

RESEARCH ARTICLE

Assessment of genetic variability in eggplant (*Solanum melongena* L.) genotypes for disease resistance and yield parameters

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Abstract

Eggplant is a globally important vegetable crop valued for its nutritional and economic significance. However, its productivity is often constrained by various biotic stresses particularly susceptibility to Phomopsis blight, causing significant economic losses and threatening food security. This study aims to identify genetically distinct genotypes with enhanced disease resistance and yield to support sustainable eggplant breeding efforts. This research evaluated genetic variability among 33 eggplant genotypes, focusing on resistance to Phomopsis blight. The evaluation was conducted during the Spring-Summer and *Khari*f seasons, of 2022-at the Vegetable Research Farm, Lovely Professional University, Punjab India and laid out in a Randomized Block Design in triplicates. The pooled analysis of variance revealed significant differences among genotypes for key traits. High phenotypic and genotypic variance (>50%) were observed for average fruit weight (g), percent disease index (PDI) for leaf & fruit at 21st day after inoculation (DAI) (%) and percent leaf area diseased (%). High phenotypic (PCV) and genotypic coefficient of variation (GCV) (>20%) were recorded for characters including fruit yield plant⁻¹ (kg), lesion size on fruits (cm²), average fruit weight (g), PDI for fruit at 7th, 14th & 21st DAI (%) and PDI for leaf at 7th, 14th & 21st DAI (%). A narrow difference between GCV and PCV indicated that phenotypic variability was primarily genetic. High heritability (>60%) with a substantial genetic advance (>30%) as a percentage of the mean (GAM) at 5% underscored the potential for improvement through targeted selection, driven by additive genetic effects. These findings provide valuable insights into breeding programs targeting disease-resistant and high-yielding eggplant varieties. Future studies should investigate molecular mechanisms underlying disease resistance to refine breeding strategies.

Keywords

eggplant breeding; genetic variability; Phomopsis blight; SDGs; *Solanum melongena*

Introduction

Eggplant (*Solanum melongena* L.; 2n = 2x = 24) is one of the popular solanaceous vegetable crops globally. Unripe eggplant fruits are consumed as vegetables and are a part of many culinary preparations (1,2). Indo-China or India is believed to be the center of eggplant diversity (3,4). Numerous eggplant cultivars exhibit considerable diversity in their morphology (such as vigour, growth habit, fruit

size, shape and colour), physiology (including water requirements and flowering time) and biochemical characteristics (like fruit bitterness). Hence there is significant potential for improvement of its various horticultural characteristic (5-7). By harnessing the inherent diversity within the crop's genetic pool, breeders can identify and develop varieties that thrive in specific agro-climatic zones. Low yields in eggplant are attributed to several challenges like biotic factors like pests (e.g., shoot and fruit borer, aphids), diseases (e.g., *Phomopsis* blight, bacterial wilt), abiotic stresses (such as temperature extremes, water stress) and inadequate management practices (1,2).

The development of improved eggplant cultivars is the need to ensure food security for the rapidly growing population. Genetic diversity is vital for eggplant crop improvement in many ways, such as disease resistance, adaptability and improved yield (27). Thus, it helps breeders to identify diverse germplasm, facilitating the development of resilient varieties. Genetic improvement of any crop depends on the amount of genetic variability present in the population. Germplasm serves as a valuable source of base population, providing a wider scope for variability (8,9). Therefore, the collection of diverse germplasms and thorough knowledge about the nature and magnitude of variability are necessary. Identifying elite lines with high genetic variability, heritability and genetic advancement is crucial for breeding programs. Additionally, selecting diverse parental combinations can help to develop superior progenies and introduce desirable traits into the existing genetic base (9-11, 27). The presence of high heritability on its own is not enough to ensure effective selection in segregating generations. It must be accompanied by substantial genetic advance information (12,13).

This research presents a thorough analysis of 33 distinct genotypes of eggplant, meticulously screened and evaluated for resistance against *Phomopsis* blight disease. The research aims to evaluate the genetic variability among eggplant genotypes to develop effective breeding strategies that leverage the inherent diversity within the breeding population.

