

Outbreak Reports

Investigation of a Fatal Imported Case of Melioidosis — Jingmen City, Hubei Province, China, May 2026

Kun Sun^{1,2,&}; Man Liu^{3,&}; Xinyang Zhou⁴; Dan Wu⁵; Ziheng Chen⁶; Qi Chen^{3,#}; Yang Wu³

Summary

What is already known about this topic?

Melioidosis, caused by the bacterium *Burkholderia pseudomallei* (*B. pseudomallei*), is endemic in tropical coastal regions.

What is added by this report?

This report describes a fatal imported case of sequence type 55 (ST55) melioidosis from Hainan Province. The patient developed sepsis and multiple organ failure and died within 2 days after admission; the diagnosis was confirmed only after death.

What are the implications for public health practice?

Clinicians in nonendemic areas should consider melioidosis in febrile travelers, obtain a thorough travel history, and use rapid polymerase chain reaction (PCR) diagnostics. Strengthening clinical awareness and laboratory capacity is essential for early detection and improved outcomes.

sequence type 55 (ST55). Based on the patient's epidemiological history, the case was classified as imported from Hainan Province.

Conclusion: This case underscores the need for clinicians in nonendemic regions to consider melioidosis in febrile travelers, obtain a thorough travel history, and use rapid molecular diagnostics, including polymerase chain reaction (PCR). Strengthening clinical awareness and laboratory capacity is essential to improve patient outcomes and public health preparedness.

On May 30, 2026, the Jingmen Center for Disease Control and Prevention (CDC) reported a positive blood culture for *Burkholderia pseudomallei* (*B. pseudomallei*) from a patient at Jingmen People's Hospital who died on May 25. The Hubei CDC immediately initiated an epidemiological investigation to identify the infection source and implement control measures to prevent further transmission.

ABSTRACT

Introduction: Melioidosis, caused by *Burkholderia pseudomallei* (*B. pseudomallei*), is endemic in tropical coastal regions. We report a fatal imported case of melioidosis in Hubei Province, China.

Methods: Clinical and epidemiological data were collected through a retrospective review of electronic medical records and semi-structured interviews with attending physicians and family members. Whole-genome sequencing (WGS) was performed for molecular source tracing.

Results: The patient had fever and palpitations for 2 weeks while in Hainan Province. On illness day 17 (hospital day 1), sepsis and acute kidney injury were evident at admission. Empiric imipenem/cilastatin, the first-line agent for severe *B. pseudomallei* infection, was initiated; however, the patient died of multiple organ failure 2 days later. *B. pseudomallei* was identified only after death, from blood culture. Multilocus sequence typing (MLST) identified the clinical isolate as

INVESTIGATION AND RESULTS

The 59-year-old man denied a history of diabetes or chronic kidney disease. However, ultrasonography on May 23 showed findings consistent with chronic kidney disease and bilateral renal calculi. On May 7, while in Hainan Province, he developed fever and fatigue with dizziness, palpitations, chest tightness, and nausea. His symptoms did not improve after treatment at a local clinic, and he returned to Jingmen on May 20.

At 15:56 on May 23, he presented to a county hospital with intermittent fever (38.3 °C), palpitations, chest tightness, and oliguria. On admission, his creatinine (CREA) was 1,711.3 µmol/L, indicating acute kidney failure and a critical condition, and procalcitonin (PCT) was 23.2 ng/mL, indicating severe infection. Empiric imipenem/cilastatin was initiated.

Nucleic acid and serological tests ruled out common pathogens (Supplementary Table S1, available at <https://weekly.chinacdc.cn/>), and a blood culture was performed.

On May 24, his condition deteriorated to sepsis with multiorgan dysfunction, and his family requested transfer to the municipal hospital. Tests that afternoon showed a marked decrease in white blood cell count (WBC, $1.11 \times 10^9/L$), severe thrombocytopenia [platelet count (PLT), $72 \times 10^9/L$], and elevated inflammatory markers, including C-reactive protein (CRP, 202.45 mg/L) and interleukin-6 (IL-6, >4,000 pg/mL). Hepatic injury worsened, with alanine aminotransferase (ALT) at 120 U/L and aspartate aminotransferase (AST) at 388 U/L. Renal function remained poor, with CREA at 823.5 $\mu\text{mol/L}$ and estimated glomerular filtration rate (eGFR) at 5.52 mL/min per 1.73 m^2 . Myocardial injury was evident, with B-type natriuretic peptide (BNP) >5,000 pg/mL and creatine kinase-myocardial band (CK-MB) at 81 U/L. Urinalysis showed proteinuria (++) , hematuria (++) , and bacteriuria (286.9/ μL), suggesting concurrent urinary tract involvement. Imipenem/cilastatin was continued.

