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RESEARCH ARTICLE

Evaluation of blackgram [*Vigna mungo* (L.) Hepper] genotypes for salinity tolerance at the seedling stage

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Abstract

Salinity is a significant environmental stress limiting factor in blackgram (*Vigna mungo*) production, necessitating the identification of saline-tolerant genotypes for sustainable cultivation. This study was conducted at the National Pulses Research Centre (NPRC), Vamban, in 2019 and 2020 to test the tolerance of blackgram genotypes to salinity under a hydroponic system. The experiment was laid out in a randomised complete block design with two replications. Five genotypes were initially tested at salt levels ranging from 11 to 15 dSm^{-1} and 13 dSm^{-1} was identified as the critical level for screening. 100 blackgram genotypes were subsequently evaluated at 13 dSm^{-1}, which led to the identification of seven highly saline-tolerant genotypes. Further validation trials were conducted using these seven VBN 8 genotypes and two susceptible checks (VBN 6 and CO 6). The results confirmed that five genotypes *viz.,* ACM BG 14-001, VBG 18-071, VBG 18-080, VBG 19-005 and VBG 19-010, exhibited strong tolerance to salinity, with survival rates exceeding 75% at 13 dSm^{-1}. These genotypes may be tested in saline-affected areas for potential release as a new variety. Additionally, they can serve as donors in breeding programs for saline tolerance. This study's findings contribute to identifying resilient genotypes that may enhance productivity in salt-affected soils and ensure food security.

Keywords: hydroponics; salinity; screening; survival rate

Introduction

Blackgram [*Vigna mungo* (L.) Hepper] is a self-pollinated short-duration crop that is domesticated from *Vigna mungo* var. *sylvestris* (1-3). It fixes 42 kg of nitrogen per hectare per year and reduces the input cost for farmers. This crop is a key protein source in a cereal-based diet. It is easy to digest, so it does not cause flatulence. In India, the blackgram is cultivated in over 4.63 million hectares, with an average production of 2.78 mt and productivity of 600 kg/ha (4). Agricultural land in arid and semi-arid regions faces major threats like soil degradation, sodification and salinisation. They follow drought and erosion (5). About 6% of cultivable land worldwide has salinity; around 54% of soil has sodicity (6). Researchers classify soil salinity as primary (natural) or secondary (human-made). These two causes raise the salinity by 10% per year (7). Over half of all arable land could become salinised by 2050 (8). It severely harms vegetation, biodiversity and soil fertility, leading to the desertification of productive arable lands, which occurs as a consequence (9-11).

Salinity stress is a major constraint to agricultural productivity that accumulates excessive concentrations of soluble salts in both soil and water, which harms crop yield. It reduces germination percentage and weakens seedlings (12). It also shortens shoot and root length and reduces total biomass. Salt damage causes symptoms like necrosis (13). It starts with burning on leaf margins, then chlorosis. Leguminous crops are sensitive to salinity and vary in their tolerance (14). Salinity tolerance is a complex trait. It varies by genotype, growth stage and organ in crops. Monocotyledon cereal crops exhibit a biphasic response to salinity. High salt levels cause plants to slow their growth. They do this by closing stomata and stopping cell growth. After a week of salinity exposure, toxic ions accumulate in the cytoplasm (15). Salinity harms rhizobia, the agent of nodulation in pulse crops (16). So, nodulation decreases.

Traditional field screening for salinity tolerance can be time-consuming, expensive and influenced by several environmental factors (17-19). Hydroponics screening has emerged as a valuable technique for rapidly and efficiently evaluating the response of blackgram genotypes to salinity stress (17, 20). This method offers several advantages, including precise control of environmental conditions, ease of nutrient management and the ability to assess root-shoot growth and development (21-23). Numerous studies have employed hydroponics to screen blackgram genotypes for salinity tolerance (24). These studies have investigated the effects of different salinity levels on various growth parameters, such as germination rate, seedling growth, root and shoot length, biomass accumulation and physiological

responses (25-27). By carefully controlling the salinity levels in the hydroponic solution, researchers can effectively identify the genotypes that exhibit superior performance under stress conditions (21). Hydroponics screening allows for the simultaneous evaluation of many genotypes, making it a powerful tool for screening and selection (28, 29). This approach can accelerate breeding by identifying promising genotypes for further assessment in field trials.