Materials and Methods

2.1 Experimental site and resources

The assessment of variability was carried out during the Spring-Summer and *Kharif* seasons, of 2022 at the Vegetable Research Farm, Lovely Professional University, Punjab, India. The geographical coordinates of the research site are N 31°15'19.45" latitude and E 75°42'20.73" longitude, with an average elevation of 252 m above mean sea level (MSL). A total of 33 genotypes of eggplant (as stated in Table 1) [30 Indigenous Collection (IC) + 3 commercial varieties (namely, Pusa Bhairav, Pant Samrat and Pant Rituraj used as standard checks)] were screened out against the *Phomopsis* blight disease and their performance was evaluated in Randomized Block Design in triplicates.

Table 1. Details of diverse genotypes considered in the study

Genotypes	Particulars	Sources
G ₁	IC090121	NBPGR, New Delhi
G ₂	IC090132	NBPGR, New Delhi
G ₃	IC090144	NBPGR, New Delhi
G ₄	IC090146	NBPGR, New Delhi
G ₅	IC090781	NBPGR, New Delhi
G ₆	IC090785	NBPGR, New Delhi
G ₇	IC090791	NBPGR, New Delhi
G ₈	IC090806	NBPGR, New Delhi
G ₉	IC090810	NBPGR, New Delhi
G ₁₀	IC090828	NBPGR, New Delhi
G ₁₁	IC090839	NBPGR, New Delhi
G ₁₂	IC090871	NBPGR, New Delhi
G ₁₃	IC090887	NBPGR, New Delhi
G ₁₄	IC090905	NBPGR, New Delhi
G ₁₅	IC090907	NBPGR, New Delhi
G ₁₆	IC090915	NBPGR, New Delhi
G ₁₇	IC090931	NBPGR, New Delhi
G ₁₈	IC090940	NBPGR, New Delhi
G ₁₉	IC090942	NBPGR, New Delhi
G ₂₀	IC090966	NBPGR, New Delhi
G ₂₁	IC099676	NBPGR, New Delhi
G ₂₂	IC099703	NBPGR, New Delhi
G ₂₃	IC099723	NBPGR, New Delhi
G ₂₄	IC099726	NBPGR, New Delhi
G ₂₅	IC099670	NBPGR, New Delhi
G ₂₆	IC099691	NBPGR, New Delhi
G ₂₇	IC099731	NBPGR, New Delhi
G ₂₈	IC104076	NBPGR, New Delhi
G ₂₉	IC104083	NBPGR, New Delhi
G ₃₀	IC104089	NBPGR, New Delhi
G ₃₁	Pusa Bhairav	IARI, New Delhi
G ₃₂	Pant Samrat	GBPUA&T, Uttarakhand
G ₃₃	Pant Rituraj	GBPUA&T, Uttarakhand

2.2 Transplanting

Healthy seedlings of these genotypes were transplanted at 60 × 45 cm spacing on the prepared ridges. As suggested in 'The Package of Practices for Cultivation of Vegetables-2021' by Punjab Agricultural University, Ludhiana, Punjab, India, all the essential cultural practices for eggplant cultivation were followed (14).

2.3 Disease screening and parameters

Disease screening was done *via* artificial inoculation of *Phomopsis vexans*. To facilitate inoculation, mother culture of *P. vexans* (Saccardo & Sydow) Harter (Fungal No., 7222) was collected from the Indian Type Culture Collection (ITCC), Division of Plant Pathology, Indian Agricultural Research Institute (IARI), New Delhi. Then finally a spore suspension (70 mL with 5 × 10⁶ spores/mL) was prepared and inoculation was done twice on the 10 randomly marked plants of each genotype (15). Five out of 10 were inoculated first at 15 days after transplanting (DAT) *i.e.*, at the vegetative stage and rest five were at the fruiting stage, with the slow pressure release of spore suspension using a hand sprayer. Disease scoring was done based on the recording of various disease parameters *viz.*,

- percent leaf incidence (PLI) (%)
- percent fruit incidence (PFI) (%),
- percent leaf area diseased (PLAD)-eye estimation (%),
- percent fruit area diseased (PFAD)-eye estimation (%),
- percent disease index (PDI) (a measure of the severity of disease symptoms expressed as a percentage of the total

plant area affected) for leaf and fruit on the 7th, 14th and 21st day after inoculation (DAI) (%) and

- lesion size on fruits (cm²) (15, 16-19).

