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Review Article

Synergistic Biological Control of Bacterial Leaf Blight of Rice by *Trichoderma, Pseudomonas* and *Bacillus*

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ABSTRACT

Bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *oryzae,* is one of the most destructive diseases affecting rice production worldwide. With the growing demand for environmentally friendly and sustainable agricultural practices, microbial antagonist-based biological control has emerged as a promising alternative to synthetic chemical pesticides. This review comprehensively evaluates the efficacy and mechanisms of three widely studied biocontrol agents, i.e. *Trichoderma*, *Pseudomonas* and *Bacillus,* in the management of BLB disease of rice. These biocontrol agents suppress the pathogen through multiple mechanisms, including the production of antimicrobial compounds, competition for nutrients and ecological niches, promotion of plant growth and activation of host plant defence responses. Numerous studies have demonstrated that the

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application of these beneficial microorganisms significantly reduces pathogen proliferation, disease lesion length, disease incidence and disease severity, while improving grain yield and overall crop performance. Furthermore, the combined application of these biocontrol agents has shown greater effectiveness in disease suppression and yield enhancement than the use of individual agents alone, indicating synergistic interactions among them. Overall, this review highlights the considerable potential application of *Trichoderma*, *Pseudomonas* and *Bacillus* species as sustainable and effective biological control agents for the long-term management of BLB disease. Their integration into rice production systems offers a promising strategy for integrated disease management, improved crop productivity and reduced reliance on synthetic chemical pesticides.

Keywords: Bacillus spp., bacterial leaf blight, biological control, disease severity, rice, *Pseudomonas* spp. *Trichoderma* spp., yield

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most important staple food crops, providing the primary source of nutrition for more than half of the global population. It is the second most widely produced cereal crop, with an annual global production of approximately 645 million tonnes. Rice is cultivated in at least 114 countries, with nearly 90% of global production originating from Asian countries (Sharif et al., 2014). Beyond its role in food production, rice is deeply embedded in the economies, cultures, and livelihoods of many regions, making it indispensable to global agriculture and food security (Asma et al., 2023).

Despite its global importance, rice production is increasingly threatened by numerous biotic and abiotic stresses. Among the biotic constraints, Bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is one of the most destructive diseases affecting rice worldwide (Adedibu et al., 2024) and causes severe damage to millions of hectares of rice fields annually and can result in yield losses of up to 75% under severe disease outbreaks (Adedibu et al., 2024). Consequently, effective disease management strategies are essential to minimise yield losses and ensure sustainable rice production.

Various approaches have been employed to manage BLB, including chemical control, resistant cultivars, and biological control. Chemical pesticides and antibiotics have traditionally been used to suppress the disease. However, their effectiveness under field conditions has often been inconsistent due to differences in the sensitivity of *Xoo* pathogenic races to chemical treatments (Yasmin et al., 2017). Moreover, the continuous and excessive application of pesticides and antibiotics has accelerated the emergence of resistant pathogen populations. This reduces the long-term effectiveness of these chemicals while raising environmental and public health concerns.

The cultivation of resistant rice varieties has been regarded as one of the most effective and environmentally friendly approaches for BLB management (Teja et al., 2025).

Nevertheless, this strategy also has several limitations under field application. Improving resistance against one pathogen may inadvertently increase the plant's susceptibility to other diseases (Teja et al., 2025). Furthermore, breeding disease-resistant cultivars requires balancing resistance with desirable agronomic traits, as resistance genes may negatively influence yield, grain quality, or other important characteristics (Oliva et al., 2019; Teja et al., 2025). Additional challenges, including linkage drag and limited resistance durability due to the emergence of new pathogenic races, will further complicate the development of durable resistant cultivars (Teja et al., 2025).

In response to these challenges, biological control using beneficial microorganisms has emerged as a promising and environmentally sustainable alternative for BLB management. Biocontrol agents (BCAs) and plant growth-promoting microorganisms (PGPMs) suppress plant pathogens through multiple mechanisms while simultaneously enhancing plant growth and health (Ashwini et al., 2023). These microorganisms produce a wide range of bioactive secondary metabolites, including siderophores, rhamnolipids, antibiotics, lytic enzymes, and volatile organic compounds (VOCs), which could inhibit pathogen growth through various mechanisms. They also enhance host resistance by activating plant defence responses, thereby reducing disease development (Teja et al., 2025). In addition to disease suppression, many beneficial microorganisms stimulate root and shoot development, improve nutrient uptake and promote overall plant growth, contributing to higher crop productivity (Do et al., 2023). For example, volatile organic compounds (VOCs) produced by *Bacillus* species exhibit strong antibacterial activity by inducing reactive oxygen species (ROS) accumulation and oxidative stress in plant pathogens (Ali et al., 2023). Beneficial microorganisms such as *Trichoderma* spp., *Pseudomonas* spp., and *Bacillus* spp. have demonstrated broad-spectrum activity against numerous foliar and soil-borne pathogens, including *Phytophthora* spp., *Rhizoctonia solani*, *Xanthomonas* spp. and *Pythium* spp. (Teja et al., 2025). Among these beneficial microorganisms, *Trichoderma* spp. are widely recognised for their ability to suppress plant diseases through the production of antimicrobial metabolites and the activation of plant defence mechanisms. Studies have demonstrated that *Trichoderma* significantly reduces BLB severity by inducing the rice immune system while simultaneously producing antimicrobial compounds that directly inhibit *Xoo* (Islam et al., 2023; Teja et al., 2025).

Similarly, *Pseudomonas* species, particularly *P. aeruginosa*, have shown considerable potential as biological control agents against BLB. These bacteria produce a diverse array of antimicrobial compounds, including hydrogen cyanide, phenazines, and siderophores, which effectively inhibit the growth of *Xoo*. In addition, *Pseudomonas* spp. enhance nutrient availability and induce systemic resistance in rice plants, thereby improving plant growth and increasing resistance to disease (Thammasittirong et al., 2025). *Bacillus* species also play an important role in promoting plant health and suppressing plant diseases.

Several species, including *B. amyloliquefaciens*, produce bioactive lipopeptides with strong antibacterial activity against *Xoo*. Besides directly suppressing the pathogen, *Bacillus* spp. enhance nutrient uptake, stimulate plant growth, and improve the overall vigour and productivity of rice plants (Banluehan & Tunchai, 2025).

This review aims to comprehensively evaluate the synergistic effects and biocontrol efficacy of *Trichoderma* spp., *Pseudomonas* spp., and *Bacillus* spp. in the biological management of bacterial leaf blight (BLB) of rice. These three genera were selected because they are well represented in both the commercial biopesticide industry and the existing BLB-specific research literature, accounting for a substantial proportion of currently marketed microbial biocontrol products (De Pessemier et al., 2026). Moreover, they represent distinct and complementary groups of biological control agents (BCAs) with diverse modes of action, including antibiosis, antibiotic and siderophore production, and lipopeptide-mediated antagonism. Collectively, these mechanisms provide broad functional diversity and offer considerable potential for effective BLB management. Other promising genera, such as *Streptomyces* and *Paenibacillus*, have also demonstrated biocontrol potential; however, the available BLB-specific evidence for these microorganisms remains comparatively limited. Therefore, they are beyond the scope of the present review. Overall, this manuscript provides a comprehensive assessment of the effectiveness of fungal and bacterial BCAs against BLB, with particular emphasis on their disease-suppression mechanisms, plant growth-promoting activities, and potential to enhance rice yield. The review further discusses their role in reducing reliance on synthetic pesticides and promoting sustainable rice production.

