

## International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693  
ISSN Online: 2617-4707  
NAAS Rating (2025): 5.29  
IJABR 2025; SP-9(11): 632-633  
[www.biochemjournal.com](http://www.biochemjournal.com)  
Received: 20-09-2025  
Accepted: 23-10-2025

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## Inheritance and allelism of bacterial wilt resistance in brinjal (*Solanum melongena* L.)

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DOI: <https://www.doi.org/10.33545/26174693.2025.v9.i11Sh.7223>

### Abstract

Bacterial wilt caused by *Ralstonia solanacearum* is one of the most destructive diseases of brinjal (*Solanum melongena* L.), particularly in tropical and subtropical regions. The disease causes sudden wilting and collapse of plants, leading to severe yield losses and instability in production. Chemical and cultural control measures are largely ineffective due to the soil-borne nature and wide host range of the pathogen. Consequently, host plant resistance is regarded as the most reliable, economical, and eco-friendly approach for disease management. Understanding the inheritance of resistance and the allelic relationship among resistance sources is essential for the effective utilization of resistant genotypes in breeding programmes. The present study was undertaken to investigate the inheritance and allelism of bacterial wilt resistance in selected brinjal genotypes. Three resistant genotypes, SMn6n7, IC0598430 and CARIn1, were used, with CARIn1 serving as a common resistant parent. Crosses were made between CARIn1 and the other two genotypes, and the resulting F<sub>1</sub>s were selfed to generate F<sub>2</sub> populations. Evaluation under sick plot conditions revealed complete resistance in parents, F<sub>1</sub>s and F<sub>2</sub> populations, with no segregation for susceptibility. The absence of segregation confirmed the allelic nature of bacterial wilt resistance genes among the tested genotypes. The findings indicate limited genetic diversity for resistance and emphasize the need to identify novel resistance sources to achieve durable bacterial wilt resistance in brinjal breeding programmes.

**Keywords:** Brinjal, bacterial wilt, *Ralstonia solanacearum*, inheritance, allelism, disease resistance

### Introduction

Brinjal (*Solanum melongena* L.) is an important vegetable crop widely cultivated in India and other parts of the world. It contributes significantly to nutritional security, farm income and employment generation. Despite its importance, brinjal productivity is severely constrained by several biotic stresses, among which bacterial wilt caused by *Ralstonia solanacearum* is one of the most devastating diseases (Sidhu and Dhatt, 2007) [4]. Bacterial wilt is characterized by sudden wilting of plants without prior yellowing, browning of vascular tissues, and eventual death of the plant. The pathogen survives in soil, crop residues and alternate hosts, making its management extremely difficult. Favorable environmental conditions such as high temperature and soil moisture aggravate disease incidence, resulting in yield losses ranging from moderate to complete crop failure in endemic regions (Manda *et al.*, 2020) [3].

Management of bacterial wilt through chemical, cultural and biological methods has met with limited success. Crop rotation and soil amendments provide only partial control, while chemical treatments are uneconomical and environmentally hazardous. In this context, host plant resistance offers the most effective, sustainable and farmer-friendly solution for managing bacterial wilt in brinjal (Yuliar *et al.*, 2015) [5].

Boukema (1980) [1] investigated for the resistance to pepper strains of TMV in five *Capsicum chinense* accessions (PI 152225, 159236, 315008, 315023, and 315024) and found that resistance was inherited monogenically and partially dominant. The resistance genes in these accessions are allelic to each other and to the known alleles L<sub>1</sub> and L. Several resistant genotypes have been identified in cultivated brinjal and related *Solanum* species. However, the inheritance of resistance varies depending on the genetic background, and resistance

sources may share common genes. Knowledge of allelic relationships among resistance genes is crucial for breeding programmes, as crossing genotypes with identical resistance genes does not increase genetic diversity. Allelism tests using resistant  $\times$  resistant crosses help determine whether resistance genes are identical or non-allelic. The present investigation was therefore undertaken to study the inheritance and allelic relationship of bacterial wilt resistance in selected brinjal genotypes.