Furthermore, hydroponics can be used to study the underlying mechanisms of salt tolerance by enabling the analysis of root exudates, nutrient uptake and gene expression analysis (30, 31). To breed a salt-tolerant crop, it is essential to understand the genetics and mechanisms of salt tolerance. Reliable screening methods and appropriate selection indices are necessary for the success of breeding programmes aimed at improving salinity tolerance. Many studies exist on salt tolerance in cereal crops. However, the mechanisms of salt tolerance in legumes are still unclear. Researchers have conducted limited studies on screening salt and its mechanisms in legumes. This article aims to identify a reliable method for testing salinity tolerance in blackgram using hydroponics and to screen for saline tolerance among 100 blackgram genotypes.

Materials and methods

Plant materials

Five blackgram genotypes were used to standardise the screening protocol. The genotypes are ADT 6, VBN 6, VBN 8, VBG 19-002 and VBG 19-010. The screening was done in 2019-20 at the National Pulses Research Centre (NPRC), Vamban, under the Glasshouse facility. The genotypes ADT 6, VBN 6 and VBN 8 are released varieties for cultivation in Tamil Nadu, India. At the same time, VBG 19-002 and VBG 19-010 are advanced breeding lines developed from a cross between *Vigna mungo* and *Vigna mungo* var. *sylvestris*. The 100 genotypes listed in Table 1 were screened for salinity tolerance at 13 dSm^{-1}. These included both breeding lines and varieties. The identified highly saline-tolerant genotypes were further tested along with two susceptible genotypes to confirm their superiority.

Experimental design

All experiments were conducted using a randomised complete block design with two replications.

Screening protocol

The screening used the IRRI protocol for the experimental protocol and nutrient preparation (32). Styrofoam sheets with 22 × 22 × 3 cm dimensions were used to create the experimental setup. Eighty identical holes were drilled with uniform spacing (Fig. 1). The sterilised seeds were germinated using the roll-towel method for three days. Healthy seedlings were then transferred to the styrofoam sheets placed on Yoshida nutrient solution. One seedling was placed in each hole without damaging the roots. A total of 20 seedlings per genotype per replication was maintained. At 18 days after sowing, the genuine leaf emerged (the three-leaf stage). Salt stress was imposed in the Yoshida nutrient solution using different concentrations of NaCl. Initial screening with electrical conductivity (EC) level from 0 to 20 dSm^{-1} showed a critical salinity range of 10 to 15 dSm^{-1} (data not shown). The study

Fig 1. Screening for salinity tolerance in blackgram under the hydroponic method.

adopted five different EC levels of 11, 12, 13, 14 and 15 dSm^{-1} to determine a critical level. The subsequent screening adopted a salinity level of 13 dSm^{-1}.

Data collection

On the 7th day after salinisation, two traits were measured - shoot length (cm) and survival rate (%). For further screening, only the survival rate (%) was used.

Statistical analysis

Analysis of variance was carried out for each trait. The means were compared using the least significant difference method. Mean Function Value (MFV) was used to test salt tolerance. It is a fuzzy evaluation method (33). The MFVs of genotypes ranged from 0 to 1. Here, 0 is the lowest and 1 the highest expression of a trait at a specific salinity. Salinity tolerance has five categories. They are based on the average ($\bar{X}$) and the standard deviation (SD) of the MFV. These categories are listed below. The data were analysed using the STAR package developed by IRRI, Philippines.

