

sporotrichosis (10). Cats with sporotrichosis should be kept indoors and apart from other cats in the home to reduce the potential for further transmission. In conclusion, increased awareness of sporotrichosis in cats and the potential for zoonotic transmission could help veterinary professionals more quickly recognize and treat feline cases and take precautions to prevent human acquisition in the veterinary setting.

Acknowledgments

We gratefully acknowledge the cat owners as well as the veterinary technician who shared her experience for this report. We also acknowledge Dr. Karen Wu for facilitating the initial connection between the Kansas veterinary office and CDC.

This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy (e.g., 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. §241(d); 5 U.S.C. §552a; 44 U.S.C. §3501 et seq).

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References

- Rossow JA, Queiroz-Telles F, Caceres DH, Beer KD, Jackson BR, Pereira JG, et al. A One Health approach to combatting *Sporothrix brasiliensis*: narrative review of an emerging zoonotic fungal pathogen in South America. *J Fungi (Basel)*. 2020;6:247. <https://doi.org/10.3390/jof6040247>
- Rees RK, Swartzberg JE. Feline-transmitted sporotrichosis: a case study from California. *Dermatol Online J*. 2011;17:2. <https://doi.org/10.5070/D30459K1JB>
- Reed KD, Moore FM, Geiger GE, Stemper ME. Zoonotic transmission of sporotrichosis: case report and review. *Clin Infect Dis*. 1993;16:384-7. <https://doi.org/10.1093/clind/16.3.384>
- de Miranda LHM, Silva JN, Gremião IDF, Menezes RC, Almeida-Paes R, Dos Reis ÉG, et al. Monitoring fungal burden and viability of *Sporothrix* spp. in skin lesions of cats for predicting antifungal treatment response. *J Fungi (Basel)*. 2018;4:92. <https://doi.org/10.3390/jof4030092>
- Reis ÉG, Schubach TMP, Pereira SA, Silva JN, Carvalho BW, Quintana MSB, et al. Association of itraconazole and potassium iodide in the treatment of feline sporotrichosis: a prospective study. *Med Mycol*. 2016;54:684-90. <https://doi.org/10.1093/mmy/myw027>
- Gremião IDF, Martins da Silva da Rocha E, Montenegro H, Carneiro AJB, Xavier MO, de Farias MR, et al. Guideline for the management of feline sporotrichosis caused by *Sporothrix brasiliensis* and literature revision. *Braz J Microbiol*. 2021;52:107-24. <https://doi.org/10.1007/s42770-020-00365-3>
- Barnacle JR, Chow YJ, Borman AM, Wyllie S, Dominguez V, Russell K, et al. The first three reported cases of *Sporothrix brasiliensis* cat-transmitted sporotrichosis outside South America. *Med Mycol Case Rep*. 2023;39:14-7. <https://doi.org/10.1016/j.mmcr.2022.12.004>
- Yingchanakiat K, Limsivilai O, Sunpongsri S, Niyomtham W, Lugsomya K, Yurayart C. Phenotypic and genotypic characterization and antifungal susceptibility of *Sporothrix schenckii sensu stricto* isolated from a feline sporotrichosis outbreak in Bangkok, Thailand. *J Fungi (Basel)*. 2023;9:590. <https://doi.org/10.3390/jof9050590>
- Welsh RD. Sporotrichosis. *J Am Vet Med Assoc*. 2003;223:1123-6. <https://doi.org/10.2460/javma.2003.223.1123>
- Crothers SL, White SD, Ihrke PJ, Affolter VK. Sporotrichosis: a retrospective evaluation of 23 cases seen in northern California (1987-2007). *Vet Dermatol*. 2009;20:249-59. <https://doi.org/10.1111/j.1365-3164.2009.00763.x>

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***Burkholderia thailandensis* Isolated from Infected Wound, Southwest China, 2022**

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DOI: <http://doi.org/10.3201/eid3005.230743>

We report a clinical isolate of *Burkholderia thailandensis* 2022DZh obtained from a patient with an infected wound in southwest China. Genomic analysis indicates that this isolate clusters with *B. thailandensis* BPM, a human isolate from Chongqing, China. We recommend enhancing monitoring and surveillance for *B. thailandensis* infection in both humans and livestock.