On the morning of May 25, overt disseminated intravascular coagulation (DIC) developed, with platelet count falling to $26 \times 10^9/L$ and D-dimer increasing to 13.11 $\mu\text{g/mL}$ (Supplementary Table S2, available at <https://weekly.chinacdc.cn/>). The family then opted to withdraw treatment. He was discharged at 10:00 and died at home at 12:00 that day.

On May 26, the county hospital's blood culture identified *B. pseudomallei* but was not reported to the

local CDC. On May 30, the municipal hospital's blood culture also identified *B. pseudomallei* and was reported to the municipal CDC (Figure 1). On May 31, the assembled sequence was uploaded to PubMLST (<https://pubmlst.org>; ID: 7855). Comparison of the seven housekeeping genes (*ace*, *gltB*, *gmhD*, *lepA*, *lipA*, *narK*, *ndh*) yielded sequence type 55 (ST55). Phylogenetic analysis of strain HB26JM070BP01 with 65 domestic and geographically proximate *B. pseudomallei* strains assessed evolutionary relationships. It clustered most closely with strain 35 from Dongfang City, Hainan Province, isolated in 2019, at a distance of 3,349 single-nucleotide polymorphisms (SNPs) (Figure 2; Supplementary Table S3, available at <https://weekly.chinacdc.cn/>).

From March through May 20, the patient weeded betel nut nurseries in Hainan Province. Whether he had skin wounds was unknown; however, exposure to warm, moist soil remained a possible route of infection. After returning to Jingmen, he had no symptoms suggestive of bacterial shedding, such as cough, sputum, or vomiting. He lived in a self-built rural house with an independent septic tank, acceptable sanitation, and no obvious pollutants. Bathroom wastewater drained directly into the septic tank. His brother delivered all meals, and no visitors or contacts were recorded before hospitalization. During hospitalization, medical procedures and laboratory testing could have generated aerosols. After he died at home, his brothers bathed the body, and the wastewater drained through the bathroom floor drain into the septic tank. They placed the body in a paper

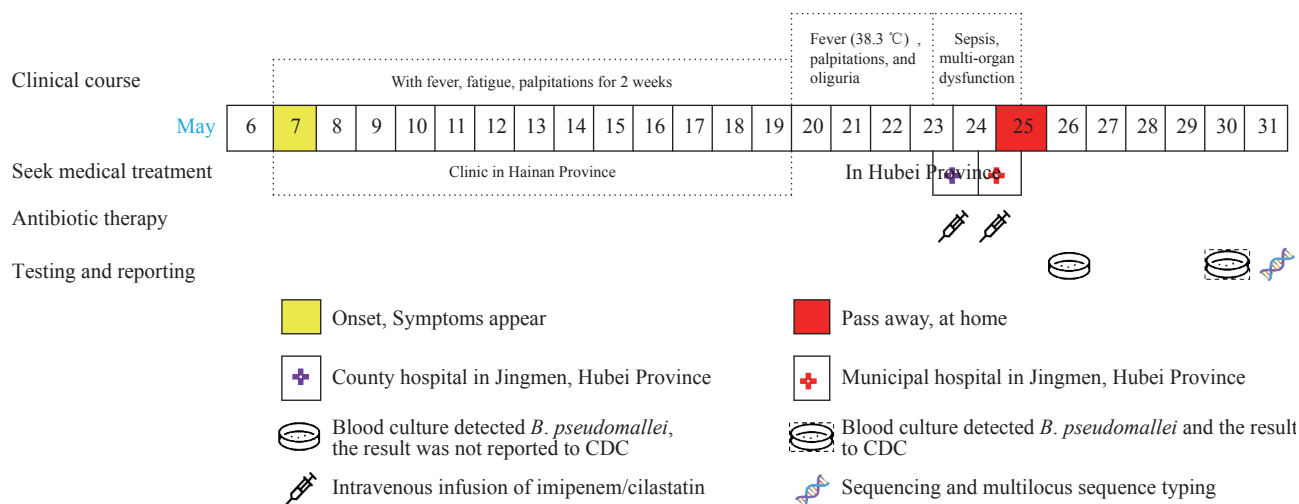


FIGURE 1. The timeline shows the clinical course, antimicrobial therapy, and pathogen identification for a fatal imported case of melioidosis in Hubei, China, 2026.