Biocontrol Potential of *Trichoderma* spp. Against BLB Disease

Disease Control Efficacy

Trichoderma spp. have shown considerable promise as BCA against a wide range of soil-borne plant diseases (Bastakoti et al., 2017; Kumar et al., 2019). Numerous studies have demonstrated their effectiveness in controlling various plant diseases, including collar rot, root rot, stem rot and sheath blight, offering an environmentally friendly alternative to synthetic chemical pesticides (Kumar et al., 2020). In addition, *Trichoderma* spp. have been reported to effectively suppress important soil-borne pathogens such as *Fusarium solani*, *Rhizoctonia solani*, and *Sclerotium rolfsii* (Bastakoti et al., 2017). Beyond disease suppression, *Trichoderma* is widely recognised as a versatile BCA because of its dual role in controlling phytopathogens and promoting plant growth, making it an important component of sustainable agricultural systems (Kumar et al., 2020). Meanwhile, Sutthisa et al. (2024) reported that several *Trichoderma* isolates enhanced the germination rate and biomass accumulation of rice seedlings, demonstrating their plant growth-promoting potential.

For management of BLB, foliar spray and soil application are the most commonly used delivery methods and have been shown to effectively reduce disease severity while improving plant health (Kalboush et al., 2017). Kamaruzzaman et al. (2021) reported that different *Trichoderma* strains exhibited in-vitro inhibition of *Xoo*, with inhibition percentages ranging from 70 to 81%. Similarly, Gangwar and Sinha (2010) screened 52 *Trichoderma* isolates and found that 23 isolates, including *T. virens*, *T. hamatum* and *T. harzianum,* achieved complete (100%) inhibition of *Xoo* growth. Among these, *T. harzianum* exhibited the strongest antagonistic activity through the production of both volatile and non-volatile antimicrobial compounds. These findings highlight the significant potential of *Trichoderma* spp. as sustainable biological control agents for the management of BLB in rice. Their ability to suppress pathogens while simultaneously promoting plant growth makes them promising candidates for incorporation into integrated disease management strategies.

Several isolates have been reported to minimise lesion length significantly. In rice leaves treated with 27 µgmL^{-1} *Trichokonins* A (TKA), lesion length decreased by 82.2% compared with untreated controls (Meehae et al., 2023; Zhang et al., 2022). Efficacy tests showed that rice treated with TKA yielded disease lesion lengths of about 3.8 cm compared to 21.2 cm in untreated rice (Zhang et al., 2022). Furthermore, Islam et al. (2023) reported that *T. asperellum* strain BDISOF08 decreased disease lesions by up to 87.5%. Details of the findings were reported in Table 1.

Table 1
Effect of Trichoderma *spp. on reduction of lesion length of bacterial leaf blight disease of rice*

***Trichoderma* spp.**	**Reduction of Lesion Length (%)**	**References**
T. asperellum,	87.5	Islam et al., 2023
T. paraviridescens,	75	
T. erinaceum	60.4	
T. longibrachiatum	82.2	Zhang et al., 2022; Teja et al., 2025; Meehae et al., 2023
Trichoderma consortia	70	Teja et al., 2025

Trichoderma treatment using the seed priming method resulted in a 75% reduction in lesion length (Islam et al., 2023). Although the percentage of disease reduction was not explicitly indicated in the report, this finding is sufficient to indicate the potential of *Trichoderma* as a BCA. On the other hand, application of *Trichoderma* as a consortium resulted in a 70% lesion length reduction when it was compared to the control treatment (Teja et al., 2025). This further demonstrates *Trichoderma's* effectiveness and synergistic response in controlling BLB of rice.

Trichoderma have shown significantly decrease in disease severity under practical applications (Zhang et al., 2022). Similarly, a field study by Gangwar (2013) revealed that *T. harzianum* managed to reduce disease severity by 59% in comparison to the untreated controls. In the study, among other isolates, *Trichoderma* isolate 40 and *T. virens* showed decreases in disease from 48-58% (Jena et al., 2022). Under field settings, the combination of foliar sprays and root dips containing *T. viride* decreased disease severity by 40% (Mandal et al., 2017). Details of the disease control efficacy report against BLB were summarised in Table 2. The application rate is a significant challenge; T. *harzianum* with high application rates (4-8 g/L) has been proven to be more successful in managing disease than lower rates, as demonstrated by Khan and Sinha (2007).

Table 2
Disease control efficacy of Trichoderma *spp. in controlling bacterial leaf blight disease of rice*

***Trichoderma* spp.**	**Disease Control Efficacy (%)**	**References**
Trichoderma harzianum	48-59	Jena et al., 2022
Trichoderma spp.	48.3	
Trichoderma virens	58	
Trichoderma viride (foliar + root dip)	40	Mandal et al., 2017
Trichoderma atroviride	81	Prismantoro et al., 2024

Trichoderma also impacts plant growth and yield. For example, *T. harzianum* has led to significantly less disease incidence while increasing grain yield. *T. harzianum* was reported to enhance grain yield from 29.67 g/plant (control) to 48.74 g/plant (Jena et al., 2022). The efficacy of *Trichoderma* may vary between isolates or strains, but all the strains or isolates tested have shown high yields. Jena et al. (2022) reported that *T. harzianum* IRRI-5 was the most efficient isolate and yielded the tallest plants with the highest number of filled grains and the highest yield per rice plant. Under controlled settings, *T. harzianum* has been shown to enhance yield properties such as the number of tillers and panicles. Number of grains per panicle and total grain yield were also improved significantly (Teja et al., 2025).

Mode of Action of Trichoderma spp.

Trichoderma spp. suppress phytopathogens through several complementary mechanisms. Their effectiveness against BLB disease infection results from a combination of direct antagonism, plant defence activation and plant growth promotion, as illustrated in Figure 1.

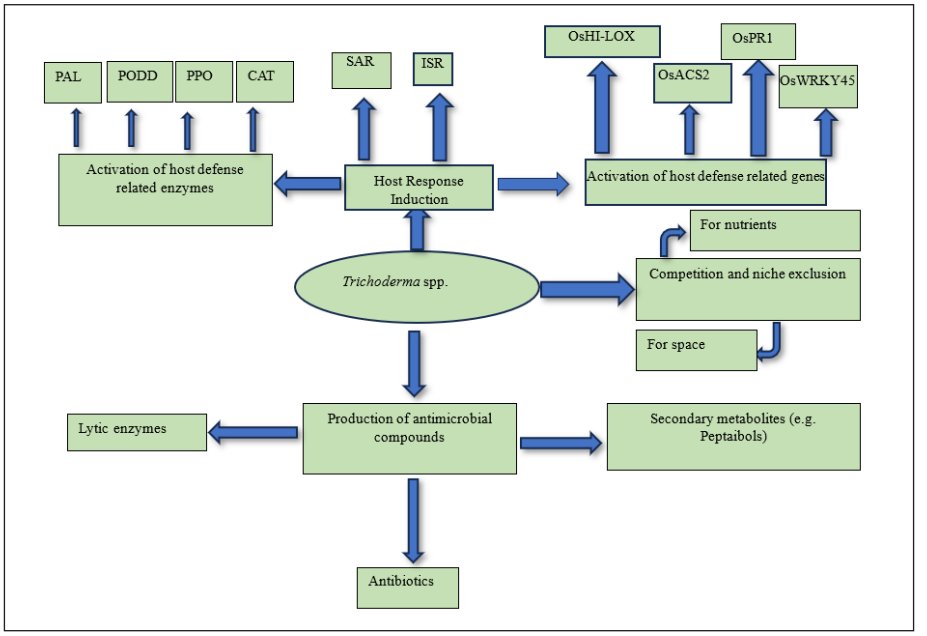

Figure 1. Illustration of the mechanisms of action of *Trichoderma* spp. for controlling bacterial leaf blight disease of rice