Range	Categories
$Xi \geq \bar{X} + 1.64$ SD	Highly saline tolerant
$\bar{X} + 1$ SD $\leq Xi \leq \bar{X} + 1.64$ SD	Saline tolerant
$\bar{X} - 1$ SD $\leq Xi \leq \bar{X} + 1$ SD	Moderately saline tolerant
$\bar{X} - 1.64$ SD $\leq Xi \leq \bar{X} - 1$ SD	Saline susceptible
$Xi \leq \bar{X} - 1.64$ SD	Highly saline susceptible

Results and Discussions

Identification of the critical EC level for salinity screening

To conduct extensive salinity tolerance screening, it is crucial to determine the critical salinity level. This critical level should be able to differentiate between tolerant and susceptible genotypes. To determine this level, five genotypes with varying backgrounds were screened at five levels of salinity (11, 12, 13, 14 and 15 dSm^{-1}). Shoot length (cm), survival percentage and mean functional values (MFVs) were estimated at different salinity levels for all genotypes.

Shoot length (cm)

Table 2 shows the shoot length (cm) at different salinity levels. It also includes the membership function value (MFV) and means. Of the genotypes tested, VBG 19-010 had the longest shoots. They measured 19.60 cm at the lowest salt level (11 dSm^{-1}). It also

Table 1. List of blackgram genotypes.

S. No	Genotypes	Parentage	Source
1.	ACM BG 14–001	CO 5 × VBN (Bg) 4	AC and RI, TNAU, Madurai
2.	ACM BG 16–017	Mutant from MDU 1(500 Gy)	AC and RI, TNAU, Madurai
3.	ACM BG 18–009	ACM BG 14–001 × MDU 1	AC and RI, TNAU, Madurai
4.	Mash 1008	SML-32 and Mash 1	PAU, Ludhiana
5.	Mash 114	Mash 338 × RBI 1	PAU, Ludhiana
6.	PU 11–25	UPU 97–10 × KU 96–3	GBPUA andT, Pantnagar
7.	PU 14–28	PI 31 × MASH 1008	GBPUA andT, Pantnagar
8.	SPS 5	-	IIPR, Kanpur
9.	SUG 1137	KUG 269 × UG 563	RRS, PAU, Gurdaspur
10.	TU 94–2	TPU 3 × TAUs	Trombay Mumbai
11.	TU 68	TU 94–1 × *Vigna mungo* var. *sylvestris*	Trombay Mumbai
12.	VBG 12–110	Mash 114 × Vamban 3	NPRC, TNAU, Vamban
13.	VBG 13–003	KU 216 × Vamban 3	NPRC, TNAU, Vamban
14.	VBG 14–016	VBN (Bg) 4 × PU 133–19	NPRC, TNAU, Vamban
15.	VBG 17–007	VBN (Bg) 5 × MDU 1	NPRC, TNAU, Vamban
16.	VBG 17–012	VBN (Bg) 4 × Uttara	NPRC, TNAU, Vamban
17.	VBG 17–019	ADT 5 × DU 1	NPRC, TNAU, Vamban
18.	VBG 17–026	KUG 365 × MDU 1	NPRC, TNAU, Vamban
19.	VBG 17–029	VBN (Bg) 5 × TU 17–14	NPRC, TNAU, Vamban
20.	VBG 18–040	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
21.	VBG 18–041	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
22.	VBG 18–042	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
23.	VBG 18–043	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
24.	VBG 18–044	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
25.	VBG 18–045	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
26.	VBG 18–046	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
27.	VBG 18–047	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
28.	VBG 18–048	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
29.	VBG 18–050	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
30.	VBG 18–051	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
31.	VBG 18–052	VBN (Bg) 4 × Mash 114	NPRC, TNAU, Vamban
32.	VBG 18–054	VBN (Bg) 4 × PU 11–14	NPRC, TNAU, Vamban
33.	VBG 18–055	VBN (Bg) 4 × PU 11–14	NPRC, TNAU, Vamban
34.	VBG 18–056	VBN (Bg) 4 × PU 11–14	NPRC, TNAU, Vamban
35.	VBG 18–057	VBN 8 × Mash 114	NPRC, TNAU, Vamban
36.	VBG 18–058	VBN 8 × LBG 652	NPRC, TNAU, Vamban
37.	VBG 18–059	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
38.	VBG 18–060	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
39.	VBG 18–061	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
40.	VBG 18–062	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
41.	VBG 18–063	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
42.	VBG 18–064	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
43.	VBG 18–065	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
44.	VBG 18–066	VBN 8 × TU 99–2	NPRC, TNAU, Vamban
45.	VBG 18–067	VBN 8 × VBG 11–053	NPRC, TNAU, Vamban
46.	VBG 18–068	VBN 8 × VBG 11–053	NPRC, TNAU, Vamban
47.	VBG 18–069	VBN 8 × VBG 11–053	NPRC, TNAU, Vamban
48.	VBG 18–070	VBN 8 × VBG 11–053	NPRC, TNAU, Vamban
49.	VBG 18–071	VBN 8 × VBG 11–053	NPRC, TNAU, Vamban
50.	VBG 18–072	VBN 6 × Mash 1008	NPRC, TNAU, Vamban