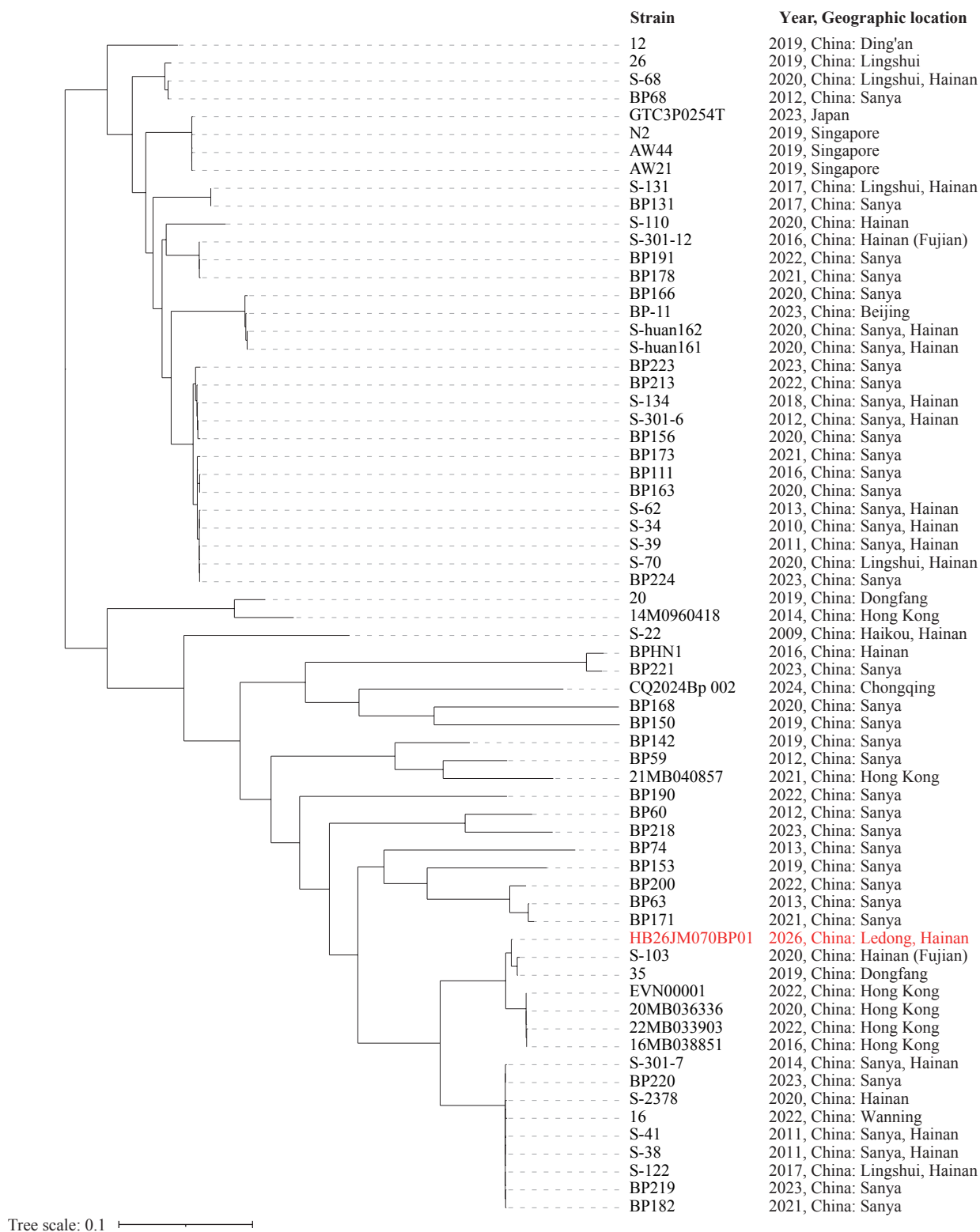


FIGURE 2. The phylogenetic tree comprises 66 *Burkholderia pseudomallei* strains.

coffin and transported it to a crematorium.