Note. PAL = Phenylalanine Ammonia-Lyase; POD = Peroxidase; PPO = Polyphenol Oxidase; CAT = Catalase; SAR = Systemic Acquired Resistance; ISR = Induced Systemic Resistance; OsHI-LOX = *Oryza sativa* Herbivore-Induced Lipoxygenase; OsPR1 = *Oryza sativa* Pathogenesis-Related Protein 1; OsACS2 = *Oryza sativa* 1-Aminocyclopropane-1-Carboxylate Synthase 2; OsWRKY45 = *Oryza sativa* WRKY Transcription Factor 45

Systemic acquired resistance (SAR) and induced systemic resistance (ISR) are the terms used to describe how *Trichoderma* spp. boost the immune system of the rice plant (Table 3). Phenylalanine ammonia-lyase (PAL), polyphenol oxidase (PPO), catalase (CAT), and peroxidase (POD) are important defence-related enzymes that are activated to suppress disease infection. By reinforcing cell walls with lignin and phenolic compounds, detoxifying reactive oxygen species and synthesising antimicrobial chemicals, these enzymes help plants become less vulnerable to bacterial invasion (Islam et al., 2023). Concurrently, *Trichoderma* induces enhancement of genes related to salicylic acid (SA) and jasmonic acid (JA) signalling pathways necessary for the host defence system. Key genes are OsHI-LOX (lipoxygenase for the JA pathway), OsACS2 (ethylene biosynthesis), OsPR1 and OsPR10 (pathogenesis-related proteins) and OsWRKY45, OsWRKY62 and OsWRKY71 (transcription factors for defence). When these genes are upregulated, the rice plants enter a "primed" state that allows them to fight against the pathogen more quickly and effectively (Islam et al., 2023).

Table 3
Application of different effective strains/isolates of Trichoderma *against Bacterial Leaf Blight of rice*

Strains/Isolates	Mechanisms of Action	Efficacy of Disease Control	Evidence Level	Application Conditions/ Method	References
T. longibrachiatum SMF2 (Trichokonins A, TKA)	Direct antibacterial compound disrupts Xoo cell integrity, causing protein/ nucleic acid leakage	Lesion length reduced by 82.2% at 27 µg/mL TKA; MIC = 54 µg/mL	Laboratory (purified compound applied via detached-leaf/in-planta assay, not whole-plant field or greenhouse trial)	Purified antimicrobial compound (TKA); pathogenicity assays on rice leaves	Zhang et al. (2022)
Native *Trichoderma* isolates (BDISOF67, BDISOF91, BDISOF08, BDISOF09)	ISR: enhanced PAL, PPO, CAT, POD; upregulated SA/ JA defence genes	Enzyme activity increases (PAL 4.27×, PPO 1.77×, CAT 3.53×, POD 1.57×); lesion reduction % not reported	Greenhouse/pot trial	Rhizosphere-isolated strains; whole-plant inoculation to assess induced resistance	Islam et al. (2023)
T. harzianum (phylloplane isolate)	Field-formulated antagonism; possible volatile/non-volatile metabolite involvement	Field disease severity reduced by 48.26% and 59.22%	Field trial	Fungal bioagent formulation applied in field across seasons	Gangwar (2013)
T. harzianum, T. hamatum, T. virens, and other isolates	In-vitro antagonism via volatile/non-volatile metabolites	Up to 100% inhibition of Xoo radial growth (dual culture); up to 55.5% inhibition (diffusion, non-volatile extract, 6.25%)	Laboratory (in vitro)	Dual-culture and metabolite diffusion assays	Gangwar & Sinha (2010)
T. asperellum TAIK1 (as part of consortium)	Combined antagonism and growth promotion/induced defence (not fully resolved)	61.13% disease decrease with consortium (individual isolate contribution not separated)	Greenhouse	Native isolates applied in vivo; growth/disease assessment	Kannan et al. (2021)
T. harzianum IRRI-2 to IRRI-6 (IRRI-5 best)	In-vitro antibiosis; growth stimulation via seed treatment	IRRI-5 and IRRI-2 most effective; disease reduction % not reported	Greenhouse/pot trial	Seed treatment, then *Xoo* inoculation, then disease/ yield assessment	(Jena et al., 2022)

Note. Xoo = *Xanthomonas oryzae* pv. *oryzae*; TKA = Trichokonins A; MIC = Minimum Inhibitory Concentration; PAL = Phenylalanine Ammonia-Lyase; PPO = Polyphenol Oxidase; CAT = Catalase; POD = Peroxidase; SA = Salicylic Acid; JA = Jasmonic Acid; OsPR1 = *Oryza sativa* Pathogenesis-Related Protein 1; OsPR10 = *Oryza sativa* Pathogenesis-Related Protein 10; OsWRKYs = *Oryza sativa* WRKY Transcription Factors; OsHI-LOX = *Oryza sativa* Herbivore-Induced Lipoxygenase; OsACS2 = *Oryza sativa* 1-Aminocyclopropane-1-Carboxylate Synthase 2; IRRI = International Rice Research Institute

Certain strains of *Trichoderma* can directly inhibit the growth of *Xoo* by producing antibiotics, lytic enzymes, and secondary metabolites (including peptaibols) (Islam et al., 2023; Zhang et al., 2022). In the rhizosphere and phyllosphere, *Trichoderma* outcompete pathogens for nutrients and space (Figure 1), hence lowering the establishment and colonisation of pathogens (Islam et al., 2023; Prismantoro et al., 2024).

Biocontrol Potential of *Pseudomonas* spp. Against BLB Disease

Disease Control Efficacy

Exemplary potential has been shown by *Pseudomonas* to serve as biocontrol agents in sustainable agriculture. *P. oryziphila* demonstrates effective antagonistic action against *Xoo* and successfully inhibits its dispersal and growth in rice tissue (Yang et al., 2021). Research revealed that specific strains of *Pseudomonas*, such as *Pseudomonas sp. Rh323* demonstrates significant antagonistic effects against *Xoo*. In-vitro studies showed that this strain could efficiently inhibit the pathogen's growth, resulting in better plant health and higher yields in rice crops (Rangarajan et al., 2003; Yasmin et al., 2016). Certain strains of *Pseudomonas* have been shown in studies to considerably shorten the length of lesions on rice plants. Based on the findings of Rangarajan et al., (2003) treatment with *Pseudomonas* isolates, the lesion length decreased by 15-74% in normal soil and 82% in saline soil. *P. fluorescens* P-7 reduced lesion length in treated plants from 20.37 cm in the control treatment to 18.5 cm (Rangarajan et al., 2003). The severity of BLB is another parameter that is lessened considerably by *Pseudomonas* spp. treatment. Numerous studies have shown that *Pseudomonas* strains are successful in both lab and field settings. In field trials, foliar application of *P. aeruginosa BRp3* decreased the severity of BLB from 83% in the infected control to 43%. This efficacy was equivalent to the streptocyclin treatment (39%) (Yasmin et al., 2017). Inoculation with another strain, *Pseudomonas* sp. *Rh323* resulted in 80% disease reduction under field and greenhouse trials. *Pseudomonas* sp. Rh323-treated plants additionally showed increased plant dry weight, shoot and root length, and increased activity of defence-related enzymes (e.g., catalase, phenylalanine ammonia-lyase, and peroxidase), which are linked to induced systemic resistance (Yasmin et al., 2016).

Pseudomonas have demonstrated encouraging outcomes in boosting yield. *Pseudomonas* have been shown in numerous trials to be effective in lowering the severity of BLB and increasing grain yield (Gokil, 2013; Jeyalakshmi et al., 2010). *Pseudomonas* has been used in practical applications to significantly increase grain and straw yields. One study concluded that the use of *Pseudomonas* consortia in the field trials increased grain yield significantly by 31% and straw output by 10% compared to plots that were not infected (Yasmin et al., 2016). *Pseudomonas aeruginosa BRp3* inoculation increased

grain yield by 51% and straw yield by 55% in certain trials compared to non-inoculated controls (Yasmin et al., 2017). Even under pathogen pressure, *Pseudomonas* sp. application in BLB-infected rice fields has been shown to increase grain yield by up to 31% and straw yield by 10% compared to non-inoculated controls (Yasmin et al., 2016). Yasmin et al. (2016) also found that yield improvements were achieved using 20% less chemical fertiliser, indicating the effectiveness and sustainability of the approach.

