

***Burkholderia glumae* in rice: Climate-driven epidemiology, advanced detection techniques and AI-enhanced predictive forecasting models**

HAMOOD U REHMAN^{1,2}, NORIDA MAZLAN^{1,3*}, SITI IZERA ISMAIL^{2,3},
NUR AZURA HUSIN⁴

¹Department of Agriculture Technology, Faculty of Agriculture, Universiti Putra Malaysia, Selangor, Malaysia

²Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, Selangor, Malaysia

³Laboratory of Climate-Smart Food Crop Production,

Institute of Tropical Agriculture and Food Security, Universiti Putra Malaysia, Selangor, Malaysia

⁴Department of Computer Science, Faculty of Computer Science and Information Technology, Universiti Putra Malaysia, Selangor, Malaysia

*Corresponding author: noridamz@upm.edu.my

Citation: Rehman H., Mazlan N., Ismail S.I., Husin N.A. (2026): *Burkholderia glumae* in rice: Climate-driven epidemiology, advanced detection techniques, and AI-enhanced predictive forecasting models. Plant Protect. Sci., 62: 318–339.

Abstract: Bacterial panicle blight (BPB), caused by *Burkholderia glumae*, is a major and rising threat to global rice production. Its severity is heightened by climate change, with outbreaks driven by high temperatures and humidity during the vulnerable flowering stage. Current management is hampered by delayed detection and a disconnect between diagnostic tools and predictive models. This review synthesises advances across climatology, molecular biology, and computational agriculture to address this gap. We analyse climate-driven disease dynamics, precise molecular diagnostics, and the emergence of AI for real-time image-based detection and weather-based forecasting. The novel contribution of this work is the proposal of an Integrated Multimodal AI Framework (IMAF) that converges these domains. The IMAF links climate modelling, sensor data, and computer vision to enable proactive, climate-resilient disease forecasting and decision support. This synthesis represents a critical paradigm shift from reactive management to intelligent, predictive intervention. We conclude with a roadmap for developing and deploying such integrated systems to enhance global rice resilience.

Keywords: BPB prediction; artificial intelligence in agriculture; plant pathogen forecasting; sustainable rice production

Rice (*Oryza sativa* L.) is one of the most important staple crops, providing over 50% of the world's caloric intake and serving as the primary food source for billions of people, particularly in Asia, where it constitutes nearly half of daily caloric consumption (Dorairaj-Govender 2023;

Supported by the Malaysia Research University Network, UPM Grant No. 553931, the Project title "Development of bacterial panicle blight prediction model through abiotic factors and determination of resistant rice variety on the disease".

© The authors. This work is licensed under a Creative Commons Attribution-NonCommercial 4.0 International (CC BY-NC 4.0).

Table 1. Bacterial diseases of rice and their pathogens

Plant Part	Diseases	Bacterial Pathogens
Seedling	Seedling blight	<i>Burkholderia plantarii</i>
	Bacteria brown stripe of rice (BBSR)	<i>Pseudomonas syringae</i> pv. <i>panici</i> <i>Acidovorax avenae</i> subsp. <i>avenae</i>
	Bacteria blight (BB) or bacteria leaf blight (BLB)	<i>Pantoea ananatis</i> , <i>Pantoea stewartii</i> subsp. <i>indologenes</i> , <i>Pantoea ananatis</i> , <i>Pantoea agglomerans</i> , <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>
Foliar	Bacteria leaf streak (BLS)	<i>X. oryzae</i> pv. <i>oryzicola</i>
	Halo blight	<i>Pseudomonas syringae</i> pv. <i>oryzae</i>
	Sheath brown rot	<i>Pseudomonas fuscovaginae</i>
Leaf sheath and grain rot	Sheath rot	<i>Pseudomonas syringae</i> pv. <i>syringae</i>
	Bacteria panicle blight (BPB)	<i>Burkholderia glumae</i> or <i>B. gladioli</i>
	Bacteria palea browning	<i>Erwinia herbicola</i> , <i>Pantoea ananatis</i> , <i>Enterobacter cloacae</i>
Culm and root	Bacteria foot rot	<i>Erwinia chrysanthemi</i> , <i>Dickeya zeae</i>

Source: Ngalamat et al. (2023)

Rezvi et al. 2023). Global rice production reached 758.5 mil. t in 2020, with more than 90% of cultivation occurring in tropical and subtropical regions (Wu et al. 2023). However, the sustainability of rice production is increasingly threatened by biotic and abiotic stressors, which collectively reduce yields by 20–40% annually (Sandalio et al. 2022; Bao 2023). Among bacterial diseases (Table 1) Bacterial Panicle Blight (BPB), caused by *Burkholderia glumae*, has emerged as a severe constraint to rice production, with yield losses reaching up to 75% under favourable conditions.

BPB was first reported in Japan in the 1950s and has since spread to major rice-producing regions, including Southeast Asia, Latin America, and the southern United States (Paz-Carrasco et al. 2018). The virulence of *B. glumae* is largely attributed to toxoflavin. This phytotoxin disrupts plant cellular processes, triggering a complex interaction between biotic and abiotic stressors (Sabri et al. 2023), as depicted in Figure 1. The link between abiotic stresses and enhanced susceptibility to *B. glumae* is explicitly demonstrated at the molecular level by Mizobuchi et al. (2023), who identified RBG1res as a key MAPKKK gene that confers resistance by negatively regulating ABA, a hormone central to drought and heat stress signalling. This finding provides direct mechanistic evidence that stress-induced ABA accumulation can compromise immune pathways, thereby increasing BPB susceptibility. Further, integrative studies, such as those by Iqbal et al. (2023), delineate how abiotic stress responses intersect with pathogen virulence regula-

tion, thereby affecting defensive signalling cascades and modulating disease outcomes. These studies advance beyond correlative observations by identifying specific genetic and biochemical nodes linking abiotic stress and disease resistance, supporting the necessity for breeding programs targeting both stress tolerance and BPB resistance concurrently. This toxin significantly enhances disease severity by interfering with plant defence mechanisms and accelerating infection (Kumar et al. 2023a). Environmental factors, particularly high nighttime temperatures (28–35 °C) and relative humidity levels exceeding 90%, further accelerate BPB progression (Ortega et al. 2021). As climate change intensifies, these conditions are becoming more frequent, leading to an increased geographical spread of BPB and complicating disease control measures. Quantitative models project that a 1 °C increase in average growing-season temperature could elevate the probability of BPB outbreaks by 20–40% in major rice-producing regions, with proportional increases in yield loss (Shew et al. 2019).

Traditional methods for BPB detection rely on symptomatic identification, which occurs late in the infection cycle and limits the effectiveness of timely interventions. While molecular diagnostic techniques such as polymerase chain reaction (PCR) and loop-mediated isothermal amplification (LAMP) have improved detection precision by targeting the toxoflavin biosynthesis gene cluster (toxABCDE), these approaches remain time-consuming, labour-intensive, and require specialised equipment, restricting their application

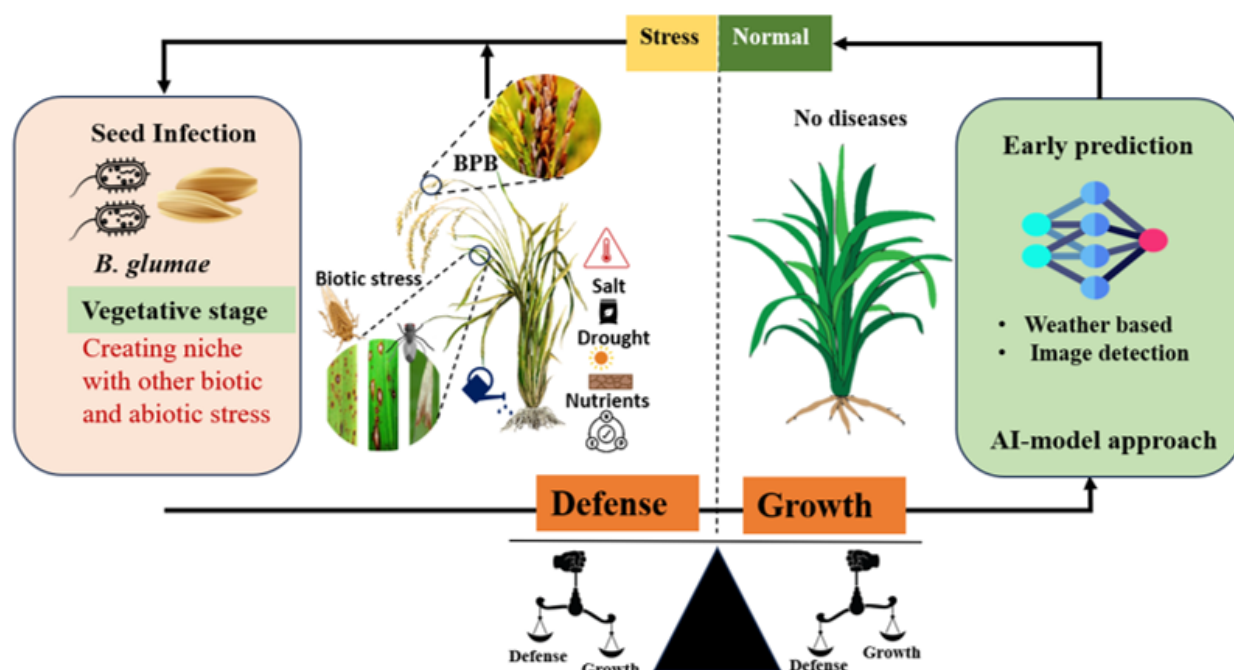


Figure 1. Conceptual model of *Burkholderia glumae* infection dynamics under biotic-abiotic stress interplay and the intervention point for AI-driven management

The diagram illustrates two potential pathways for a rice plant under stress. The pathway (green) represents proactive management: early detection of conducive conditions or pre-symptomatic infection via AI-based tools (weather modelling and image detection) triggers timely defensive interventions (e.g., targeted bactericide application), allowing the plant to maintain resource allocation toward growth and achieve high yield. The pathway (red) represents disease progression without intervention: combined abiotic stresses (e.g., heat, drought) weaken plant defences, increasing susceptibility to *B. glumae* infection. The pathogen, aided by a stress-compromised host, causes Bacterial Panicle Blight (BPB), resulting in significant yield loss. The model highlights AI's role in intercepting the disease cycle before irreversible damage occurs

in resource-limited settings (Simhadri et al. 2024). Recent advancements in artificial intelligence (AI) and predictive analytics have transformed disease detection and management in agriculture. Convolutional neural networks (CNNs) and You Only Look Once (YOLO) models have demonstrated remarkable accuracy in identifying BPB through image-based analysis, enabling real-time monitoring of infected fields (Quoc et al. 2024). These AI-driven frameworks integrate hyperspectral imaging and remote sensing data to detect disease markers before visible symptoms appear, allowing for early intervention (Simhadri et al. 2024). Additionally, as depicted in Figure 1, weather-based predictive models, such as BGRcast, leverage pathogen biology and meteorological data to forecast BPB outbreaks, equipping farmers with timely, data-driven insights for disease mitigation (Balaska et al. 2023).

