



RESEARCH ARTICLE

Screening soil-borne disease resistance in wild and cultivated eggplant accessions for grafting and rootstock breeding

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Abstract

Brinjal (*S. melongena* L.), a crucial dietary staple in South and Southeast Asia, faces severe yield losses from soil-borne wilt diseases caused by *Fusarium oxysporum* f. sp. *melongenae* (Fusarium Wilt), *Ralstonia solanacearum* (Bacterial Wilt), and *Sclerotium rolfsii* (Southern Blight), with losses up to 81% in India. To address this, 14 *Solanum* germplasms, including seven wild species and seven cultivated varieties, were screened for resistance to FW, BW, and SB during Kharif 2024 at the ICAR-Indian Institute of Vegetable Research, Varanasi, India, aiming to identify robust rootstocks for sustainable disease management and also a source for resistance in the rootstock breeding program. Disease severity was evaluated using the disease index at 10, 20, 30, and 40 days after inoculation and quantified cumulatively via the AUDPC under controlled conditions. Among the germplasms, *S. torvum* exhibited exceptional resistance across all pathogens, recording the lowest disease index at 40 days after inoculation (BW: 9.33%; SB: 53.33%; FW: 32.00%) and AUDPC (BW: 210.0; SB: 500.0; FW: 380.0), highlighting its potential as a superior rootstock. Similarly, *S. sisymbriifolium*, *S. incanum*, and accession IC-111056 showed strong resistance, particularly to BW and SB, while cultivars Surya, Solemel, and Zippy were highly susceptible, underscoring their vulnerability. Identifying the susceptibility of Surya through field trials across diverse agro-ecological zones is essential to validate the stability of resistance, as pathogen strains and environmental conditions vary regionally. The present experiment underscores advancements in rootstock breeding, highlighting significant progress in developing bacterial wilt-resistant eggplant through the identification of promising resistant accessions, contributing to global efforts for sustainable cultivation and rootstock breeding program in brinjal.

Keywords: AUDPC, Bacterial wilt, Disease index, Fungal wilt, *Solanum melongena*, *Solanum torvum*, Wild species.

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Introduction

Brinjal (*Solanum melongena* L.), commonly known as eggplant or aubergine, is a vital crop in tropical and subtropical regions, particularly South and Southeast Asia, where it supports food security, nutrition, and livelihoods for smallholder farmers (Akanksha et al., 2023; Athya et al., 2024). Rich in dietary fiber, B-complex vitamins, and antioxidants such as nasunin and chlorogenic acid, brinjal is a dietary staple with global production exceeding 55 million tons annually, of which India contributes approximately 25% (FAO, 2023). However, soil-borne wilt diseases caused by *Fusarium oxysporum* f. sp. *melongenae* (Fusarium Wilt), *Ralstonia solanacearum* (Bacterial Wilt), and *Sclerotium rolfsii* (Southern Blight) severely constrain yields, with bacterial wilt causing losses up to 81% in India (Ramesh et al., 2022). *Fusarium oxysporum* f. sp. *melongenae* is a xylem-colonizing fungus that forms persistent chlamydospores, disrupting

water and nutrient transport and leading to wilting and plant death (Gordon and Martyn, 1997; Chung, 2012). *Ralstonia solanacearum*, a highly aggressive soil-borne bacterium, infects over 200 plant species and thrives in warm, humid conditions, forming biofilms that enhance its environmental persistence (Hayward, 1991; Geninand Denny, 2012). *Sclerotium rolfsii*, a necrotrophic fungus, causes rapid basal tissue decay under high moisture and temperature, resulting in plant collapse (Mondal et al., 2013). These pathogens pose significant challenges in regions with intensive monoculture and limited access to advanced disease management tools.

Conventional disease management strategies, including chemical treatments, crop rotation, and soil solarization, are often ineffective due to pathogen persistence, monoculture and practical constraints. Chemical controls risk environmental pollution and residue accumulation (Aktar et al., 2009), while crop rotation is hindered by land scarcity and the broad host range of *R. solanacearum* (Rai et al., 2014). Soil solarization and organic amendments are cost-prohibitive and inconsistent across regions (Gamliel et al., 2000). Breeding for resistance offers a long-term solution but is challenged by the polygenic nature of resistance and regional pathogen variability, delaying resistant cultivar development (Lebeau et al., 2013; Cucu et al., 2025).

Grafting onto resistant rootstocks provides a sustainable, immediate alternative, combining disease resistance with desirable scion traits (King et al., 2008; Polat and Gebologlu, 2025). Wild *Solanum* species, such as *S. torvum*, *S. sisymbriifolium*, and *S. incanum*, are valuable resistance sources due to co-evolutionary adaptations, including enhanced secondary metabolite production and vascular barriers (Syfert et al., 2016; Namisy et al., 2019). Systematic screening of wild and cultivated *Solanum* germplasms for resistance to the wilt disease complex (FW, BW, SB) for rootstock development can enhance yield stability (HendraNurdika et al., 2023; Du et al., 2024) and also identify sources for resistance in cultivated and cross-compatibility species. This study aimed to evaluate 14 *Solanum* germplasms (7 wild, 7 cultivated) against soil-borne diseases (bacterial wilt, *Fusarium* wilt, and southern blight) under controlled conditions to identify resistant sources for rootstock breeding.