Mode of Actions of Pseudomonas spp.

Rice bacterial leaf blight can be effectively controlled by *Pseudomonas* species by suppressing the pathogen and promoting plant health through a variety of ways (Figure 2 and Table 4):

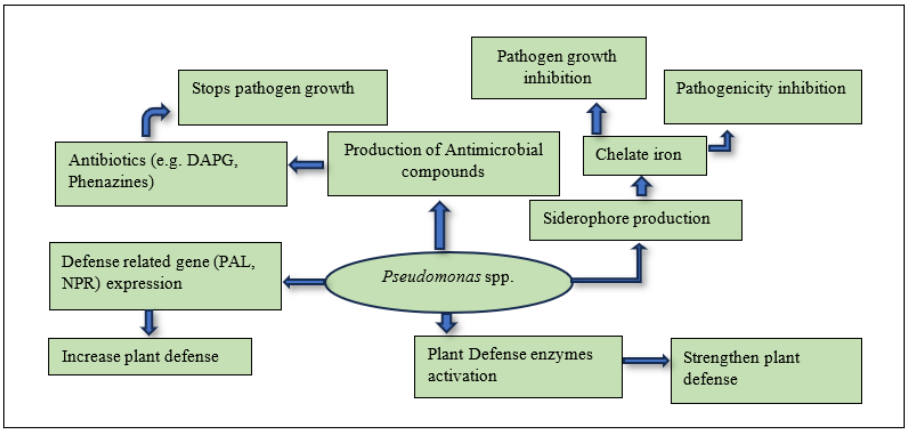

Figure 2. Illustration of the mechanisms of action of *Pseudomonas* for controlling bacterial leaf blight of rice
Note. DAPG = 2,4-Diacetylphloroglucinol; PAL = Phenylalanine Ammonia-Lyase; NPR = Nonexpressor of Pathogenesis-Related Genes 1

Antibiotics including 2,4-diacetylphloroglucinol (DAPG), phenazines, pyocyanin and pyochellin are produced by specific strains of *Pseudomonas* (Figure 2). These substances actually stop the BLB pathogen from growing (Velusamy et al., 2006; Yasmin et al., 2016, 2017). *Pseudomonas* spp. secretes siderophores that chelate iron. These inhibit the pathogen's growth and pathogenicity by depriving it of vital iron (Yasmin et al., 2016; 2017). Moreover, when rice was inoculated with *Pseudomonas* strains, defence-related enzymes such as catalase, phenylalanine ammonia-lyase, peroxidase, and polyphenol oxidase become more active. This strengthens the plant's defences against infection. Certain strains increase rice's systemic resistance by inducing the expression of defence-related genes (PAL, NPR1, etc.) (Elsharkawy et al., 2022; Yasmin et al., 2016).

Table 4
Application of different effective strains/isolates of Pseudomonas *against Bacterial Leaf Blight of rice*

Strains/Isolates	Mechanisms of Action	Efficacy of Disease Control	Evidence Level	Application Conditions/ Method	References
Pseudomonas spp. Rh323 (as part of a 4-strain consortium: E227, E233, Rh269, Rh323)	Siderophore production, phosphate solubilization; induction of plant defence enzymes (confirmed for Rh323 individually: +86% peroxidase, +53% catalase, plus PAL/PPO activity)	Co-inoculation of the consortium reduced diseased leaf area by ~80%, improved shoot length by 31%, root length by 41%, and plant dry weight by 60% versus the infected control; rhizosphere colonisation persisted up to 21 days	Laboratory (in vitro screening) + Greenhouse (net-house pot trial) + Field (consortium yield trial)	Seed inoculation and co-inoculation were investigated in growth-room, greenhouse (net house), and field consortium applications.	Yasmin et al., 2016
P. aeruginosa BRp3	Multiple secondary metabolites (siderophores, 1-hydroxy-phenazine, pyocyanin, pyochelin, rhamnolipids, HAQs); induction of plant defence enzymes	Consistent pathogen reduction in rice; grain yield +51%, straw yield +55% vs. non-inoculated control	Greenhouse (net-house pots) + Field	Used as an inoculant in net-house pot trials and field experiments (28 m^2 plots); CLSM verified rhizosphere colonisation under both sterilised and field conditions	Yasmin et al., 2017
Pseudomonas spp. E227, E233	Plant growth-promoting characteristics and siderophore production (in vitro)	In-vitro inhibition zones vs. *Xoo* (1-19 mm across strains); antagonists that enhanced plant health under stress	Laboratory (in vitro screening) + Field (as part of the same consortium trial as Rh323)	Extracted from rhizosphere, assessed in vitro, and used in seed/ co-inoculation consortia in field and greenhouse experiments	Yasmin et al., 2016
P. fluorescens BCA3; *Geobacillus thermoparaffinivorans* BCA12 (endophytic isolates)	Fluorescent pseudomonad/ endophytic bacterial antagonism (in vitro)	Strong in-vitro inhibitory zone vs. *Xoo*, ~35 mm (nutrient agar assay)	Laboratory (in vitro screening only)	Endophytic bacteria isolated from paddy roots/leaves; screened via nutrient-agar plate antagonism assay; molecular ID by 16S rRNA	Halim et al., 2020

Table 4 (*continued*)

Strains/Isolates	Mechanisms of Action	Efficacy of Disease Control	Evidence Level	Application Conditions/ Method	References
P. aeruginosa MML2212	Production of phenazine-1-carboxamide antibiotic	In-vitro antimicrobial activity vs. *Xoo*, comparable to/slightly exceeding the antibiotic rifamycin	Laboratory only (purified-compound assay)	Purified compound tested via laboratory antibacterial assays; no field disease percentage reported	Shanmugaiah et al., 2010
P. oryziphila strain 1257	LgrD-dependent nonribosomal peptides and other antimicrobial metabolites; motility/ colonization traits	Strong antagonism against *Xoo* pathovars; suppressed pathogen migration/ proliferation in rice tissue; field trial confirmed efficient biocontrol of bacterial leaf streak (BLS)	Laboratory (mutagenesis/ in vitro) + Greenhouse + Field; note: primarily tested against X. *oryzae* pv. *oryzicola* (leaf streak), not pv. *oryzae* (blight) specifically	Biosynthetic determinants identified via genome sequencing and mutagenesis; tested in vitro, in planta, greenhouse, and field trials	Yang et al., 2021

Note. Xoo = *Xanthomonas oryzae* pv. *oryzae*; CLSM = Confocal Laser Scanning Microscopy; HAQs = 4-Hydroxy-2-Alkylquinolines; BCA = Biological control agent; BLB = Bacterial leaf blight

**P. aeruginosa* is a recognised opportunistic human pathogen associated with hospital-acquired infections and is listed as a priority antimicrobial-resistance-threat organism. It is also naturally prevalent in agricultural soils, where surveyed strains frequently carry virulence and antibiotic-resistance determinants (Licea-Herrera et al., 2024). Accordingly, the efficacy data reported for BRp3 above should be read alongside this biosafety context: agricultural deployment of *P. aeruginosa*-based inoculants warrants strain-level risk screening and is subject to greater regulatory scrutiny than non-pathogenic *Pseudomonas* species (e.g., *P. fluorescens*) discussed elsewhere in this review

