stress by lowering the osmotic water potential. The study's results are consistent with those of Veer & Sharma (2010), who reported that under circumstances of water deficiency stress, black gram seedlings' fresh weight rapidly decreased.

In the case of root fresh weight, reduction of water potential showed a considerable decrease in the fresh weight of roots of seedlings all genotypes. It varied between 0.64 - 0.82, 0.43 - 0.78, 0.26-0.62 and 0, 12-0.43, respectively, for -0.7 bar, -1 bar, -2 bar and -4 bar. At the elevated stress level (-4.0 bar), the genotypes G29, G27, G16, and G8 performed better in respect of higher RRFW (0.43, 0.40, 0.36, 0.34 with 57.34, 59.65, 63.60, and 66.00% reduction, respectively) followed by G2 (0.33 with 67%) and G12 (0.32 with 68% reduction). Genotypes G1, G13, G19 and G3 showed relatively lower values (0.12, 0.19, 0.19 and 0.23) and corresponding higher reduction (88, 80.75, 81.40 and 77.17%), respectively, due to elevated stress (-4.0 bar) (Table 9). According to the current research, the RRFW dropped as stress levels rose. The decrease, however, differed depending on the stress levels and genotype types under study. Increased levels of drought stress decreased the fresh weight of the shoots and roots, according to Shitole & Dhumal (2012). This reduction in fresh weight may be the result of metabolic abnormalities brought on by stress and the production of reactive oxygen species (ROS). The varying responses to moisture stress in terms of tolerance level may account for the significant decreases in seedling development across the genotypes in terms of fresh weight of shoots and roots (Sunil *et al.*, 2016; Rajwinder et al., 2017).

3.2.3 Relative shoot and root dry weight

The relative shoot and root dry weights (RSDW) significantly decreased as a result of reducing PEG water potential (Tables 10 and 11). The results showed that as the PEG content increased, there was a substantial decrease in RSDW in all genotypes. The RSDW of seedlings from all genotypes ranged between 0.54 and 0.81 under a pressure of -0.7 bars. Furthermore, the RSDW at higher stress levels was comparatively lower, ranging from 0.37 to 0.69 at -1.0 bar, 0.22 to 0.59 at -2.0 bar, and 0.0 to 0.39 at -4.0 bar. In addition, at higher stress level (-4.0 bar), the genotypes G29, G27 and G16 attained the highest RSDW (0.39, 0.38, 0.34) with 61.00, 62.00 and 66.00% reduction, followed

Table 8. Relative shoot fresh weight (mg) of mungbean genotypes as induced by PEG 6000

Genotypes	-0.7 bar	% D	-1 bar	% D	-2 bar	% D	-4 bar	% D
G1	0.59	40.70	0.25	57.84	0.19	81.00	0.00	100.00
G2	0.78	21.76	0.52	33.54	0.41	59.33	0.24	75.65
G3	0.63	37.00	0.27	57.14	0.23	77.00	0.14	86.16
G4	0.66	34.00	0.39	41.34	0.28	72.00	0.17	83.00
G5	0.72	28.00	0.46	35.49	0.37	63.44	0.19	80.82
G6	0.68	32.00	0.44	35.96	0.36	63.53	0.22	77.63
G7	0.69	31.00	0.42	38.71	0.33	67.00	0.21	79.00
G8	0.84	16.00	0.58	30.95	0.43	57.00	0.28	72.27
G9	0.69	31.23	0.37	46.20	0.29	71.00	0.20	80.00
G10	0.65	35.00	0.39	40.03	0.29	70.88	0.16	84.00
G11	0.65	35.00	0.31	52.31	0.30	70.00	0.20	80.00
G12	0.73	27.00	0.47	35.62	0.40	60.38	0.24	75.58
G13	0.61	39.00	0.27	55.74	0.21	79.00	0.13	87.00
G14	0.74	25.64	0.43	42.17	0.37	62.60	0.25	75.44
G15	0.78	21.62	0.52	33.65	0.39	61.31	0.25	74.66
G16	0.76	24.00	0.54	28.95	0.47	53.20	0.26	73.69
G17	0.67	33.00	0.35	47.76	0.28	72.00	0.17	83.00
G18	0.73	27.00	0.38	47.75	0.28	72.45	0.16	84.00
G19	0.61	39.00	0.29	52.46	0.27	72.97	0.14	85.61
G20	0.71	29.00	0.40	43.66	0.29	71.15	0.16	84.09
G21	0.64	35.53	0.40	37.96	0.34	66.00	0.19	81.00
G22	0.73	27.00	0.38	48.29	0.29	70.89	0.16	83.67
G23	0.67	32.77	0.41	39.02	0.35	64.68	0.20	79.89
G24	0.69	31.23	0.39	43.82	0.30	70.00	0.19	81.21
G25	0.70	29.82	0.36	48.71	0.31	69.00	0.19	80.88
G26	0.75	25.20	0.43	42.51	0.37	62.50	0.22	77.58
G27	0.80	20.00	0.57	28.75	0.49	51.31	0.27	72.73
G28	0.69	31.00	0.42	39.29	0.37	62.67	0.17	83.13
G29	0.82	18.00	0.61	25.61	0.50	50.21	0.31	69.00
G30	0.73	26.76	0.48	34.17	0.35	65.30	0.21	78.84
G31	0.74	25.72	0.48	34.83	0.33	67.27	0.20	79.75
G32	0.68	32.34	0.46	32.07	0.35	64.53	0.23	77.25
G33	0.72	27.81	0.48	34.02	0.30	69.72	0.16	83.52
Mean				0.41				
CV (%)				2.18				
LSD (0.05)				0.03				
MSerror				0.0003				
LS				**				