Burkholderia thailandensis is a member of the *Burkholderia pseudomallei* complex and is generally considered nonpathogenic (1). Initially identified in Thailand, *B. thailandensis* was distinguished from *B. pseudomallei* by its ability to assimilate arabinose (2). Similar to *B. pseudomallei*, *B. thailandensis* is frequently found in soil and water, especially in rice paddies (3,4). Although invasive infections caused by *B. thailandensis* are rare worldwide, recent reports have documented cases of suppurative infections, such as wound infections, cellulitis, and tissue abscesses (5,6). Previously, we identified a strain of *B. thailandensis* BPM that caused a human infection in Chongqing, southwest China (7). In this study, we report another clinical isolate of *B. thailandensis* that we obtained in Dazhu, Sichuan, southwest China, from an infected wound resulting from a cut inflicted by a farm tool in 2022.

A 61-year-old male farmer who had untreated type 2 diabetes mellitus reported a 1-month history of pain and swelling in his left knee. He had injured the middle toe of his left foot with a plow a month earlier, and redness, swelling, and pain developed below the left knee joint. Despite a week of antimicrobial treatment at a local community health center, his symptoms did not improve. In December 2022, the patient began to experience weakness in his right lower limb,

and he later fell, sustaining an injury to his left lower limb. During this period, he experienced lower-limb weakness and exhibited symptoms related to the central nervous system. He sought care and was admitted to the orthopedics department of Dazhu County People's Hospital (Dazhou, China) for treatment of a left lower-limb injury and a left-foot diabetic foot infection. However, because his central nervous system symptoms worsened, he was transferred to the neurology department and receive a diagnosis of osteomyelitis and demyelinating disease. *B. thailandensis* strain 2022DZh was obtained from a deep-tissue specimen during surgical debridement of the infected wound on the left foot (Appendix Figure 1, <https://wwwnc.cdc.gov/EID/article/30/5/23-0743-App1.pdf>). The initial empirical antimicrobial therapy consisted of cefradine. However, the hospital laboratory tested the isolate 2022DZh using the VITEK 2 COMPACT system (bioMérieux, <https://www.biomerieux.com>) and identified it as *B. pseudomallei*, leading to a switch to intravenous meropenem treatment (Appendix Table 1). Despite treatment with meropenem, the patient's condition continued to deteriorate; he died 3 days after applying for discharge.

Subsequently, the isolate 2022DZh was submitted to the laboratory for confirmatory identification.

