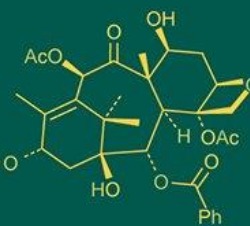
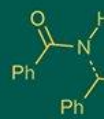


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Evaluation of bitter gourd (*Momordica charantia* L.) genotypes for yield performance and powdery mildew resistance

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Abstract

An experiment was conducted to screen bitter gourd (*Momordica charantia* L.) genotypes for yield performance and powdery mildew resistance under protected conditions. The study was carried out during the Late Rabi season of 2025 at the College of Horticulture, Bagalkot, Karnataka, to identify genotypes combining desirable yield attributes with tolerance to powdery mildew. A total of 51 bitter gourd genotypes collected from diverse sources were evaluated in a Randomized Complete Block Design (RCBD) with two replications. Powdery mildew severity was assessed under artificial epiphytotic conditions at different stages of crop growth, and yield-related traits were recorded at harvest.

The results revealed considerable variability among the genotypes with respect to powdery mildew reaction and yield performance. Disease severity increased progressively with crop age; however, distinct differences were observed in the extent of infection among genotypes. Several genotypes exhibited comparatively lower disease severity, while others showed high levels of susceptibility. Yield per vine varied widely among the genotypes, indicating substantial genetic diversity for productivity-related traits. Genotypes recording high to very high fruit yield (≥ 1.5 kg per vine) were identified, even under disease pressure, suggesting better adaptability and yield stability. A combined evaluation of powdery mildew reaction and yield performance enabled the identification of approximately 10-12 promising genotypes, which expressed superior yield potential along with relatively better tolerance to powdery mildew.

The study highlights the effectiveness of screening under protected epiphytotic conditions for identifying elite genotypes. The promising genotypes identified in the present investigation can be utilized as potential donor parents in future breeding programmes aimed at developing high-yielding and powdery mildew-tolerant bitter gourd cultivars, thereby contributing to sustainable production and disease management.

Keywords: Bitter gourd, *Momordica charantia*, powdery mildew, *Podosphaera xanthii*, genotype screening, yield traits, disease resistance

Introduction

Bitter gourd (*Momordica charantia* L.) is an important cucurbitaceous vegetable crop cultivated widely in tropical and subtropical regions for its nutritional, medicinal and economic significance (Singh *et al.*, 2013) [8]. The fruits are rich in vitamins, minerals and bioactive compounds and are valued for their role in traditional medicine (Hassan *et al.*, 2019). Despite its importance, the productivity of bitter gourd remains relatively low, mainly due to its susceptibility to several biotic stresses.

Among the biotic constraints, powdery mildew caused by *Podosphaera xanthii* is one of the most destructive diseases affecting bitter gourd cultivation (Kumar *et al.*, 2008) [6]. The disease appears at different stages of crop growth and is characterized by white powdery fungal growth on leaf surfaces, leading to reduced photosynthetic efficiency, premature leaf senescence and poor fruit development. Under favourable environmental conditions, powdery mildew can cause severe yield losses, making it a major concern for growers (Kumar *et al.*, 2020) [7].

Chemical control of powdery mildew is often uneconomical and environmentally undesirable, and repeated fungicide applications may result in residue problems and the

development of resistant pathogen strains (Chinthan *et al.*, 2021) ^[1]. Therefore, the use of host plant resistance is considered the most effective, economical and sustainable strategy for managing powdery mildew. Identification of tolerant genotypes through systematic screening is a prerequisite for developing improved varieties.

Screening of diverse germplasm under protected conditions not only helps in identifying sources of disease tolerance but also facilitates the selection of genotypes with superior yield performance under disease pressure Kutty and Dharmatti (2004) ^[5]. However, comprehensive screening studies involving a large number of bitter gourd genotypes under uniform conditions are limited. In this context, the present investigation was undertaken to screen bitter gourd genotypes for yield performance and powdery mildew resistance, with the objective of identifying promising genotypes suitable for use in breeding programmes and sustainable crop improvement.

Materials and Methods

The experiment was conducted during the Late Rabi season of 2025 at the College of Horticulture, Bagalkot, Karnataka, India. The experimental site is located in the Northern Dry Zone of Karnataka and is characterized by a semi-arid climate with moderate temperature and low relative humidity during the cropping period. The soil of the experimental field was well-drained red loamy soil with moderate fertility status.

A total of 51 bitter gourd (*Momordica charantia* L.) genotypes collected from diverse sources were evaluated for yield performance and powdery mildew resistance. The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications to minimize experimental error. Each genotype was planted in a plot consisting of multiple plants, maintaining a spacing of 120 cm × 90 cm between rows and plants. Healthy seeds of each genotype were sown in nursery beds, and 15-day-old seedlings were transplanted into the pots. Recommended agronomic practices such as irrigation, nutrient management, staking and intercultural operations were followed uniformly for all genotypes throughout the crop growth period.