Biocontrol Potential of *Bacillus* spp. Against BLB Disease

Disease Control Efficacy

In sustainable agriculture, the application of *Bacillus*-based biocontrol agents provides a cost-effective and environmentally safe substitute for chemical pesticides (Shafi et al., 2017). *Bacillus* strains have been successful in suppressing *Xoo* and enhancing rice plant growth in a variety of experiments. *Bacillus* showed 50-58% inhibition against *Xoo* under greenhouse experiments and produced substantially increased plant biomass (El-Shakh et al., 2015). According to Putra and Giyanto (2014), seed treatment with *Bacillus* and *Actinomycetes* boosted seedling emergence and reduced the *Xoo* population up to 89%. Certain strains of *Bacillus* were found to secrete peptolytic enzymes that inhibited 70.9% of the growth of *Xoo* (Sousheel et al., 2021). Another study identified a strain of *B. subtilis* D13 that released volatile chemicals that markedly reduced *Xoo* colony diameter and motility (Xie et al., 2018). Additionally, *B. amyloliquefaciens* has shown antibacterial activity to *Xoo*, with the reported inhibition values of approximately 61% (Elshakh et al., 2016). Antibody potentials for *B. amyloliquefaciens* strain C2-1 against *Xoo* also showed good activity with zones of inhibition of approximately 7.4-8.9 mm over 7 days; with 14 days' action inhibition, it reduced infection by almost 60% in greenhouse testing (Meehae et al., 2023). Banluehan and Tunchai (2025) demonstrated that a number of *Bacillus* strains had high antibacterial activity, generating zones of inhibition of *Xoo* with diameters up to about 30 mm, in a dual-culture test. Reduction in disease symptoms or pathogen growth depends on strain and circumstance, with some strains showing in-vitro inhibition zones up to 30 mm and more than 60% of disease suppression in planta (Ooi et al., 2022). However, *Bacillus* strains decreased lesions between 54.7-85.3% under controlled conditions.

Disease severity has also been reduced by *Bacillus* species. It has demonstrated a significant decrease in disease severity in field trials (40-52%). For example, *Bacillus* KFP-5, KFP-7, and KFP-17 strains have been successful in decreasing BLB severity levels and stimulating rice growth (Rais et al., 2018). Endophytic *Bacillus* strains have shown the ability to reduce the severity of BLB disease (Ooi et al., 2022). The use of *B. subtilis* var. *amyloliquefaciens* (FZB 24) through different methods reduced BLB severity by 40% under glasshouse tests (Nagendran et al., 2013).

Besides these, there are promising results from Bacillus species in reducing BLB and enhancing crop productivity. Study reveals that *B. subtilis* bioformulations lower BLB incidence by 21% and possibly raise yield by as much as 50% (Wartono et al., 2015). Fresh weight and dry weight of the plant increased significantly due to the application of *B. subtilis* and *B. amyloliquefaciens*; fresh weight increased from 50.03% to 73.11%, and

dry weight increased from 64.11% to 86.65% (Ku Asmah & Sapak, 2020). Higher plant height, more tillers, longer roots, and higher chlorophyll content were all observed in treated rice plants (Ku Asmah & Sapak, 2020). Although certain yield increases were not always statistically significant, field application of antagonistic bacteria, such as *Bacillus* sp., increased grain production by up to 31% and straw yield by 10% above non-inoculated plots (Yasmin et al., 2016).

Mode of Actions of Bacillus spp.

BLB of rice is predominantly controlled by *Bacillus* species through a variety of mechanisms, such as host plant defense responses being triggered, competition for resources and habitats, generation of antimicrobial chemicals, and antagonism against *Xoo* (Figure 3).

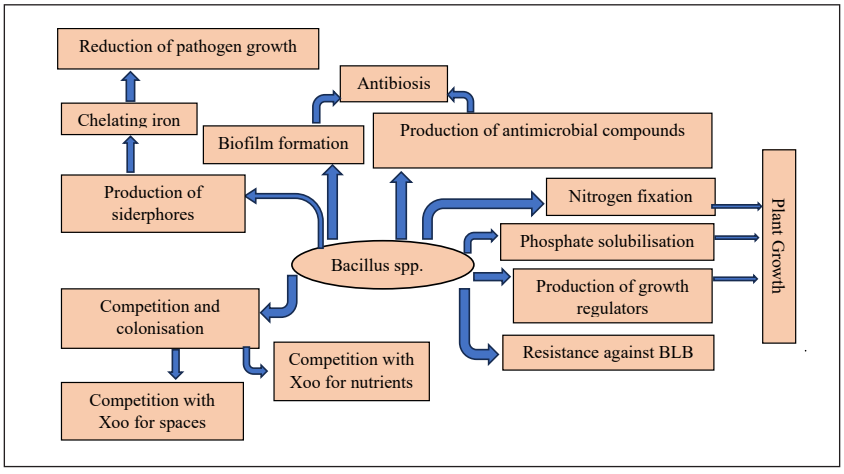

Figure 3. Illustration of mechanisms of action of *Bacillus* spp. for controlling bacterial leaf blight disease of rice

Key antimicrobial compounds produced by *Bacillus* spp., including toxins, siderophores, proteases, and antibiotics, contribute to preventing *Xoo* from growing and causing disease. For instance, the antimicrobial peptides bacitracin A and polymyxin B, which inhibit BLB pathogens, are produced by *B. subtilis* UiTMB1 (Ku Asmah & Sapak, 2020) (Table 5). It has been discovered that *Brevibacillus laterosporus* SN19-1 suppresses *Xoo* biofilm formation and enzymatic activity, leading to elevated reactive oxygen species and pathogen cellular damage (Su et al., 2024). *Bacillus* colonises in rice tissues, which then take up ecological niches and compete with *Xoo* for nutrients and space. As a result, the pathogen's capacity to cause infection is diminished. Research revealed that BLB was suppressed by high population densities of *Bacillus* sp. in rice leaf tissues (Ku Asmah & Sapak, 2020).

Table 5
Application of different effective strains/isolates of Bacillus *against bacterial leaf blight of rice*

Strains/ Isolates	Mechanisms of Action	Efficacy of Disease Control	Evidence Level	Application Conditions/ Method	References
Bacillus amyloliquefaciens A1, A2, A3 (endophytic isolates)	Carries genes for bacillomycin, fengycin, iturin, surfactin; culture filtrates inhibit growth/ biofilm and trigger plant defense/Induced Systemic Resistance	50.29-57.86% inhibition rate against *Xoo* in greenhouse; fresh weight increased 50.03-73.11%, dry weight increased 64.11-86.65%	Laboratory (in vitro antagonism/ fungal tests) Greenhouse trial	Selected endophytic strains applied in greenhouse/pot experiments; culture filtrates and live-cell applications	El-shakh et al., 2015
Bacillus velezensis Bv-303	Cell-free supernatant (CFS) antibiosis; metabolites stable to heat, acid, alkali, and ultraviolet (UV)	In-vitro growth inhibition 85.7-88.0%; in-planta leaf spray of cell-culture broth (CCB) caused 63% disease suppression.	Laboratory (in vitro)	Oxford-cup diffusion assay in vitro; *in vivo* leaf spray of cell-culture broth (CCB), cell-free supernatant (CFS), or cell suspension water (CSW); CCB is most effective	Liu et al., 2023
Bacillus subtilis UiTMB1	Antagonistic metabolites and plant growth promotion; induced systemic resistance	Glasshouse disease severity index 3.43 (treated) vs. 8.40 (untreated)	Laboratory (detached-leaf assay) Greenhouse trial	Laboratory bacterial assays and detached-leaf technique; glasshouse seed/foliar treatments prior to pathogen inoculation	Ku Asmah and Sapak, 2020
Bacillus BTH-22	Antibiosis (bacteriostatic)	Inhibition of *Xoo* growth: 3.9 cm on Nutrient Agar	Laboratory (in vitro only)	In-vitro nutrient agar antagonism assays (CRD, 6 replications)	Sayekti et al., 2025
Bacillus BTH-31a	Antibiosis (bacteriostatic)	Inhibition of *Xoo* growth: 9.3 cm on Nutrient Agar	Laboratory (in vitro)	In-vitro nutrient agar antagonism assays (CRD, 6 replications)	Sayekti et al., 2025
Bacillus Rh219 (rhizosphere isolate)	"Multiple plant growth-promoting and biocontrol traits assessed jointly, including siderophore production, phosphate solubilisation, IAA production, and antagonistic activity".	In-vitro inhibition zones 1-19 mm; the co-inoculation consortium reduced diseased leaf area by 80% vs. the infected control	Laboratory (in vitro screening), Field (consortium application tested in field trial),	Rhizosphere isolation, seed inoculation and co-inoculation in greenhouse/field trials; dual-culture and in-planta co-inoculation	Yasmin et al., 2016