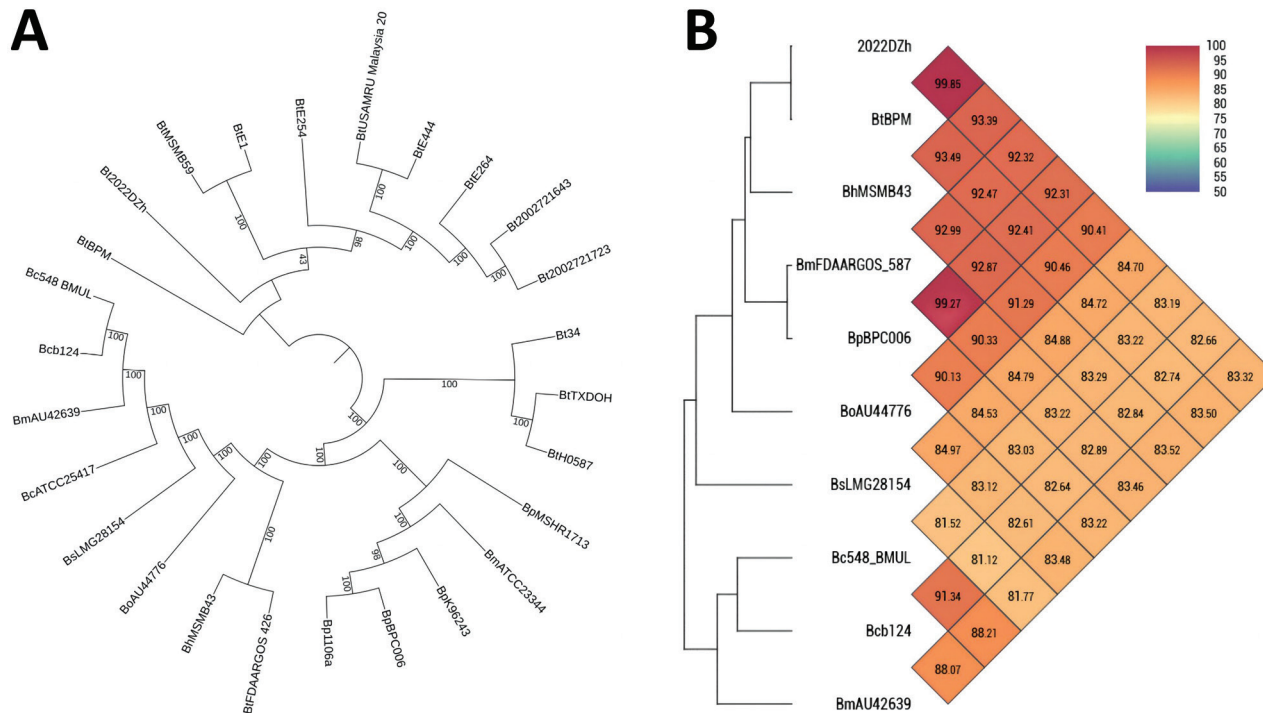


Figure. Analysis of the single-copy gene phylogenetic tree and average nucleotide identity for genomes of *Burkholderia thailandensis* 2022DZh from a patient in Dazhu, Sichuan, China, and other isolates from *Burkholderia* species. A) Single-copy gene phylogenetic tree created using the genomes of *B. thailandensis* 2022DZh and 25 other isolates from various *Burkholderia* species. B) Average nucleotide identity heatmap developed using genomes of *B. thailandensis* 2022DZh and 9 other isolates from various *Burkholderia* species.

Results of arabinose assimilation testing of isolate 2022DZh by API 20NE system (bioMérieux) were positive, consistent with the biochemical characteristics of *B. thailandensis* (Appendix Figure 2). We extracted DNA from the isolate 2022DZh for confirmation and further characterization. We performed 16S rRNA gene sequencing of 2022DZh using nucleotide BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), revealing 100% similarity with *B. thailandensis* BPM (Appendix Figure 3). The nucleotide sequences of the 2 chromosomes of isolate 2022DZh are >99.5% consistent with those of *B. thailandensis* E264 and *B. thailandensis* E254 (Appendix Table 2). We conclusively identified isolate 2022DZh as *B. thailandensis* based on our phenotypic and molecular data. We deposited the genome sequences of *B. thailandensis* strain 2022DZh into GenBank (accession nos. CP141809.1 and CP141811.1).

For phylogenetic analysis, we compared the genome of *B. thailandensis* 2022DZh with a reference panel of publicly available *Burkholderia* species genomes (Appendix Table 3). The single-copy gene phylogenetic tree analysis indicated that *B. thailandensis* 2022DZh clusters with *B. thailandensis* BPM (Figure, panel A). The results of average nucleotide identity revealed that *B. thailandensis* 2022DZh also clusters with *B. thailandensis* BPM; genome identity was 99.85%. However, when compared with *B. pseudomallei* BPC006, genome identity was 92.31% (Figure, panel B), consistent with the commonly used 95% threshold for distinguishing species. Through multilocus sequence type analysis (<https://pubmlst.org/organisms/burkholderia-pseudomallei>) (8), we determined that *B. thailandensis* 2022DZh and *B. thailandensis* BPM both belong to sequence type 76. In addition, there appears to be no known epidemiologic link between *B. thailandensis* 2022DZh and *B. thailandensis* BPM; they are geographically separated by a significant distance of ≈ 200 km (Appendix Table 3).