Environmental swabs ($n=54$) were collected from his residence ($n=13$; high-touch surfaces, toilet, and other sites), county and municipal hospitals ($n=39$; high-touch surfaces and other sites), and the garbage station ($n=2$; a stretcher and a towel) (Table 1). Blood samples ($n=37$) were obtained from healthcare workers ($n=30$), individuals in direct contact with the deceased ($n=3$),

TABLE 1. The environmental sampling results from Jingmen, Hubei Province, China, 2026.

Sampling location	Total	The number of nucleic acid-positive	The number of nucleic acid-negative
Patient's residence	13	0	13
Garbage station	2	0	2
County hospital			
Department of infectious diseases	3	0	3
Laboratory department	10	0	10
Municipal hospital			
Ambulance	10	0	10
ICU	9	0	9
Laboratory department	7	0	7

Abbreviation: ICU=Intensive Care Unit

and family members ($n=4$). All samples tested negative for *B. pseudomallei* by polymerase chain reaction (PCR).

PUBLIC HEALTH RESPONSE

After the report, public health authorities initiated an epidemiological investigation, identified and monitored close contacts in healthcare, visitation, medical, and funeral settings, collected and tested environmental and clinical samples, and provided health education. Terminal disinfection targeted the septic tank, surfaces exposed to the patient, hospital wards, and transport vehicles.

No symptoms were observed among at-risk personnel during the 21-day monitoring period.

DISCUSSION

This is the first fatal imported melioidosis case reported in Jingmen, Hubei Province. The patient had resided in Hainan Province, where melioidosis is endemic. In 2024, Wuhan, Hubei Province, reported another imported case from Hainan Province, whose isolate was sequence type 46 (ST46), the predominant genotype circulating there (1). Together, these cases suggest that, although melioidosis is not endemic in Hubei, cross-regional importation poses a tangible risk warranting strengthened clinical awareness and public health surveillance.

The isolate belonged to ST55. Molecular epidemiological surveys have consistently identified ST55 as a predominant sequence type of *B. pseudomallei* in Hainan Province, accounting for 8.2% (10/122) – 13.2% (12/91) of clinical isolates, mainly in southwestern Hainan (2–4). He worked in Ledong

County, in southwestern Hainan, consistent with the reported distribution of ST55. His weed control work involved exposure to warm, moist soil, conditions that may facilitate *B. pseudomallei* infection.

The current case shared epidemiological exposures with the Wuhan case, including comparable age, farm work in Hainan Province, high-temperature and high-humidity environments, and daily contact with moist soil and surface water. However, the clinical courses and outcomes differed markedly. In that case, initial symptoms were periumbilical and joint pain, and blood culture confirmed the diagnosis on fever day 3, allowing timely imipenem administration and a favorable outcome (1). In contrast, he had intermittent fever for more than 2 weeks and had already developed sepsis and acute kidney failure by illness day 17, at presentation to the county hospital. Although imipenem, the first-line agent for severe *B. pseudomallei* infection (5), was initiated that day, the optimal therapeutic window had likely been missed, and he died of multiple organ failure. These findings underscore the importance of early pathogen screening and prompt intensified anti-infective therapy, particularly for patients with unexplained fever or sepsis returning from endemic regions.

The clinical manifestations of melioidosis are typically nonspecific and can resemble the common cold, pneumonia, sepsis, or tuberculosis (6–7). Here, he was treated at a local clinic in Hainan Province for nearly 2 weeks without improvement and subsequently presented to county and municipal hospitals in Hubei Province. At admission, he was critically ill, and blood cultures were obtained to identify the causative agent. However, *B. pseudomallei* was identified only after his death. This course highlights insufficient diagnostic awareness among primary care physicians, including

those in endemic areas. Blood culture, the diagnostic mainstay, is also time-consuming and has limited sensitivity, further complicating diagnosis (7–8).

Although autochthonous cases have been reported in inland provinces such as Anhui and Jiangxi, melioidosis remains extremely rare there (9). Healthcare workers in nonendemic regions may therefore have limited awareness of melioidosis and seldom include it in the differential diagnosis for febrile patients. Because melioidosis is not a legally notifiable infectious disease in China, medical institutions may also be less aware of the need to report it. This can delay the public health response and increase the risk of pathogen carriers shedding bacteria in nonendemic areas.