Materials and Methods

Plant material and experimental design

The experiments were conducted during Kharif 2024 at the ICAR-IIVR, Varanasi, India, to assess resistance in 14 *Solanum* genotypes against *Fusarium oxysporum* f. sp. *melongenae* (FW), *Ralstonia solanacearum* (BW), and *Sclerotium rolfsii* (SB). The genotypes included seven wild species (*S. incanum*, *S. gilo*, *S. macrocarpon*, *S. torvum*, *S. virginianum*, *S. sisymbriifolium*, *S. laciniatum*) and seven cultivated varieties (IC-354557, IC-111056, Arka Neelkanth, Salato, Solemel,

Zippy, Surya). The study was conducted in a Completely Randomized Block Design with three replicates.

Pathogen cultivation

Virulent strains (*F. oxysporum* f. sp. *melongenae* NAIMCC-F-3272, *R. solanacearum* NAIMCC-B-01496, *S. rolfsii* NAIMCC-F-04171) were sourced from the ICAR-NBAIM, Mau, India. Fungal strains (*F. oxysporum* f. sp. *Melongenae* and *Sclerotium rolfsii*) were cultured on potato dextrose agar (PDA) at 30°C for 7 days, followed by potato dextrose broth (PDB) at 37°C with 120 rpm shaking for 24 hours. *R. solanacearum* was cultured on nutrient agar at 28°C for 48 hours and multiplied in nutrient broth. Fungal cultures were stored at 4°C, and bacterial cultures at room temperature.

Soil preparation and inoculation

Soil mixed with FYM (8:2 ratio) was sterilized using 5% formalin, covered for 48 hours, and aerated for 72 hours. Sterilized soil along with compost and FYM in 3:1:1 ratio was placed in pots and glasses containing 25-day-old seedlings each. Inoculation followed the root-dip method, roots were slightly injured by trimming the base and dipped in 5% sucrose solution for 5 minutes, then in pathogen suspensions (1.5×10^8 cfu/mL for *R. solanacearum*, 1.0×10^6 cfu/mL for *F. oxysporum* f. sp. *Melongenae* and *S. rolfsii*, adjusted to 0.3 OD at 600 nm) for 30 minutes. 5 ml of inoculum was used per plant.

Disease assessment

Experiments were conducted in a growth chamber at 21°C (day)/18°C (night) with 75–80 % humidity. Wilt symptoms were recorded weekly for 40 days post-inoculation using a modified 1–5 scale (Winstead and Kelman, 1952; Hussain et al., 2005) (Figure 1). Pathogen identity was confirmed through re-isolation and microscopy, adhering to Koch's postulates (Bhunjun et al., 2021). Disease index (%) was calculated following McKinney (1923), and AUDPC was computed to quantify cumulative disease severity (Shaner and Finney, 1977).

Statistical analysis

Data were pooled across replicates due to consistent resistance patterns. Analysis of variance (ANOVA) and Tukey's HSD test ($p = 0.05$) were performed using SPSS (version 16.0, IBM Corp., Armonk, NY, USA) to identify significant differences in resistance among genotypes.

Results

Resistance to *Ralstonia solanacearum* (BW), *Sclerotium rolfsii* (SB), and *Fusarium oxysporum* f. sp. *melongenae* (FW) was evaluated in 14 *Solanum* germplasms during Kharif 2024 at the ICAR-Indian Institute of Vegetable Research, Varanasi, India. Disease severity was quantified using the disease index (%) at 10, 20, 30, and 40 days after inoculation (DAI)



Figure 1: Disease Assessment on 1-5 scale

Table 1: Disease index (DI, %) and AUDPC for *Ralstonia solanacearum* (BW) in *Solanum* germplasm