51.	VBG 18–073	VBN 6 × Mash 1008	NPRC, TNAU, Vamban
52.	VBG 18–074	VBN 6 × Mash 1008	NPRC, TNAU, Vamban
53.	VBG 18–075	VBN 6 × Mash 1008	NPRC, TNAU, Vamban
54.	VBG 18–076	VBN 6 × Mash 1008	NPRC, TNAU, Vamban
55.	VBG 18–077	VBN 6 × Mash 1008	NPRC, TNAU, Vamban
56.	VBG 18–079	VBN (Bg) 7 × Mash 114	NPRC, TNAU, Vamban
57.	VBG 18–080	VBN 8 × VBG 11–053	NPRC, TNAU, Vamban
58.	VBG 19–001	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
59.	VBG 19–002	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
60.	VBG 19–003	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
61.	VBG 19–004	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
62.	VBG 19–005	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
63.	VBG 19–006	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
64.	VBG 19–007	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
65.	VBG 19–008	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
66.	VBG 19–009	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
67.	VBG 19–010	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
68.	VBG 19–011	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
69.	VBG 19–012	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
70.	VBG 19–013	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
71.	VBG 19–014	BDR-1×*Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
72.	VBG 19–015	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
73.	VBG 19–016	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
74.	VBG 19–017	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
75.	VBG 19–018	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
76.	VBG 19–019	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
77.	VBG 19–020	BDR-1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
78.	VBG 19–021	MDU 1 × Mash 1008	NPRC, TNAU, Vamban
79.	ADT 3	Pureline selection from Tirunelveli	TRRI, TNAU, Aduthurai
80.	ADT 5	Pureline selection from Kanpur variety	TRRI, TNAU, Aduthurai
81.	ADT 6	Vamban 1 × VBG 04–2006	TRRI, TNAU, Aduthurai
82.	APK 1	ADT 2 × RU 1	RRS, TNAU, Aruppukottai
83.	CO 5	Pureline selection from Musiri type	TNAU, Coimbatore
84.	CO 6	DU 2 × VB 20	TNAU, Coimbatore
85.	KKM 1	COBG 643 × Vamban 3	V.O.C. Chidambaranar ACandRI, TNAU, Killikulam
86.	LBG 752	LBG 402 × LBG 20	ANGRAU andhra Pradesh
87.	LBG 787	LBG 685 × IPU 98–1	ANGRAU andhra Pradesh
88.	MDU 1	ADB 2003 × VBG 66	AC and RI, TNAU, Madurai
89.	TMV 1	Midhi Ulundu × KM 1	ORS, TNAU, Tindivanam
90.	Vamban 1	KM-1 × 476–1	NPRC, TNAU, Vamban
91.	Vamban 2	Mutant from T9	NPRC, TNAU, Vamban
92.	Vamban 3	LBG 402 × LBG 17	NPRC, TNAU, Vamban
93.	VBN (Bg) 4	CO 4 × PDU 102	NPRC, TNAU, Vamban
94.	VBN (Bg) 5	Vamban 1 × UK 17–1	NPRC, TNAU, Vamban
95.	VBN 6	Vamban 1 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
96.	VBN (Bg) 7	Vamban 3 × *Vigna mungo* var. *sylvestris*	NPRC, TNAU, Vamban
97.	VBN 8	Vamban 3 × VBG 04–008	NPRC, TNAU, Vamban
98.	VBN 9	Mash 114 × Vamban 3	NPRC, TNAU, Vamban
99.	VBN 10	VBN 1 × UH 04–04	NPRC, TNAU, Vamban
100.	VBN 11	PU 31 × CO 6	NPRC, TNAU, Vamban