Screening for powdery mildew was carried out under artificial epiphytotic conditions without the application of fungicides in order to allow natural disease development (Fig.1). Powdery mildew symptoms were observed on leaves, and disease severity was recorded at different crop growth stages. Disease assessment was carried out using visual scoring, and the Percent Disease Index (PDI) was calculated.

$$PDI = \frac{\text{Sum of all numerical rating}}{\text{No. of leaves observed} \times \text{Maximum rating}} \times 100$$

Further, the Area Under Disease Progress Curve (AUDPC) was computed to quantify disease progression over time. Yield and yield-related traits were recorded from randomly selected plants of each genotype. The observations included fruit length (cm), average fruit weight (g), number of fruits per vine and fruit yield per vine (kg). The recorded data were subjected to analysis of variance (ANOVA) to determine the significance of variation among genotypes. The statistical analysis was performed following standard procedures to identify genotypes with superior performance.

Experimental results

The screened bitter gourd genotypes exhibited wide variation in powdery mildew incidence and severity under protected conditions (Table 1). Disease severity increased progressively with crop age, as reflected by higher percent disease index (PDI) values at later observation stages. However, considerable differences were observed among genotypes in the rate and extent of disease development. Some genotypes showed early disease onset with rapid disease progression, whereas others exhibited delayed infection and relatively lower disease severity. The variation observed in AUDPC values further confirmed differential responses of genotypes to powdery mildew infection.

Based on disease reaction, the genotypes were categorized into highly susceptible and susceptible classes, with only a few genotypes showing comparatively lower disease intensity. The presence of genotypes with relatively lower disease progression indicates the availability of useful genetic variability for powdery mildew tolerance within the germplasm.

Significant differences were also recorded among genotypes for yield and yield-related traits (Table 2). Fruit yield per vine varied from 0.17 kg to 2.29 kg, indicating substantial variability in yield potential. Genotypes such as Dharg Local-1, UHSBP-215-1, IC-68275-3 and Katali Vaibhav-3 recorded very high fruit yield (>2.0 kg per vine), whereas genotypes with severe disease infection generally recorded lower yield. Mean fruit length and average fruit weight also differed significantly among genotypes, contributing to variation in yield performance.

A combined evaluation of powdery mildew reaction and yield performance enabled the identification of 11 promising genotypes (Table 1). These genotypes exhibited high to very high fruit yield despite showing susceptibility or high susceptibility to powdery mildew, indicating their ability to maintain yield under disease pressure. Such genotypes represent valuable genetic material for further evaluation and utilization.

Discussion

The significant variation observed among bitter gourd genotypes for powdery mildew reaction and yield performance can be attributed to inherent genetic differences among the genotypes. Differences in disease severity and AUDPC values suggest variation in host-pathogen interaction mechanisms, such as delayed disease onset or slower disease progression (Jeger and Rollinson, 2001) ^[4]. Similar variability in powdery mildew response among bitter gourd and other cucurbit crops has been reported earlier, highlighting the importance of germplasm screening Campbell and Madden (1990) ^[2].

The negative impact of powdery mildew severity on yield performance was evident in the present study, as genotypes with higher disease severity generally recorded lower fruit yield. Powdery mildew infection reduces photosynthetic efficiency and limits assimilate availability for fruit development, ultimately affecting yield. However, some genotypes maintained high yield even under severe disease pressure, indicating better adaptability and yield stability.

The identification of high-yielding genotypes such as Dharg Local-1, UHSBP-215-1 and IC-68275-3, despite their susceptibility to powdery mildew, suggests that yield performance is influenced not only by disease resistance but also by inherent yield potential. Such genotypes can be

effectively utilized as donor parents for improving yield, while disease resistance can be incorporated through hybridization with tolerant sources.

Overall, the results emphasize the effectiveness of systematic screening under protected conditions for

identifying elite genotypes combining superior yield performance and adaptability under disease stress. The integration of disease screening with yield evaluation provides a strong foundation for future bitter melon breeding programmes.