This comprehensive review moves beyond summarising isolated advances to provide a novel synthesis at the intersection of climate science,

pathogen biology, and computational intelligence. While previous reviews have detailed BPB pathology, epidemiology, and distribution, this work critically evaluates the evolution from statistical models to AI-driven forecasting systems. It uniquely proposes the Integrated Multimodal AI Framework (IMAF) as a cohesive roadmap. The IMAF converges climatic, molecular, and imaging data streams to enable proactive, climate-resilient decision support. While structured as an analytical review article, it has been formatted as a Short Communication to concisely present the state of the art and propose conceptual integrations for future research directions. The integration of AI-driven disease detection, predictive analytics, and molecular diagnostics represents a transformative paradigm for BPB management. By enhancing early detection capabilities and improving forecasting accuracy, these synergistic technologies provide a proactive strategy to safeguard rice production against climate-driven pathogen dynamics. As global tem-

peratures continue to rise, the confluence of AI, remote sensing, and molecular diagnostics will be indispensable for developing climate-resilient disease management strategies (Faizal Azizi et al. 2022).

BPB: PATHOGEN AND EPIDEMIOLOGY

B. glumae, the primary causative agent of BPB, presents a significant global challenge to rice production, impacting both yield and grain quality. Originally identified in Japan in the 1950s (Goto et al. 1956), BPB has spread across various rice-growing regions, including Asia, the Americas, and tropical climates, where it causes severe yield losses, sometimes exceeding 50% in affected fields (Ramachandran et al. 2021). The global distribution of BPB pathogens indicates that *B. glumae* is the predominant threat, with occasional reports of *B. gladioli* in rice production (Figure 2). Outbreaks in Louisiana and Arkansas reported yield losses of 40–50% during the 1990s and 2010, while similar damage occurred in Malaysia (Ramachandran et al. 2021) and tropical Asia under favourable conditions of high humidity and temperature (Echeverri-Rico et al. 2021).

BPB primarily spreads through seed transmission, with bacteria rapidly multiplying during seed soaking and colonising young plants under warm, humid conditions. This environmental de-

pendence, especially at temperatures above 40 °C, underscores the growing threat of BPB under changing climatic conditions (Pérez-Suárez et al. 2022). In addition, the disease progresses through asymptomatic colonisation of the leaf sheath, which serves as a pool for further plant infection, leading to symptoms such as grain rot, panicle discolouration, and reduced grain-filling. Studies have highlighted flowering stages as critical periods of infection due to increased susceptibility to high humidity (Li et al. 2016). Moreover, the genomic flexibility of *B. glumae* within the *Burkholderiaceae* family enables its survival in various environments, including soil, plant debris, and alternate hosts such as peppers, tomatoes, and eggplants (Nandni et al. & Vishunavat 2019). As shown in Figure 2, *B. glumae* has been reported in 23 regions, whereas *B. gladioli* has been recorded in 7 regions, with 5 regions reporting both species, further emphasising the need for targeted disease management strategies. This adaptability, coupled with its seed-borne nature, necessitates further research to develop effective management strategies for BPB under changing global conditions.

SEED-BORNE NATURE OF *B. GLUMAE*

B. glumae is unequivocally established as a seed-borne pathogen, with contaminated rice seeds

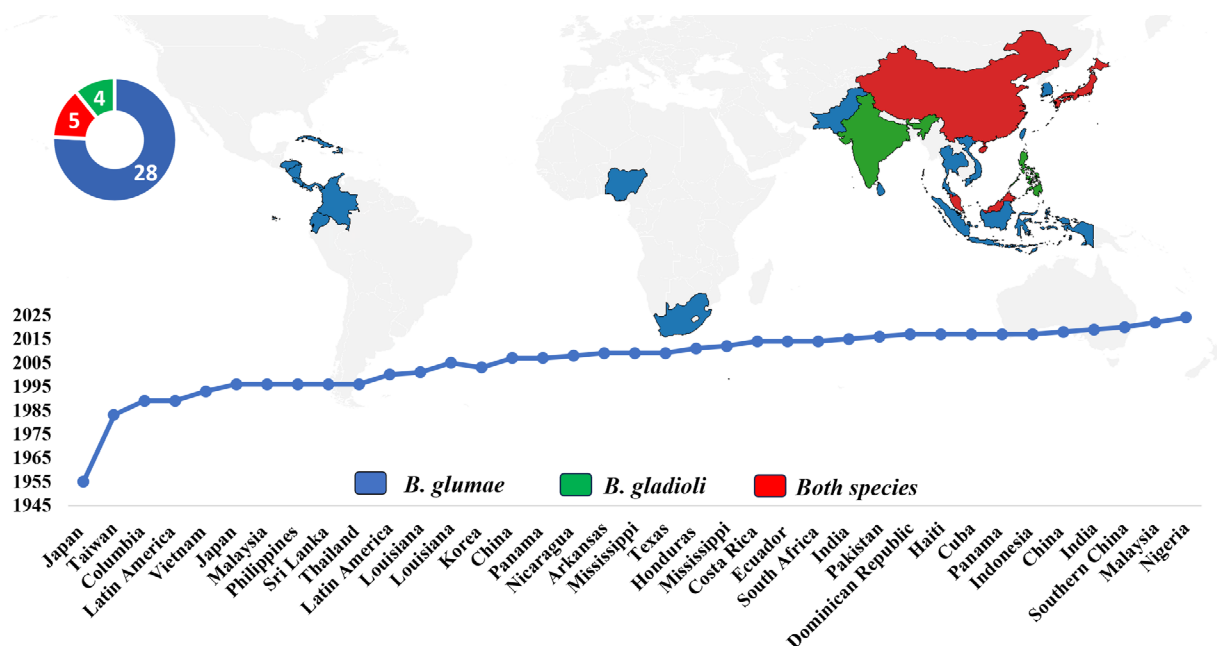


Figure 2. Distribution of Bacterial panicle blight (BPB) pathogens in rice production: predominance of *Burkholderia glumae* as a major threat, with occasional reports of *B. gladioli*

serving as the primary inoculum source for both field-level epidemics and transcontinental dissemination (Chompa et al. 2022). The pathogen exhibits remarkable persistence in seed tissues, demonstrating 91% bacterial recovery immediately post-harvest, with a gradual decline to 28% after 12 months of storage, maintaining viable inoculum for subsequent growing seasons (Gowda et al. 2021). This extended survival capacity, coupled with detection of approximately 2×10^5 CFU per seed, underscores the critical quarantine significance of BPB and explains its rapid proliferation across rice-producing regions from Southeast Asia to the Americas (Gowda et al. 2021; Zhang et al. 2022).

TRANSMISSION DYNAMICS AND INFECTION PATHWAYS

Seed-to-seedling transmission constitutes the fundamental disease cycle, in which infected seeds yield symptomatic seedlings exhibiting rot and growth inhibition within 7–10 days post-germination (Kouzai & Akimoto-Tomiya 2022). Epidemiological studies identify boot leaf initiation and panicle emergence as critical infection windows, with approximately 81% disease incidence under optimal environmental conditions of 28–32 °C and ~95% relative humidity (Gowda et al. 2021). The panicle stage demonstrates vulnerability, as artificial inoculations at 45 days after transplanting consistently produce severe panicle blight symptoms and grain discolouration across susceptible cultivars (Priyadarsini et al. 2023). This transmission pathway is further exacerbated

by warm, humid conditions that characterise major rice-growing regions, facilitating both seed infection and subsequent disease development.

SYMPTOMS OF BPB

According to Azizi et al. (2022), BPB often exhibits symptoms that can be confused with those caused by abiotic stresses such as drought, extreme heat, or chemical toxicity. However, research has identified specific BPB-related symptoms that primarily manifest during the reproductive phase of rice under conditions of high humidity and elevated night temperatures (Mulaw et al. 2018; Ramachandran et al. 2021). Severe BPB outbreaks are characterised by symptoms such as glume discolouration, inflorescence sterility, and grain rot, which can result in significant yield losses (Zarbafti et al. 2019). The disease predominantly affects the flag leaves and the leaves. Notably, *B. glumae* often colonises the leaf sheath asymptotically, complicating early detection (Wamishe et al. 2015). Kernel blighting, marked by kernels turning from white to light grey with dark brown edges, is typically the first visible symptom of an infection (Nandakumar et al. 2009). As infection progresses, the pathogen multiplies within the panicle, leading to floral infections and, ultimately, grain rot (Azzahra et al. 2024). These symptoms are depicted in Figure 3, which illustrates the field symptoms of *B. glumae* in rice from Sungai Besar, Selangor, Malaysia. The figure highlights the characteristic straw-coloured or discoloured spikelets and rotting grains, which are caused by the pathogen entering the lemma and palea (Riera-Ruiz et al. 2018).



Figure 3. Field Symptoms of *Burkholderia glumae* in rice from Sungai Besar, Selangor, Malaysia

In severe outbreaks, additional symptoms include extensive sterility, grain rot and poor grain filling, which can lead to significant yield losses of up to 40% during extreme epidemics (Savary et al. 2012; Sandalio et al. 2022). Disease progression is distinct across different stages of rice growth. For example, during the nursery stage, BPB manifests as seedling blight, characterised by leaf chlorosis and stunted root development (Chompa et al. 2022). As plants mature, panicle blight intensifies during panicle emergence, with infected florets often exhibiting brown or grey discolouration at their bases. This leads to aborted kernels and sterile grains, significantly lowering yields under both controlled and field conditions (Ortega et al. 2021). A unique diagnostic feature of BPB, distinguishing it from abiotic stresses, such as heat stress, is the presence of green rachis within blighted florets (Nandni et al. 2019; Sanya et al. 2022). During early-stage infections, some healthy grains may still be visible. However, as the infection worsens, saprophytic fungi often colonise the spikelet, causing discolouration and grain rot (Ortega et al. 2021). BPB symptoms also extend to leaf sheaths and stems, where reddish-brown linear lesions with necrotic centres may develop, potentially leading to sheath and stem rot (Azzahra et al. 2024). These symptoms, such as those in Japan and parts of Southeast Asia, are common in areas with high humidity and temperature (Song et al. 2024).

Regional studies have further clarified BPB symptomatology. For example, in North India, the disease causes discoloured glumes, spikelet sterility and grain rot during early planting phases, significantly impacting grain filling and overall yield (Mondal 2016). Similarly, in Malaysia, outbreaks during 2017 and 2018 were marked by straw-coloured panicles and poorly filled grains, affecting up to 50% of rice crops (Ramachandran et al. 2021). As shown in Figure 3, these symptoms underscore the devastating effects of BPB in tropical and subtropical climates, where high humidity and moderate temperatures exacerbate the disease's progression (Gowda et al. 2022). The ability of *B. glumae* to colonise plant tissues asymptotically and multiply rapidly under favourable conditions poses significant challenges for detection and management (Wamishe et al. 2015; Mulaw et al. 2018). Early recognition of symptoms like those depicted in Figure 3 is de-

tailed for justifying yield losses and controlling disease spread effectively.