**= 1% level of significance; % D= Percent decrease; LS, Level of significance

Table 9. Relative root fresh weight (mg/seedling) of mungbean genotypes as induced by PEG 6000

Genotypes	-0.7 bar	% D	-1 bar	% D	-2 bar	% D	-4 bar	% D
G1	0.64	35.59	0.45	54.93	0.26	74.42	0.12	88.00
G2	0.80	20.39	0.61	39.00	0.49	51.00	0.33	67.00
G3	0.66	33.52	0.44	56.00	0.33	67.42	0.23	77.17
G4	0.74	26.18	0.63	37.27	0.39	61.17	0.24	76.07
G5	0.76	24.35	0.55	44.52	0.44	55.74	0.24	75.74
G6	0.78	22.15	0.64	36.00	0.47	52.88	0.26	73.57
G7	0.74	26.49	0.56	44.00	0.42	57.80	0.29	71.39
G8	0.81	18.67	0.69	31.00	0.51	49.00	0.34	66.00
G9	0.77	23.24	0.67	33.48	0.48	52.00	0.25	75.00
G10	0.75	24.98	0.48	52.00	0.37	63.21	0.25	74.77
G11	0.78	21.80	0.55	44.91	0.42	58.48	0.31	68.86
G12	0.79	21.41	0.66	34.00	0.54	46.00	0.32	68.00
G13	0.69	31.00	0.45	55.05	0.34	65.89	0.19	80.75
G14	0.75	25.15	0.62	37.96	0.39	60.51	0.25	74.52
G15	0.77	23.00	0.69	31.00	0.58	42.00	0.31	69.14
G16	0.82	17.93	0.70	30.00	0.60	40.00	0.36	63.60
G17	0.77	23.19	0.69	31.45	0.32	68.00	0.24	76.00
G18	0.77	22.96	0.46	53.55	0.35	64.95	0.25	75.27
G19	0.64	35.66	0.43	57.17	0.33	66.51	0.19	81.40
G20	0.78	22.06	0.64	36.21	0.35	65.31	0.24	75.54
G21	0.78	22.24	0.68	32.03	0.49	50.51	0.31	68.81
G22	0.70	30.16	0.60	39.67	0.50	50.05	0.31	69.08
G23	0.77	23.14	0.68	31.64	0.34	66.00	0.32	67.73
G24	0.75	24.66	0.64	36.23	0.35	65.00	0.26	74.29
G25	0.78	21.55	0.69	31.34	0.38	62.00	0.33	67.37
G26	0.78	22.43	0.69	30.63	0.32	68.00	0.26	74.00
G27	0.79	21.00	0.72	28.00	0.61	38.70	0.40	59.65
G28	0.76	23.90	0.58	41.80	0.33	67.00	0.28	71.58
G29	0.81	19.00	0.78	22.00	0.62	37.98	0.43	57.34
G30	0.70	30.11	0.65	35.14	0.39	60.63	0.25	74.53
G31	0.75	24.58	0.49	50.53	0.39	60.78	0.25	75.37
G32	0.77	22.53	0.54	46.36	0.37	63.00	0.27	73.24
G33	0.75	25.05	0.67	33.21	0.38	62.20	0.22	78.00
Mean				0.51				
CV (%)				3.22				
LSD (0.05)				0.04				
MSerror				0.0007				
LS				**				

**= 1% level of significance; % D= Percent decrease; LS, Level of Significance

Table 10. Relative shoot dry weight (mg/seedling) of mungbean genotypes as induced by PEG 6000