One limitation of this study is that we did not attempt to identify related isolates of *B. thailandensis* from environmental samples in this region of southwest China. Further studies are needed to identify the primary molecular mechanisms underlying the pathogenicity of *B. thailandensis* 2022DZh and to determine its molecular and evolutionary relationships with other strains of *B. thailandensis* (9).

In conclusion, our findings underscore that *B. thailandensis* can cause serious infections, and clinical practitioners should be aware of this type of infection (10). Therefore, we strongly recommend enhancing monitoring and surveillance for *B. thailandensis* infection in both humans and livestock.

This work was supported by the National Natural Science Foundation of China (82072348) and the Youth Project of the National Natural Science Foundation of China (82002113).

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References

- Ronning CM, Losada L, Brinkac L, Inman J, Ulrich RL, Schell M, et al. Genetic and phenotypic diversity in *Burkholderia*: contributions by prophage and phage-like elements. *BMC Microbiol.* 2010;10:202. <https://doi.org/10.1186/1471-2180-10-202>
- Lertpatanasuwan N, Sermsri K, Petkaseam A, Trakulsomboon S, Thamlikitkul V, Suputtamongkol Y. Arabinose-positive *Burkholderia pseudomallei* infection in humans: case report. *Clin Infect Dis.* 1999;28:927-8. <https://doi.org/10.1086/517253>
- Birnie E, van 't Hof S, Bijnsdorp A, Mansaray Y, Huizenga E, van der Ende A, et al. Identification of *Burkholderia thailandensis* with novel genotypes in the soil of central Sierra Leone. *PLoS Negl Trop Dis.* 2019;13:e0007402. <https://doi.org/10.1371/journal.pntd.0007402>
- Hall CM, Stone NE, Martz M, Hutton SM, Santana-Propper E, Versluis L, et al. *Burkholderia thailandensis* isolated from the environment, United States. *Emerg Infect Dis.* 2023;29:618-21. <https://doi.org/10.3201/eid2903.221245>
- Gee JE, Elrod MG, Gulvik CA, Haselow DT, Waters C, Liu L, et al. *Burkholderia thailandensis* isolated from infected wound, Arkansas, USA. *Emerg Infect Dis.* 2018;24:2091-4. <https://doi.org/10.3201/eid2411.180821>
- Glass MB, Gee JE, Steigerwalt AG, Cavuoti D, Barton T, Hardy RD, et al. Pneumonia and septicemia caused by *Burkholderia thailandensis* in the United States. *J Clin Microbiol.* 2006;44:4601-4. <https://doi.org/10.1128/JCM.01585-06>
- Chang K, Luo J, Xu H, Li M, Zhang F, Li J, et al. Human infection with *Burkholderia thailandensis*, China, 2013. *Emerg Infect Dis.* 2017;23:1416-8. <https://doi.org/10.3201/eid2308.170048>
- Tuanyok A, Mayo M, Scholz H, Hall CM, Allender CJ, Kaestli M, et al. *Burkholderia humptydoensis* sp. nov., a new species related to *Burkholderia thailandensis* and the fifth member of the *Burkholderia pseudomallei* complex. *Appl Environ Microbiol.* 2017;83:e02802-16. <https://doi.org/10.1128/AEM.02802-16>
- Li J, Zhong Q, Li J, Chong HM, Wang LX, Xing Y, et al. Genomic features and virulence characteristics of a rare *Burkholderia thailandensis* strain causing human infection. *J Med Microbiol.* 2023;72:72. <https://doi.org/10.1099/jmm.0.001688>
- Cossaboom CM, Marinova-Petkova A, Stryko J, Rodriguez G, Maness T, Ocampo J, et al. Melioidosis in a resident of Texas with no recent travel history, United States. *Emerg Infect Dis.* 2020;26:1295-9. <https://doi.org/10.3201/eid2606.190975>

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Article DOI: <http://doi.org/10.3201/eid3005.230743>