Table 2. Mean and membership function values of shoot length (cm) for different salinity levels.

Genotypes	11 dSm^{-1}		12 dSm^{-1}		13 dSm^{-1}		14 dSm^{-1}		15 dSm^{-1}	
	Shoot length (cm)	MFV	Shoot length (cm)	MFV	Shoot length (cm)	MFV	Shoot length (cm)	MFV	Shoot length (cm)	MFV
ADT 6	19.17 ab	0.95	19.98 ab	0.68	23.25 ab	1.00	19.43 ab	0.82	17.80 ab	0.65
VBN 6	11.77 c	0.00	12.50 c	0.00	16.25 c	0.00	15.20 c	0.00	14.10 c	0.00
VBN 8	19.23 a	0.95	23.50 a	1.00	21.95 a	0.81	20.38 a	1.00	19.80 a	1.00
VBG 19–002	17.53 b	0.74	18.02 b	0.50	22.52 b	0.90	17.56 b	0.46	16.25 b	0.38
VBG 19–010	19.60 a	1.00	21.70 a	0.84	23.04 a	0.97	20.13 a	0.95	19.70 a	0.98

Mean values with similar letters had no significant difference (P≤0.05); MFV: mean functional value.

had the highest MFV of 1.00 at this salinity. It was followed by VBN 8, with a shoot length of 19.23 cm. At the highest salinity (15 dSm^{-1}), VBN 8 and VBG 19-010 outperformed the other genotypes. Genotypes showed the most significant MFV values of 1.00 and 0.98. This suggests that these two genotypes have greater tolerance to high salinity levels. Genotype VBN 6 had the lowest shoot length at all salinity levels. Additionally, VBN 6 also exhibited the lowest MFV value of 0.00. These findings suggest that VBN 6 is less tolerant to salinity than other genotypes. Salt stress significantly decreases shoot length and biomass by reducing photo-synthesis and increasing the respiration rate in growing plants (19).

Survival rate (%)

Table 3 displays survival rates for different salinity levels (%) and MFV. Generally, an increase in salinity leads to a decrease in survival percentage. However, plants died ultimately at salinity levels of 14 and 15 dSm^{-1}. There was 0% survival. At salinity levels of 11, 12 and 13 dSm^{-1}, genotype VBG 19-010, followed by VBN 8, had the highest survival and MFV. Across all salinity levels, VBN 6 showed the lowest MFV and survival percentage.

In blackgram, higher salinity levels typically lead to reduced survival rates. This is because high salt concentrations create osmotic stress on the plants, hindering their growth and limiting their ability to absorb water and essential minerals (34). This stress also restricts the expansion of the cytoplasm and vacuoles within the plant cells. Additionally, ion toxicity from excessive salt disrupts the ionic balance. These adverse effects of salinity stress are supported by several studies (35-37). Due to the salinity stress, salinity-sensitive plants have stunted shoots and reduced leaf area, leading to a decreased survival rate as salinity increases (38, 39).