This case has several implications for public health practice in nonendemic regions. First, healthcare providers should maintain a high index of suspicion for melioidosis in febrile patients returning from endemic regions, including southern China and Southeast Asia, particularly those with reported skin wounds and exposure to contaminated soil or water. Second, clinical laboratories in nonendemic regions need diagnostic capacity, including rapid molecular methods such as PCR, to correctly identify *B. pseudomallei* and reduce turnaround time. Third, training in disease recognition and reporting should be strengthened at all levels of medical institutions, particularly county-level hospitals, community health service centers, and primary clinics that may encounter rare or emerging infectious diseases. Finally, CDCs in inland provinces should incorporate melioidosis into travel-related disease surveillance and develop rapid response plans for imported cases.

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* Corresponding author: Qi Chen, qc15671670160@163.com.

¹ Changsha Center for Disease Control and Prevention (Changsha Health Comprehensive Supervision and Law Enforcement Bureau),

Changsha City, Hunan Province, China; ² Chinese Field Epidemiology Training Program, Chinese Center for Disease Control and Prevention & Chinese Academy of Preventive Medicine, Beijing, China; ³ Hubei Provincial Center for Disease Control and Prevention, Wuhan City, Hubei Province, China; ⁴ Jingmen Center for Disease Control and Prevention, Jingmen City, Hubei Province, China; ⁵ Shayang Center for Disease Control and Prevention, Jingmen City, Hubei Province, China; ⁶ Wuxue Center for Disease Control and Prevention, Huanggang City, Hubei Province, China.

& Joint first authors.

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SUPPLEMENTARY MATERIALS

Laboratory Testing Methods

Nucleic Acid Test

Target genes: Real-time fluorescence PCR targeted the 115 bp fragment of the orf2 gene in type III secretion system gene cluster 1 (TTS1) of *B. pseudomallei*. Primers and probes: PCR used primer and probe sequences targeting TTS1-orf2 reported by Novak et al (1). Amplification with Rotor Gene was performed as follows: initial denaturation at 94 °C for 10 min, then 45 cycles of 94 °C for 15 s and 60 °C for 1 min. Cycle threshold (Ct): Samples with a Ct <40 were considered positive.

Genomic DNA Extraction and Sequencing

Total genomic DNA was extracted from inactivated *B. pseudomallei* strains using a bacterial genomic DNA extraction kit [Tiangen Biochemical Technology (Beijing) Co., Ltd., item number DP302]. DNA concentration and OD 260/280 ratio were measured with a NanoDrop Lite spectrophotometer, and DNA integrity and quality were assessed by 1.5% agarose gel electrophoresis. DNA that passed these checks was used directly for library construction, without PCR amplification. Paired-end sequencing was then performed on an Illumina MiSeq platform with a read length of 150 bp (PE150). Sequencing followed standard procedures, and raw data were output in FASTQ format for subsequent bioinformatics analysis.

Multilocus Sequence Typing (MLST)

The assembled sequence was aligned using the PubMLST *B. pseudomallei* MLST database (pubmlst.org/bpseudomallei) to determine the sequence type (ST). The isolated strain was identified as ST55.

Phylogenetic Analysis Method

Genomic Acquisition of Bacterial Strains

A search was conducted in the NCBI Genomes database using *B. pseudomallei* as the keyword, and genomes from China and from geographically proximate countries and regions were screened. Genomic contigs, integrity, and other indicators were also used for screening. Finally, 65 bacterial genomes were included, and the target genome

SUPPLEMENTARY TABLE S1. Hospital-based laboratory findings from nucleic acid and serum antibody testing for pathogens.

Sampling time	Test item	Report time	Method	Results
May 23, 16:13	Respiratory syncytial virus	May 24, 15:03	IgM antibody test	Negative (-)
	Adenovirus			
	Legionella pneumophila			
	Mycoplasma pneumoniae			
	Chlamydia pneumoniae			
	Dengue virus	May 24, 15:49	PCR	Negative (-)
	Chikungunya virus			
	Novel Bunyavirus			
	Influenza A virus			
	Influenza B virus			
May 24, 14:22	Hemorrhagic fever with renal syndrome virus	May 24, 17:03	IgM antibody test	Negative (-)
	Epstein-Barr virus DNA	May 26, 08:18	PCR	Negative (-)
	<i>Burkholderia pseudomallei</i>	May 26, 08:47	Blood culture	Positive (+)
May 24, 14:22	<i>Burkholderia pseudomallei</i>	May 30, 10:08	Blood culture	Positive (+)

Abbreviation: IgM=immunoglobulin M; PCR=polymerase chain reaction.