In addition, yield attributing characters such as average fruit weight (g) and fruit yield plant⁻¹ (kg) were also observed.

2.4 Analysis of variance

The data acquired in both the seasons for various disease and yield characters of 33 diverse eggplant genotypes were subjected to analysis of variance (ANOVA) to determine significance and critical difference (CD) was calculated at $P=0.05$ and 0.01 to separate the means of replicate for significance (20).

2.5 Analysis of genetic variability

In this study range, general mean, genetic parameters such as variance, coefficient of variation, heritability in a broad sense (h^2_{bs}), genetic advance (GA) and genetic advance presented as mean at 5% (GAM) were estimated. The genotypic (GV) (σ^2_g), phenotypic (PV) (σ^2_p) and environmental variance (EV) (σ^2_e) were classified as high (>50%), medium (20-50%) and low (<20%) as proposed by Johnson and his colleagues (23). The phenotypic (PCV), genotypic (GCV) (which indicates the extent of variation in a trait due to genetic differences) and environmental coefficients of variation (ECV) were estimated as high (>20%), moderate (10-20%) and low (<10%) as suggested by Burton and DeVane (21) and Sivasubramanian and Menon (22). According to Burton and DeVane (21) and Johnson and his colleagues (23), heritability in the broad sense (h^2_{bs}) was classified as high (>60%), moderate (30-60%) and low (<30%), while the expected genetic advance (GA) resulting from the selection of 5 percent superior individuals was categorized as high (>30%), moderate (10-30%) and low (<10%).

2.6 Statistical analysis

The data analysis was performed using Windostat version 9.3 (IndoStat Services, Hyderabad) and R software version 4.2.

Results and Discussion

3.1 Analysis of variance

The pooled ANOVA results revealed significant variability among genotypes for the studied characters (Table 2). The presence of an ample amount of variability is essential for effective selection to improve crop yield and other characteristics. Significant variability for the studied characters in the diverse eggplant genotypes was observed by 8,12,13,24,28,29,30.

3.2 Analysis of genetic variability

3.2.1 Range and general mean : Based on the pooled data findings regarding range and general mean depicted in Fig. 1 revealed that character average fruit weight (g) exhibited the greatest phenotypic range of variation (46.24 to 129.48) and the highest general mean (55.26 g), followed by PDI-for leaf at 21st DAI (%) (13.05 to 65.61, 42.4 %), PLAD-eye estimation (%) (14.20 to 66.23, 41.31 %), PDI-for fruit at 21st DAI (%) (11.27 to 62.52, 39.7 %), PFAD-eye estimation (%) (12.60 to 62.77, 37.61 %), PLI (%) (7.10 to 38.43, 24.61 %), PDI for leaf at 14th DAI (%) (7.18 to 36.09, 23.33 %), PFI (%) (5.22 to 32.20, 22.45 %), PDI-for fruit at 14th DAI (%) (4.23 to 23.45, 14.89 %), PDI-for leaf at 7th DAI (%) (2.94 to 14.76, 9.54 %), PDI-for fruit at 7th DAI (%) (1.97 to 10.95, 6.95 %), fruit yield plant⁻¹ (kg) (0.53 to 4.08, 1.12 kg) and lesion size on fruits (cm²) (0.23 to 2.08, 0.99 cm²).