Genotype VBN 6 was found to be highly sensitive to salinity. It exhibited the lowest values at all levels of salinity. The consistently low values observed for VBN 6 across all salinity treatments suggest a limited capacity to cope with osmotic and ionic stress. It had detrimental effects on plant growth, including disrupted cellular processes and decreased survival rate. Conversely, genotypes VBN 8 and VBG 19-010 were classified as saline-tolerant due to their high scores based on their survival rate. It indicates the presence of mechanisms enabling them to mitigate salinity's negative impacts, including osmotic adjustment, efficient ion exclusion or compart-mentalisation and enhanced antioxidant defence systems. The survival rate (%) showed that 14 and 15 dSm^{-1} salinity levels have resulted in complete mortality. It could not distinguish between the genotypes for their salinity tolerance level. However, genotypes VBN 8 and VBG 19-010 showed over 50% plant survival at 13 dSm^{-1}. Hence, 13 dSm^{-1} is the optimal salinity level for screening purposes and is crucial for the efficient and reliable selection of tolerant genotypes. Among traits, survival rate (%) can be used to identify saline tolerance. MFV provides a convenient and objective metric for comparing the genotypes, potentially integrating multiple aspects of plant growth into a single value. The strong correlation between MFV based on survival rate and overall salinity tolerance suggests that this simplified approach can be effectively used in screening programmes.

Screening of advanced breeding lines and varieties of blackgram

Table 4 presents the survival rate (%) and MFV of 100 blackgram genotypes. Survival rates ranged from 0% to 78%. No genotype had 100% survival. Of the 100 genotypes, only three survived at least 75%. They are VBG 18-071, VBG 18-080 and VBG 19-010. Nine genotypes, including ACM BG 14-001 and VBN 8, had a 50% to 75% survival rate. Twenty-six genotypes had a 25% to 50% survival rate. The remaining 62 genotypes exhibited less than 25% survival. Most of the genotypes showed a decrease in survival rate under 13 dSm^{-1}. Similar findings were reported on survival rate (%) (24). The highest MFV value was 1.00 in VBG 18-071. The lowest MFV value was 0.00. Based on the classification using MFV, seven genotypes were identified as highly saline-tolerant (17). They were ACM BG 14-001, VBG 18-071, VBG 18-080, VBG 19-005, VBG 19-007, VBG 19-010 and Vamban 3. They had a high MFV (>0.70). These genotypes hold considerable promise as potential candidates for direct utilisation in breeding programs or as sources of valuable genes for salt tolerance. It

Table 3. Mean and membership function values of plants' survival rate (%) for different salinity levels.

Genotypes	11 dSm^{-1}		12 dSm^{-1}		13 dSm^{-1}		14 dSm^{-1}		15 dSm^{-1}	
	Survival (%)	MFV	Survival (%)	MFV	Survival (%)	MFV	Survival (%)	MFV	Survival (%)	MFV
ADT 6	37.50 b	0.50	35.00 a	0.52	0.00 b	0.00	0.00 a	0.00	0.00 a	0.00
VBN 6	0.00 c	0.00	0.00 b	0.00	0.00 b	0.00	0.00 a	0.00	0.00 a	0.00
VBN 8	65.70 a	0.87	63.35 a	0.95	54.80 a	0.91	0.00 a	0.00	0.00 a	0.00
VBG 19–002	54.80 ab	0.72	41.65 a	0.62	10.00 b	0.17	0.00 a	0.00	0.00 a	0.00
VBG 19–010	75.70 a	1.00	66.70 a	1.00	60.40 a	1.00	0.00 a	0.00	0.00 a	0.00

Mean values with similar letters had no significant difference (P≤0.05); MFV: mean functional value.