SUPPLEMENTARY TABLE S2. Dynamic changes in hospital-based laboratory test results for the case.

Test item	Reference range	County People's Hospital		Municipal People's Hospital	
		May 23, 16:13	May 24, 05:48	May 24, 14:00–17:00	May 25, 07:00–08:00
Inflammatory/infectious markers					
PCT (ng/mL)	≤0.5	23.20 ↑	35.31 ↑	57.92 ↑↑	54.80 ↑↑
IL-6 (pg/mL)	≤7.0	358.56 ↑	>5,000 ↑	>4,000 ↑	>4,000 ↑
CRP (mg/L)	≤8.0	110.10 ↑	–	202.45 ↑↑	–
Fer (ng/mL)	27–375	>1,500 ↑	–	–	1,685.30 ↑↑
Blood routine					
WBC (×10 ⁹ /L)	3.5–9.5	9.08	3.32 ↓	1.11 ↓↓	2.22 ↓
RBC (×10 ¹² /L)	4.3–5.8	1.8↓	2.6↓	2.5↓	2.17↓
NEUT (%)	45–75	97.6 ↑	98.2 ↑	94.4 ↑	93.2 ↑
LYM (%)	20–50	1.3 ↓	0.9 ↓	5.5 ↓	4.2 ↓
HGB (g/L)	130–175	54 ↓↓	76 ↓	71 ↓	66 ↓
PLT (×10 ⁹ /L)	125–350	149	110 ↓	72 ↓↓	26 ↓↓↓
DIC trend					
PT (s)	11.5–14.5	15.3 ↑	–	26.3 ↑↑	39.7 ↑↑↑
APTT (s)	29.0–42.0	41.3	–	85.4 ↑↑	80.8 ↑↑
INR	0.8–1.2	1.19	–	2.34 ↑↑	3.95 ↑↑
FIB (g/L)	2.0–4.0	3.84	–	3.12	1.24 ↓↓
DD (μg/mL)	<0.5	11.53 ↑	–	12.32 ↑	13.11 ↑
FDP (μg/mL)	≤5	–	–	50.74 ↑↑	51.65 ↑↑
Liver and kidney function and myocardial injury					
CREA (μmol/L)	57–97	1,711 ↑↑	860.3 ↑↑	823.5 ↑↑	–
BUN (mmol/L)	1.7–8.3	50.76 ↑↑	27.07 ↑↑	27.04 ↑↑	–
eGFR (mL/min per 1.73m ²)	≥90	2.17 ↓↓	5.08 ↓↓	5.52 ↓↓	–
ALT (U/L)	9–50	32	–	120 ↑↑	–
AST (U/L)	8–40	67 ↑	–	388 ↑↑↑	–
LDH (U/L)	135–225	457 ↑	715 ↑	777 ↑↑	–
CK (U/L)	24–190	473 ↑	460 ↑	836 ↑↑	–
CK-MB (U/L)	0–24	22	29 ↑	81 ↑↑	–
hs-cTnl (ng/L)	0–18.5	–	667.0 ↑↑	–	–
hs-cTnT (pg/mL)	≤20.0	–	–	–	299.7 ↑↑
N-terminal pro-BNP (pg/mL)	≤210.64	>35,000 ↑	>35,000 ↑	–	–
BNP (pg/mL)	≤100	–	–	>5,000 ↑↑	–
Electrolyte/acid-base					
K ⁺ (mmol/L)	3.5–5.3	3.73	3.09 ↓	3.18 ↓	–
Na ⁺ (mmol/L)	135–150	128.3 ↓	137.5	135.3 ↓	–
CO ₂ CP (mmol/L)	20–29	7.7 ↓↓	6.8 ↓↓	–	–
Ca ²⁺ (mmol/L)	2.1–2.9	1.63 ↓	2.60	2.08 ↓	–
Urinalysis					
Urine PRO	Negative (–)	–	–	(++)	–
Urine Occult BLD	Negative (–)	–	–	(++)	–
Urine RBC (pcs/μL)	≤10	–	–	15.40 ↑	–