By reducing the pathogen's access to iron, the iron-chelating substances like *Bacillus* inhibit pathogen growth. The formation of siderophores by a number of *Bacillus* strains contributes to their hostile actions. (Banluehan & Tunchai, 2025; Ooi et al., 2022). Nitrogen fixation, phosphate solubilisation, and the synthesis of growth regulators like indole-3-acetic acid (IAA) are among the characteristics of many *Bacillus* strains that promote plant growth and increase plant resilience against BLB (Ooi et al., 2022; Su et al., 2024).

Bacillus species induce plant innate immunity of rice plants, particularly induced systemic resistance (ISR) through jasmonic acid and ethylene signaling pathways, making them more resistant to BLB infection. To illustrate these processes, it has been shown in studies that *Bacillus* treatments enhance resistance and reduce disease severity before pathogen challenge (Shrestha et al., 2016). The antagonism against *Xoo* is mainly due to non-ribosomally produced metabolites, specifically difficidin and bacilysin. Gene knockout studies in *B. amyloliquefaciens* FZB42 showed that these two compounds are the most active agents suppressing *Xoo*. They damage the cell wall and membrane structure of the pathogen and downregulate genes involved in virulence, cell division and cell-wall synthesis (Wu et al., 2015).

INTEGRATED DISEASE MANAGEMENT PROGRAM

The successful deployment of *Trichoderma* spp., *Pseudomonas* spp. and *Bacillus* spp. for managing BLB of rice depends on strategic integration into the existing crop management system. Rather than relying on a single application method, an integrated approach should be adopted to maximise disease suppression and plant health benefits. The following methods should be followed for successful integration:

Seed and Seedling Treatment

Seed treatment is the most effective and widely used method for the integration of BCAs. Soaking seeds in BCA suspensions before sowing, for example, *T. harzianum* at 1×10^7 spores/mL and *P. fluorescens* at 1×10^8 CFU/mL, was recommended by Sai Teja et al. (2026). However, these concentrations should not be considered universal recommendations, as they may vary depending on the strain, formulation, application method, and environmental conditions. Research on basmati rice demonstrated that seed treatment with a microbial consortium (*T. harzianum* + *T. asperellum* + *P. fluorescens*) achieved maximum inhibition of BLB incidence (48.56%), disease intensity (52.42%), and lesion length (45.41%) compared to untreated controls (Sai Teja et al., 2026).

Another method is soaking 30-day-old seedlings for 20 minutes in BCA suspensions before transplanting (Sai Teja et al., 2026). The recommended concentrations are *Trichoderma* spp. at 1×10^7 spores/mL; *Pseudomonas* at 1×10^8 CFU/mL; *Bacillus* spp. at

comparable densities (Sai Teja et al., 2026). In case of foliar application, it is recommended to spray BCA suspensions at 0.1% concentration (1×10^7-10^8 CFU/mL or spores/mL) using knapsack sprayers (Sai Teja et al., 2026). In one field trial, foliar application of a BCA consortium formulation showed disease control efficacy comparable to the chemical standard (streptocycline + copper oxychloride) (Sai Teja et al., 2026). This result is based on a single study and should therefore be considered preliminary evidence rather than a generalised conclusion. Broader validation across field sites, seasons, and rice-growing regions is needed before foliar application of BCA consortia can be considered a reliable and comparable alternative to chemical control.

BCA Consortium Formulations

Single-strain inoculants often show inconsistent performance due to environmental variability, largely because an introduced strain must establish itself within a competitive, heterogeneous soil and phyllosphere microbiome, and can be readily outcompeted, suppressed, or inactivated by abiotic stress once alone (Negi et al., 2024). Consortium approaches address this limitation not simply by "adding more agents," but through specific ecological mechanisms that single strains cannot achieve on their own:

- **Niche Complementarity and Functional Redundancy:** Different BCA species or genera occupy different ecological niches (root surface versus internal tissue versus phyllosphere) and are dependent on different resources, and therefore group members can share more of the plant-associated habitat jointly and not compete with each other (Maciag et al., 2023). Functional redundancy (that is, multiple members of the consortium are capable of performing a particular biocontrol task such as antibiosis or ISR induction) provides some buffer; if one strain does not perform well in a given environment and another sub-group can take care of it, the overall anti-pathogen effect is maintained in a variety of field conditions (Maciag et al., 2023; Negi et al., 2024).
- **Metabolic Cooperation:** Consortium members can perform cross-feeding and complementary metabolic activity, where the metabolic byproducts or niche-modifying activity of one strain creates more favorable conditions for another, leading to increased defense-related outputs than either organism can produce independently. This is consistent with studies showing that miniature microbial consortia enhance plant defense signaling cascades and activate genes that encode multiple metabolic pathways (the phenylpropanoid pathway, phenylalanine ammonia-lyase pathway, total phenolics, proline accumulation, and pathogenesis-related proteins) more effectively than single-strain inoculation (Negi et al., 2024).
- **Improved Rhizosphere and Phyllosphere Colonisation:** Because consortium members can help establish each other (e.g., one strain will change local pH, exudate content, or microbiota competition before a second strain arrives) multi-strain products

generally result in much more consistent and extensive root or leaf colonisation than single strains and thus should be the basis for long-term biocontrol activities as opposed to one-off antagonistic events (Maciag et al., 2023).

- **Enhanced Resilience to Environmental Fluctuation:** Consortium members frequently differ in their optimal temperature, moisture, and pH ranges, a multi-strain formulation is more likely to retain at least partial activity across the range of conditions encountered in the field than a single strain optimised for one narrow set of conditions. This approach directly addresses the environmental-variability problem that motivates consortium use in the first place (Negi et al., 2024). Furthermore, combined mechanisms rather than single efficacy effects could explain why consortium approaches are reported to provide synergistic growth promotion effects more than single-strain treatments (Hasan Naqvi et al., 2025; Sai Teja et al., 2026).

LIMITATIONS AND PRACTICAL CHALLENGES OF BIOLOGICAL CONTROL

Although *Trichoderma, Pseudomonas* and *Bacillus* spp. have shown great potential in BLB management as discussed in detail in this review, their application as biological control agents is always limited. Their application limitations and challenges on ecological, technical and regulatory in nature, are discussed below:

Inconsistent Field Performance

One of the most fundamental limitations of biological control agents (BCAs) is the substantial disparity between their performance under laboratory or greenhouse conditions and their effectiveness in the field. Although in-vitro studies frequently demonstrate strong antagonistic activity, for example, *P. fluorescens* has been reported to inhibit *Xoo* by 59.84%, while microbial consortia achieved 68.56% inhibition under laboratory conditions (Sharma & Bora, 2022). Such efficacy does not always translate into consistent disease suppression under field conditions. For instance, *P. fluorescens* strain PDY7 reduced BLB severity by 58.83% in greenhouse experiments but achieved only 51.88% suppression under field conditions (Velusamy et al., 2013). This difference highlights the complexity of field environments, where BCA's performance is influenced by numerous interacting biotic and abiotic factors, including temperature, humidity, rainfall, soil properties, microbial competition, host physiology, and pathogen population dynamics. Inconsistent field performance has been consistently identified as a major challenge in the application of beneficial microorganisms, including *Trichoderma*, *Bacillus*, and *Pseudomonas* spp. (Gusly et al., 2026; Qadeer et al., 2025; Raju & Punamalai, 2025). The challenge is further complicated by the unpredictable nature of interactions among different BCA strains. For example, combinations of *T. harzianum* and *P. fluorescens* have been reported to exhibit both

antagonistic and synergistic interactions against BLB, indicating that combining multiple BCAs does not necessarily result in improved disease control (Jambhulkar et al., 2018). Therefore, the effectiveness of BCA-based disease management depends not simply on the presence of highly antagonistic microorganisms, but on their ability to survive, establish, multiply, and maintain effective interactions with the host plant and pathogen under dynamic field conditions (Senapati et al., 2022). Improving field consistency will consequently require greater emphasis on strain selection, compatibility testing, formulation stability, application timing, environmental adaptation, and optimisation of delivery systems.