Genotypes	-0.7 bar	% D	-1 bar	% D	-2bar	% D	-4 bar	% D
G1	0.55	45.05	0.41	59.00	0.22	78.49	0.00	100.00
G2	0.68	32.00	0.64	36.00	0.59	41.00	0.30	70.00
G3	0.54	46.00	0.43	57.00	0.30	70.00	0.18	82.00
G4	0.69	30.79	0.56	44.00	0.43	57.00	0.30	70.27
G5	0.77	22.61	0.61	39.00	0.44	56.00	0.20	80.00
G6	0.76	24.15	0.57	43.00	0.36	64.00	0.25	75.00
G7	0.78	22.33	0.62	38.00	0.46	54.00	0.29	71.00
G8	0.80	20.00	0.69	31.00	0.35	65.00	0.31	69.00
G9	0.70	29.79	0.58	42.00	0.31	69.00	0.21	79.00
G10	0.71	29.00	0.51	49.00	0.38	62.00	0.26	74.00
G11	0.79	21.00	0.64	36.00	0.34	66.00	0.22	78.00
G12	0.73	26.58	0.63	37.00	0.49	51.00	0.29	70.91
G13	0.67	32.93	0.37	63.00	0.27	73.00	0.19	80.99
G14	0.76	24.40	0.51	49.00	0.36	64.00	0.29	71.24
G15	0.80	20.00	0.46	54.00	0.34	66.00	0.23	77.00
G16	0.78	22.12	0.61	39.00	0.40	60.00	0.34	66.00
G17	0.71	29.29	0.50	50.00	0.39	61.00	0.29	70.93
G18	0.58	42.00	0.48	52.00	0.32	68.00	0.20	80.00
G19	0.67	33.00	0.45	55.00	0.27	73.00	0.17	82.96
G20	0.65	35.00	0.55	45.00	0.35	65.00	0.28	72.02
G21	0.70	30.00	0.53	47.00	0.37	63.00	0.25	75.00
G22	0.68	31.76	0.48	52.00	0.38	62.00	0.30	70.14
G23	0.72	28.00	0.55	45.00	0.31	69.00	0.24	76.00
G24	0.78	21.62	0.50	50.00	0.33	67.00	0.28	72.00
G25	0.75	24.68	0.59	41.00	0.38	62.00	0.30	70.00
G26	0.81	19.48	0.60	40.00	0.31	69.00	0.24	76.00
G27	0.78	22.36	0.67	33.00	0.57	43.00	0.38	62.00
G28	0.70	30.00	0.66	34.00	0.45	55.00	0.28	72.20
G29	0.81	19.00	0.69	31.00	0.58	42.00	0.39	0.61
G30	0.73	26.58	0.63	37.00	0.41	59.00	0.28	71.62
G31	0.77	22.78	0.60	40.00	0.42	58.00	0.30	70.35
G32	0.70	29.92	0.55	45.00	0.37	63.00	0.23	77.00
G33	0.77	22.57	0.50	50.00	0.39	61.00	0.28	72.00
Mean				0.48				
CV (%)				6.34				
LSD (0.05)				0.07				
MSerror				0.0021				
LS				**				

**= 1% level of significance; % D= Percent decrease; LS, Level of significance

Table 11. Relative root dry weight (mg/seedling) of mungbean genotypes as induced by PEG 6000

Genotypes	-0.7 bar	% D	-1 bar	% D	-2 bar	% D	-4 bar	% D
G1	0.76	24.17	0.55	44.88	0.37	63.00	0.09	90.82
G2	0.80	20.00	0.72	28.48	0.49	50.51	0.34	65.51
G3	0.75	25.00	0.57	42.89	0.40	60.00	0.26	74.46
G4	0.78	22.00	0.69	31.20	0.49	50.57	0.27	72.97
G5	0.74	26.00	0.69	31.45	0.49	50.57	0.28	71.72
G6	0.79	20.85	0.62	38.43	0.47	52.98	0.29	71.47
G7	0.75	25.00	0.68	31.63	0.43	56.78	0.31	68.97
G8	0.85	15.00	0.71	29.44	0.51	49.20	0.36	64.00
G9	0.76	24.00	0.63	36.74	0.48	52.13	0.33	66.53
G10	0.73	27.00	0.62	38.00	0.47	53.44	0.28	72.35
G11	0.74	26.00	0.68	32.07	0.47	53.46	0.33	66.58
G12	0.81	18.74	0.64	35.96	0.51	49.00	0.34	66.00
G13	0.66	34.00	0.57	42.76	0.40	60.05	0.25	75.33
G14	0.79	21.00	0.66	34.00	0.50	50.00	0.34	65.55
G15	0.80	19.75	0.68	32.00	0.48	52.37	0.32	67.86
G16	0.84	16.00	0.73	27.00	0.52	48.04	0.36	64.00
G17	0.74	26.00	0.63	37.00	0.49	51.00	0.34	66.00
G18	0.83	16.84	0.68	32.47	0.42	57.76	0.28	72.26
G19	0.69	31.00	0.59	41.00	0.39	61.35	0.27	73.00
G20	0.77	23.00	0.70	30.00	0.49	50.61	0.31	68.88
G21	0.78	21.71	0.63	36.99	0.48	52.46	0.27	72.54
G22	0.78	21.69	0.65	35.23	0.47	53.44	0.33	66.81
G23	0.78	21.97	0.68	32.14	0.48	51.61	0.29	71.50
G24	0.80	20.37	0.67	32.70	0.48	51.79	0.28	71.97
G25	0.77	23.17	0.61	39.14	0.42	58.44	0.30	70.00
G26	0.82	17.66	0.70	30.01	0.41	58.57	0.27	73.03
G27	0.83	17.00	0.76	24.39	0.56	44.22	0.38	61.93
G28	0.81	19.28	0.67	32.63	0.41	58.88	0.32	68.30
G29	0.87	13.00	0.76	24.00	0.56	43.73	0.38	61.97
G30	0.81	18.86	0.65	35.35	0.43	57.10	0.35	65.22
G31	0.78	22.00	0.70	30.00	0.47	52.70	0.33	66.94
G32	0.78	22.45	0.69	31.13	0.45	55.40	0.33	66.86
G33	0.79	21.21	0.63	37.00	0.49	50.65	0.28	71.61
Mean				0.55				
CV (%)				7.37				
LSD (0.05)				0.09				
MSerror				0.0031				
LS				**				

**= 1% LS; % D= Percent decrease; LS, Level of Significance

by G8 (0.31 with 69.00% reduction), while genotypes G1, G19, G3 and G13 had relatively low values of RSDW with 100, 82.96, 82.00 and 80.99% reduction over control, respectively. According to these results, G29, G27, G16 and G8 were the most tolerant of water stress, and G1, G19, G3 and G13 proved to be the most sensitive genotypes to water deficit stress when considering RSDW. These results were in close conformity with earlier findings in mungbean (Sunil *et al.*, 2016; Rajwinder et al., 2017), *Cassia angustifolia* (Shitole & Dhumal, 2012) and soybean (Sadeghi et al., 2011), where it was reported that increasing water deficit stress levels remarkably decreased RSDW. The increment of drought and salt stress caused a progressive reduction in the shoot dry weight in legumes, which may be due to the osmotic effect that hampered the seedling growth and resulted in lower shoot dry weight (Meo, 2000).