Continued

Test item	Reference range	County People's Hospital		Municipal People's Hospital	
		May 23, 16:13	May 24, 05:48	May 24, 14:00–17:00	May 25, 07:00–08:00
Urine WBC (pcs/ μ L)	≤ 12	–	–	73.30 $\uparrow$	–
Urine Bacteria Count (pcs/ μ L)	≤ 130	–	–	286.90 $\uparrow$	–

Note: $\uparrow$ and $\downarrow$ indicate values above and below the reference range, respectively; two or three arrows indicate progressively greater deviation. – = not tested.

Abbreviation: PCT=procalcitonin; IL-6=interleukin-6; CRP=C-reactive protein; Fer=ferritin; WBC=white blood cell; RBC=red blood cell; NEUT=neutrophil percentage; LYM=lymphocyte percentage; HGB=hemoglobin; PLT=platelet; DIC=disseminated intravascular coagulation; PT=prothrombin time; APTT=activated partial thromboplastin time; INR=international normalized ratio; FIB=fibrinogen; DD=D-dimer; FDP=fibrin/fibrinogen degradation products; CREA=creatinine; BUN=blood urea nitrogen; eGFR=estimated glomerular filtration rate; ALT=alanine aminotransferase; AST=aspartate aminotransferase; LDH=lactate dehydrogenase; CK=creatinine kinase; CK-MB=creatinine kinase-myocardial band; hs-cTnI=high-sensitivity cardiac troponin I; hs-cTnT=high-sensitivity cardiac troponin T; BNP=B-type natriuretic peptide; PRO=protein; BLD=blood.

SUPPLEMENTARY TABLE S3. Single-nucleotide polymorphism (SNP) distances between strain HB26JM070BP01 and 65 *Burkholderia pseudomallei* strains.

Strain	SNP distance	Strain	SNP distance
35	3,349	12	18,232
S-103	4,145	26	18,370
EVN00001	4,888	S-68	18,456
20MB036336	4,896	BP68	18,462
16MB038851	4,903	Reference	18,586
22MB033903	4,947	AW44	18,587
BP220	8,382	AW21	18,589
S-122	8,385	N2	18,594
S-301-7	8,389	BP156	18,607
S-38	8,390	BP-11	18,670
BP219	8,391	S-huan161	18,678
S-2378	8,392	S-huan162	18,679
S-41	8,397	S-39	18,681
BP182	8,399	S-34	18,682
16	8,554	S-62	18,683
BP63	12,694	S-70	18,694
BP200	13,063	BP166	18,702
BP171	13,270	S-110	18,723
BP153	13,992	BP224	18,752
BP74	15,085	14M0960418	18,897
BP60	15,608	BP223	18,897
S-22	15,785	BP163	18,937
BP218	16,004	BP111	18,945
BP190	16,111	BP173	18,966
BP142	16,352	BP213	18,984
21MB040857	16,552	S-134	19,004
BP59	16,850	S-301-6	19,006
S-301-12	17,290	BP150	19,043
BP191	17,606	CQ2024Bp_002	19,166
BP178	17,663	BP168	19,789
BP131	18,063	BPHN1	20,370
S-131	18,063	BP221	20,703
20	18,095		

(HB26JM070BP01) was added. The recommended GTC3P0254T strain (GCF030297255.1) in the NCBI Genomes database was used as the reference genome for SNP analysis.

SNP and Phylogenetic Analysis

SNP analysis of the genomes of the included strains was performed using Snippy (version 4.6.0; Melbourne, Australia). Short-sequence alignment was performed with BWA (version 0.7.18-r1243), mutation detection with FreeBayes (version 1.3.6; Boston, USA), and distance matrices of core and inter-strain SNPs were constructed with Snippy. After recombinant regions were removed using Gubbins (version 2.4.1; Hinxton, UK), phylogenetic analysis was conducted using IQ-TREE2 (version 2.4.0; Vienna, Austria) based on the GTR+ASC model, and 1,000 bootstrap tests were performed. The phylogenetic tree was visualized with iTOL (<https://itol.embl.de/>).

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