Formulation Stability and Shelf Life

Biocontrol efficacy depends heavily on formulation type and storage conditions. *Trichoderma*-based commercial formulations, for instance, often have shelf lives of only about 3-4 months under standard storage, with propagule viability declining due to poor carrier selection, moisture exposure, or UV degradation (Otithi et al., 2026). Comparable viability and stability challenges apply to *Bacillus* and *Pseudomonas* formulations, where maintaining cell viability during storage and after field application remains a recognised obstacle for commercialisation (Schisler et al., 2004).

Environmental Dependency

BCA performance is highly dependent on local environmental and edaphic conditions rather than a fixed strain property. *Pseudomonas*-mediated lesion-length reduction, for example, has been reported to range from 15-74% in normal soil but to 82% in saline soil (Rangarajan et al., 2003), suggesting that the same strain can work very differently depending on soil chemistry. More generally, temperature, moisture, pH and soil type have a direct impact on BCA establishment and activity (Iqbal, 2026), meaning that a strain validated in one set of conditions may not perform as well elsewhere without local validation.

Interactions with Indigenous Microbiota

Introduced BCAs are not on their own and can be actively inhibited by the native soil and plant microbial community. Colonisation and persistence are known bottlenecks, with many inoculants failing to keep up with native microbiota, being preyed on by protists, or the timing of the initial application (Iqbal, 2026). These interactions can go beyond competition: in one instance, the local Stenotrophomonas maltophilia bacterium has been found to destroy *Bacillus*-produced lipopeptide antibiotics (iturin, fengycin, surfactin), which can negatively impact the biocontrol activity of the introduced BCA after colonisation (Iqbal, 2026). This shows that colonisation alone is not always sufficient to sustain the presence of the BCA, since the resident microbes can react with the active compounds of the BCA after colonisation has been successful.

Strain Compatibility in Consortium Formulations

As discussed earlier in this review on consortium approaches, compatibility between BCA species is not guaranteed and is usually medium and condition-dependent. *Bacillus velezensis* has been shown to completely inhibit *Trichoderma virens* growth in nutrient-rich synthetic media, and the same two strains are fully compatible under conditions similar to the rhizosphere (Izquierdo-García et al., 2020). Consortium design cannot safely assume that combining multiple effective single-strain BCAs will produce an effective combined formulation without empirical compatibility screening

Regulatory Barriers, Biosafety and Commercialisation

Registration of microbial biopesticides is slower and more uncertain than chemical pesticides because live organisms require more safety data. This is especially true for *Pseudomonas aeruginosa* (e.g., strain BRp3, an opportunistic human pathogen found in agricultural soils, which requires strain-level biosafety testing before being used in the field (Licea-Herrera et al., 2024), and the regulatory scrutiny and field performance remain an issue for *Pseudomonas*-based products (Giovanardi et al., 2025). By contrast, *Trichoderma* is the most established and commercially known species (registered since the late 1980s and now the most widely commercialised fungal BCA in the world (Otithi et al., 2026), and *Bacillus* and *Pseudomonas* are both still lacking in BLB-specific applications. No such product is the most developed for BLB control by a commercial product registered here so far, and the regulatory and biosafety pathways are still underdeveloped in comparison to the research base.

Sources of Variation in Disease Control Efficacy

The wide range of disease reduction percentages reported in studies in this review (e.g. *Bacillus* lesion reduction covering 54.7-85.3%, *Pseudomonas* lesion reduction covering 15-82%) is not noise, and these are specific sources of variation which the manuscript should talk about, rather than presenting the numbers as a simple list:

1. **Pathogen Strain/Race Variability-** *Xoo* itself is genetically diverse across regions, and isolates differ in virulence and in resistance genes they can overcome, meaning a BCA's apparent success is partly a function of the *Xoo* population it was tested against, not the BCA itself (Adedibu et al., 2024)
2. **Rice Species/Varieties/Genotypes-** Host genetic background affects both baseline susceptibility and how strongly ISR-related defense pathways respond to microbial priming; consortium efficacy has been shown to differ between rice varieties tested under otherwise identical conditions (e.g., different outcomes between the Inpari 33 and Ciherang varieties reported by Teja et al., 2025).

3. **Environmental and Edaphic Conditions-** Soil salinity, pH, and moisture significantly change BCA performance, as evidenced by *Pseudomonas* lesion length loss from 15-74% in normal soil to 82% in saline soil (Rangarajan et al., 2003). The organism is more robust and performs better under one specific stress condition, rather than uniformly across all soils.
4. **Application Method and Timing-** Seed priming, seedling dip, soil application, and foliar spray are not interchangeable, and the same *Trichoderma* isolate may show a significantly different lesion-length reduction depending on the delivery method e.g., 75% via seed priming versus other values from other methods (Islam et al., 2023) and the effects are generally stronger when applied prior to infection rather than after infection is established.
5. **Dose and Formulation-** As mentioned in the field-efficacy discussion, higher application rates (e.g., T. *harzianum* at 4-8 g/L) dominate over lower rates (Khan & Sinha, 2007), and formulation quality influences the number of viable propagules actually delivered to the target tissue.
6. **Strain-Level Metabolic Variability-** Even within a species, individual strains vary in which antimicrobial compounds, siderophores, or enzymes they produce and in what quantity, which is why single-species efficacy ranges are often as wide as or wider than the ranges between genera (Ngalimat et al., 2021).

FUTURE PROSPECTIVES

The future of BLB disease management is moving beyond single-strain applications and to more sophisticated integrated approaches that incorporate the advances in nanotechnology, plant pathology, breeding, biotechnology, microbial ecology and precision agriculture. *Trichoderma* spp*., Bacillus* spp*.,* and *Pseudomonas* spp. have demonstrated measurable efficacy for BLB disease control under field conditions, but previous research indicates the need for new directions and technology to further progress in field application that would revolutionise their use in the future (Hasan Naqvi et al., 2025; Teja et al., 2025). A big way forward is from single-strain inoculants to synthetic microbial consortia (consortia of microbial communities of mutually active biocontrol agents). This approach remains largely experimental, but has shown early promise in addressing some of the field-performance limitations associated with existing single-strain BCAs (Kayla et al., 2026).