ISOLATION AND IDENTIFICATION OF *B. GLUMAE*

For the detection of *B. glumae*, isolation is a crucial step. Studies follow well-established microbiological protocols for this purpose. Plant samples, particularly from infected panicles or leaf sheaths, are cut into 4–5 cm-long pieces and surface-sterilised by immersion in 3% sodium hypochlorite or 70% ethanol for 1 minute (Alvarez et al. 2023). Following surface sterilisation, the samples are rinsed with sterile distilled water to remove any residual disinfectant (Riera-Ruiz et al. 2018). One gram of the sterilised tissue is mashed in sterile peptone water, and 200 µL of the suspension is plated onto semi-selective King's B agar medium (Singh et al. 2015; Hasibuan et al. 2018). Nandakumar et al. (2009) incubated these plates at 28–37 °C for 2 days. Isolates were selected from representative colony types in each sample and streaked onto King's B broth (KBB) plates to obtain pure cultures of the pathogen. Pure cultures of isolates were stored in KBB with 30% glycerol at –70 °C (Alvarez et al. 2023).

MORPHOLOGICAL DETECTION

A comprehensive review of 12 studies confirms that the morphological characteristics of *B. glumae* are consistently observed using a combination of morphological and biochemical methods. Extensive studies, including those by Ashfaq et al. (2016), Gowda et al. (2022), Darmawan et al. (2023), and Singh et al. (2015), demonstrate the reliability of these techniques. In all these studies, colonies of *B. glumae* were grown on King's B agar, a nutrient-rich medium that enables monitoring of key colony features. This method is one of the most widely used, with colonies incubated for 48 h at 28 °C. During this period, colonies of *B. glumae* appear round and convex, with entire edges, and range in colour from greyish white to yellow. Certain isolates produce a yellow-green water-soluble pigment called toxoflavin, which is recognised as a virulence factor of *B. glumae*. Figure 4 illustrates symptomatic seeds from Ma-

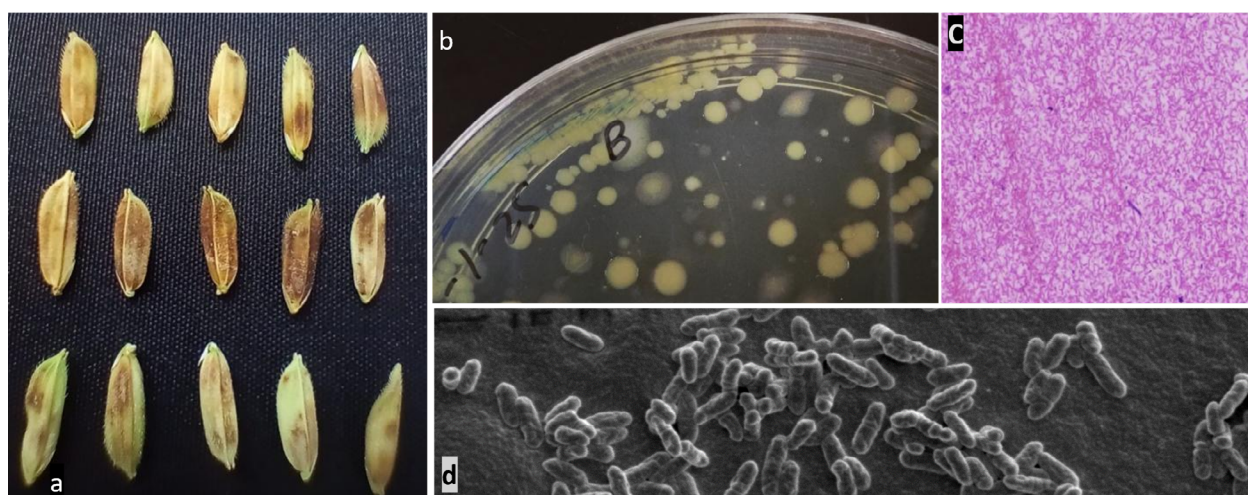


Figure 4. Phenotypic, microscopic, and ultrastructural characteristics of *Burkholderia glumae* associated with bacterial panicle blight of rice

(A) Symptomatic seeds from Malaysian rice granaries; (B) *Burkholderia glumae* reared colony on NA medium; (C) *B. glumae* under the light microscope showing pink colour after gram staining; (D) *B. glumae* under the scanning electron microscope

Malaysian rice granaries and colonies of *B. glumae* reared on nutrient agar (NA) medium, showcasing the distinct colony morphology observed in these studies. Microscopically, the bacterium is rod-shaped with rounded tips, measuring 0.5–0.7 μm in diameter and 1.5–2.0 μm in length (Coenye et al. 2000). Gram staining confirms the bacterium's Gram-negative nature, with red or pink cells visible under light microscopy at 1 000 $\times$ magnification (Schaad 2008). These observations were first documented by Chompa et al. (2022) using a scanning electron microscope (SEM), which provided detailed images of non-sporulating, rod-shaped cells measuring 1.5–2.5 μm in length. The smooth, rounded ends of *Burkholderia* cells are characteristic of this genus. The presence of flagella, a key morphological feature that facilitates bacterial motility, is depicted in Figure 4. These structures enable *B. glumae* to move within host tissues and colonise plant surfaces effectively. Advanced microscopy techniques, such as SEM, reveal the flagella's structure, which is critical for understanding the pathogen's ability to invade and spread under favourable environmental conditions. This feature plays a pivotal role in its virulence and pathogenicity, as documented by Bashir et al. (2024).

Biochemical and physiological testing must consistently identify *B. glumae* and distinguish it from other rice bacterial pathogens. These assays leverage the bacterium's unique metabolic

and structural characteristics, providing comprehensive diagnostic tools for disease management. Important assays include the KOH solubility test, catalase test, toxoflavin production assay, and colony morphology evaluation on selective media; all other important tests are shown in Table 2 with their possible results. These findings are supported by Darmawan et al. (2023), who demonstrated consistent results for isolates collected from ten regions in South Sulawesi, Indonesia.

MOLECULAR DETECTION

The use of molecular detection techniques has significantly enhanced the identification and quantification of *B. glumae* in rice. Advanced methods such as digital PCR (dPCR), real-time PCR (qPCR), conventional PCR, and loop-mediated isothermal amplification (LAMP) offer varying degrees of sensitivity and specificity (Table 3). Among these, qPCR is widely recognised for its high precision, with assays capable of detecting *B. glumae* at concentrations as low as 1 CFU per reaction (Kim et al. 2012). The 16S rRNA gene is a common target, though primers for the 16S-23S ITS region or virulence genes (e.g., *tox* operon, *rhs*) provide greater specificity (Fang et al. 2009; Kumar et al. 2023b). Digital PCR (dPCR) offers a tenfold increase in sensitivity over qPCR, enabling absolute quantification

Table 2. Biochemical and physiological characterisation of *Burkholderia glumae*

Test	Result	Outcomes	References
KOH solubility test	Positive	Produces mucoid reaction with adhesive filaments, confirming Gram-negative nature	Schaad (2008); Ramachandran et al. (2021); Darmawan et al. (2023)
Gram staining	Negative	Appears red (Gram-negative) due to a thin peptidoglycan layer	Schaad (2008); Hasibuan et al. (2018)
Catalase test	Positive	Produces bubbles due to the catalase enzyme breaking down hydrogen peroxide	Singh et al. (2015); Ashfaq et al. (2016); Bashir et al. (2024)
Oxidase test	Negative	No colour change, indicating absence of cytochrome c oxidase	Singh et al. (2015); Ashfaq et al. (2016); Darmawan et al. (2023)
Anaerobic growth test	Negative	No growth in oxygen-deprived environments, confirming a strict aerobic nature	Ashfaq et al. (2016); Darmawan et al. (2023)
Toxoflavin production assay	Variable	Some isolates produce bright yellow toxoflavin, while others do not.	Darmawan et al. (2023)
Fluorescent pigment production	Negative	No fluorescence under UV light, distinguishing it from other pathogens	Darmawan et al. (2023)
Colony colour on YDC medium	White/greyish	Colonies appear white or greyish white, unlike those of pigment-producing bacteria	Darmawan et al. (2023)
Colony texture	Circular, convex	Colonies are smooth, circular, and convex with entire margins	Ramachandran et al. (2021); Bashir et al. (2024)
Nitrate reductase test	Positive	Reduces nitrate to nitrite, indicated by a red colour change	Singh et al. (2015); Bashir et al. (2024)
Cell shape	Rod-shaped	Microscopic observation reveals rod-shaped cells	Bashir et al. (2024)

without a standard curve and proving invaluable for low-biomass samples like seeds (Zhang et al. 2022). While conventional PCR remains a useful tool for characterisation, its lower sensitivity (detection limit of $\sim 10^4$ CFU/mL) limits its utility for early detection (Fang et al. 2009). LAMP provides a rapid, isothermal alternative suitable for field labs, but requires meticulous primer design to avoid cross-reactivity (Faizal Azizi et al. 2022). Table 3 provides a comprehensive overview of research-grade molecular techniques used to detect and characterise *B. glumae*, detailing target genes and specific research outcomes.

COMPARATIVE ANALYSIS OF MOLECULAR DETECTION METHODS FOR FIELD DEPLOYMENT

While the techniques summarised in Table 3 demonstrate high analytical performance in controlled settings, their translation to field applications for on-farm or point-of-care diagnosis

is constrained by practical limitations of cost, time, technical complexity, and infrastructure requirements. A critical comparison of the most pertinent methods (Table 4) highlights these trade-offs. For instance, dPCR and qPCR achieve exceptional sensitivity ($1\text{--}10^2$ CFU) and specificity but require sophisticated, expensive thermocyclers and skilled technicians, confining their use to centralised laboratories. This creates a diagnostic lag, delaying management decisions. Conversely, LAMP reduces reliance on precision instruments and can yield results in under an hour, offering a more viable path for field-deployable kits. However, its susceptibility to carryover contamination and the current lack of commercially validated, user-friendly kits for *B. glumae* remain significant hurdles.