Germplasm	<i>Ralstonia solanacearum</i> (BW)				
	10 DAI	20 DAI	30 DAI	40 DAI	AUDPC
<i>S. gilo</i>	4.00±0.00 ^{abc}	17.33±1.33 ^{cd}	45.33±2.67 ^f	66.67±3.53 ^g	1470.0 ± 30.0 ^{gh}
<i>S. incanum</i>	1.33±1.33 ^a	13.33±1.33 ^c	21.33±1.33 ^{bc}	26.67±1.33 ^{cd}	730.0 ± 26.5 ^d
<i>S. lacinatum</i>	6.67±1.33 ^{bcde}	22.67±2.67 ^e	40.00±2.31 ^f	76.00±2.31 ^g	1560.0 ± 52.0 ^h
<i>S. macrocarpon</i>	5.33±1.33 ^{abcd}	21.33±1.33 ^{de}	24.00±0.00 ^{bcd}	64.00±2.31 ^f	1200.0 ± 30.0 ^f
<i>S. sisymbirifolium</i>	2.67±1.33 ^{ab}	6.67±1.33 ^{ab}	5.33±1.33 ^a	24.00±2.31 ^{bc}	380.0 ± 52.9 ^b
<i>S. virginianum</i>	6.67±1.33 ^{bcde}	18.67±1.33 ^{de}	25.33±1.33 ^{cd}	52.00±4.62 ^e	1100.0 ± 36.1 ^f
<i>S. torvum</i>	2.67±1.33 ^{ab}	2.67±1.33 ^a	5.33±1.33 ^a	9.33±3.53 ^a	210.0 ± 60.0 ^a
IC-354557	2.67±1.33 ^{ab}	6.67±1.33 ^{ab}	6.67±1.33 ^a	36.00±2.31 ^d	490.0 ± 36.1 ^c
IC-111056	1.33±1.33 ^a	8.00±0.00 ^b	5.33±1.33 ^a	16.00±2.31 ^{ab}	330.0 ± 17.3 ^b
Arka Neelkanth	8.00±0.00 ^{cde}	18.67±1.33 ^{de}	20.00±0.00 ^b	65.33±3.53 ^f	1130.0 ± 10.0 ^f
Salato	9.33±1.33 ^{de}	17.33±1.33 ^{cd}	24.00±0.00 ^{bcd}	29.33±3.53 ^{cd}	910.0 ± 26.5 ^e
Solemel	6.67±1.33 ^{bcde}	22.67±1.33 ^e	28.00±0.00 ^d	48.00±2.31 ^e	1170.0 ± 17.3 ^f
Zippy	6.67±1.33 ^{bcde}	29.33±1.33 ^f	34.67±1.33 ^e	54.67±3.53 ^e	1420.0 ± 36.1 ^g
	10.67±1.33 ^e	37.33±1.33 ^g	41.33±1.33 ^f	68.00±4.62 ^g	1770.0 ± 30.0 ⁱ

Numbers in the same column followed by the same alphabet are not significantly different for the turkey test at $\alpha=5\%$

and cumulative severity via the AUDPC over a 40-day period under controlled conditions. DI and AUDPC values for BW, SB, and FW are presented in Tables 1, 2, and 3, respectively.

***Ralstonia solanacearum* (BW) resistance**

BW disease severity increased progressively from 10 to 40 DAI across all germplasm (Table 1). At 10 DAI, *S. incanum* and IC-111056 exhibited the lowest DI (1.33), followed by *S. sisymbirifolium* and *S. torvum* (2.67), while Surya recorded the highest (10.67). By 40 DAI, *S. lacinatum* showed the highest DI (76.00), followed by Surya (68.00) and *S. gilo* (66.67). Conversely, *S. torvum* displayed the lowest DI (9.33), followed by IC-111056 (16.00) and *S. sisymbirifolium* (24.00), indicating strong resistance to bacterial wilt. AUDPC values ranged from 210.0 (*S. torvum*) to 1770.0 (Surya), with low values for IC-111056 (330.0), *S. sisymbirifolium* (380.0), and IC-354557 (490.0), and high values for *S. lacinatum* (1560.0) and *S. gilo* (1470.0).

***Sclerotium rolfsii* (SB) resistance**

SB disease severity escalated from minimal at 10 DAI to severe by 40 DAI (Table 2). At 10 DAI, *S. gilo*, *S. incanum*, *S. sisymbirifolium*, *S. torvum*, IC-354557, and IC-111056 showed no symptoms (0.00), while *S. lacinatum*, *S. virginianum*, Arka Neelkanth, and Solemel recorded the highest DI (4.00). By 40 DAI, Solemel exhibited the highest DI (93.33), followed by Arka Neelkanth (89.33) and *S. gilo* (72.00). *S. sisymbirifolium* displayed the lowest DI (13.33), followed by IC-111056 (34.67) and *S. macrocarpon* (36.00), indicating robust resistance to southern blight. AUDPC values ranged from 280.0 (*S. sisymbirifolium*) to 1750.0 (Solemel), with low values for IC-111056 (460.0), *S. torvum* (500.0), and IC-354557 (710.0), and high values for Surya (1440.0) and *S. gilo* (1420.0).

***Fusarium oxysporum* f. sp. *melongenae* (FW) resistance**

FW disease severity varied across time points, reflecting differential susceptibility (Table 3). At 10 DAI, *S. incanum*, *S.*

Table 2: Disease Index (DI, %) and AUDPC for *Sclerotium rolfsii* (SB) in *Solanum* germplasms

