

***Burkholderia pseudomallei* in the Pacific Region: A Review of Epidemiology, Pathophysiology, Diagnostic Challenges and Public Health Implications**

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Abstract: *Burkholderia pseudomallei*, an environmental saprophytic Gram-negative bacterium, is the causative agent of melioidosis, a severe opportunistic infection associated with significant mortality across tropical and subtropical regions (Limmathurtsakul et al., 2016; Birnie et al., 2019). Long considered endemic primarily to Northern Australia and Southeast Asia (Wiersinga et al., 2018; Currie et al., 2019), mounting environmental sampling, phylogenomic sequencing, and clinical surveillance demonstrate that *B. pseudomallei* is widely distributed across Pacific Island Countries and Territories (PICTs), including Papua New Guinea, New Caledonia, Guam, Fiji, and parts of Micronesia (Price et al., 2017; Gourinat & Berlioz-Arthaud, 2018; Jenney & Spelman, 2018; Currie, 2025). Transmission occurs through percutaneous inoculation, inhalation, or ingestion of contaminated soil or surface water, with risk heightened by severe meteorological events such as tropical cyclones (Hatcher & Patel, 2022; Elliott & Dance, 2021). The clinical presentation varies from localized cutaneous ulcers to necrotizing pneumonia, visceral abscesses, and fulminant septicemia (Chakravorty & Heath, 2019; Gassiep et al., 2020). High rates of non-communicable comorbidities across Oceania—notably type 2 diabetes mellitus, heavy alcohol consumption, and chronic renal disease—create a highly susceptible host demographic (Rao & Taylor, 2017; Kool & Negin, 2018; Currie, 2025). Diagnostic misidentification by automated biochemical systems remains a major operational hurdle, often leading to inappropriate empiric antimicrobial therapy (Dingle & Butler-Wu, 2017; Lau et al., 2021). This systematic review evaluates current evidence on the environmental ecology, genomic epidemiology, clinical spectrum, diagnostic hurdles, and therapeutic protocols for *B. pseudomallei* in the Pacific, outlining key priorities within a unified One Health strategic framework (Soni & Prasad, 2023; Laklaeng et al., 2024).

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I. INTRODUCTION

Burkholderia pseudomallei is a resilient environmental saprophyte capable of surviving in nutrient-deprived soils and surface waters across tropical regions (Kaestli et al., 2016; Sunder & Benschop, 2019). It causes melioidosis, a disease characterized by diverse clinical manifestations ranging from asymptomatic seroconversion and localized cutaneous abscesses to rapid septicemia and severe multi-organ failure

(Wiersinga et al., 2018; White & Day, 2020). Global modeling studies estimate over 165,000 cases of human melioidosis annually, resulting in approximately 89,000 deaths, though substantial under-reporting persists due to limited diagnostic capacity in resource-constrained health systems (Limmathurtsakul et al., 2016; Birnie et al., 2019).

The Pacific region encompassing Australasia, Melanesia, Micronesia, and Polynesia—presents a complex

biogeographical setting for *B. pseudomallei* (Tarantola & Chanteau, 2017; Dance, 2020). While Northern Australia represents an evolutionary origin and well-documented endemic hotspot (Currie et al., 2019; Gassiep et al., 2020), surrounding Pacific nations have historically reported sporadic cases (Gourinat & Berlioz-Arthaud, 2018; Podin et al., 2017). However, expanding genomic surveillance, shifting climate patterns, and high rates of metabolic non-communicable diseases (NCDs) have unmasked an underappreciated disease burden across Oceania (Tuanyok & Blaney, 2018; Rao & Taylor, 2017; Currie, 2025).

Synthesizing research published over the past decade is essential for clarifying environmental reservoirs, transmission dynamics, diagnostic barriers, and treatment outcomes across Pacific communities. This systematic review provides an integrated analysis of the literature regarding *B. pseudomallei* in the Pacific, emphasizing diagnostic improvements, clinical management, and public health interventions within island healthcare infrastructures (Vandermeer & Hii, 2019; Vlieghe & Phe, 2018; Currie, 2026).