The primary challenges for field deployment of molecular methods are: (i) Sample preparation complexity: Efficient DNA extraction from plant tissue in non-laboratory conditions is a major bottleneck. (ii) Cost-prohibitive instrumentation: The capital cost of devices like

Table 3. Details of molecular techniques used for the detection and characterisation of *Burkholderia glumae* in rice

Molecular Technique	Target gene	Outcomes	References
Mismatch amplification mutation assay (MAMA PCR)	GyrA (Ser83Arg, Ser83Ile)	Discriminated oxolinic acid (OA)-resistant <i>Burkholderia glumae</i> and differentiated it from other <i>Burkholderia</i> spp. in rice seeds	Maeda et al. (2007)
PCR, biolog GN2, fatty acid analysis	16S rDNA, 16S-23S rDNA ITS	Identified <i>B. glumae</i> and <i>B. gladioli</i> as causative agents of BPB in rice	Nandakumar et al. (2009)
Real-time PCR, SYBR green dye	16S-23S rDNA ITS	Developed an overly sensitive real-time PCR assay for detecting <i>B. glumae</i> in rice seeds and plants	Fang et al. (2009)
SYBR green real-time PCR, Bio-PCR	rhs family gene	Developed a rapid and specific real-time PCR method with species-specific primers to detect <i>B. glumae</i> in rice seed samples	Kim et al. (2012)
PCR, whole-genome sequencing	16S-23S rDNA ITS, gyrB	Comparative analysis of <i>B. glumae</i> and <i>B. gladioli</i> revealed distinct virulence factors affecting rice yield	Fory et al. (2014)
Droplet digital PCR (dPCR), SYBR Ggreen qPCR	rhs family protein gene (BG1 primer pair)	EvaGreen dPCR assay developed for seed-borne <i>B. glumae</i> . 10-fold higher sensitivity than SYBR Green qPCR; detection limit: 2×10^2 CFU/seed	Zhang et al. (2022)
PCR-based sequencing (16S rRNA), tox gene cluster profiling	16S rRNA, 11 tox genes (toxRABCDE, toxFGHIJ)	BG1 strain showed a complete tox gene cluster, correlated with high virulence Reliable method for identifying <i>B. glumae</i>	Kumar et al. (2023b)
BOX-PCR, ERIC-PCR, rep-PCR, gyrB gene phylogeny	gyrB (and DNA fingerprinting)	Identified phyletic groups of <i>B. glumae</i> ; higher virulence in BG1 & BG3, lower in BG7 & BG10; strains grouped by region	Kumar et al. (2023b)
BOX-PCR, VNTR, recA, toxB	recA, toxB sequences	47 isolates identified as <i>B. glumae</i> ; BOX-PCR revealed 38 genomic profiles: 7 VNTR haplotypes; significant variability in virulence	Valdez-Nuñez et al. (2024)
PCR-based sequencing (16S rRNA, gyrB)	16S rRNA, gyrB	Pathogen confirmed through PCR and sequencing; geographic region-specific clustering of strains in India	Sreenayana et al. (2024)

real-time PCR systems is often beyond the reach of extension services or smallholder cooperatives. (iii) Technical expertise requirement: Interpreting amplification curves or gel electrophoresis results requires training not commonly available at the field level. (iv) Scalability and throughput: Processing large numbers of samples, as required for seed certification, is slow and labour-intensive with most current field-amenable methods.

Future development must focus on integrated, sample-to-answer systems that combine rapid, crude extraction methods with stabilised LAMP or recombinase polymerase amplification (RPA) reagents in lyophilised formats. Coupling these with simple visual (colourimetric) or lateral-flow readouts could dramatically improve field applica-

bility. The goal is to shift the sensitivity-specificity curve from the laboratory bench to the farmer's field without prohibitive cost increases, a crucial step for enabling real-time, data-driven BPB management decisions.

GENOMIC INSIGHTS INTO *B. GLUMAE* PATHOGENICITY

The first complete genome sequence of *B. glumae* BGR1 provided crucial insights into its virulence mechanisms. The genome comprises two chromosomes and four plasmids, with chromosome 2 harbouring key pathogenicity-related genes, including those involved in the type III protein secretion system

Table 4. Comparative summary of key molecular detection methods for *Burkholderia glumae*: Sensitivity, specificity, and field applicability

Method	Sensitivity	Specificity	Time to result	Field applicability	Key limitations for field use	Cost
Conventional PCR	Moderate (10 ³ –10 ⁴ CFU/mL)	Moderate-high (primer-dependent)	3–6 h	Low	Requires gel electrophoresis; low sensitivity; high contamination risk	\$
Real-time PCR (qPCR)	High (1–10 CFU/reaction)	Very high	1.5–2.5 h	Medium	Requires expensive thermocycler & trained operator; lab dependent	\$\$
Digital PCR (dPCR)	Very high (0.1–1 CFU/reaction)	Very high	2–3 h	Low	Very high instrument cost; complex data analysis; strictly lab based	\$\$\$
Loop-mediated isothermal amplification (LAMP)	High (10 ² –10 ³ CFU/reaction)	High (primer design critical)	30–60 min	Medium-high	Isothermal (simple heater); visual detection possible; but prone to aerosol contamination	\$
Enzyme-linked immunosorbent assay (ELISA)	Low-moderate (10 ⁴ –10 ⁵ CFU/mL)	Moderate (cross-reactivity possible)	4–6 h	Medium	Requires specific antibodies; not for early detection; lab-based protocols	\$\$

CFU – Colony forming unit; ITS – Internal transcribed spacer; relative cost: \$ – low, \$\$ – medium, \$\$\$ – high

and toxoflavin biosynthesis (Lim et al. 2009; Wang et al. 2023). Toxoflavin, a major virulence factor, is regulated by quorum sensing and plays a critical role in disease manifestation. *B. glumae* also produces other yellow pigments, such as reumycin and fervenulin, which may further contribute to its pathogenicity. The regulatory network governing toxoflavin production includes the toxABCDE and toxFGHI operons, controlled by the LysR-type transcriptional activator ToxR and the quorum-sensing regulator TofR (Kim et al. 2004). Additionally, the quorum-sensing system involves the synthesis of autoinducers N-hexanoyl homoserine lactone (C6-HSL) and N-octanoyl homoserine lactone (C8-HSL), which activate toxJ expression, linking quorum sensing to toxoflavin biosynthesis and pathogenicity (Kim et al. 2013). Comparative genomic studies of *B. glumae* with related *Burkholderia* species have revealed evolutionary adaptations, such as genome rearrangements and the presence of unique CRISPR/Cas systems, further highlighting the need for species-specific control strategies (Xie et al. 2025).

INFECTION PROCESS AND DETECTION CHALLENGES

The infection dynamics of *B. glumae* in rice plants have been extensively studied using real-

time fluorescence quantitative PCR and GFP-labelled strains. Li et al. (2016) found that *B. glumae* primarily colonises the growing points of rice plants, with the highest bacterial populations observed in the uppermost leaf during the two-leaf stage. The pathogen population declines after this stage but resurges during the booting phase, leading to panicle outbreaks. The infection pattern involves initial colonisation of lateral root vascular bundles, followed by systemic spread to leaf sheaths and leaves, resulting in curling and wilting symptoms. Diagnosing *B. glumae* infections remains challenging due to symptom similarities with abiotic stress factors, such as thermal or water stress (Gowda et al. 2022). Traditional culture-based methods and serological assays (e.g., ELISA) are prone to environmental variability, require expert handling, and lack the speed needed for in-season intervention. While molecular and biosensor techniques offer superior specificity, their practical deployment faces significant hurdles related to cost, technical complexity, and field robustness, as critically analysed in the preceding section (see Comparative Analysis of Molecular Detection Methods for Field Deployment).

Additionally, studies have confirmed that *B. glumae* can survive in stored rice seeds for extended periods, with maximum recovery (91%) observed

just after harvest (Gowda et al. 2022). This highlights the importance of robust seed treatment and storage strategies. Future research should focus on developing multiplex PCR assays targeting multiple genes, such as *gyrB* and *rpoD*, to enhance the specificity and accuracy of *B. glumae* detection (Maeda et al. 2006).

INNOVATIVE APPROACHES TO *B. GLUMAE* DETECTION AND FORECASTING

Controlling BPB remains a significant challenge due to the pathogen's environmental adaptability and the limitations of traditional detection and management strategies. Antibiotics and chemical controls are often avoided due to environmental and resistance concerns, while biological controls have shown unreliable results (Ngalimat et al. 2021). Consequently, the scientific community has pivoted toward computational solutions, catalysing the development of sophisticated forecasting frameworks and AI-driven detection methodologies that offer unprecedented precision in pathogen identification and outbreak prediction.

PARADIGM SHIFTS IN ML-DRIVEN PLANT PATHOLOGY: FROM STATIC CLASSIFICATION TO DYNAMIC FORECASTING SYSTEMS

The role of machine learning (ML) in plant pathology is undergoing a significant transition – from classifying curated images to forecasting disease risk in real field environments. This shift marks a change in both objective and methodology, driven by advances in model architecture, multimodal data integration, and hybrid system design. For BPB in rice, these trends offer a practical roadmap toward more robust and deployable forecasting tools. Below, we synthesise key developments, anchoring them in representative studies that illustrate the field's trajectory.

EVOLVING ARCHITECTURES: BALANCING ACCURACY WITH PRACTICALITY

Model design has increasingly emphasised deployability. Early applications often relied on large,

generic networks, but recent work focuses on lightweight, purpose-built architectures suited to resource-limited settings. For instance, Kundu et al. (2021) developed a shallow CNN that drastically reduced parameter counts and training time while maintaining high accuracy, demonstrating that efficient models can perform effectively without extensive computational overhead, a critical consideration for field deployment.

To handle complex real-world scenarios such as distinguishing between diseases with similar symptoms, more sophisticated ensemble and attention-based approaches have emerged. Meena et al. (2022), for example, combined multiple architectures with Squeeze-and-Excitation blocks to improve discrimination among several rice diseases. This reflects a broader move toward models that not only classify but also prioritise diagnostically relevant features, reducing errors in visually ambiguous cases.

Meanwhile, the systematic use of transfer learning has provided a structured way to leverage pre-trained models. Prabu Kanna et al. (2023) compared several state-of-the-art networks for cauliflower disease identification, illustrating how evidence-based selection can identify optimal architectures for specific agricultural contexts. Together, these studies highlight a maturing design philosophy: the goal is no longer maximal accuracy alone, but an optimal balance of performance, efficiency, and applicability.

FROM STANDALONE MODELS TO INTEGRATED MANAGEMENT SYSTEMS

A defining trend in recent years is the integration of ML into end-to-end agricultural management systems. Rather than operating in isolation, machine learning is increasingly embedded within IoT-enabled pipelines that automate data collection, analysis, and alerting. Kundu et al. (2021) exemplified this with a drone-based sensing system that captures field imagery and environmental data, processes it on edge devices, and delivers alerts effectively, moving ML from the lab into the operational loop.

Perhaps even more relevant for forecasting is the rise of hybrid or physics-informed modelling, which combines mechanistic understanding with data-driven learning. Fenu and Mallocci (2019) demonstrated this approach by integrating weath-

er-driven process models with neural networks and support vector machines to predict potato late blight, achieving strong performance while retaining interpretability. For BPB, such a framework could embed the established BGRcast logic within an adaptive ML layer, creating a system that is both knowledge-guided and data-refined.

Concurrently, the scope of ML tasks in pathology has broadened. Following the progression noted in surveys such as Dhaka et al. (2021), the field has moved beyond simple classification toward localisation and severity estimation. This advance enables more granular recommendations, such as distinguishing early infection stages or quantifying disease progression, which are essential for timely, targeted intervention.

SYNTHESIS: A CONCEPTUAL FRAMEWORK FOR BPB FORECASTING

These paradigm shifts collectively inform a design strategy for next-generation BPB forecasting. An effective system might integrate:

A **data layer** employing cost-effective sensors and imagery platforms, inspired by IoT frameworks like that of Kundu et al. (2021), to capture field-specific microclimate and panicle data.