Table 4. Mean and MFV values for survival rate (%) of blackgram genotypes at 13 dSm^{-1}.

S. No.	Genotype	Survival (%)	MFV	S. No.	Genotype	Survival (%)	MFV
1.	ACM BG 14–001	71.25	0.91 HT	51.	VBG 18–073	33.33	0.43
2.	ACM BG 16–017	12.50	0.16	52.	VBG 18–074	0.00	0.00
3.	ACM BG 18–009	45.83	0.59 T	53.	VBG 18–075	25.00	0.32
4.	Mash 1008	6.25	0.08	54.	VBG 18–076	45.83	0.59 T
5.	Mash 114	6.25	0.08	55.	VBG 18–077	50.00	0.64 T
6.	PU 11–25	0.00	0.00	56.	VBG 18–079	33.33	0.43
7.	PU 14–28	6.25	0.08	57.	VBG 18–080	77.00	0.99 HT
8.	SPS 5	20.00	0.26	58.	VBG 19–001	28.57	0.37
9.	SUG 1137	25.00	0.32	59.	VBG 19–002	37.50	0.48
10.	TU 94–2	0.00	0.00	60.	VBG 19–003	33.04	0.42
11.	TU 68	0.00	0.00	61.	VBG 19–004	33.93	0.43
12.	VBG 12–110	28.57	0.37	62.	VBG 19–005	74.11	0.95 HT
13.	VBG 13–003	31.25	0.40	63.	VBG 19–006	30.95	0.40
14.	VBG 14–016	0.00	0.00	64.	VBG 19–007	54.76	0.70 HT
15.	VBG 17–007	18.75	0.24	65.	VBG 19–008	14.58	0.19
16.	VBG 17–012	7.14	0.09	66.	VBG 19–009	36.67	0.47
17.	VBG 17–019	0.00	0.00	67.	VBG 19–010	75.00	0.96 HT
18.	VBG 17–026	0.00	0.00	68.	VBG 19–011	0.00	0.00
19.	VBG 17–029	20.83	0.27	69.	VBG 19–012	19.64	0.25
20.	VBG 18–040	13.39	0.17	70.	VBG 19–013	0.00	0.00
21.	VBG 18–041	26.79	0.34	71.	VBG 19–014	39.58	0.51
22.	VBG 18–042	33.33	0.43	72.	VBG 19–015	50.00	0.64 T
23.	VBG 18–043	0.00	0.00	73.	VBG 19–016	45.83	0.59 T
24.	VBG 18–044	12.50	0.16	74.	VBG 19–017	0.00	0.00
25.	VBG 18–045	7.14	0.09	75.	VBG 19–018	0.00	0.00
26.	VBG 18–046	0.00	0.00	76.	VBG 19–019	0.00	0.00
27.	VBG 18–047	13.39	0.17	77.	VBG 19–020	42.86	0.55 T
28.	VBG 18–048	10.00	0.13	78.	VBG 19–021	0.00	0.00
29.	VBG 18–050	0.00	0.00	79.	ADT 3	0.00	0.00
30.	VBG 18–051	0.00	0.00	80.	ADT 5	6.25	0.08
31.	VBG 18–052	0.00	0.00	81.	ADT 6	0.00	0.00
32.	VBG 18–054	0.00	0.00	82.	APK 1	12.50	0.16
33.	VBG 18–055	0.00	0.00	83.	CO 5	0.00	0.00
34.	VBG 18–056	13.39	0.17	84.	CO 6	0.00	0.00
35.	VBG 18–057	0.00	0.00	85.	KKM 1	0.00	0.00
36.	VBG 18–058	0.00	0.00	86.	LBG 752	0.00	0.00
37.	VBG 18–059	50.00	0.64 T	87.	LBG 787	0.00	0.00
38.	VBG 18–060	0.00	0.00	88.	MDU 1	28.57	0.37
39.	VBG 18–061	0.00	0.00	89.	TMV 1	0.00	0.00
40.	VBG 18–062	0.00	0.00	90.	Vamban 1	6.25	0.08
41.	VBG 18–063	0.00	0.00	91.	Vamban 2	39.29	0.50
42.	VBG 18–064	0.00	0.00	92.	Vamban 3	71.25	0.91 HT
43.	VBG 18–065	0.00	0.00	93.	VBN (Bg) 4	50.00	0.64 T
44.	VBG 18–066	0.00	0.00	94.	VBN (Bg) 5	43.75	0.56 T
45.	VBG 18–067	14.58	0.19	95.	VBN 6	0.00	0.00
46.	VBG 18–068	25.00	0.32	96.	VBN (Bg) 7	0.00	0.00
47.	VBG 18–069	32.50	0.42	97.	VBN 8	50.00	0.64 T
48.	VBG 18–070	0.00	0.00	98.	VBN 9	12.50	0.16
49.	VBG 18–071	78.00	1.00 HT	99.	VBN 10	8.50	0.11
50.	VBG 18–072	42.86	0.55 T	100.	VBN 11	35.71	0.46