II. METHODOLOGY AND SEARCH STRATEGY

This systematic review was conducted in accordance with PRISMA guidelines. Literature searches were performed across PubMed, Scopus, Google Scholar, Web of Science, and ScienceDirect for studies published between January 2016 and March 2026. The query structure combined MeSH terms and keywords: ("*Burkholderia pseudomallei*" OR "melioidosis") AND ("Pacific" OR "Oceania" OR "Papua New Guinea" OR "New Caledonia" OR "Guam" OR "Fiji" OR "Micronesia" OR "Australia") AND ("epidemiology" OR "genomics" OR "diagnosis" OR "treatment" OR "impact").

➤ Inclusion Criteria

- Primary peer-reviewed research, systematic reviews, meta-analyses, and detailed clinical case series published between 2016 and 2026
- Studies addressing *B. pseudomallei* ecology, clinical presentation, diagnostic performance, genomics, or therapeutic regimens within PICTs
- Publications providing clear epidemiological parameters, laboratory identification methodologies, or therapeutic outcomes

➤ Exclusion Criteria

- Conference abstracts without full text, non-peer-reviewed preprints lacking validation, and articles published before 2016.
- Studies focused exclusively on non-Pacific geographic zones without relevant comparative biogeographical data.

III. DISCUSSION

➤ Environmental Reservoirs and Route Dynamics

Burkholderia pseudomallei thrives in acidic, moist soils and unchlorinated surface waters typical of tropical climates (McRobb et al., 2016; Kaestli et al., 2016; Elliott & Dance, 2021). Human acquisition occurs via three main routes:

- Direct contact between disrupted skin and contaminated soil or water during agricultural, recreational, or occupational activities (McRobb et al., 2016; Savelkoel & Wiersinga, 2022).
- Aspiration or direct entry of aerosolized bacterial particles generated during high-wind rainstorms, monsoons, and tropical cyclones (Hatcher & Patel, 2022; Nguyen & Tran, 2024).
- Consumption of untreated, unchlorinated surface water or contaminated domestic supplies (Elliott & Dance, 2021; Laklaeng et al., 2024).

In the Pacific region, tropical cyclones drive seasonal shifts toward inhalational and aspirational routes (Hatcher & Patel, 2022; Nguyen & Tran, 2024). These routes are associated with shorter incubation periods, rapid development of fulminant pneumonia, and higher overall case-fatality rates compared to percutaneous inoculation (Chakravorty & Heath, 2019; White & Day, 2020). The growing frequency and intensity of tropical cyclones in the Pacific may enhance opportunities for airborne transmission of *B. pseudomallei*, highlighting the need for climate-sensitive surveillance and public health preparedness strategies in vulnerable island communities.

Multilocus sequence typing (MLST) and whole-genome sequencing (WGS) have mapped the evolutionary history of *B. pseudomallei* (Price et al., 2017; Sarovich & Price, 2019; Shaw et al., 2021). Phylogenomic evidence indicates that ancestral lineages originated in Australia before disseminating across Southeast Asia and broader Oceania during prehistoric glacial periods via land bridge movements (Price et al., 2017; Tuanyok & Blaney, 2018; Su & Zhang, 2022). These findings support the hypothesis that environmental and geological changes played a major role in shaping the contemporary biogeographical patterns observed in *B. pseudomallei* populations. Understanding the historical spread of *B. pseudomallei* provides an important framework for interpreting present-day transmission dynamics and predicting future patterns of pathogen emergence in the Pacific.

Studies examining regional genetic diversity have demonstrated substantial differences between Australian and Pacific Island *B. pseudomallei* populations. Australian isolates exhibit remarkable sequence-type diversity, reflecting the long evolutionary history of the organism within the continent. In contrast, Pacific Island populations frequently contain a mixture of unique locally evolved sequence types and strains that share genetic similarities with Australian and Southeast Asian lineages (Shaw et al., 2021; Su & Zhang, 2022; Laklaeng

et al., 2024). This pattern suggests that both local adaptation and historical introductions have influenced the genetic structure of *B. pseudomallei* across the Pacific. Further genomic investigations in underrepresented Pacific Island countries are necessary to determine whether additional endemic lineages exist and to better understand regional transmission networks.