A **hybrid forecasting core** merging BGRcast logic with a machine learning model, following the physics-informed approach of Fenu and Mallocci (2019), to generate dynamic, locally adapted risk indices.

A **diagnostic module** using robust visual models perhaps drawing on ensemble strategies like Meena et al. (2022) to verify symptoms and estimate severity from panicle imagery.

A **decision-support interface** that delivers actionable alerts to farmers, closing the loop from data to decision.

SYNTHESIS AND TRANSITION TO BPB APPLICATIONS

The progression from standalone classifiers to integrated forecasting systems reflects the growing maturity of ML in plant pathology. Early applications, such as the ANN-based yield-prediction model developed by Anitha and Chakravarthy (2018), demonstrated the poten-

tial of computational tools in agriculture. Today, the focus has shifted toward systems that are not only accurate but also deployable, interpretable, and actionable.

For BPB research, this means prioritising the development of hybrid models that leverage both biological knowledge and field data, creating well-annotated panicle image datasets to train robust visual models, and validating forecasting prototypes across diverse agroecological settings. By building on the architectural and integrative advances illustrated in the studies above, the path forward is clear: toward reliable, accessible tools that help manage disease more precisely, sustainably, and effectively.

STATISTICAL MODELS FOR WEATHER-BASED BPB FORECASTING

The BGRcast model, developed by Lee et al. (2015), is a weather-driven forecasting tool for predicting BPB risk. The model calculates daily environmental conductiveness (C_i) using daily minimum temperature and average relative humidity, and divides BPB development into three phases: lag, inoculum build-up, and infection (Figure 5). Thresholds of $C_{inc} = 0.3$ (inoculum build-up phase) and $C_{inf} = 0.5$ (infection phase) guide advisories for bactericide sprays at the pre- and post-heading stages. Initial validations achieved 71.4% detection accuracy with a 47.6% false alarm ratio. Subsequent research by Kim et al. (2020) extended the model's applicability by demonstrating that numerical weather prediction (NWP) data from the Unified Model (UM) could replace automated weather station (AWS) data as an input source. High correlation coefficients (R^2) were observed between UM- and AWS-based estimates of C_{inc} and C_{inf} . Additionally, pre-heading and post-heading warnings achieved a probability of detection (POD) of 98.18% and 95.22%, respectively. These results suggest that integrating UM-based weather data enables earlier and more accurate disease management decisions. This innovation enhances the model's usability by enabling broader use in regions without AWS infrastructure. Further refining the model, Echeverri-Rico et al. (2021) identified minimum nighttime temperatures above 23 °C during the 10 days post-flowering as a critical factor for BPB incidence in tropical regions. This highlights the potential

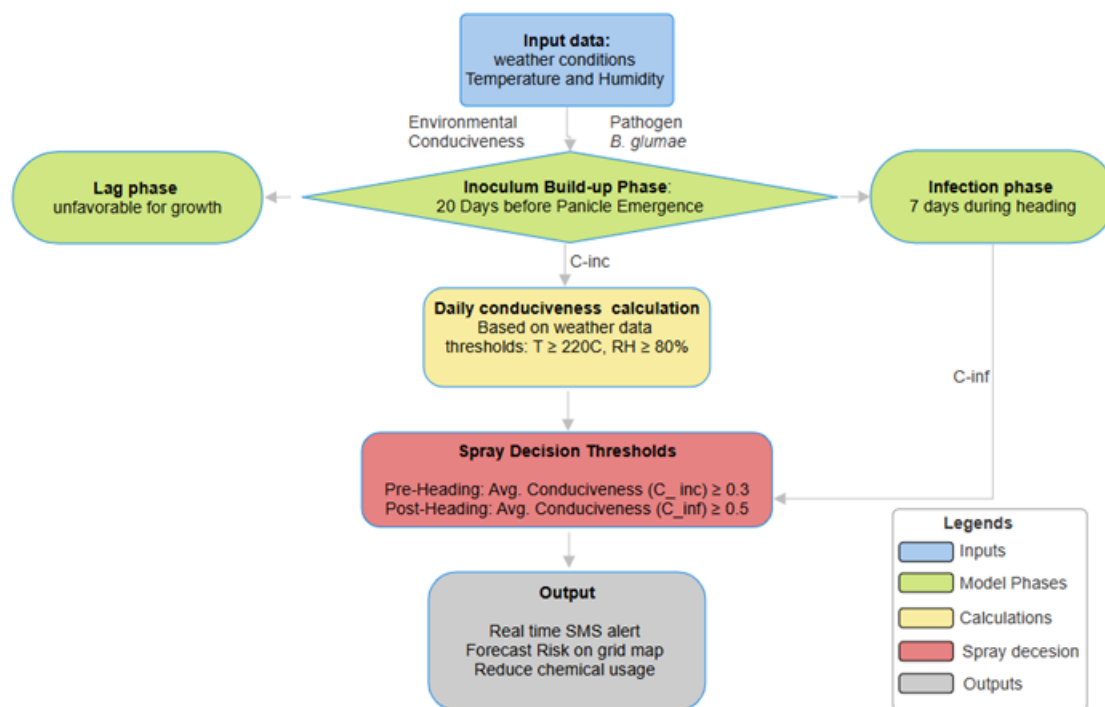


Figure 5. Bacterial grain rot (BGR) cast model's framework for forecasting Bacterial panicle blight (BPB) risk. The model incorporates environmental inputs, calculates daily conduciveness, and uses threshold-based spray decision advisories to optimise BPB management

for future iterations of BGRcast to incorporate region-specific thresholds, improving its accuracy in tropical climates. By adapting to such unique environmental conditions, BGRcast can evolve into a globally relevant forecasting tool.

The economic and environmental implications of BPB, as explored by Shew et al. (2019), underscore the importance of tools like BGRcast. Driven by warm and humid conditions, BPB is likely to intensify with climate change, leading to substantial economic losses. Projections indicate that the climatically suitable area for *B. glumae* could expand by 15–30% under a 2 °C warming scenario, significantly increasing the population at risk of infection. For instance, a 1 °C warming scenario could reduce U.S. rice exports by 3.4%, affecting food availability for 2.17 mil. people annually. Strategies such as breeding BPB-resistant rice and advancing forecasting tools, such as BGRcast, are critical for mitigating these impacts. The integration of NWP data and regional climatic considerations positions BGRcast as an effective tool for sustainable rice production amidst increasing climate variability. Future research should focus on incorporating additional climatic thresholds and expanding its applicability to diverse agroecological zones, ensuring its global relevance in combating BPB and securing food production.

AI-BASED INNOVATIONS IN DISEASE DETECTION AND FORECASTING OF *B. GLUMAE*

The transition from climatic decision-support models such as BGRcast to AI-based systems marks a paradigm shift in precision phytopathology. While models like BGRcast have proven effective in simulating weather–pathogen interactions and identifying risk periods, their scope remains constrained by empirically derived parameters. The integration of AI into rice pathology extends these foundations by enabling automated feature extraction, image-based diagnosis and predictive analytics that transcend static climatic thresholds, thereby providing a dynamic and scalable framework for *B. glumae* management.

COMPARATIVE ANALYSIS OF EXISTING AI FRAMEWORKS FOR *B. GLUMAE* DETECTION

To understand the evolution of AI tools for BPB, it is helpful to examine three key approaches. These methods show a clear progression from highly ac-

curate laboratory techniques to more practical, field-ready systems.

EARLY DETECTION IN THE LAB: HYPERSPECTRAL IMAGING

One of the first attempts to use AI for BPB detection analysed rice seeds using hyperspectral cameras (Baek et al. 2019). This method can detect biochemical changes caused by the bacteria before visible symptoms appear, achieving over 90% accuracy. Its main strength is this early, non-destructive detection. However, the need for expensive, lab-bound equipment makes it difficult to use for routine field monitoring.

TOWARD FIELD APPLICATION: REAL-TIME IMAGE DETECTION

To move detection out of the lab, researchers have adapted object detection models like YOLO to analyse images of rice grains (Quach et al. 2023). These models can identify and locate infected grains in a photo within milliseconds, making them suitable for drones or mobile phones. This speed comes with a trade-off: while good at finding diseased grains (84.5% mAP), their accuracy can be affected by changes in lighting and background clutter in real field conditions.

BUILDING SCALABLE SYSTEMS: MOBILE-OPTIMISED MODELS

The most deployable systems aim to strike a balance between accuracy and practicality. For example, transfer-learning-based pre-trained ResNet50 model was trained to diagnose multiple rice diseases, including BPB, from leaf images with over 92% accuracy (Sahasranamam et al. 2024). Crucially, the model was optimised to run on smartphones and drones. While a major step forward, its performance on leaf images requires further testing on panicle imagery from diverse field environments.

SYNTHESIS AND TRAJECTORY

Together, these studies mark a clear path. Research has moved from sensitive but stationary

lab equipment (TRL 3-4) to fast field detectors that sacrifice some accuracy (TRL 5-6), and finally to accurate, mobile-optimised systems (TRL 6-7). The consistent goal is to create tools that are both reliable and realistic for farmers to use.

ADVANCEMENT BEYOND TRADITIONAL SCOUTING

This shift to AI-driven tools addresses major limitations of traditional disease scouting, which relies on manual, visual inspection. AI systems can process vast amounts of data consistently, reduce human error and bias, and identify subtle symptoms that the eye might miss. They transform disease surveillance from a manual, reactive task into a scalable, predictive process.

A critical consideration emerging from this comparison is the cost-effectiveness and hardware accessibility for the ultimate end-users: smallholder farmers. This practical dimension creates a clear trade-off. Hyperspectral imaging, while superb for early, lab-based seed screening, requires prohibitively expensive speciality cameras (often over 10 000 USD) and stable lighting, limiting its use to institutions. YOLO-based drone scouting offers a powerful field solution but demands a significant upfront investment in the drone platform, computing hardware, and operator training. In contrast, the most promising path for direct, widespread farmer engagement may lie in CNN models optimised for mobile deployment [e.g., TensorFlow Lite (Google LLC)]. By leveraging smartphones devices already in farmers' pockets, this approach dramatically lowers the barrier to entry, offering a pragmatic balance of adequate accuracy, real-time feedback, and minimal marginal cost. Therefore, the choice of technology is not merely a performance decision but a strategic one that must align with the economic realities and infrastructure of the target farming community.

These practical constraints underscore the need to move beyond comparing individual tools to understanding the core functional roles of different AI architectures within a management pipeline. Therefore, while Table 4 compares specific implementations, Table 5 provides a synthesised taxonomy of the underlying architectures. It classifies models by their primary function: diagnosis, real-time scouting, or forecasting and compares their key performance characteristics, technology readiness level (TRL), and specific value for BPB management. This framework clarifies

Table 5. Performance comparison of representative Bacterial panicle blight (BPB) detection technologies from case studies

Core methodology	Dataset focus	Accuracy/ mAP	Deployment potential	TRL	Primary strength	Limitation	References
Hyperspectral imaging + SVM/PLS-DA	Seed spectral data	> 90%	Laboratory prototype	3–4	Early detection via spectral biomarkers	High cost; poor field portability	Baek et al. (2019)
YOLOv5/ YOLOv7 object detection	Grain/panicle images	84.5% mAP@50	Drone/ real-time detection	5–6	Fast detection; localised diagnosis	Sensitive to illumination/ background noise	Quach et al. (2023)
Fine-tuned ResNet50 CNN	Multi-disease leaf dataset (incl. BPB)	92.83% accuracy	TFLite deployment on mobile/drone	6–7	High accuracy; mobile-ready	Limited field validation; trained on leaves not panicles	Sahasranamam et al. (2024)

TRL – technology readiness level scale (1–9)

the complementary strengths of convolutional neural networks (CNNs), You Only Look Once (YOLO) models, and Long Short-Term Memory (LSTM) networks. Understanding this taxonomy is fundamental for designing integrated, next-generation decision-support systems that are not only technically sound but also economically viable and scalable (Table 6).