3.2.2 Genotypic (GV), phenotypic (PV) and environmental variance (EV) : The pooled analysis results (Table 3), revealed that GV and PV were higher than EV, indicating pre-dominance of non-genetic factors. In comparison between GV and PV, the magnitude of PV was higher. However, the observed difference between these two for all the studied characters was narrow. The maximum GV was observed for the character average fruit weight (g) (346.67) followed by PDI-for leaf at 21st DAI (%) (121.36), PDI for fruit at 21st DAI (%) (114.20) and PLAD-eye estimation (%) (50.10). While the moderate magnitude of GV was reported for the characters like PFAD-eye estimation (%) (43.57), PDI-for leaf at 14th DAI (%) (36.72), PLI (%) (22.72) and PFI (%) (21.96). However, the

Table 2. Results of combined analysis of variance for various diseases and yield characters in diverse eggplant genotypes

ANOVA Summary							
S. No.	Source		Replication	Mean Sum of Squares			
	Degrees of	freedom		Treatment	G × E	Error	Total
			2	32	32	128	197
1.	PLI (%)		0.57	137.39**	0.00	0.19	22.45
2.	PFI (%)		0.02	131.94**	0.00	0.18	21.55
3.	PLAD-eye estimation (%)		0.34	301.07**	0.00	0.45	49.21
4.	PFAD-eye estimation (%)		0.06	261.73**	0.00	0.31	42.72
5.	PDI-for leaf at 7 th DAI (%)		0.01	36.94**	0.46**	0.06	7.26
6.	PDI-for leaf at 14 th DAI (%)		1.16	220.73**	7.36**	0.41	55.52
7.	PDI-for leaf at 21 st DAI (%)		0.38	729.53**	0.00	1.16	119.27
8.	PDI-for fruit at 7 th DAI (%)		0.01	21.01**	0.43**	0.04	4.51
9.	PDI-for fruit at 14 th DAI (%)		0.22	96.45**	3.88**	0.16	25.38
10.	PDI-for fruit at 21 st DAI (%)		1.39	686.00**	0.00	1.20	112.24
11.	Lesion size on fruits (cm ²)		0.00	1.07**	0.00	0.00	0.17
12.	Average fruit weight (g)		2.38	2082.45**	0.00	2.49	339.93
13.	Fruit yield plant ⁻¹ (kg)		0.00	4.31**	0.00	0.00	0.70

values showing with ** are significant at a 1 percent level of significance

DAI = day after inoculation

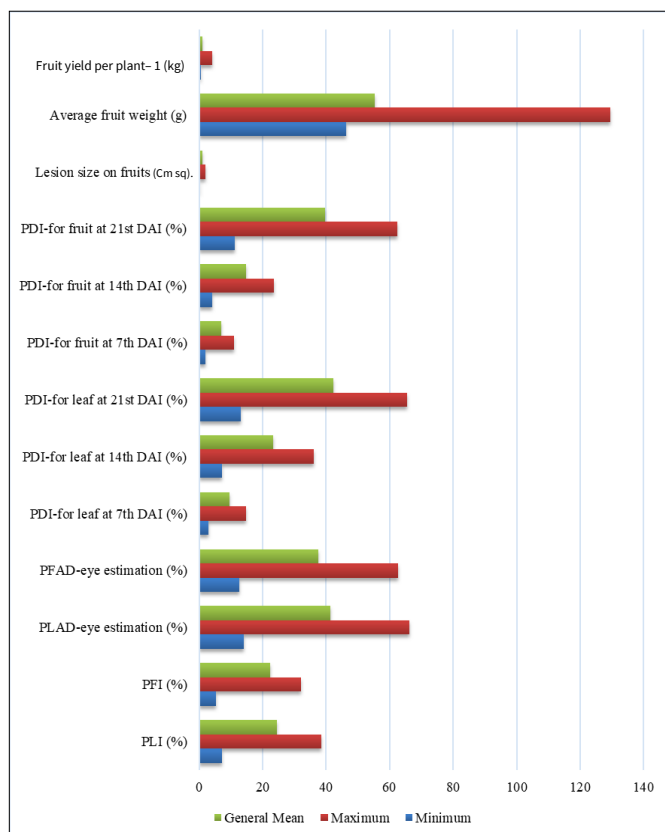


Fig. 1. Graphical presentation of general mean and range related to various disease and yield parameters.

minimum was noticed in characters such as PDI-for fruit at 14th DAI (%) (16.03), PDI-for leaf at 7th DAI (%) (6.14), PDI-for fruit at 7th DAI (%) (3.50), fruit yield plant⁻¹ (kg) (0.72) and lesion size on fruits (cm²) (0.18).