HT - highly saline tolerant, **T** - saline tolerant; **MFV**: mean functional value.

had effective mechanisms for the detrimental effects of salinity. Eleven genotypes were saline-tolerant. These genotypes also possess a beneficial gene that could contribute to the improved salt tolerance. They could be utilised in combination breeding approaches to pyramid desirable traits and develop even more resilient varieties. The rest were moderately tolerant or susceptible. Their poor performance under salinity indicates a lack of effective mechanisms for the stress.

Confirmation of salinity tolerance

Screening of 100 genotypes resulted in the identification of seven highly tolerant genotypes. These seven highly saline-tolerant genotypes, two susceptible genotypes, VBN 6 and CO 6 and a popular variety (VBN 8) were again screened to confirm their salinity tolerance. The results showed that ACM BG 14-001, VBG 18-071, VBG 18-080, VBG 19-005, VBG 19-010 and Vamban 3 had high saline tolerance.

They had a 70% survival rate at 13 dSm^{-1}, as shown in Table 5. The susceptible genotypes VBN 6 and CO 6 did not survive at this salinity level (13 dSm^{-1}), while the popular variety VBN 8 had a 50 to 63% survival rate.

Table 5. Survival rate (%) of select blackgram genotypes at 13 dSm^{-1}.

Sl. No.	Genotypes	Survival (%)	
		I	II
1	ACM BG 14–001	71.25	75.63
2	VBG 18–071	78.00	81.00
3	VBG 18–080	77.00	80.00
4	VBG 19–005	74.11	76.00
5	VBG 19–007	54.76	59.00
6	VBG 19–010	75.00	75.00
7	Vamban 3	71.25	74.00
8	VBN 8	50.00	63.00
9	VBN 6	0.00	0.00
10	CO 6	0.00	0.00

Conclusion

The study concluded that 13 dSm^{-1} is the critical salinity level to identify salinity tolerance in blackgram. Among the 100 screened genotypes, seven exhibited high saline tolerance. They are ACM BG 14-001, VBG 18-071, VBG 18-080, VBG 19-005, VBG 19-007, VBG 19-010 and Vamban 3. Of these genotypes, ACM BG 14-001, VBG 18-071, VBG 18-080, VBG 19-005 and VBG 19-010 confirmed their saline tolerance in another trial. They had a survival rate of over 75% at 13 dSm^{-1}. Hence, these genotypes can be evaluated in saline-affected areas to release as varieties. Additionally, they can serve donors in saline tolerance breeding programs.

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Authors' contributions

PP and NM conceived and designed the experiments. PP performed the experiments. SA, BV, SP, SA and DP provided suggestions on experiments. PP analysed the data and prepared the original draft. NM reviewed the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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