Conversely, under a water potential of -0.7 bar, the relative root dry weight (RRDW) of each seedling ranged from 0.66 to 0.87. At stress levels of -1.0, -2.0, and -4.0 bars, RRDW ranged from 0.55 to 0.76, 0.37 to 0.56, and 0.09 to 0.38, respectively, indicating an increasing degree of root dry weight loss with higher stress levels (Table 11). These results indicated that the root dry weight was adversely affected by increasing PEG concentrations. The results indicated that at higher stress levels (-4.0 bar) the G29, G27, G16 and G8 showed higher RRDW (0.38, 0.38, 0.36 and 0.36 with 61.97, 61.93, 64.00 and, 64.00% reduction, respectively) followed by G2 (0.34 with 65.51% reduction), and G12 (0.34 with 66% reduction). The lowest relative values were found in the G1, G3, G13 and G19 genotypes which were 0.09, 0.26, 0.25 and 0.27 with 90.82, 74.46, 75.33 and 73.00% reductions from their control, respectively. The current research was in agreement with an earlier report conducted by Gamze et al. (2005), who reported that the shoot and root dry weights of pea seedlings decreased due to the increase of PEG-induced drought stress. Many plant breeders have used dry root weight (DRW) as selection criteria for drought resistance. However, the genotypes' varying responses in terms of moisture stress tolerance may account for the significant drops in dry matter production of shoot and root. The outcomes are consistent with the cases of sunflower (Meo, 2000) and sorghum (Bibi et al., 2010; Ali et al., 2011).

3.3 Effects of PEG 6000 induced water potentials on the vigor index (VI) of mungbean genotypes

The vigor index (VI) of all the studied genotypes was significantly decreased by the stress levels of -0.7 bar, -1 bar, -2 bar and -4 bar (Table 12). Poor vigor index may be the consequence of PEG-induced osmotic stress's harmful effects on seed germination and seedling development. It ranged from 1713.38 to 3253.18, 1060.17 to 2286, 673.92 to 1754.02, 281.61 to 1200.63 and 0 to 760.30, respectively, in the control (0 bar), -0.7 bar, -1 bar, -2 bar and -4 bar. The genotypes G27, G29, G16 and G8 gave the highest VI values (760.30, 739.28, 658.37 and 610.75) with the lowest reduction (73.48, 70.48, 74.64 and 77.22%, respectively) at higher stress level (-4 bar) compared with their control. Genotypes G1, G19, G3 and G13 produced the lowest VI values (0.00, 138.05, 145.57, and 151.50) which meant the highest reduction (100, 93.09, 93.65 and 93.56%, respectively). The vigor index decreased as the water potential decreased. However, the results indicated that the genotypes G29, G27, G16 and G8 showed a significantly lower reduction of VI over control followed by G12 and G2, while G1, G3, G13 and G19 presented a higher reduction due to different stress levels. In comparison to low water potential (a stress condition), a high-water potential (0) significantly boosted the

Table 12. Vigor index (VI) of mungbean genotypes as induced by PEG 6000

Genotypes	Control	-0.7bar	% R	-1 bar	% R	-2 bar	% R	-4 bar	% R
G1	2234.13	1180.68	47.15	673.92	69.84	281.61	87.40	0.00	100.00
G2	2236.50	1705.13	23.76	1245.13	44.33	853.87	61.82	444.02	80.15
G3	2291.45	1273.35	44.43	696.48	69.61	377.43	83.53	145.57	93.65
G4	2325.35	1468.55	36.85	973.08	58.15	612.32	73.67	215.83	90.72
G5	2214.80	1368.37	38.22	939.95	57.56	523.50	76.36	225.68	89.81
G6	2658.57	1666.93	37.30	1091.87	58.93	671.03	74.76	345.00	87.02
G7	2392.30	1542.15	35.54	1074.58	55.08	746.73	68.79	356.39	85.10
G8	2681.28	1934.73	27.84	1534.72	42.76	1125.17	58.04	610.75	77.22
G9	1984.03	1319.78	33.48	933.95	52.93	480.35	75.79	286.05	85.58
G10	2340.02	1554.75	33.56	993.48	57.54	609.33	73.96	421.21	82.00
G11	1776.82	1229.53	30.80	767.17	56.82	470.90	73.50	207.38	88.33
G12	2167.28	1690.70	21.99	1192.03	45.00	734.72	66.10	452.98	79.10
G13	2352.07	1259.83	46.44	729.93	68.97	319.27	86.43	151.50	93.56
G14	2000.70	1304.85	34.78	929.73	53.53	630.53	68.48	275.10	86.25
G15	2000.32	1393.82	30.32	1022.00	48.91	594.47	70.28	344.70	82.77
G16	2595.80	1939.83	25.27	1505.67	42.00	1029.85	60.33	658.37	74.64
G17	2402.88	1433.60	40.34	956.22	60.21	659.80	72.54	338.83	85.90
G18	2441.40	1469.17	39.82	869.17	64.40	586.98	75.96	336.25	86.23
G19	1998.60	1093.05	45.31	700.68	64.94	295.27	85.23	138.05	93.09
G20	1716.43	1123.27	34.56	741.03	56.83	501.03	70.81	238.23	86.12
G21	2754.70	1857.73	32.56	1145.22	58.43	741.12	73.10	407.48	85.21
G22	3002.20	1961.28	34.67	1393.33	53.59	858.70	71.40	453.97	84.88
G23	3253.18	2267.85	30.29	1549.10	52.38	984.90	69.73	436.80	86.57
G24	2050.88	1452.35	29.18	955.60	53.41	600.97	70.70	330.18	83.90
G25	1941.60	1319.60	32.04	887.35	54.30	561.48	71.08	282.73	85.44
G26	1747.50	1169.85	33.06	768.80	56.01	505.98	71.05	283.45	83.78
G27	2866.42	2286.00	20.25	1754.02	38.81	1200.63	58.11	760.30	73.48
G28	2193.37	1392.17	36.53	922.38	57.95	619.72	71.75	309.40	85.89
G29	2504.70	1957.18	21.86	1632.05	34.84	1072.23	57.19	739.28	70.48
G30	1814.10	1204.60	33.60	753.85	58.44	466.25	74.30	311.27	82.84
G31	1758.43	1167.52	33.60	779.10	55.69	523.38	70.24	283.37	83.89
G32	2116.23	1384.33	34.59	910.57	56.97	577.60	72.71	348.87	83.51
G33	1713.38	1060.17	38.12	707.33	58.72	443.70	74.10	197.63	88.47
Mean				1153.26					
CV (%)				12.82					
LSD (0.05)				0.61					
MSerror				0.1420					
LS				**					