On the other hand, the highest magnitude of PV was found for the character average fruit weight (g) (347.97) followed by PDI-for leaf at 21st DAI (%) (122.03), PDI for fruit at 21st DAI (%) (114.56) and PLAD-eye estimation (%) (50.34). Whereas, a moderate level of PV was observed for various characters like PFAD-eye estimation (%) (43.72), PDI-for leaf at 14th DAI (%) (36.91), PLI (%) (23.23) and PFI (%) (22.07). The lowest PV was noticed in several characters including PDI-for fruit at 14th DAI (%) (16.18) followed by PDI-for leaf at 7th DAI (%) (6.18), PDI-for fruit at 7th DAI (%) (3.51), fruit yield plant⁻¹ (kg) (0.72) and lesion size on fruits (cm²) (0.18). However, characters such as lesion size on fruits (cm²) shared the magnitude of 0.18 while fruit yield plant⁻¹

(kg) had 0.72 at both GV and PV, suggesting these traits are entirely determined by genetic factors and it has no environmental influence ($\sigma^2_e = 0$) on the expression. In this scenario, the heritability in the broad sense (H^2_{bs}) is equal to 1 ($H^2 = \sigma^2_g / \sigma^2_p = 1$). It can be concluded that selecting based on the phenotypic expression of these traits would be both effective and reliable for achieving genetic improvement. Consequently, these findings hold significant importance for plant breeding programs. These results were in agreement with several other researches done on eggplant (7,8,12,25,26,28). The presented findings indicate that mass selection, or pedigree selection can be an effective breeding strategy to exploit this additive variance. In addition, hybrid breeding to exploit both additive and non-additive genetic variance and integrating genomic tools with it can enhance the precision of selection. In contrast, the EV was found low in magnitude for all the studied characters, indicating that these traits will exhibit stable performance across different environments, enhancing the reliability of selection outcomes.

3.2.3 Genotypic (GCV), phenotypic (PCV) and environmental (ECV) coefficient of variation :

The pooled analysis results revealed that the magnitude of PCV was consistently higher, while ECV was reported lower among the coefficient of variation for all the considered characters (Table 3). However, the difference between PCV and GCV values was narrow for all the studied characters, showing less influence of external factors. Thus, simple selection can be employed in the early generation to exploit available variation and phenotype-based selection will be effective to improve these traits.

The pooled analysis results related to GCV exhibited the highest magnitude for the characters like fruit yield plant⁻¹ (kg) (75.48 %) followed by lesion size on fruits (cm²) (42.85 %), average fruit weight (g) (33.69 %), PDI-for fruit at 21st DAI (26.92 %), PDI-for fruit at 7th DAI (26.9 %), PDI-for fruit at 14th DAI (26.89 %), PDI-for leaf at 14th and 21st DAI (25.98 %) and PDI-for leaf at 7th DAI (25.97 %). Whereas, a moderate level of GCV was observed for the characters like PLAD-eye estimation (%) (17.78 %) followed by PFAD-eye estimation (%) (17.55 %), PFI (%) (16.73 %) and PLI (%) (16.16 %).

Table 3. Pooled analysis results related to estimated variability components for various diseases and yield contributing characters in diverse eggplant genotypes