Currently, researchers are working to create "core microbiota" (the minimum set of microbes essential for plant health) and engineer them into stable synthetic communities for commercial use (Hasan Naqvi et al., 2025) . This is a transition from biological control to microbiome-based crop protection. The viability and shelf-life of BCAs in field conditions are still key issues. Two innovative approaches are being developed to address this: i) nanoencapsulation of microbial probiotics is a way to enhance resilience

to environmental conditions and preserve long-term viability (Hasan Naqvi et al., 2025). This prevents BCAs from desiccation and UV radiation, and competitive displacement by native soil microbes. However, several challenges continue to limit the practical application of nanoencapsulated BCAs, including high production costs, difficulties in scale-up, variable release kinetics, complex regulatory approval pathways, and uncertainties regarding the environmental persistence, biosafety, and potential non-target effects of nanomaterials. These limitations suggest that nanoencapsulated BCAs should still be regarded as an emerging technology rather than a field-ready approach for large-scale agricultural application (Narmatha et al., 2026). ii) genetic engineering approaches, these strategies are being explored at two levels: individual-strain engineering and whole-microbiome engineering, with the former currently being more established. At the individual-strain level, genetic modification of selected *Trichoderma*, *Bacillus* and *Pseudomonas* strains aims to enhance the production of antimicrobial compounds, improve root colonisation, and increase tolerance to environmental stresses (Ke et al., 2021). In contrast, engineering entire core microbial communities rather than individual strains remains largely experimental and conceptual, with substantial technical and ecological challenges yet to be resolved (Ke et al., 2021).

Recent studies have demonstrated the potential of engineered microorganisms for disease management. For example, the transgenic rice line UvScd1 was reported to upregulate defense-related genes and induce lesion-mimic phenotypes without compromising yield. In field experiments, *B. subtilis* engineered to produce the fungal effector UvScd1 also demonstrated control efficacy against several major rice diseases, including BLB, following foliar application (Wang et al., 2026). Nevertheless, these findings should not be interpreted as evidence that UvScd1-producing *B. subtilis* is immediately suitable for large-scale field deployment. The application of genetically modified biocontrol agents (GM-BCAs) in agriculture remains subject to significant ecological, biosafety, and regulatory concerns. The environmental release of self-replicating GM-BCAs could potentially facilitate horizontal gene transfer to indigenous microorganisms and alter the composition and functioning of soil and phyllosphere microbial communities, with potentially unpredictable long-term consequences beyond controlled experimental conditions (Lerner et al., 2026). Moreover, containing engineered, self-replicating organisms is inherently more challenging than controlling non-living chemical inputs. Although various biocontainment strategies are being investigated, including approaches designed to restrict the survival or persistence of engineered microorganisms outside their intended application sites, these technologies remain under development and have yet to be established as universally reliable and field-proven solutions (Lerner et al., 2026). Therefore, further research is required to establish the efficacy, environmental safety, genetic stability, containment, and regulatory feasibility of GM-BCAs before their widespread agricultural application can be considered.

Moreover, 16S rRNA amplicon sequencing and metagenomic analysis are being used to identify microbial communities associated with healthy rice plants and disease-suppressive soils (Hasan Naqvi et al., 2025). This reveals which native strains are most effective in specific agroecological contexts. Healthy rice rhizospheres are richer in microbial diversity and enriched in antibiotic production, siderophore biosynthesis and nutrient cycling genes (Hasan Naqvi et al., 2025). The number of microbial species present does not necessarily determine the effectiveness of disease suppression. Rather, the functional traits and activities of the microbial community may be more important. A study comparing disease-suppressive and disease-conducive soils demonstrated that suppressive soils did not necessarily contain the same bacterial species; instead, they shared similar functional genes, particularly those associated with siderophore production and other pathogen-suppressive activities. This finding suggests that disease suppression depends less on microbial diversity per se and more on the presence of microorganisms with specific beneficial functions. Thus, a rice field containing microorganisms capable of producing antibiotics, chelating iron, and cycling essential nutrients may provide greater protection against pathogens, not simply because it harbours a greater number of microbial species, but because the microbial community possesses the appropriate functional capabilities (Tracanna et al., 2021). Furthermore, native BCAs have been reported to exhibit greater effectiveness than non-native strains in terms of environmental adaptation, host colonisation, and competition for nutrients and ecological niches (Hasan Naqvi et al., 2025). This advantage may be attributed to their better adaptation to local environmental conditions and their ability to compete effectively for available resources. However, contrasting evidence indicates that introduced or non-native strains can perform equally well, or even better, when formulation and application strategies are properly optimised. For example, field trials in maize demonstrated that several *Bacillus* strains originating from outside the target location provided strong and consistent disease suppression. Their success appeared to depend more on formulation quality, application method, compatibility with the host plant, and adaptation to the prevailing environmental conditions than on their geographical origin (Arteaga-Ojeda et al., 2026). Similarly, research on *Trichoderma* has shown that the performance of the same strain can vary substantially depending on formulation type, with fresh formulations outperforming dry formulations in some cases. These findings highlight that formulation quality and delivery technology may be more critical determinants of BCA efficacy than whether a strain is native or non-native (Riaz et al., 2026). Combining genomics, transcriptomics, proteomics, and metabolomics will allow for the selection of strains with proven functional traits and decrease the trial-and-error approach in BCA development (Kayla et al., 2026).

Genetic resistance and biocontrol combination is a major future direction. CRISPR/Cas9 technology has already been used to develop BLB-resistant rice by editing susceptibility genes at all levels. At the individual level, editing the promoter regions of SWEET14 and

Xa13 (a SWEET11 allele) has been shown to confer resistance by preventing pathogen effectors from activating these genes (Yu et al., 2021). More broadly, Oliva et al. (2019) edited the promoters of all three clade-III susceptibility genes SWEET11, SWEET13, and SWEET14 simultaneously based on TALE-binding site analysis of 63 *Xoo* strains, and produced broad-spectrum resistant rice lines (Kitaake, IR64, and Ciherang-Sub1) without the yield degradation associated with resistance breeding. A similar multiplexed-editing approach was shown to successfully develop resistant rice lines against 133 Xoo strains (Xu et al., 2019). In the context of the SWEET gene family, recessive resistance gene Xa5 is a different animal (i.e., it is involved with a basal transcription factor subunit OsTFIIAγ5) that Xoo's TALEs need to activate susceptibility genes, not the single susceptibility gene in question. TALEN-based editing of the corresponding dominant TFIIAγ5 allele significantly reduced Xoo susceptibility in many mutant lines, making this gene a better target for gene editing than single-SWEET gene editing (Han et al., 2020). More advanced breeding is in process to produce transgene-free and edited rice lines through multiplexed selection, making it easier to get regulatory approval and public acceptance (Yu et al., 2021). Genetically resistant varieties can serve as the foundation for integrated disease management (IDM). BCAs can be used as complementary protection against pathogens that are able to overcome certain resistant genes. This integrated approach reduces selection pressure for resistance to either strategy alone.

CONCLUSION

BLB is a major global threat to rice production, as severe yield losses can undermine food security, particularly in major rice-producing countries and regions. The emergence of pathogen strains resistant to chemical pesticides, the adverse environmental impacts associated with excessive pesticide use, and the genetic limitations encountered in developing durable disease-resistant rice varieties have highlighted the urgent need for sustainable and effective alternatives. Based on empirical evidence, biological control can increase rice yield by up to 50%, reduce disease severity by more than 80%, shorten lesion length up to 87.5%, and suppress the growth of *Xoo* up to 80%. The efficacy of these BCAs can be further enhanced when they are applied in combination, resulting in synergistic effects and greater disease suppression compared with their individual application. The integration of *Trichoderma*, *Pseudomonas* and *Bacillus* spp. into integrated disease management programmes represents an environmentally friendly, sustainable, and promising approach for BLB management. Their adaptability, multifunctionality, and diverse modes of action can contribute to overall crop health and productivity while reducing reliance on chemical pesticides. To facilitate their wider adoption by farmers and integration into national rice disease management programmes, further research is needed to optimise formulation technologies, delivery systems and field-scale application strategies.

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CONSENT FOR PUBLICATION

The article contains no such material that may be unlawful, defamatory, or that would, if published, in any way whatsoever, violate the terms and conditions as laid down in the agreement.

CONFLICT OF INTERESTS

The authors declare that there are no conflicts of interest related to this article.

AVAILABILITY OF DATA AND MATERIALS

Not applicable.

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