INTEGRATED MULTIMODAL AI FRAMEWORK (IMAF) FOR *B. GLUMAE* DETECTION AND FORECASTING

Effectively managing BPB is difficult. Farmers and agronomists need to spot the disease early,

tell it apart from other problems, predict when it will strike, and act quickly, all while dealing with unpredictable weather. Current tools often tackle only one of these tasks at a time. The Integrated Multimodal AI Framework (IMAF) proposed here is designed to connect these steps into a single, intelligent system. Its workflow, from data collection to decision support, is shown in Figure 6.

The system starts by solving a basic problem: getting a reliable, consistent picture of the field. The IMAF's initial modules automate these using drones and sensors to collect and clean images and weather data. This data standardisation is the essential first step, ensuring the AI has a trustworthy foundation, much like a doctor needs clear tests before a diagnosis.

Table 6. Taxonomy and comparative profile of core artificial intelligence/machine learning (AI/ML) architectures for Bacterial panicle blight (BPB) management

Model architecture	Primary task (role)	Performance & speed	TRL for BPB	Value for BPB management
Convolutional neural networks (CNNs) e.g., ResNet, EfficientNet	Image classification (diagnosis)	Accuracy: high (90–99% on clean data); speed: medium; optimised versions (TFLite) enable mobile use	5–6	Provides high-confidence diagnostic confirmation from leaf or panicle imagery; the foundation for transfer learning
YOLO models (object detection)	Real-time detection & localization (field scouting)	mAP: moderate-high (80–90%+); speed: very fast (real-time). Ideal for edge computing (drones, phones)	6–7	Enables automated, real-time counting and mapping of infected grains in field conditions; crucial for monitoring.
Long Short-Term Memory (LSTM) Networks	Temporal forecasting (risk prediction)	Accuracy: potentially high (> 95% R^2); speed: slow (batch processing)	4–5	Models' disease-weather relationships over time to generate actionable outbreak risk forecasts
Traditional ML/statistical models (e.g., SVM, BGRcast)	Rule-based forecasting/classification (baseline)	Accuracy: moderate (70–95%); speed: very fast, low-cost	7–9	Offers interpretable, physics-based risk thresholds; establishes a reliable operational baseline

TRL – technology readiness level scale (1–9); AI – artificial intelligence; ML – machine learning

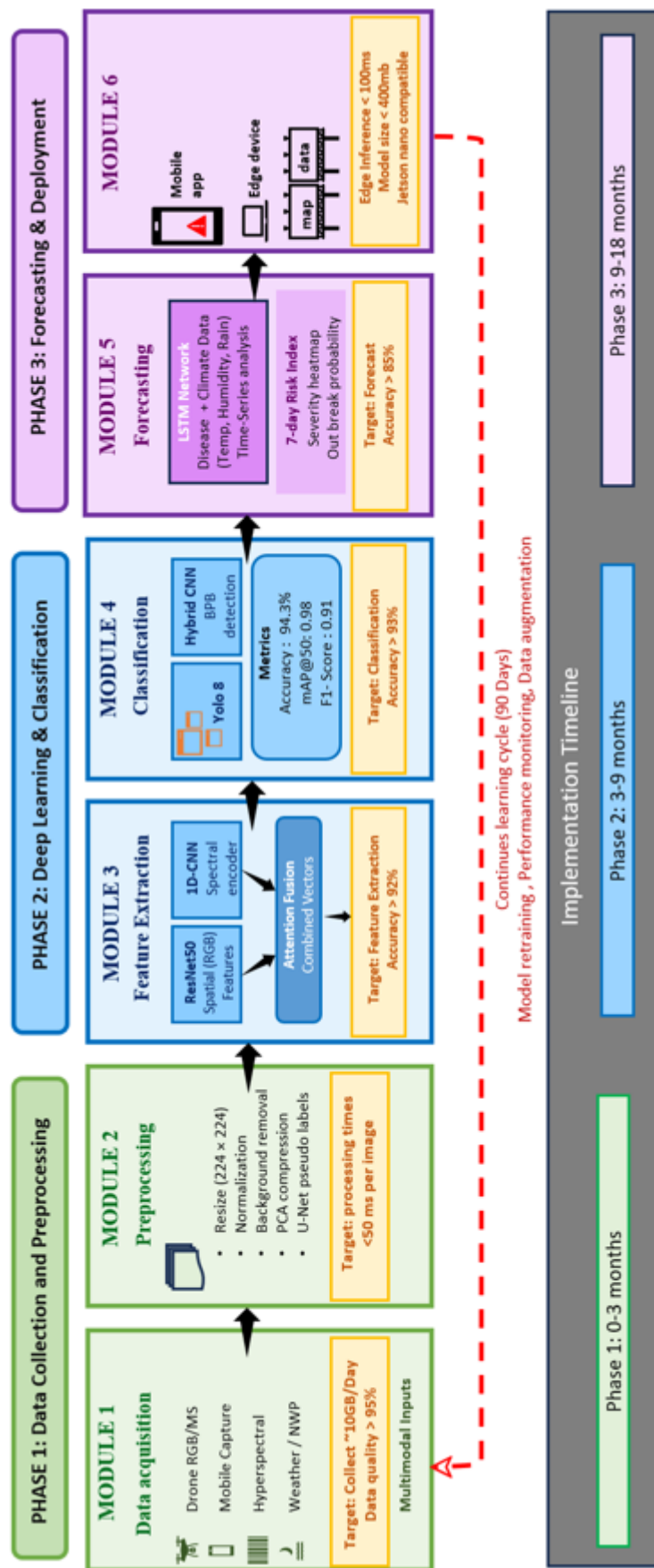


Figure 6. Architecture and implementation timeline of the proposed Integrated Multimodal AI Framework (IMAF) for BPB detection and forecasting. The IMAF integrates multimodal data through five sequential modules (M1–M5) across three development phases (0–18 months). M1: Data acquisition collects drone-based imagery (RGB/multispectral), mobile particle photos, hyperspectral seed data, and weather parameters from Numerical Weather Prediction (NWP) models. M2: Preprocessing standardises and cleans inputs via resizing (224 × 224), colour normalisation, and Principal Component Analysis (PCA). M3: Feature extraction uses a dual-stream backbone (ResNet50 CNN for spatial features; 1D-CNN for spectral features) fused with climate data via an attention mechanism. M4: Disease classification and localisation employs a YOLOv8 object detector to identify symptomatic panicle regions, followed by a hybrid CNN for severity estimation. M5: Forecasting and risk modelling integrates spatial infection data with climate streams in a Long Short-Term Memory (LSTM) network to generate 7-day risk forecasts. The system operates on a hybrid cloud-edge architecture with a continuous 90-day learning cycle for model retraining. Key performance targets for each phase are indicated within the modules.

With reliable data, the next challenge is accurate diagnosis. The IMAF tackles this by analysing field data from multiple angles at once. It looks at visual patterns, subtle spectral clues, and current weather, then combines these to confirm BPB, pinpoint its location, and estimate severity. This precise detection enables targeted treatment.

The framework's key innovation is its shift from reaction to forecasting. By analysing how current infections interact with weather forecasts, it predicts outbreak risk over the next week, giving farmers a critical head start. For this system to move from concept to field-ready tool, development must follow a validation pathway tied to increasing technology readiness. We propose an 18-month, three-phase plan: Phase 1 (0–3 months) establishes the foundation through dataset standardisation and prototype development, achieving lab-scale validation. Phase 2 (3–9 months) focuses on refining the AI models and integrating modules, validated through controlled testing against performance benchmarks. Phase 3 (9–18 months) is dedicated to multi-location trials across diverse rice-growing regions. This stage tests the system's real-world accuracy, robustness, and usability, ensuring it meets the needs of farmers under varying conditions.

Finally, the best tool is useless if the advice doesn't reach the farmer in time. The IMAF delivers insights via simple dashboards and is designed to learn each new field data point continuously, making the system smarter, keeping its advice accurate season after season. The IMAF integrates detection, diagnosis, forecasting, and delivery into one adaptive loop. By following a structured validation pathway, it is designed to evolve from a proof-of-concept into a practical, decision-ready tool that offers a clear, actionable path to protecting rice harvests from BPB.

THE DATA IMBALANCE PROBLEM

Real-world agricultural datasets are inherently skewed; images of healthy plants vastly outnumber those with disease symptoms. For episodic diseases like BPB, this imbalance is acute. Models trained on such data risk becoming biased, learning to excel at identifying "healthy" while failing to detect critical, rare infections, a fundamental challenge in machine learning known as learning from imbalanced data (He & Garcia 2009). In plant disease detection,

this can severely limit a model's ability to recognise early or subtle symptoms (Ashurov et al. 2025). While resampling techniques offer partial solutions, they can lead to overfitting or data loss, making models especially fragile against the very symptoms where early intervention is most valuable.

THE DOMAIN ADAPTATION GAP

A model trained in one location often fails in another due to domain shift, with changes in lighting, cultivars, camera angles, or field backgrounds. This is a recognised bottleneck in scaling agricultural computer vision systems (Upadhyay et al. 2025). A system achieving high accuracy on a research station may perform poorly in a farmer's field just kilometres away, as visual symptoms interact with local conditions. This lack of generalizability necessitates techniques that allow models to adapt without costly, full retraining on new datasets from every target environment.

THE INTERPRETABILITY ("BLACK BOX") DILEMMA

For adoption, farmers and agronomists must trust AI diagnoses. This is challenging because deep learning models typically function as "black boxes", offering a prediction without clear reasoning for why a specific particle was flagged as diseased. This opacity is a recognised barrier to trust and practical action in agricultural settings (Pai et al. 2025). Explainable AI (XAI) tools are therefore crucial for bridging this gap. Methods like Grad-CAM (Selvaraju et al. 2017) and SHAP (Lundberg & Lee 2017) address this by providing visual explanations, such as heatmaps that highlight the image regions most influential to the model's decision. This capability allows plant pathologists to validate the AI's reasoning, for instance, by confirming it focused on a true lesion rather than a shadow or artefact. Integrating such interpretability is essential for building the expert confidence and user trust required for successful field deployment.

These challenges are interconnected. Imbalanced data teaches models to rely on fragile features, worsening domain failure. Complex models that might generalise better are harder to interpret. Therefore, future work must prioritise curated, di-

verse datasets, robust domain adaptation methods, and built-in explainability to transition AI from a promising lab tool to a trusted field partner.