Germplasm	<i>Sclerotium rolfsii</i> (SB)				
	10 DAI	20 DAI	30 DAI	40 DAI	AUDPC
<i>S. gilo</i>	0.00±0.00 ^a	9.33±1.33 ^b	49.33±3.53 ^g	72.00±2.31 ^d	1420.0 ± 50.0g
<i>S. incanum</i>	0.00±0.00 ^a	9.33±1.33 ^b	28.00±2.31 ^e	50.67±3.53 ^c	940.0 ± 10.0de
<i>S. lacinatum</i>	4.00±0.00 ^c	4.00±0.00 ^a	5.33±1.33 ^a	68.00±2.31 ^d	680.0 ± 10.0c
<i>S. macrocarpon</i>	1.33±1.33 ^{ab}	16.00±2.31 ^c	17.33±1.33 ^{bc}	36.00±2.31 ^b	780.0 ± 45.8c
<i>S. sisymbirifolium</i>	0.00±0.00 ^a	5.33±1.33 ^{ab}	6.67±1.33 ^a	13.33±1.33 ^a	280.0 ± 36.1a
<i>S. virginianum</i>	4.00±0.00 ^c	9.33±1.33 ^b	14.67±1.33 ^b	68.00±2.31 ^d	900.0 ± 17.3d
<i>S. torvum</i>	0.00±0.00 ^a	1.33±1.33 ^a	5.33±1.33 ^a	53.33±3.53 ^c	500.0 ± 36.1b
IC-354557	0.00±0.00 ^a	5.33±1.33 ^{ab}	6.67±1.33 ^a	70.67±4.81 ^d	710.0 ± 65.6c
IC-111056	0.00±0.00 ^a	5.33±1.33 ^{ab}	8.00±0.00 ^a	34.67±3.53 ^b	460.0 ± 36.1b
Arka Neelkanth	4.00±0.00 ^c	21.33±1.33 ^d	22.67±1.33 ^d	89.33±3.53 ^e	1360.0 ± 36.1fg
Salato	2.67±1.33 ^{bc}	17.33±1.33 ^c	21.33±1.33 ^{cd}	56.00±2.31 ^c	1020.0 ± 34.6e
Solemel	4.00±0.00 ^c	30.67±1.33 ^e	37.33±1.33 ^f	93.33±3.53 ^e	1750.0 ± 50.0g
Zippy	1.33±1.33 ^{ab}	29.33±1.33 ^e	36.00±0.00 ^f	36.00±2.31 ^b	1260.0 ± 34.6f
Surya	2.67±1.33 ^{bc}	33.33±1.33 ^e	37.33±1.33 ^f	48.00±2.31 ^c	1440.0 ± 17.3g

Numbers in the same column followed by the same alphabet are not significantly different for the turkey test at α=5%)

Table 3: Disease Index (DI, %) and AUDPC for *Fusarium oxysporum* f. sp. *melongenae* (FW) in *Solanum* germplasms

Germplasm	<i>Fusarium oxysporum</i> f. sp. <i>melongenae</i> (FW)				
	10 DAI	20 DAI	30 DAI	40 DAI	AUDPC
<i>S. gilo</i>	2.67±1.33 ^{ab}	10.67±2.67 ^{bc}	25.33±1.33 ^{de}	30.67±1.33 ^b	790.0 ± 70.0de
<i>S. incanum</i>	0.00±0.00 ^a	12.00±2.31 ^{bc}	21.33±1.33 ^{bc}	16.00±2.31 ^a	620.0 ± 36.1c
<i>S. lacinatum</i>	5.33±1.33 ^{bc}	6.67±1.33 ^{ab}	5.33±1.33 ^a	29.33±3.53 ^b	440.0 ± 26.5ab
<i>S. macrocarpon</i>	2.67±1.33 ^{ab}	16.00±2.31 ^{cd}	24.00±0.00 ^{cd}	70.67±4.81 ^d	1150.0 ± 36.1f
<i>S. sisymbirifolium</i>	0.00±0.00 ^a	6.67±1.33 ^{ab}	5.33±1.33 ^a	66.67±2.67 ^d	680.0 ± 40.0cd
<i>S. virginianum</i>	6.67±1.33 ^c	10.67±1.33 ^{bc}	25.33±1.33 ^{de}	32.00±2.31 ^b	830.0 ± 40.0e
<i>S. torvum</i>	0.00±0.00 ^a	4.00±2.31 ^a	5.33±1.33 ^a	32.00±4.62 ^b	380.0 ± 80.0a
IC-354557	0.00±0.00 ^a	6.67±2.67 ^{ab}	6.67±1.33 ^a	50.67±3.53 ^c	580.0 ± 78.1bc
IC-111056	0.00±0.00 ^a	6.67±1.33 ^{ab}	5.33±1.33 ^a	53.33±4.81 ^c	580.0 ± 55.7bc
Arka Neelkanth	6.67±1.33 ^c	21.33±1.33 ^d	20.00±0.00 ^b	70.67±3.53 ^d	1200.0 ± 34.6f
Salato	8.00±0.00 ^c	20.00±0.00 ^d	24.00±0.00 ^{cd}	73.33±3.53 ^d	1270.0 ± 26.5f
Solemel	5.33±1.33 ^{bc}	30.67±1.33 ^e	28.00±0.00 ^e	33.33±1.33 ^b	1170.0 ± 0.0f
Zippy	6.67±1.33 ^c	29.33±1.33 ^e	34.67±1.33 ^f	89.33±3.53 ^e	1680.0 ± 34.6h
Surya	8.00±0.00 ^c	33.33±1.33 ^e	41.33±1.33 ^g	34.67±1.33 ^b	1440.0 ± 17.3g