**= 1% level of significance; % R= Percent reduction; LS, Level of Significance

metabolic processes necessary for germination and raised the activity of alpha and beta-amylase enzymes, boosting SG and subsequently leading to a rise in the vigor index (Kaur et al., 2005). Furthermore, research has shown a strong correlation between seed quality, mean germination time (MGT) and germination speed (Khan, 1980; Rumbaugh & Pendry, 1990). A lower MGT is indicative of higher seed vigor and quality. The rate of germination is also a reliable indication of the seed vigor index, according to other researchers (Khan, 1980; Falleri, 1994).

3.4 Traits association

Estimates of the phenotypic and genotypic correlation coefficients of all pairs of germination and seedling-associated traits are presented in Tables 13 & 14. The results showed that most of the germination and seedling traits were either positively and negatively associated with each other, but the association was strong and significant.

3.4.1 Correlation among germination-related traits

Germination percentage (GP) was positively and significantly associated with the traits like CEG, SG and VI but negatively correlated with MGT (Table 13). CEG showed a positive association with SG and VI whereas it showed a negative association with MGT. SG showed a positive correlation with VI. It is clear from the results that MGT was negatively associated with other traits. This was probably due to the increased MGT with the increase of stress levels; while other traits showed a decreased performance with stress levels.

Table 13. Genotypic (lower diagonal) and phenotypic (upper diagonal) correlation of different germination-related traits

Traits	GP	CEG	MGT	SG	VI
GP		0.74^{**}	-0.74^{**}	0.97^{**}	0.78^{**}
CEG	0.89^{**}		-0.99^{**}	0.89^{**}	0.85^{**}
MGT	-0.50^{**}	-0.74^{**}		-0.89^{**}	-0.85^{**}
SG	0.97^{**}	0.84^{**}	-0.32^{ns}		0.86^{**}
VI	0.88^{**}	0.88^{**}	-0.41^{*}	0.91^{**}	

*5% level of significance, **1% level of significance, GP= Germination percentage, CEG= Coefficient of germination, MGT= Mean germination time, SG= Speed of germination, VI=Vigor index

3.4.2 Correlation among seedling-related traits

There was a significant positive relation observed among shoot traits (*viz.,* SL, SFW and SDW) as well as among the root traits (viz., RL, RFW and RDW). On the contrary, a negative and significant association were found between shoot and root traits (Table 14). The results revealed that shoot and root traits performed differentially under stress. Generally, shoot and root traits showed a positive association but it might be the stress which played a role in their differential performance. According to Varma (2016), in order for selection for the simultaneous enhancement of many qualities to be successful, it is important to understand how these features relate to one another. Furthermore, selection for one favorable characteristic will inherently be sufficient for another if two favorable qualities are connected. As a result, correlation analysis offers details on the kind and strength of the relationship between the characteristics of various components. This is beneficial for any crop development effort when selecting appropriate genotypes.