FUTURE RESEARCH ROADMAP

To operationalise the proposed IMAF and advance AI applications for *B. glumae* epidemiology, future research should focus on progressive validation and large-scale deployment within sustainable rice ecosystems. The immediate priority is to establish a unified Rice Panicle Disease Database (RPD-DB) that integrates UAV, field, and hyperspectral imagery, annotated for disease severity. Such a standardised repository will enable transparent benchmarking and facilitate reproducible cross-model comparisons using metrics such as accuracy, F1-score, and inference latency.

Subsequent research should enhance model adaptability and real-time performance through domain adaptation and lightweight optimisation. Adversarial and few-shot learning methods can bridge the domain gap between controlled and field conditions. At the same time, quantisation and pruning of the IMAF will reduce inference time by up to 50% on embedded systems such as Jetson Nano and Raspberry Pi (NVIDIA), supporting rapid decision-making in smallholder contexts.

To transition the IMAF from a research prototype to a trusted operational tool, future work must embed explainable AI (XAI) at its core. Integrating methods such as Grad-CAM or SHAP into IMAF's Disease Classification Module is critical for two reasons. First, for farmer adoption: generating simple visual reports (e.g., heatmaps on field images) that show why a panicle was flagged builds the necessary trust for farmers to act on the system's alerts. Second, for regulatory compliance: as digital tools become part of formal Integrated Pest Management (IPM) programs, demonstrating that the IMAF's decisions are based on agronomically valid symptoms rather than data artefacts will be essential for certification. Therefore, future validation of the IMAF must include evaluating not only its accuracy but also the clarity and reliability of its explanations for end users.

Multi-location field trials across Southeast Asia are essential to validate climatic robustness and confirm generalizability under variable weather conditions. Integration of the LSTM-based risk forecast-

ing module with empirical systems such as BGRcast will yield a hybrid platform that combines climate thresholds with deep learning intelligence.

The practical deployment of integrated frameworks like the IMAF directly supports key Sustainable Development Goals (SDGs). By enabling precise, early detection of BPB, such systems can mitigate severe yield losses, directly contributing to SDG 2 (Zero Hunger). Furthermore, by optimising input use, these tools advance SDG 12 (Responsible Consumption and Production), potentially reducing the environmental footprint of rice cultivation, a significant global source of greenhouse gas emissions and water use (Wang et al. 2023; Chapagain & Hoekstra 2011). The forecasting component is particularly crucial for SDG 13 (Climate Action), as it helps farmers adapt their management to the specific weather conditions that exacerbate BPB outbreaks (Echeverri-Rico et al. 2021).

To translate this potential into a measurable on-farm impact, multi-location field trials across Southeast Asia are essential to validate climatic robustness and confirm generalizability under variable weather conditions. Integration of the LSTM-based risk forecasting module with empirical systems such as BGRcast will yield a hybrid platform that combines climate thresholds with deep learning, providing a scalable pathway to achieve these sustainability benefits.

CONCLUSION

The increasing prevalence of *B. glumae* and its role in BPB present a significant and growing challenge to global rice production, particularly in tropical and subtropical regions. Climate change is intensifying this threat by creating optimal conditions for pathogen proliferation, especially during the critical panicle emergence stage. While traditional detection methods have proven inadequate for timely intervention, leading to substantial yield losses, molecular techniques such as PCR and LAMP offer greater sensitivity and specificity. However, their resource-intensive nature often limits practical field application. Consequently, a paradigm shift towards intelligent solutions is necessary. AI and ML offer a powerful foundation for a new management framework. By leveraging the strengths of convolutional neural networks (CNNs), support vector machines

(SVMs), and other hybrid models, robust systems can be developed for accurate BPB detection, forecasting, and control. The integration of these AI models with IoT-enabled sensors and drone-based imaging can enable real-time monitoring and facilitate early intervention. In summary, the integration of AI-driven tools with climate data and field sensors represents the most promising pathway for sustainable BPB management. Such innovative approaches have the potential to address yield losses directly, optimise crop management strategies, and thereby safeguard global food security.

Acknowledgment

We are grateful to the Ministry of Higher Education and Universiti Putra Malaysia for providing financial support through the Malaysia Research University Network (MRUN) research Grant. MRUN/ITAFOS/2022 (Vote No. 5539310) to conduct the research project.

REFERENCES

- Alvarez E., Latorre M. (2023): Bacterial blight of *Bracharia* caused by *Burkholderia glumae* in Colombia. Open Journal of Plant Science (in press). Available at: <https://doi.org/10.17352/ojps.000052>.
- Anitha P., Chakravarthy T. (2018): Agricultural crop yield prediction using artificial neural network with feed forward algorithm. International Journal of Computer Sciences and Engineering, 6: 178–181.
- Ashfaq M., Haider M.S., Ali A., Ali M., Saleem I., Mubashar U. (2016): Morphological characterisation of endophytic bacterial strains isolated from discolored rice grain. Pakistan Journal of Phytopathology, 28: 1–8.
- Ashurov A.Y., Al-Gaashani M.S., Samee N.A., Alkanhel R., Atteia G., Abdallah H.A., Muthanna M.S.A. (2025): Enhancing plant disease detection through deep learning: a Depthwise CNN with squeeze and excitation integration and residual skip connections. Frontiers in Plant Science, 15: 1505857.
- Azzahra R.S.N.A., Miranti M., Prismantoro D., Mohd Suhaimi N.S., Alizadeh M., Mispan M.S., Doni F. (2024): Bacterial panicle blight caused by *Burkholderia glumae*: a major disease in rice cultivation. Cogent Food & Agriculture, 10: 2381600.
- Baek I., Kim M.S., Cho B.K., Mo C., Barnaby J.Y., McClung A.M., Oh M. (2019): Selection of optimal hyperspectral wavebands for detection of discolored, diseased rice seeds. Applied Sciences, 9: 1027.
- Balaska V., Adamidou Z., Gasteratos A. (2023): Sustainable crop protection via robotics and artificial intelligence solutions. Machines, 11: 774.
- Bao J. (2023): Rice. In: Shewry P.R., Koxsel H., Taylor J.R.N. (eds): ICC Handbook of 21st Century Cereal Science and Technology. Amsterdam, Academic Press, San Diego: 145–151.
- Bashir Y.R., Sani Z.R., Abdulazeez U.S. (2024): Morphological, biochemical and molecular characterisation of the causal agent of bacterial panicle blight disease of rice (BPB) in selected rice production zones of Zamfara state. International Journal of Science for Global Sustainability, 10: 138–145.
- Chapagain A.K., Hoekstra A.Y. (2011): The blue, green and grey water footprint of rice from production and consumption perspectives. Ecological Economics, 70: 749–758.
- Chompa S.S., Akter A., Sadeq A.B.M., Rahman M.E., Rashid H.O., Ibnat N., Hossain M.B. (2022): An overview of major bacterial diseases of rice and management strategies for their control in Malaysia. Global Scientific Journals, 10: 1074–1102.
- Coenye T., Gillis M. (2000): *Pseudomonas antimicrobica* Attafuah and Bradbury 1990 is a junior synonym of *Burkholderia gladioli* (Severini 1913) Yabuuchi et al. 1993. International Journal of Systematic and Evolutionary Microbiology, 50: 2135–2139.
- Darmawan A.A., Sahlan F.K., Nurmujahidin N. (2023): Morpho-physiological characterisation of bacterial grain rot in rice seed from Gowa regency, South Sulawesi. In: Darmawan A.A., Kuswinanti T., Asman A. (eds): IOP Conference Series: Earth and Environmental Science, 1230: 012114.
- Dhaka V.S., Meena S.V., Rani G., Sinwar D., Ijaz M.F., Woźniak M. (2021): A survey of deep convolutional neural networks applied for prediction of plant leaf diseases. Sensors, 21: 4749.
- Dorairaj D., Govender N.T. (2023): Rice and paddy industry in Malaysia: Governance and policies, research trends, technology adoption and resilience. Frontiers in Sustainable Food Systems, 7: 1093605.
- Echeverri-Rico J., Petro E., Torres E.A. (2021): Understanding the complexity of disease-climate interactions for rice bacterial panicle blight under tropical conditions. PLoS ONE, 16: e0252061.
- Faizal Azizi M.M., Lau H.Y. (2022): Advanced diagnostic approaches developed for the global menace of rice diseases: A review. Canadian Journal of Plant Pathology, 44: 627–651.
- FAO, WFP (2025): 2025 Global Report on Food Crises. Food and Agriculture Organization of the United Nations & World Food Programme. Available at: <https://www.fao.org/publications>