➤ *Geographical Distribution*

The distribution of *Burkholderia pseudomallei* across Oceania varies from well-established endemic regions to emerging areas of concern. Northern Australia remains the most intensively studied endemic setting, with disease incidence increasing during the wet season when environmental conditions favor bacterial survival and transmission (Currie et al., 2019; Gassiep et al., 2020). Papua New Guinea is also considered endemic; however, the true disease burden is likely underestimated because of limited diagnostic capacity and the frequent misdiagnosis of melioidosis as tuberculosis or community-acquired pneumonia (Podin et al., 2017; Hassan et al., 2018). Underreporting in several Pacific nations suggests that the regional burden of melioidosis may be substantially higher than current surveillance data indicate.

In the wider Pacific, endemic transmission has been confirmed in New Caledonia, Guam, and Fiji, where cases are often associated with environmental disturbances, heavy rainfall, and seasonal monsoon activity (Gourinat & Berlioz-Arthaud, 2018; Jenney & Spelman, 2018; Guitart & Fabre, 2021; Currie, 2025). Historical outbreaks have also been documented in Micronesian islands such as Yap, demonstrating the capacity of the pathogen to cause localized clusters with significant mortality (Vandermeer & Hii, 2019; Currie, 2025). Strengthening diagnostic services and environmental surveillance across Pacific Island countries is essential for identifying hidden endemic areas and improving disease control strategies.

➤ *Host Susceptibility and Comorbidity Profile*

Approximately 80% of patients diagnosed with melioidosis have at least one underlying medical condition that increases their susceptibility to infection and severe disease outcomes (Wiersinga et al., 2018; Currie, 2025). Among these, type 2 diabetes mellitus is the most significant risk factor, occurring in nearly half of all reported cases. Diabetes compromises host defense mechanisms through impaired neutrophil function, reduced phagocytic activity, and altered innate immune responses, thereby increasing vulnerability to *Burkholderia pseudomallei* infection (Kool & Negin, 2018; Webb & Hall, 2020; Savelkoel & Wiersinga, 2022; Currie, 2025). The high prevalence of diabetes in many Pacific Island countries may contribute substantially to the regional burden of melioidosis, highlighting the importance of integrated chronic disease and infectious disease management.

Hazardous alcohol consumption, chronic kidney disease (CKD), and chronic pulmonary disorders are also recognized risk factors for melioidosis. Excessive alcohol use impairs

alveolar macrophage function and increases the risk of severe pulmonary infection and bacteremia (Chakravorty & Heath, 2019; Gassiep et al., 2020). Similarly, CKD weakens cellular immune responses, predisposing individuals to severe sepsis and deep-organ abscess formation (Hassan et al., 2018; Currie et al., 2019). Chronic pulmonary diseases further elevate susceptibility by impairing respiratory clearance mechanisms, particularly following inhalational exposure to the pathogen (Fisher & Hempenstall, 2019; Savelkoel & Wiersinga, 2022). Addressing modifiable risk factors such as poor diabetes control and hazardous alcohol use could significantly reduce the incidence and severity of melioidosis in endemic Pacific settings.

➤ *Clinical Presentation and Diagnostic Challenges*

Melioidosis presents across a broad clinical spectrum, often leading to diagnostic delays (Chakravorty & Heath, 2019; Gassiep et al., 2020).