Table 14. Genotypic (lower diagonal) and phenotypic (upper diagonal) correlation of different seedling-related traits

Traits	SL	RL	SFW	RFW	SDW	RDW
SL		-0.67**	0.90**	-0.44**	0.97**	-0.78**
RL	-0.70**		-0.90**	0.89**	-0.70**	0.96**
SFW	0.91**	-0.92**		-0.71**	0.92**	-0.96**
RFW	-0.53**	0.92**	-0.75**		-0.44*	0.85**
SDW	0.98**	-0.71**	0.92**	-0.49**		-0.79**
RDW	-0.81**	0.99**	-0.97**	0.89**	-0.80**	

*5% level of significance, **1% level of significance, SL= Shoot length, RL= Root length, SFW= Shoot fresh weight, RFW= Root fresh weight, SDW= Shoot dry weight and RDW= Root dry weight

3.5 Principal component analysis

To investigate the genetic variations among the genotypes, principal component analysis was used, and trait-genotype biplots were created using mean relative data from different drought stress-induced PEG-6000 (Figure 1 A-D). Dimension 1 (Dim 1) accounted for 66.9% of the variance in the mungbean under the -0.07bar stress condition, and substantial positive loading scores were found in the GN, SG, SL, RDW, SG, and VI. Trait MGT had a negative loading score in Dim 1 (Figure 1A). The dimension 2 (Dim 2) under the 0.07 bar stress condition, which was related to the attributes SL, RDW, SFW, and VI, accounted for 8.8% of the variation (Figure 1A). The relationship between germination and seedling growth features was illustrated by the loading plot of Dim 1 versus Dim 2. Figure 1B shows the loading plot for the first two principal components under the -0.1 bar stress condition. The axes of RDW, CEG, VI, SL, SG, RL, SDW, and SFW traits were aligned, indicating that these traits contributed more to Dim 1 than others. The MGT trait was primarily associated with Dim 2. In the loading plot, longer vectors indicate that greater variability in the traits is explained by the first two principal components, while shorter vectors suggest that the variability of those traits is better explained by other dimensions (Rudresh et al., 2021). Additionally, the traits that point in the same direction show a positive correlation between the traits and the genotypes that point in the opposite direction show a negative association. In the current investigation, CEG and MGT had a strong negative correlation only under the -0.1 bar stress condition. The other characteristics of lodging severity had a positive correlation. The first two dimensions accounted for 82.7% of the total cumulative variance in the treatment -0.2 bar stress condition. While Dim 2 was primarily impacted by MGT, all traits showed a strong positive loading into Dim 1. Similarly, Dim 1 and Dim 2 displayed variances of 80.10 and 10.9%, respectively, under the -0.4 bar stress situation (Figure 1D). All characteristics exhibited the same trend for the analyzed values (MGT, CEG, VI, RFW, SL, SG, RL, GP, and SFW) under stress conditions. Significantly, during water deficit stress, G29, G27, G16, G8, and G2 corresponding to BMX-08010-2, BMX-08009-7, BMX-01015, BARI Mung-8, BARI Mung-2 genotypes were discovered close to the apex of the biplot, indicating that these genotypes have the distinct genetic potential of the higher tolerance to drought stress in comparison to others.

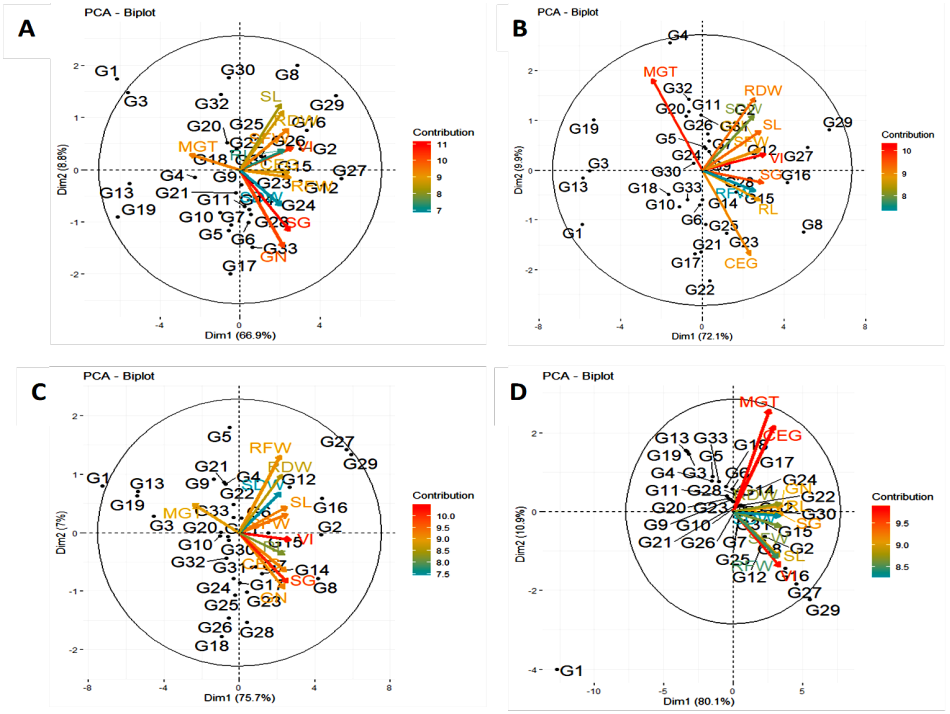

Figure 1. (A) Biplot of principal component displaying genotypic grading based on -0.07 bar using PEG-6000. (B) Biplot of principal components displaying genotypic grading based on -0.1 bar condition. (C) Biplot of principal components displaying genotypic grading based on -0.2 bar using PEG treatment condition. (D) Biplot of principal components displaying genotypic grading based on -0.4 bar through PEG treatment. GN=Germination, CEG= Coefficient of germination, MGT=Mean germination time, SG=Speed of germination, VI=Vigor index, SL=Shoot length, RL=Root length, SFW=Shoot fresh weight, RFW=Root fresh weight, SDW= Shoot dry weight and RDW= Root dry weight