Numbers in the same column followed by the same alphabet are not significantly different for the turkey test at α=5%)

sisymbirifolium, *S. torvum*, IC-354557, and IC-111056 exhibited no symptoms (0.00), while Salato and Surya recorded the highest DI (8.00). By 40 DAI, Zippy showed the highest DI (89.33), followed by Salato (73.33) and Arka Neelkanth (70.67). *S. incanum* displayed the lowest DI (16.00), followed

by *S. lacinatum* (29.33) and *S. torvum* (32.00), indicating strong resistance to *Fusarium* wilt. AUDPC values ranged from 380.0 (*S. torvum*) to 1680.0 (Zippy), with low values for *S. lacinatum* (440.0), IC-354557 (580.0), and IC-111056 (580.0), and high values for Surya (1440.0) and Salato (1270.0).

Integrated resistance profiles

S. torvum consistently exhibited superior resistance across all pathogens, with the lowest DI at 40 DAI (BW: 9.33; SB: 53.33; FW: 32.00) and AUDPC values (BW: 210.0; SB: 500.0; FW: 380.0), positioning it as a prime candidate for rootstock development. *S. sisymbirifolium* also showed strong resistance, particularly to SB (DI: 13.33; AUDPC: 280.0) and BW (DI: 24.00; AUDPC: 380.0), while *S. incanum* demonstrated notable resistance to FW (DI: 16.00; AUDPC: 620.0) and moderate resistance to BW (DI: 26.67; AUDPC: 730.0). Among cultivated genotypes, IC-111056 also displayed consistent resistance (e.g., BW: DI 16.00, AUDPC 330.0; SB: DI 34.67, AUDPC 460.0). Conversely, Surya, Solemel, and Zippy were highly susceptible, with elevated DI and AUDPC values (e.g., Surya: BW DI 68.00, AUDPC 1770.0; Solemel: SB DI 93.33, AUDPC 1750.0; Zippy: FW DI 89.33, AUDPC 1680.0). These results identify *S. torvum*, *S. sisymbirifolium*, *S. incanum*, and IC-111056 as promising rootstocks for grafting to enhance wilt resistance in brinjal cultivation and sources for rootstock breeding of resistant varieties/hybrids to wilt.

Discussion

The screening of 14 *Solanum* germplasms for resistance to *Ralstonia solanacearum* (BW), *Sclerotium rolfsii* (SB), and *Fusarium oxysporum* f. sp. *melongenae* (FW) revealed significant variation in disease resistance, with *S. torvum*, *S. sisymbirifolium*, *S. incanum*, and IC-111056 emerging as promising rootstock candidates for grafting in brinjal cultivation and also for rootstock breeding. These findings align with previous studies highlighting the potential of wild *Solanum* species as sources of resistance to soil-borne pathogens due to their co-evolutionary adaptations (Kumar et al., 2025a; Syfert et al., 2016; Namisy et al., 2019). The superior resistance of *S. torvum* across all pathogens, with consistently low DI and AUDPC values, corroborates its established use as a rootstock in tomato and brinjal for managing bacterial wilt and fusarium wilt (Kumar et al., 2025b; King et al., 2008; Du et al., 2024; Polat and Geboloğlu, 2025). Its broad-spectrum resistance likely stems from genetic mechanisms such as enhanced production of secondary metabolites (e.g., phenolics, alkaloids) and physical barriers in vascular tissues, which restrict pathogen colonization (Syfert et al., 2016).

S. sisymbirifolium exhibited exceptional resistance to SB and strong resistance to BW, suggesting its suitability as a rootstock in regions where southern blight and bacterial wilt predominate. Its resistance to SB may be attributed to lignified cell walls and antifungal compounds, which limit the necrotrophic activity of *S. rolfsii* (Mondal et al., 2013; Solares et al., 2023). Similarly, *S. incanum* showed robust resistance to FW and moderate resistance to BW, consistent with reports of its tolerance to vascular pathogens due to restricted xylem colonization (Namisy et al., 2019). IC-111056,

a cultivated variety, displayed consistent resistance across all pathogens, suggesting it may harbour introgressed resistance genes from wild relatives, a phenomenon observed in other Solanaceous crops (Lebeau et al., 2013). The high disease incidence (DI) and AUDPC values of commercial cultivars Surya, Solemel, and Zippy reveal their susceptibility to wilt diseases due to the diverse nature of pathogen strains and the complicated interactions between resistance and environmental factors. Furthermore, wilt resistance can vary depending on the specific pathogenic strains present in a particular field or geographic area (Kunwar et al., 2020; Ramesh et al., 2022). The development of resistance from wilt diseases is complex due to factors such as the polygenic and intricate inheritance of resistance, the association between resistance and reduced fruit quality (Ramesh et al., 2022; HendraNurdika et al., 2023).