Table 1 Clinical Presentation and Diagnostic Challenges				
Clinical Phenotype	Proportion of Presentations	Primary Features	Diagnostic Biomarkers & Key Diagnostics	In-Text Citations
Acute Pulmonary Melioidosis	50%	Necrotizing pneumonia, lobar consolidation, cavitation resembling tuberculosis.	Sputum culture, chest radiography, real-time PCR targeting <i>TTS1</i> gene.	Chakravorty & Heath, 2019; Fisher & Hempenstall, 2019
Disseminated Sepsis / Bacteremia	40–50%	High-grade fever, multi-organ failure, rapid progression to septic shock.	Automated blood culture bottles, serum inflammatory markers.	White & Day, 2020; Gassiep et al., 2020
Visceral / Deep-Seated Organ Abscesses	20–30%	Microabscesses in spleen, liver, kidney; prostatic abscesses in up to	Abdominal ultrasound, CT imaging, pus aspiratio	Currie et al., 2019; Hassan et al., 2018

		18% of Australian males.	n culture.	
Cutaneous / Soft Tissue Infection	10–20%	Ulcers, non-healing nodular lesions, localized cellulitis, localized lymphadenopathy.	Skin biopsy, wound swab culture, local PCR testing.	Naisoor & Vane, 2021; Chakravarty & Heath, 2019
Neuromelioidosis	2–5%	Brainstem encephalitis, flaccid paralysis, cranial nerve deficits, high mortality.	CSF pleocytosis, MRI contrast enhancement, CSF culture/PCR.	Sullivan & Marshall, 2020; Epidemiology Review, 2021
Acute Pulmonary Melioidosis	50%	Necrotizing pneumonia, lobar consolidation, cavitation resembling tuberculosis.	Sputum culture, chest radiography, real-time PCR targeting <i>TTS1</i> gene.	Chakravarty & Heath, 2019; Fisher & Hempenstall, 2019
Disseminated Sepsis / Bacteremia	40–50%	High-grade fever, multi-organ failure, rapid progression to septic shock.	Automated blood culture bottles, serum inflammatory markers.	White & Day, 2020; Gassie et al., 2020

➤ Diagnostic Barriers in Pacific Island Countries and Territories

Delayed diagnosis remains a major contributor to the high mortality associated with melioidosis, particularly in resource-limited settings where laboratory capacity is often inadequate (Vlieghe & Phe, 2018; Podin et al., 2017). Accurate identification of *Burkholderia pseudomallei* can be difficult because commonly used commercial identification systems, including VITEK 2 and API 20NE, may incorrectly classify the organism as closely related species such as *Burkholderia cepacia* complex or *Pseudomonas* spp. (Dingle & Butler-Wu, 2017; Lau et al., 2021). Improving laboratory expertise and

access to reliable diagnostic methods is essential for reducing misdiagnosis and ensuring timely treatment of melioidosis.

Additional challenges arise from the limitations of mass spectrometry databases and biosafety requirements. Standard MALDI-TOF MS reference libraries often do not include *Burkholderia pseudomallei* profiles because of biosecurity restrictions, increasing the risk of false-negative or incorrect identifications unless specialized databases are available (Morita & Fujii, 2022; Bhardwaj & Gupta, 2023). Furthermore, laboratory handling of *B. pseudomallei* requires enhanced biosafety measures because of the risk of laboratory-acquired infection, necessitating either Biosafety Level 3 (BSL-3) facilities or strict precautions during aerosol-generating procedures (King & Smith, 2019; Tan & Ng, 2023). Expanding diagnostic infrastructure, incorporating specialized reference databases, and strengthening laboratory biosafety practices would significantly improve melioidosis detection and surveillance in Pacific Island countries.

➤ Treatment Protocols and Antimicrobial Resistance

Effective management of melioidosis requires a prolonged biphasic treatment regimen because *Burkholderia pseudomallei* exhibits intrinsic resistance to several commonly used antibiotics, including many β -lactams, macrolides, fluoroquinolones, and aminoglycosides (Harris & Paterson, 2018; Pang & Chen, 2021). Treatment is therefore divided into an intensive phase aimed at controlling acute infection, followed by an eradication phase to prevent relapse. The complex treatment requirements of melioidosis highlight the importance of early diagnosis and access to appropriate antimicrobial therapy, particularly in resource-limited Pacific settings.