3.6 Hierarchical clustering analysis using heatmaps

A heat map with hierarchical clustering analysis (HCA) illustrates the magnitude of a phenomenon as color in two dimensions, displaying how the phenomenon is clustered according to their relative expression patterns. Therefore, it can be an effective tool in the investigation of complex relationships between different traits in different environments (Meena et al., 2020). Plotting a heat map using hierarchical clustering analysis and taking into account the mean relative characteristics performance of the 33 mungbean genotypes allowed for the identification of the critical qualities needed to assess water deficiency stress resistance. Based on the degree of correlation between germination and seedling development characteristics under conditions of water deficiency stress, a heat map dendrogram was used to group mungbean genotypes into different groups. Two dendrogram types were created: a vertically positioned characteristics dendrogram and a horizontally positioned genotype dendrogram (Figure 2). By dividing the characteristics into three separate groups, and the hierarchical clustering showed the heterogeneity of traits for each genotype (Figure 2).

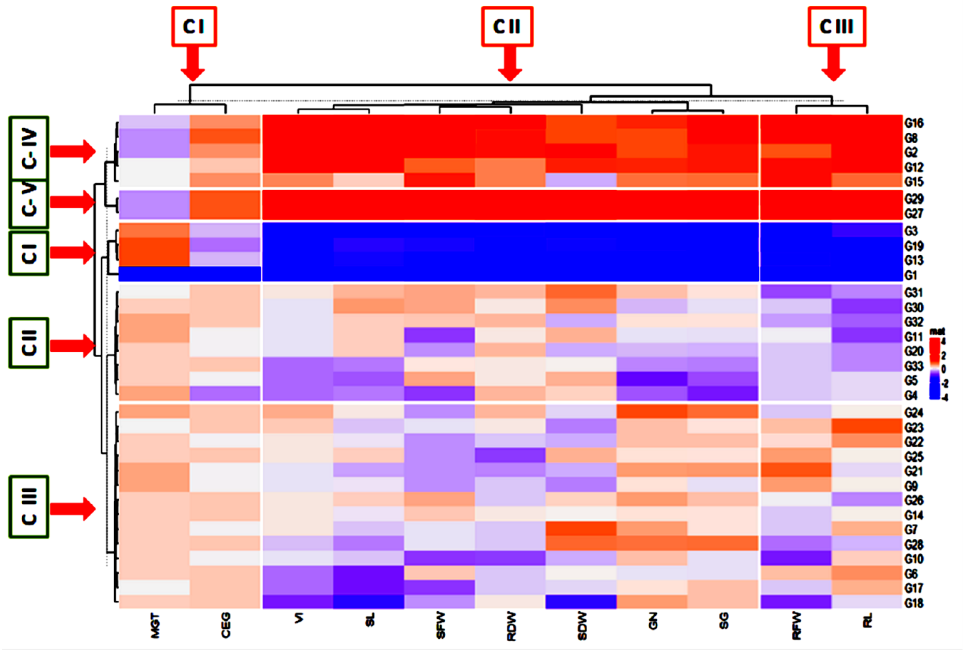

Figure 2. Heat map dendrogram partitioning mungbean genotypes into several clusters based on the range of the relationship of germination and seedling growth traits under water deficit stress conditions. The hierarchical clustering (method = ward. D2 and distance = Euclidean) indicates trait and genotype association. The color (from blue to red) and intensities indicate the extent of expression level which was adjusted based on the relationship among genotypes and traits. Deeper blue represents susceptibility, and darker red color represents tolerance to water deficit stress.GN=Germination, CEG= Coefficient of germination, MGT=Mean germination time, SG=Speed of germination, VI=Vigor index, SL=Shoot length, RL=Root length, SFW=Shoot fresh weight, RFW=Root fresh weight, SDW= Shoot dry weight and RDW= Root dry weight.

Cluster I included traits such as MGT and CEG, while cluster III comprised traits like RL and RFW. While the rest of the traits were grouped into cluster II in which most of the genotypes exhibited a reduction in trait value under water deficit conditions imposed by PEG-6000. The studied mungbean genotypes were divided into five groups based on color intensity: cluster I includes the most susceptible genotypes like G1, G13, G19 and G3 corresponding to BARI Mung-1, BU Mung-4, BMX-05001 and BARI Mung-3, respectively. The drought stress tolerant genotypes such as G29, G27, G16, G8, G2, G12, and G15 corresponding to BMX-08010-2, BMX-08009-7, BMX-01015, BARI Mung-8, BARI Mung-2, BU Mung-2, and BMX-01007 were plotted in cluster V and cluster IV, of which G29 and G27 presented as the most tolerant. The rest of the genotypes were plotted in clusters II and III. The heatmap cluster analysis shows the nature of the grouping between genotypes with color intensity; it is regarded as one of the best methods for analyzing the genotypes under different contexts (Nazari & Pakniyat, 2010; Dehbalaei et al., 2013; Liu et al., 2015; Sakinah et al., 2021). Therefore, it is advised to examine mungbean resistance to PEG-6000-imposed drought stress by this method.