- Fang Y., Xu L.H., Tian W.X., Huai Y., Yu S.H., Lou M.M., Xie G.L. (2009): Real-time fluorescence PCR method for detection of *Burkholderia glumae* from rice. *Rice Science*, 16: 157–160.
- Fenu G., Mallocci F.M. (2019): An application of machine learning technique in forecasting crop disease. In: Fenu G., Mallocci F. M. (eds): *Proceedings of the 3rd International Conference on Big Data Research*, New York: 76–82.
- Fory P.A., Triplett L., Mosquera G.M. (2014): Comparative analysis of two emerging rice seed bacterial pathogens. *Phytopathology*, 104: 436–444.
- Goto K., Ohata K. (1956): New bacterial diseases of rice (brown stripe and grain rot). *Annals of the Phytopathological Society of Japan*, 21: 46–47.
- Gowda H.R.A., Tripathi R., Vishunavat K. (2022): Morphological and molecular characterisation of *Burkholderia glumae* causing panicle blight of paddy. *Physiological and Molecular Plant Pathology*, 117: 101755.
- Hasibuan M., Safni I., Lubis K. (2018): Morphological characterisation of several strains of the rice-pathogenic bacterium *Burkholderia glumae* in North Sumatra. In: *IOP Conference Series: Earth and Environmental Science*, Bristol, 122: 012044.
- He H., Garcia E.A. (2009): Learning from Imbalanced Data. *IEEE Transactions on Knowledge and Data Engineering*, 21: 1263–1284.
- Iqbal A., Nwokocha G., Tiwari V., Barphagha I.K., Grove A., Ham J.H., Doerrler W.T. (2023): A membrane protein of the rice pathogen *Burkholderia glumae* required for oxalic acid secretion and quorum sensing. *Molecular Plant Pathology*, 24: 1400–1413.
- Kanna G.P., Kumar S.J., Kumar Y., Changela A., Woźniak M., Shafi J., Ijaz M.F. (2023): Advanced deep learning techniques for early disease prediction in cauliflower plants. *Scientific Reports*, 13: 18475.
- Kim B.K., Cho M.S., Park D.S. (2012): Rapid and specific detection of *Burkholderia glumae* in rice seed by real-time bio-PCR using species-specific primers based on an *Rhs* family gene. *Plant Disease*, 96: 577–580.
- Kim H.S., Do K.S., Park E.W. (2020): Application of numerical weather prediction data to estimate infection risk of bacterial grain rot of rice in Korea. *Plant Pathology Journal*, 36: 54–66.
- Kim J., Kim J.G., Hwang I. (2004): Quorum sensing and the LysR-type transcriptional activator ToxR regulate toxoflavin biosynthesis and transport in *Burkholderia glumae*. *Molecular Microbiology*, 54: 921–934.
- Kim S., Park J., Seo Y.S. (2013): RNAseq-based transcriptome analysis of *Burkholderia glumae* Quorum sensing. *Plant Pathology Journal*, 29: 249–259.
- Kumar S., Mondal K.K., Mani C. (2023a): phylogenetic analysis, molecular characterization and virulence profiling based on toxoflavin gene of an Indian BG1 strain of *Burkholderia glumae* causing panicle blight of rice. *3 Biotech*, 13: 1–16.
- Kumar S., Mondal K.K., Mani C. (2023b): Genetic and pathogenic diversity analysis of *Burkholderia glumae* strains from Indian hot spot regions causing bacterial panicle blight of rice (*Oryza sativa* L.). *Tropical Plant Pathology*, 48: 139–153.
- Kundu N., Rani G., Dhaka V.S., Gupta K., Nayak S.C., Verma S., Woźniak M. (2021): IoT and interpretable machine learning based framework for disease prediction in pearl millet. *Sensors*, 21: 5386.
- Lee Y.H., Ko S.J., Park E.W. (2015): BGRcast: A disease forecast model to support decision-making for chemical sprays to control bacterial grain rot of rice. *Plant Pathology Journal*, 31: 350–362.
- Li L., Wang L., Huang S.W. (2016): Infection process of *Burkholderia glumae* before booting stage of rice. *Journal of Phytopathology*, 164: 825–832.
- Lim J.Y., Lee T.H., Hwang I. (2009): Complete genome sequence of *Burkholderia glumae* BGR1. *Journal of Bacteriology*, 191: 3758–3759.
- Lundberg S.M., Lee S.I. (2017): A unified approach to interpreting model predictions. In: *Advances in Neural Information Processing Systems 30 (NIPS 2017)*, Red Hook, New York: 4765–4774.
- Maeda Y., Shinohara H. (2006): Phylogenetic study and multiplex PCR-based detection of *Burkholderia plantarii*, *Burkholderia glumae* and *Burkholderia gladioli* using *GyrB* and *RpoD* sequences. *International Journal of Systematic and Evolutionary Microbiology*, 56: 1031–1038.
- Maeda Y., Horita M., Hikichi Y. (2007): Analysis of sources of Oxolinic acid-resistant field strains of *Burkholderia glumae* based on Rep-PCR analysis and nucleotide sequences of *GyrB* and *RpoD*. *Journal of General Plant Pathology*, 73: 46–52.
- Meena R., Joshi S., Raghuwanshi S. (2022): Detection of varieties of diseases in rice plants using deep learning techniques. In: *2022 4th International Conference on Inventive Research in Computing Applications (ICIRCA)*, Piscataway: 664–674.
- Mizobuchi R., Sugimoto K., Tsushima S., Fukuoka S., Tsuiki C., Endo M., Sato H. (2023): A *MAPKKK* gene from rice, *RBG1res*, confers resistance to *Burkholderia glumae* through negative regulation of ABA. *Scientific Reports*, 13: 3947.
- Mondal K.K. (2016): Emerging phyto-bacterial diseases in India: research status and challenges. In: Chowdappa P., Sharma P., Singh D., Misra A.K. (eds): *Perspectives of Plant Pathology in Genomic Era*. New India Publishing Agency, New Delhi: 167–178.

- Mulaw T., Wamishe Y., Jia Y. (2018): Characterisation and in plant detection of bacteria that cause bacterial panicle blight of rice. *American Journal of Plant Sciences*, 9: 667–684.
- Nandakumar R., Shahjahan A.K.M., Rush M.C. (2009): *Burkholderia glumae* and *B. gladioli* cause bacterial panicle blight in rice in the Southern United States. *Plant Disease*, 93: 896–905.
- Nandni S., Vishunavat K. (2019): Bacterial panicle blight of rice. *Journal of Pharmacognosy and Phytochemistry*, 8: 918–922.
- Ngalimat M.S., Hata E.M., Yusof M.T. (2021): Characterisation of *Streptomyces spp.* from rice fields as a potential biocontrol agent against *Burkholderia glumae* and rice plant growth promoter. *Agronomy*, 11: 1850.
- Ngalimat M.S., Mohd Hata E., Yusof M.T. (2023): Induction of systemic resistance in rice plants against *Burkholderia glumae* infection by bioformulation of *Streptomyces spp.* under greenhouse conditions. *Biological Control*, 184: 105286.
- Ortega L., Rojas C.M. (2021): Bacterial panicle blight and *Burkholderia glumae*: From pathogen biology to disease control. *Phytopathology*, 111: 772–778.
- Pai D.G., Balachandra M., Kamath R. (2025): Explainable AI in agriculture: review of applications, methodologies, and future directions. *Engineering Research Express*.
- Paz-Carrasco L.C., Intriago-Mendoza L.D., Basso M.F., Celi-Herán R.E. (2018): Prevalence of *Burkholderia glumae* in rice crops in Ecuador. *Journal of Agricultural Science*, 10: 342–352.
- Pérez-Suárez J., Saboya N., Sullon A.A. (2022): Prediction model of the *Burkholderia glumae* pest in rice crops using machine learning and spatial interpolation. *Lecture Notes on Data Engineering and Communications Technologies*, 126: 681–694.
- Quach L.D., Quoc K.N., Ngoc H.T. (2023): Evaluating the effectiveness of YOLO models in different sized object detection and feature-based classification of small objects. *Journal of Advances in Information Technology*, 14: 907–917.
- Quoc K.N., Quach L.D. (2024): Grain rot dataset caused by *Burkholderia glumae* bacteria. *Data in Brief*, 54: 110334.
- Ramachandran K., Vijaya S.I., Zakaria L. (2021): Characterisation and identification of *Burkholderia glumae* as the causal pathogen of bacterial panicle blight of rice (*Oryza sativa* L.) in Malaysian rice granaries. *Journal of General Plant Pathology*, 87: 164–169.
- Rezvi H.U.A., Tahjib-Ul-Arif M., Brestič M. (2023): Rice and food security: Climate change implications and the future prospects for nutritional security. *Food and Energy Security*, 12.
- Riera-Ruiz C., Castro-Lara J., Cevallos-Cevallos J.M. (2018): Interactions of *Burkholderia glumae* and *B. gladioli* in symptom development in rice seeds and seedlings. *Canadian Journal of Plant Pathology*, 40: 347–357.
- Sabri S., Ab Wahab M.Z., Mohd Anuar I.S. (2023): A review of bacterial diseases of rice and its management in Malaysia. *Food Research*, 7: 120–133.
- Sahasranamam V., Ramesh T., Karthikkumar A. (2024): AI and neural network-based approach for paddy disease identification and classification. *International Research Journal of Multidisciplinary Technovation*, 6: 101–111.
- Sandalio L.M., Hossain A., Sánchez-Bermúdez M. (2022): Effects of combined abiotic stresses related to climate change on root growth in crops. *Frontiers in Plant Science*, 13: 918537.
- Sanya D.R.A., Syed-Ab-Rahman S.F., Rohr J.R. (2022): A review of approaches to control bacterial leaf blight in rice. *World Journal of Microbiology and Biotechnology*, 38.
- Savary S., Nelson A., Aunario J. (2012): Modeling and mapping potential epidemics of rice diseases globally. *Crop Protection*, 34: 6–17.
- Schaad N.W. (2008): Emerging plant pathogenic bacteria and global Warming. In: *Pseudomonas syringae* Pathovars and Related Pathogens – Identification, Epidemiology and Genomics. Springer, Dordrecht: 369–379.
- Selvaraju R.R., Cogswell M., Das A., Vedantam R., Parikh D., Batra D. (2017): Grad-CAM: Visual explanations from deep networks via gradient-based localisation. In: *Proceedings of the IEEE International Conference on Computer Vision*. IEEE Computer Society, Piscataway: 618–626.
- Shew A.M., Durand-Morat A., Thoma G. (2019): Warming increases bacterial panicle blight (*Burkholderia glumae*) occurrences and impacts on USA rice production. *PLoS ONE*, 14: e0219199.
- Simhadri C.G., Kondaveeti H.K., Ananthachari P. (2024): Deep learning for rice leaf disease detection: A systematic literature review on emerging trends, methodologies and techniques. *Information Processing in Agriculture*, 12: 151–168.
- Singh D. (2015): Identification of a seed-borne rice bacterium, *Burkholderia glumae* using cultural, morphological, and biochemical methods. *Journal of Applied and Natural Science*, 7: 562–566.
- Song T., Gupta S., Friedman J. (2024): A *Burkholderia Cenocepacia*-like environmental isolate strongly inhibits the plant fungal pathogen *Zymoseptoria Tritici*. *Applied and Environmental Microbiology*, 90: e02222–23.
- Sreenayana B., Mondal K.K., Mani C. (2024): Virulence profiling of emerging Indian strains of *Burkholderia glumae* causing panicle blight of rice. *Journal of Phytopathology*, 172: e13277.
- Upadhyay A., Chandel N.S., Singh K.P., Chakraborty S.K., Nandede B.M., Kumar M., Elbeltagi A. (2025): Deep learning

<https://doi.org/10.17221/33/2025-PPS>

- and computer vision in plant disease detection: A comprehensive review of techniques, models, and trends in precision agriculture. *Artificial Intelligence Review*, 58: 92.
- Valdez-Núñez R.A., Ramos-Luna L.C., Béna G. (2024): genetic diversity and virulence of phytopathogenic *Burkholderia glumae* strains isolated from rice cultivars in valleys of the High Jungle of Perú. *Plant Disease*, 108: 2376–2388.
- Wamishe Y. (2015): Bacterial panicle blight of rice in Arkansas. In: Arkansas Row Crops. University of Arkansas.
- Wang X., Chang X., Ma L., Bai J., Liang M., Yan S. (2023): Global and regional trends in greenhouse gas emissions from rice production, trade, and consumption. *Environmental Impact Assessment Review*, 101: 107141.
- Wu H., Zhang J., Tao F. (2023): AsiaRiceYield4km: Seasonal rice yield in Asia from 1995 to 2015. *Earth System Science Data*, 15: 791–808.
- Xie Y., Liu L., Shen X. (2025): A super convenient and specific CRISPR/Cas12a diagnostic platform for toxigenic *Burkholderia gladioli* based on virulence genes. *Food Control*, 168: 110904.
- Zarbaei S.S., Ham J.H. (2019): An overview of rice QTLs associated with disease resistance to three major rice diseases: Blast, sheath blight and bacterial panicle blight. *Agronomy*, 9: 177.
- Zhang J., Luo J., An Q. (2022): Development of droplet digital PCR assay for detection of seed-borne *Burkholderia glumae* and *B. gladioli* causing bacterial panicle blight disease of rice. *Microorganisms*, 10: 1223.

Received: March 3, 2025

Accepted: February 23, 2026

Published online: September 8, 2026