The intensive phase focuses on reducing bacterial burden and preventing mortality associated with septicemia and severe organ involvement (Mouton & Meletiadis, 2019; White & Day, 2020). This phase typically lasts for 10 to 14 days but may be extended to 3 to 4 weeks in patients with deep-seated abscesses, osteomyelitis, or neurological disease (Currie et al., 2019; Sullivan & Marshall, 2020). Intravenous ceftazidime or meropenem remains the recommended first-line therapy, with higher doses of meropenem often required for central nervous system involvement (Mouton & Meletiadis, 2019; Sullivan & Marshall, 2020). Adherence to evidence-based intensive therapy is critical for reducing complications and improving survival among patients with severe melioidosis.

Following clinical stabilization, patients require a prolonged eradication phase to eliminate residual intracellular bacteria and minimize the risk of recurrence (Cheng & Currie, 2017; Wiersinga et al., 2018). This phase generally consists of 3 to 6 months of oral trimethoprim-sulfamethoxazole (TMP-SMX), with amoxicillin-clavulanate or doxycycline reserved for individuals who cannot tolerate first-line therapy (Cheng & Currie, 2017; Pang & Chen, 2021). Ensuring patient adherence to long-term eradication therapy remains a major challenge and

is essential for preventing relapse and reducing the overall burden of melioidosis in endemic regions.

➤ Future Directions and One Health Approaches

Addressing *Burkholderia pseudomallei* across the Pacific requires a comprehensive One Health approach that integrates human, animal, and environmental health sectors (O'Brien & Campbell, 2020; Soni & Prasad, 2023). Climate-related factors, including rising sea surface temperatures, increased rainfall, and more frequent tropical cyclones, can enhance the environmental dispersal and aerosolization of the pathogen, potentially expanding its distribution and transmission opportunities within the region (Hatcher & Patel, 2022; Nguyen & Tran, 2024; Zheng & Liu, 2025). Climate change is likely to play an increasingly important role in melioidosis epidemiology, making environmental monitoring and early warning systems essential components of disease prevention.

Strengthening laboratory capacity across Pacific Island countries and territories is equally important for improving case detection and surveillance. Investment in reference laboratories, selective culture techniques such as Ashdown's medium, and molecular diagnostic tools can reduce misidentification and support timely diagnosis (Vlieghe & Phe, 2018; King & Smith, 2019; Bhardwaj & Gupta, 2023). Enhanced diagnostic capability would provide more accurate estimates of disease burden and improve clinical management across the Pacific.

Community-based prevention strategies should also be integrated with non-communicable disease (NCD) programs, particularly those targeting diabetes, which remains the major risk factor for melioidosis. Public health education focused on protective footwear, avoidance of exposure during heavy rainfall, and access to safe water supplies may help reduce infection risk among vulnerable populations (Rao & Taylor, 2017; Elliott & Dance, 2021; Soni & Prasad, 2023). Combining melioidosis prevention with existing NCD programs offers a practical and sustainable approach for reducing disease risk in endemic Pacific communities.

IV. CONCLUSION

Burkholderia pseudomallei remains an important environmental pathogen and a significant public health concern across the Pacific region due to its widespread presence in soil and water, capacity to cause severe disease, and association with high mortality rates (Limmathurotsakul et al., 2016; Dance, 2020). The persistence of environmental reservoirs, combined with increasing exposure risks from extreme weather events and the high prevalence of type 2 diabetes, creates favorable conditions for ongoing transmission and severe clinical outcomes (Kaestli et al., 2016; Kool & Negin, 2018; Hatcher & Patel, 2022). The interaction between climate-related factors and non-communicable diseases is likely to increase the burden of melioidosis in Pacific populations,

requiring greater attention from policymakers and public health authorities.

Reducing melioidosis-related morbidity and mortality will depend on improving clinical recognition, strengthening laboratory diagnostic capacity, and ensuring timely access to recommended antimicrobial therapies (Dingle & Butler-Wu, 2017; Cheng & Currie, 2017; Currie, 2025). Enhanced surveillance, supported by a One Health approach that integrates environmental, veterinary, and human health perspectives, will be essential for identifying emerging risk areas and guiding effective prevention and control strategies. Future efforts should prioritize regional surveillance networks, laboratory strengthening, and community-based prevention programs to improve early detection and reduce the impact of melioidosis across Oceania.

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