The genetic basis of resistance in wild *Solanum* species likely involves polygenic traits, including quantitative trait loci (QTLs) associated with pathogen recognition, signal transduction, and defence responses. For BW, resistance in *S. torvum* and *S. sisymbirifolium* may involve R-genes that trigger hypersensitive responses, limiting bacterial spread in vascular tissues (Genin and Denny, 2012). For FW, *S. incanum* and *S. torvum* likely possess I-genes (e.g., I-2 homologs), which confer resistance to *F. oxysporum* by recognizing fungal effectors in tomato as well (Gordon and Martyn, 1997; Chitwood-Brown et al., 2021). SR resistance in *S. sisymbirifolium* may be linked to upregulation of pathogenesis-related (PR) proteins and chitinases, which degrade fungal cell walls (Solares et al., 2023). These mechanisms warrant further investigation through genomic and transcriptomic analyses to identify specific resistance genes and pathways, facilitating marker-assisted breeding or gene editing for enhanced rootstock development (Akanksha et al., 2023).

Grafting onto resistant rootstocks like *S. torvum* offers immediate benefits to small and marginal farmers, bypassing the lengthy timelines of conventional breeding (King et al., 2008; Du et al., 2024). However, challenges such as graft incompatibility, environmental adaptability, skill and cost of grafted seedlings must be addressed (Oda, 2007). *S. torvum* is known for high compatibility with cultivated brinjal scions, but *S. sisymbirifolium* and *S. incanum* require further testing to ensure vigour and fruit quality (Polat and Geboloğlu, 2025). Field trials across diverse agro-ecological zones are essential to validate resistance stability, as pathogen strains and environmental conditions vary regionally (Athyia et al., 2024; Cucu et al., 2025). Integrating grafting with other sustainable practices, such as biocontrol agents or organic amendments, could enhance disease management while reducing reliance on chemical controls (Rai et al., 2014; Gamliel et al., 2000).

This study's controlled conditions ensured reliable resistance assessment, but limitations include the use of single pathogen strains, which may not reflect field-level strain diversity (Bhunjun et al., 2021). Future research should screen germplasms against multiple strains and incorporate molecular markers to map resistance loci (Lebeau et al., 2013). Additionally, evaluating rootstock-scion interactions under field conditions will clarify practical applications for smallholder farmers, particularly in South and Southeast Asia, where wilt diseases are prevalent (Ramesh et al., 2022).

Rootstock Breeding for *Solanum melongena*

The results of the screening trial for resistance to *Ralstonia solanacearum* (BW), *Sclerotium rolfsii* (SB), and *Fusarium oxysporum* f. sp. *melongenae* (FW), identified *S. torvum*, *S. sisymbirifolium*, *S. incanum*, and accession IC-111056 as highly resistant rootstock candidates due to their low Disease Index (DI) and Area Under the Disease Progress Curve (AUDPC). These findings align with previous reports of *S. torvum* and *S. sisymbirifolium* as robust sources of resistance to BW and FW (Daunay et al., 2001 and Kumar et al., 2025 a & b). Rootstock breeding aims to introgress these resistance traits into *S. melongena* through conventional crossing and backcrossing to recover agronomic traits like fruit yield and quality, as demonstrated by Kalloo (1993) in earlier brinjal breeding programs. Marker-assisted selection (MAS) using quantitative trait loci (QTLs) identified in *S. torvum* and *S. aethiopicum* (Toppino et al., 2020) can accelerate the development of polygenic resistance, addressing the susceptibility of cultivars like Surya, Solemel, and Zippy. Biotechnological approaches, such as CRISPR/Cas9, offer potential for precise resistance gene editing, as shown by Van Eck (2018), to counter pathogen variability noted by Prior et al. (1996). Crosses between different *S. melongena* cultivars/ accessions are generally highly successful due to their genetic similarity, as no significant reproductive barriers exist, and hybrids are fertile with high seed set and germination rates. Intraspecific hybridization is used to combine desirable traits like fruit size, yield, and disease resistance within eggplant breeding programs (Daunay et al., 1991; Behera and Singh, 2002), while interspecific hybridization between *S. melongena* and *S. torvum* is challenging due to their phylogenetic distance, with *S. torvum* belonging to the tertiary gene pool of eggplant. Research indicates limited crossability, with viable hybrids obtained primarily when *S. melongena* is used as the female parent (Plazas et al., 2016). *S. torvum* is a preferred rootstock for eggplant due to its robust resistance to soil-borne pathogens, including *Ralstonia solanacearum* (bacterial wilt), *Verticillium dahliae*, *Fusarium oxysporum* f. sp. *melongenae*, and *Meloidogyne* spp. (root-knot nematodes) (Gousset et al., 2005). However, it's irregular and slow seed germination (often <50%) hinders large-scale use. Interspecific hybrids of *S. melongena*, such as those crossed with *S. incanum* (SI ×

SM) or *S. aethiopicum* (SM × SA), provide high germination rates (≥90%) and complete graft success (100%), enhancing vigor, yield, and nematode resistance while maintaining fruit quality, while cross-compatibility of *S. melongena* with *S. incanum* due to its taxonomic proximity with *S. melongena* as member of the “*melongena* complex” (Karihaloo and Rai, 1995) enhances its role as a potential source for resistance to wilt diseases in brinjal. Further, poor germination in *S. torvum*, as observed in the study, which did not address germination challenges in *S. torvum*, a key resistant candidate, would also hinder rootstock production scalability (Gisbert et al., 2011), warranting improved seed treatments or vegetative propagation to ensure consistent rootstock production.