Characters	Variance			Coefficient of Variation (%)			h^2_{bs} (%)	GA	GAM at 5% (%)
	GV	PV	EV	GCV	PCV	ECV			
PLI (%)	22.72	23.23	0.51	16.16	16.34	2.42	97.80	9.71	32.93
PFI (%)	21.96	22.07	0.11	16.73	16.78	1.20	99.49	9.63	34.38
PLAD-eye estimation (%)	50.10	50.34	0.24	17.78	17.82	1.24	99.52	14.55	36.53
PFAD-eye estimation (%)	43.57	43.72	0.16	17.55	17.58	1.05	99.65	13.57	36.09
PDI-for leaf at 7 th DAI (%)	6.14	6.18	0.04	25.97	26.05	2.00	99.41	5.09	53.35
PDI-for leaf at 14 th DAI (%)	36.72	36.91	0.18	25.98	26.05	1.84	99.50	12.45	53.39
PDI-for leaf at 21 st DAI (%)	121.36	122.03	0.67	25.98	26.05	1.93	99.45	22.63	53.37
PDI-for fruit at 7 th DAI (%)	3.50	3.51	0.02	26.90	26.97	1.98	99.46	3.84	55.27
PDI-for fruit at 14 th DAI (%)	16.03	16.18	0.15	26.89	27.01	2.60	99.07	8.21	55.13
PDI-for fruit at 21 st DAI (%)	114.20	114.56	0.36	26.92	26.96	1.51	99.69	21.98	55.37
Lesion size on fruits (cm ²)	0.18	0.18	0.00	42.85	42.88	1.78	99.83	0.87	88.19
Average fruit weight (g)	346.67	347.97	1.30	33.69	33.76	2.06	99.63	38.28	69.27
Fruit yield plant ⁻¹ (kg)	0.72	0.72	0.00	75.48	75.58	3.86	99.74	1.74	155.29

GV = Genotypic variance; PV = Phenotypic variance; EV = Environmental variance; GCV = Genotypic coefficient of variation PCV = Phenotypic coefficient of variation; ECV = Environment coefficient of variation; h^2_{bs} = Heritability in broad sense; GA = Genetic advance; GAM at 5% = Genetic advance as percentage of mean at 5%

On the other side, a high magnitude of PCV was noticed for the characters including fruit yield plant⁻¹ (kg) (75.58 %) followed by lesion size on fruits (cm²) (42.88 %), average fruit weight (g) (33.76 %), PDI-for fruit at 14th DAI (%) (27.01 %), PDI-for fruit at 7th DAI (%) (26.97 %), PDI for fruit at 21st DAI (%) (26.96 %) and 26.05 % was for PDI-for leaf at 7th, 14th and 21st DAI (%). Whereas, the moderate level was shown by the characters viz., PLAD-eye estimation (%) (17.82 %), PFAD-eye estimation (%) (17.58 %), PFI (%) (16.78 %) and PLI (%) (16.34 %). On the other hand, the magnitude of ECV was found low for all the considered characters. PCV varied from 5.06 % (days to I harvest) to 34.39 % (seeds fruit⁻¹) whereas, GCV ranged from 4.77 % to 34.38 % for the same traits discovered (28). Both PCV and GCV showed high values for characters like leaf area, seeds fruit⁻¹, number of fruits cluster⁻¹, average fruit weight and fruit yield plant⁻¹ in eggplant genotypes. These results were following the findings of several researchers those who had worked on eggplant genotypes (7,8,12,24,25,26).

These findings offer important insights into the nature and extent of variability within the eggplant genotypes. The close alignment of PCV and GCV suggests a significant contribution of additive genetic variance to the overall phenotypic variation (28). Therefore, breeding strategies such as recurrent selection, pedigree selection, backcross breeding and hybrid breeding should be employed to enhance the genetic gain over generations. The low ECV could be indicative of a relatively stable environment or the inherent robustness of the characters.

3.2.4 Heritability (H^2_{bs}) and Genetic advance presented as mean (GAM) : The analysis of variability components in this study revealed that H^2_{bs} and GAM at 5% selection intensity were consistently high for all the characters considered (Table 3). Further, high heritability coupled with high expected genetic advance indicated the involvement of additive genetic variance, therefore selection may be effective for the improvement of these traits (28). The higher magnitude of H^2_{bs} indicates that the observed variation in these traits is predominantly due to genetic differences among genotypes, with a minimal contribution from external factors. This high genetic control suggests that these traits are reliably passed from one generation to the next, making them excellent contenders for selective breeding. However, the highest magnitude of H^2_{bs} was recorded for the characters like lesion size on fruits (cm²) (99.83 %) followed by fruit yield plant⁻¹ (kg) (99.74 %), PDI-for fruit at 21st DAI (%) (99.69 %), PFAD-eye estimation (%) (99.65 %), average fruit weight (g) (99.63 %), PLAD-eye estimation (%) (99.52 %), PDI-for leaf at 14th DAI (%) (99.50 %), PFI (%) (99.49 %), PDI-for fruit at 7th DAI (%) (99.46 %), PDI-for leaf at 21st DAI (%) (99.45 %), PDI-for leaf at 7th DAI (%) (99.41 %), PDI-for fruit at 14th DAI (%) (99.07 %) and PLI (%) (97.8%). This indicates that substantial progress can be made through selection based on these traits.