### Materials and Methods

The experimental material consisted of three bacterial wilt resistant brinjal genotypes, namely SM-6-7, IC0598430 and CARI-1. The genotype CARI-1, developed at ICAR-Central Island Agricultural Research Institute, Port Blair, Andaman and Nicobar Islands, was used as a common resistant parent. CARI-1 was crossed individually with SM-6-7 and IC0598430 to generate two resistant  $\times$  resistant crosses.

The  $F_1$  plants obtained from each cross were self-pollinated to produce respective  $F_2$  populations. The parents,  $F_1$ s and  $F_2$  populations were evaluated for bacterial wilt resistance under sick plot conditions where the soil was naturally infested with *Ralstonia solanacearum*. Standard agronomic practices were followed uniformly for all genotypes.

Plants were regularly observed for wilt symptoms throughout the crop growth period. Plants showing no wilting symptoms were classified as resistant, while plants exhibiting typical bacterial wilt symptoms were scored as susceptible. Data on resistant and susceptible plants were recorded and used to study segregation patterns and allelic relationships.

### Results and Discussion

All parental genotypes evaluated in the present study showed complete resistance to bacterial wilt, with no susceptible plants recorded under sick plot conditions. Similarly, the  $F_1$  plants derived from both crosses exhibited complete resistance, indicating dominant expression of resistance.

Evaluation of the  $F_2$  populations revealed that all plants were resistant, with no segregation for susceptibility in either cross. The segregation data of parents and  $F_2$  populations are presented in Table 1.

**Table 1:** Segregation of brinjal  $F_2$  populations based on bacterial wilt resistance

| Parent/Cross              | Generation | Resistant plants | Susceptible plants | Total plants |
|---------------------------|------------|------------------|--------------------|--------------|
| SM-6-7                    | $P_1$      | 12               | 0                  | 12           |
| CARI-1                    | $P_1$      | 10               | 0                  | 10           |
| SM-6-7 $\times$ CARI-1    | $F_2$      | 212              | 0                  | 212          |
| IC0598430                 | $P_1$      | 15               | 0                  | 15           |
| CARI-1                    | $P_1$      | 10               | 0                  | 10           |
| IC0598430 $\times$ CARI-1 | $F_2$      | 202              | 0                  | 202          |

The absence of susceptible plants and lack of segregation in the  $F_2$  populations of both crosses clearly indicate that the resistance genes present in SM-6-7 and IC0598430 are allelic to one of the resistance genes present in CARI-1. This confirms that the resistant parents share a common gene governing bacterial wilt resistance.

Such results are characteristic of allelic relationships, where resistant  $\times$  resistant crosses do not produce susceptible segregants. Similar observations have been reported earlier

in brinjal and other solanaceous crops, where lack of segregation in  $F_2$  populations confirmed allelism of resistance genes. The findings suggest that although multiple resistant genotypes are available, they may possess the same resistance gene, resulting in limited genetic diversity.

In essence, this means that the genetic resistance mechanisms in these three varieties are identical, and the resistance is controlled by the same two complementary recessive genes across all three sources. The consistent resistance in the  $F_2$  generations of these crosses provides strong evidence that the resistance genes in SM 6-7 and IC0598430 are indeed allelic to those in CARI-1, leaving no room for gene diversity among these resistant lines concerning bacterial wilt resistance. These results are in conformity with the earlier investigations of Chen *et al.* (2001) [2].

### Conclusion

The present study revealed that bacterial wilt resistance in the brinjal genotypes SM-6-7, IC0598430 and CARI-1 is governed by allelic genes. The complete absence of segregation for susceptibility in the  $F_2$  populations of resistant  $\times$  resistant crosses confirmed the allelic relationship of resistance genes among the tested genotypes. While these resistant lines are valuable for immediate use in breeding programmes, the limited genetic diversity for resistance underscores the need to identify and incorporate novel, non-allelic resistance sources. Broadening the genetic base of resistance will be essential for developing brinjal varieties with durable and long-lasting resistance to bacterial wilt.

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