3.7 Multi-trait genotype-ideotype distance index (MGIDI)

Based on the results of measuring numerous attributes, the mungbean genotypes were ranked (Figure 3). The MGIDI index identified genotypes G29, G27, G16, G8, G12, G2 and G15 from the total set of 33 genotypes, as strong performers in the studies of germination and seedling growth traits under water deficit conditions. The MGIDI index offered a view into both the strengths and weakness of each genotype, making it easier to identify ideal genotypes based on a multiple trait framework. Genotypes that contributed less to overall performance were plotted near to the center of the graph, while those contributed more were plotted near the edges (Benakanahalli et al., 2021). A MGIDI distance of 5.20 set as the cut-off point for selection intensity (Figure 3, red circle). Genotype G30, positioned near the cross-point of the axes, indicated that it may display important characteristics, despite not being a major contributor in the current evaluation. This suggests that G30 could have untapped potential that warrants further investigation. Genotypes near the cut-off point should also be given special attention, as they may show unique or valuable traits (Olivoto & Nardino, 2020). Therefore, in future research, it would be valuable to explore the contributions of genotypes close to the cut-off point in more depth. The use of the MGIDI index in plant evaluation is expected to become widespread due to its effectiveness in identifying ideal genotypes. For example, the MGIDI index has already been used successfully to select optimal strawberry genotypes (Olivoto et al., 2021).

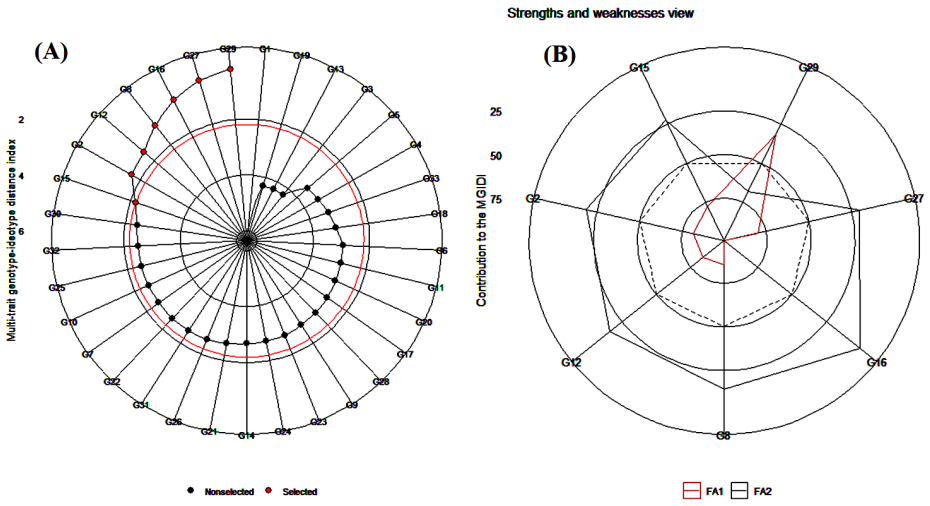

Figure 3. Genotype grading in an upward trend for the MGIDI index. (A)The chosen genotypes according to this index are displayed in red color. The centric red circle demonstrates the cross point based on selection intensity. (B) The strengths and weaknesses view of the chosen genotypes is shown as the proportion of every factor on the determined MGIDI index. The minimum of the ratio interpreted by a factor (nearer to the outside), the nearer the characters within that factor are to the *ideotype*. The dashed line shows the conceptual value if all the factors are equally responsible.

4. Conclusions

The results of the investigation showed that increasing PEG concentrations resulted in decreased germination, shoot and root length, as well as reduced fresh and dry weight. Shoot length was more negatively impacted by higher PEG levels than root length. Screening for drought-tolerant genotypes based on germination percentage, vigor index, and relative performance of various traits revealed significant findings. BARI Mung-1 failed to germinate at -4 bar pressure, indicating high susceptibility to severe water deficit stress. Conversely, genotypes BMX-08010-2, BMX-08009-7, BMX-01015, BARI Mung-8, BARI Mung-2, and BU Mung-2 exhibited greater drought tolerance, with good germination indices and strong seedling performance at -4 bar PEG concentration. In contrast, genotypes BARI Mung-1, BARI Mung-3, BU Mung-4, and BMX-05001 were more vulnerable to water shortage stress across various pressure levels (-0.7, -1, -2, and -4 bar), resulting in poorer germination rates and weaker seedling traits. Genotypes that performed better under water deficit conditions showed smaller losses in growth parameters, indicating their potential use in future drought-tolerant breeding programs. Additionally, significant correlations between various research features were observed. The main component analysis, hierarchical clustering using a heat map, and MGIDI yielded genotype selections consistent with the drought tolerance analysis. The identified drought-tolerant genotypes can be adapted to drought-prone areas, maintaining stable yields with minimal yield penalty, thus contributing to agricultural productivity, nutrient security, resilience, and sustainability in semi-arid regions. The study highlights the vital role of drought-tolerant mungbean genotypes in advancing sustainable agriculture and enhancing food security. By improving crop resilience to adverse conditions, these genotypes ensure more stable food supplies and efficient water use. Their nitrogen-fixing ability enriches soil health, reducing reliance on synthetic fertilizers. Additionally, their integration into crop rotation systems, especially with rice, enhances soil fertility and disrupts pest cycles. Mungbeans' nutritional value and economic benefits further emphasize their importance. Promoting these resilient genotypes supports sustainable farming practices, strengthens community well-being, and protects environmental health, addressing climate change challenges and securing future food sources.

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6. Conflicts of Interest

The authors have declared that they have no conflicts of interest.

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