Scion and rootstock compatibility

Graft compatibility between *S. melongena* (eggplant) scions and resistant rootstocks is essential for effective wilt management, necessitating genetic proximity to ensure vascular continuity and optimal agronomic performance. Intraspecific grafting among *S. melongena* cultivars achieves near-100% success due to their close genetic relationship, enabling the combination of vigorous root systems with high-quality scions to enhance yield and disease resistance (Moncada et al., 2013). The results highlight *S. incanum* as a compatible rootstock, corroborating Bletsos et al. (2003), who demonstrated successful *S. incanum* × *S. melongena* hybrids with minimal fruit quality trade-offs. *S. torvum*, despite its superior resistance across all pathogens, may pose compatibility challenges due to genetic divergence, as noted by Gisbert et al. (2011), potentially leading to graft failure or reduced vigour. *S. sisymbirifolium* and IC-111056 offer promising alternatives, with closer genetic alignment to *S. melongena*. Anatomical and physiological screening, as recommended by Lebeau et al. (2011), is essential to optimize xylem connectivity and scion-rootstock vigour, particularly under varying environmental conditions like high temperatures, which can influence compatibility and resistance expression.

Future directions

Future breeding programs should build on the findings by prioritizing *S. torvum*, *S. sisymbirifolium*, *S. incanum*, and IC-111056 for rootstock development, integrating resistance genes into elite *S. melongena* lines. Advanced genomic tools, such as genome-wide association studies (GWAS), can identify novel resistance loci, complementing MAS strategies outlined by Toppino et al., (2020). CRISPR/Cas9-mediated editing, as explored by Van Eck (2018), could enhance resistance stability against diverse RS strains, addressing pathogen variability (Prior et al., 1996). Overcoming germination challenges in *S. torvum* through seed priming or micropropagation, as suggested by Gisbert et al., (2011), will improve scalability. Multi-locational field trials are needed

to validate graft compatibility and resistance under diverse agro-ecological conditions, as environmental interactions can diminish resistance expression (Lebeau et al., 2011). Breeding for minimal fruit quality trade-offs, such as avoiding increased phenolic content (Kalloo, 1993) is critical to maintain market acceptance. Standardizing grafting protocols and training smallholder farmers in disease-prone regions will facilitate adoption, leveraging the resistance profiles of identified germplasms to enhance sustainable brinjal cultivation and food security.

Limitations of the brinjal wilt resistance screening study

The screening of 14 *Solanum* germplasms for resistance to *Ralstonia solanacearum* (BW), *Sclerotium rolfsii* (SB), and *Fusarium oxysporum* f. sp. *melongenae* (FW) at the ICAR-Indian Institute of Vegetable Research, Varanasi, India, provides valuable insights but has several limitations. Firstly, the study was conducted under controlled conditions, which may not fully replicate the complex environmental interactions (e.g., temperature fluctuations, soil variability) encountered in field settings, potentially affecting resistance expression, as noted by Lebeau et al. (2011). Secondly, the evaluation focused on a single isolate per pathogen, limiting insights into resistance stability against diverse strains of BW, which exhibit significant genetic variability across regions (Prior et al., 1996). Thirdly, the study did not assess graft compatibility between resistant rootstocks (*S. torvum*, *S. sisymbirifolium*, *S. incanum*, IC-111056) and commercial *S. melongena* scions, a critical factor for practical application, as highlighted by Bletsos et al. (2003). Fourthly, fruit quality traits, such as size and phenolic content, which can be affected by resistance introgression (Kalloo, 1993), were not evaluated, potentially overlooking trade-offs. Lastly, the small sample size of 14 germplasms may not fully represent the genetic diversity of *Solanum* species, restricting the identification of additional resistant sources. These limitations suggest the need for field-based trials, multi-strain pathogen testing, compatibility assessments, and broader germplasm screening to enhance the applicability of the findings for sustainable brinjal cultivation.

Conclusion

This study demonstrates that *S. torvum*, *S. sisymbirifolium*, *S. incanum*, and IC-111056 (*S. melongena*) possess significant resistance to *Ralstonia solanacearum*, *Sclerotium rolfsii*, and *Fusarium oxysporum* f. sp. *melongenae*, making them highly suitable as rootstocks for grafting in brinjal cultivation and also in a rootstock breeding program. *S. torvum* stands out for its broad-spectrum resistance, offering a robust solution for managing the wilt disease complex. These findings provide a foundation for sustainable disease management, enhancing yield stability and supporting small and marginal livelihoods in disease-prone regions. By leveraging the genetic diversity

of wild and cultivated *Solanum* germplasms, grafting technology can deliver immediate, environmentally friendly solutions, while future genomic studies and field trials will further optimize rootstock development and deployment, ensuring long-term resilience in brinjal production systems.