However, the estimates of GAM were found to be highest for the character fruit yield plant⁻¹ (kg) (155.29 %) followed by lesion size on fruits (cm²) (88.19 %), average fruit weight (g) (69.27 %), PDI-for fruit at 21st DAI (%) (55.37 %), PDI-for fruit at 7th DAI (%) (55.27 %), PDI-for fruit at 14th

DAI (%) (55.13 %), PDI-for leaf at 14th DAI (%) (53.39 %), PDI-for leaf at 21st DAI (%) (53.37 %), PDI-for leaf at 7th DAI (%) (53.35 %), PLAD-eye estimation (%) (36.53 %), PFAD-eye estimation (%) (36.09 %), PFI (%) (34.38 %) and PLI (%) (32.93 %). Together, the high heritability and genetic advance values suggest that the characters studied have considerable genetic potential and are amenable to improvement through selection. High heritability with the high GAM reported for various characters viz., fruit diameter, average fruit weight, number of primary branches plant⁻¹, yield plant⁻¹ and number of fruits plant⁻¹ are controlled by additive gene action in eggplant (12). Comparable results were documented by many researchers and their colleagues those who worked in eggplant (7,8,24,25,26,28). Further to exploit the high genetic advance, recurrent selection, pedigree selection, and marker-assisted selection (MAS) methods can be integrated into the breeding program.

Conclusion

The pooled analysis of variance components and variability assessments of the selected eggplant genotypes revealed substantial genetic variability for the studied characters. High PV and GV (>50%) were noticed for characters including average fruit weight (g), PDI-for leaf & fruit at 21st DAI (%) and PLAD-eye estimation (%). While, high PCV and GCV values (>20%), were observed for key characters viz., fruit yield plant⁻¹ (kg), lesion size on fruits (cm²), average fruit weight (g), PDI-for fruit at 7th, 14th & 21st DAI (%) and PDI-for leaf at 7th, 14th & 21st DAI (%), indicating a strong potential for effective selection and genetic improvement in breeding programs. The high heritability (>60%) coupled with high GAM (>30%) for all characters, suggests these can be reliably selected for phenotypic improvement, facilitating sustainable genetic gains. Therefore, the study highlights characters like average fruit weight (g), fruit yield plant⁻¹ (kg), PDI for leaf and fruit at 7th, 14th and 21st DAI (%) and lesion size on fruits (cm²) as the most promising traits for genetic improvement in eggplant. Future research should focus on genome-wide association studies (GWAS) to identify genetic markers for key traits and screening diverse germplasm for stress tolerance and disease resistance. Efforts should also target breeding for climate resilience and utilizing molecular tools like marker-assisted selection for precision breeding. Additionally, detailed phenotypic profiling and trait correlation studies can enhance multi-trait selection efficiency in eggplant breeding programs. Thus, this research advances sustainable development goals (SDGs) by supporting zero hunger through the development of high-yielding, disease-resistant eggplant varieties, enhancing food security. It aligns with responsible consumption and production by promoting sustainable practices and reducing food loss. Additionally, by emphasizing genetic variability for resilience traits, it contributes to climate action, enabling the breeding of climate-resilient crops. Integrating tools like GWAS and marker-assisted selection ensures sustainable genetic gains for resilient agriculture.

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Authors' contributions

EG conducted the research. VT and AK designed the technical programme and did the review and editing. SM did the data analysis. EG, B, LK and AK wrote the main manuscript text. All the authors reviewed and approved the final version of the manuscript.

Compliance with ethical standards

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