Table 1: Promising bitter melon genotypes identified based on yield performance and powdery mildew reaction

Genotype	AUDPC	Disease reaction	Fruit yield per vine (kg)	Yield performance	Remark
IC-68275-3	1554.16	HS	2.15	Very high	High yielding under disease pressure
Katali Vaibhav-3	1297.26	HS	2.03	Very high	Superior yield potential
UHSBP-215-1	1665.83	HS	2.22	Very high	Outstanding performer
Dharg Local-1	453.49	HS	2.29	Very high	Consistently high yield
Phule Green Local	1072.41	HS	1.94	High	Bold fruits and high yield
IC-505632-2	938.53	S	1.77	High	Yield-efficient genotype
IC-505632-3	1234.28	HS	1.78	High	Stable yield expression
IC-45346-1	932.80	S	1.54	High	Good yield under infection
IC-85626-1	742.25	S	1.65	High	Moderately tolerant yielder
Punjab-15	1216.24	HS	1.55	High	Good adaptability
Shar Karela	1333.46	HS	1.66	High	High yielding local type

HS-Highly susceptible; S-Susceptible.

Disease reaction based on artificial screening against powdery mildew under protected conditions.

Table 2: Mean yield performance of bitter melon genotypes under protected conditions

S. No	Genotype	Fruit length (cm)	Average fruit weight (g)	Fruit yield per vine (kg)
1	MC-1	5.33	7.85	0.17
2	MC-9	16.92	95.50	1.17
3	Katali Vaibhav	15.06	69.30	1.01
4	MC-8	15.17	89.94	0.97
5	Dharg Local	15.82	92.56	1.41
6	IC-505627	13.68	94.81	1.44
7	IC-45346	10.06	46.30	0.75
8	IC-505632	12.39	57.63	0.90
9	IC-68275	17.15	75.10	1.24
10	IC-45351	18.05	95.67	1.31
11	IC-45350	16.00	88.52	1.41
12	IC-68295	13.82	81.89	0.99
13	IC-65972	14.22	97.20	1.22
14	IC-85626	15.74	90.11	1.22
15	IC-599421	11.76	66.95	1.06
16	Katali Vaibhav-1	12.66	48.12	1.01
17	Bagalkot Local-5	13.33	56.62	0.71
18	Phule Green Local	18.33	135.95	1.94
19	UHSBP-215	15.65	77.43	1.42
20	Katali Vaibhav-2	16.92	81.85	1.03
21	Dandeli Local	18.34	98.01	1.17
22	UHSBP-415	19.19	89.12	1.53
23	Ranebennur Local-1	13.20	76.63	1.48
24	UHSBP-815	12.83	61.78	1.15
25	IC-85626-2	13.24	69.64	1.02
26	IC-68275-3	21.19	133.52	2.15
27	IC-505632-2	14.27	65.26	1.77
28	IC-45346-1	15.13	83.19	1.54
29	IC-85626-1	14.20	99.16	1.65
30	IC-418486-1	14.66	91.63	1.50
31	MC-9-80	14.79	75.28	1.07
32	Katali Vaibhav-3	15.07	106.81	2.03
33	UHSBP-215-1	23.02	177.36	2.22
34	UHSBP-K	10.18	0.00	1.61
35	MC-9-2	14.23	140.24	0.85
36	IC-45351-1	13.40	135.86	1.09
37	IC-505632-3	19.72	162.32	1.78
38	IC-45350-1	14.47	179.38	1.15
39	Dharg Local-1	20.68	215.80	2.29
40	MC-8-4	12.94	165.56	1.00
41	Ranebennur Local-1	17.35	208.08	1.40
42	Hospet Local-1	17.62	202.71	1.46
43	Hospet Local-2	12.96	103.73	1.11

44	MGL	16.01	90.72	1.18
45	MWL	13.77	77.11	1.41
46	Pant Karela	18.50	110.46	1.48
47	Punjab Local	16.20	90.49	1.35
48	Punjab-14	17.54	110.24	1.44
49	Punjab-15	16.60	103.31	1.55
50	Shar Karela	13.65	94.11	1.66
51	Taiyo	20.13	81.98	1.44
	Mean	15.35	100.87	1.33
	S. Em±	0.99	10.18	0.15
	CD @ 5%	2.83	28.92	0.31
	CV (%)	9.19	14.28	11.81



Fig 1: Overview screening of bitter gourd genotypes for powdery mildew

Conclusion

The present study revealed significant variability among bitter gourd (*Momordica charantia* L.) genotypes for powdery mildew reaction and yield-related traits under protected conditions. The screening under artificial epiphytotic conditions enabled clear differentiation of genotypes based on disease severity and AUDPC values. Considerable variation was also observed for yield attributes such as fruit length, average fruit weight, number of fruits per vine and fruit yield per vine.

Genotypes such as Dharg Local-1, UHSBP-215-1, IC-68275-3 and Katali Vaibhav-3 recorded very high fruit yield even under disease pressure, indicating their superior yield potential and adaptability. The identification of these promising genotypes provides valuable genetic resources for future breeding programmes aimed at developing high-yielding and powdery mildew tolerant bitter gourd varieties. The selected genotypes can therefore be utilized as potential donor parents for crop improvement and sustainable bitter gourd production.

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