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सारांश

बैंगन (सोलनम मेलॉन्जेना एल.) एक महत्वपूर्ण सब्जी फसल है, जिसका उत्पादन दक्षिण तथा दक्षिण-पूर्व एशिया में व्यापक रूप से होता है। यह फसल पोषण एवं आर्थिक दृष्टि से अत्यंत महत्वपूर्ण है, किंतु इसे अनेक मृदा-जनित रोगों जैसे फ्यूजेरियम ऑक्सीस्पोरम एफ. एसपी. मेलोंगेने (फ्यूजेरियम विल्ट), राल्सटोनिया सोलेनेसेरम (बैक्टीरियल विल्ट), और स्क्लेरोटियम रोलफ्सी (सदर्न ब्लाइट) के कारण भारी क्षति होती है। भारत में अकेले इन रोगों से बैंगन की उपज में लगभग 81% तक की कमी देखी गई है। इन रोगों के प्रति प्रतिरोधी रूटस्टॉक की पहचान टिकाऊ उत्पादन एवं रोग प्रबंधन हेतु एक महत्वपूर्ण रणनीति मानी जाती है। इस दिशा में वर्षा ऋतु 2024 में, भा.कृ.अ.प- भारतीय सब्जी अनुसंधान संस्थान, वाराणसी में 14 बैंगन के प्रजातियों का मूल्यांकन किया गया, जिनमें सात जंगली प्रजातियाँ (सोलनम टोरवम, सोलनम सिसिम्ब्रीफोलियम, सोलनम इनकैनम आदि) एवं सात संवर्धित किस्में (सूर्या, सोलमेल, ज़िप्पी आदि) सम्मिलित थीं। इन प्रजातियों को कृत्रिम संक्रमण के अधीन नियंत्रित परिस्थितियों में परीक्षण किया गया, और रोग की प्रगति का आकलन 10, 20, 30 एवं 40 दिनों के अंतराल पर रोग सूचकांक (डी.आई. %) तथा रोग प्रगति वक्र के अधीन क्षैलफल (ए.यू.डी.पी.सी.) के माध्यम से किया गया। परिणामों से स्पष्ट हुआ कि सोलनम टोरवम ने सभी तीन रोगजनकों के विरुद्ध सर्वाधिक प्रतिरोध प्रदर्शित किया, जिसमें 40 दिनों के बाद न्यूनतम रोग सूचकांक (बैक्टीरियल विल्ट: 9.33%; सदर्न ब्लाइट: 53.33%; फ्यूजेरियम विल्ट: 32.00%) तथा ए.यू.डी.पी.सी. मान (बैक्टीरियल विल्ट: 210.0; सदर्न ब्लाइट: 500.0; फ्यूजेरियम विल्ट: 380.0) प्राप्त हुए। इसके अतिरिक्त, सोलनम सिसिम्ब्रीफोलियम (बैक्टीरियल विल्ट डी.आई.: 24.00%, ए.यू.डी.पी.सी.: 380.0; सदर्न ब्लाइट डी.आई.: 13.33%, ए.यू.डी.पी.सी.: 280.0), सोलनम इनकैनम (फ्यूजेरियम विल्ट डी.आई.: 16.00%, ए.यू.डी.पी.सी.: 620.0), एवं आईसी-111056 (बैक्टीरियल विल्ट डी.आई.: 16.00%, ए.यू.डी.पी.सी.: 330.0) ने भी उल्लेखनीय प्रतिरोध दर्शाया। इसके विपरीत, उन्नत किस्मों जैसे सूर्या (बैक्टीरियल विल्ट डी.आई.: 68.00%, ए.यू.डी.पी.सी.: 1770.0), सोलमेल (सदर्न ब्लाइट डी.आई.: 93.33%, ए.यू.डी.पी.सी.: 1750.0) एवं ज़िप्पी (फ्यूजेरियम विल्ट डी.आई.: 89.33%, ए.यू.डी.पी.सी.: 1680.0) अत्यधिक संवेदनशील पाई गईं। यह अध्ययन सोलनम टोरवम, सोलनम सिसिम्ब्रीफोलियम, सोलनम इनकैनम एवं आईसी-111056 को बहु-रोग प्रतिरोधी रूटस्टॉक के रूप में स्थापित करता है, जो बैंगन में रूटस्टॉक आधारित प्रजनन को गति प्रदान कर सकते हैं। शोध के इन परिणामों भविष्य में मृदा-जनित रोग प्रतिरोधी एवं टिकाऊ बैंगन उत्पादन प्रणाली के विकास में महत्वपूर्ण भूमिका निभा सकते हैं।