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Burkholderia thailandensis Isolated from Infected Wound, Southwest China, 2022

Appendix

Appendix Table 1. Antibiotic susceptibility testing results of *B. thailandensis* 2022DZh

Antimicrobial	MIC	Interpretation
Amoxicillin/clavulanate	≤4	S
Ceftazidime	2	S
Imipenem	≤1	S
Tetracycline	4	S
Doxycycline	≤0.5	S
Trimethoprim/sulfamethoxazole	40	S

Appendix Table 2. The Nucleotide Sequence Database (NT) identified strain 2022DZh as *B. thailandensis**

Query_name	Query_ length	Query_ start	Query_ end	Hit_name	Hit_description	Hit_length	Hit_start	Hit_end	Aln_length	Identity
chr1	3804194	627187	941171	CP008785.1	<i>Burkholderia thailandensis</i> E264 chromosome 1, complete sequence	3986340	1022844	1336839	314053	99.90320105 20517
chr2	2860001	831328	941171	CP004382.1	<i>Burkholderia thailandensis</i> E254 chromosome 2, complete sequence	2870750	2145935	2478653	332805	99.87410044 9212
plasmid1	215545	135181	157561	CP013426.1	<i>Burkholderia</i> sp. MSMB0856 plasmid pMSMB0856, complete sequence	249331	8541	30930	22395	98.04420629 60482

*The NT database is the Nucleotide Sequence Database, and the link is <http://www.ncbi.nlm.nih.gov>

Appendix Table 3. Genomes of additional *Burkholderia* species isolates used for single-copy gene phylogenetic tree analysis and average nucleotide identity (ANI) analysis in the study of *B. thailandensis* 2022DZh

Isolate	Abbreviation	Origin	Year	Source	MLST	GenBank accession no.
<i>B. thailandensis</i> H0587	BtH0587	USA	1997	Clinical (Human)	101	NZ_CP004089.1; NZ_CP004090.1
<i>B. thailandensis</i> BPM	BtBPM	China	2013	Clinical (Human)	76	NZ_CP050020.1; NZ_CP050021.1
<i>B. thailandensis</i> E264	BtE264	Thailand	1994	Environmental (soil)	80	NZ_CP008785.1; NZ_CP008786.1
<i>B. thailandensis</i> E254	BtE254	Thailand	1992	Environmental (soil)	345	NZ_CP004381.1; NZ_CP004382.1
<i>B. thailandensis</i> E444	BtE444	Thailand	2002	Environmental (soil)	79	NZ_CP004117.1; NZ_CP004118.1
<i>B. thailandensis</i> MSMB59	BtMSMB59	Australia	2006	Environmental (soil)	669	NZ_CP004385.1; NZ_CP004386.1
<i>B. thailandensis</i> USAMRU Malaysia 20	BtUSAMRU Malaysia 20	Malaysia	2015	Unknown	80	NZ_CP004383.1; NZ_CP004384.1
<i>B. thailandensis</i> 34	Bt34	USA	2002	Unknown	73	NZ_CP010017.1; NZ_CP010018.1
<i>B. thailandensis</i> 2002721723	Bt2002721723	USA	2013	Clinical (Human)	80	NZ_CP004098.1; NZ_CP004097.1
<i>B. thailandensis</i> 2002721643	Bt2002721643	USA	2002	Unknown	80	NZ_CP009601.1; NZ_CP009602.1
<i>B. thailandensis</i> E1	BtE1	Papua New Guinea	1995	Environmental (soil)	669	NZ_LOXF00000000.1
<i>B. thailandensis</i> TXDOH	BtTXDOH	USA	2003	Clinical (Human)	101	NZ_ABBD00000000.1
<i>B. thailandensis</i> FDAARGOS_426	BtFDAARGOS_426	Malaysia	2017	Environmental (soil)	1023	NZ_CP023499.1; NZ_CP023498.1
<i>B. pseudomallei</i> K96243	BpK96243	Thailand	1993	Clinical (Human)	10	NZ_CP009538.1; NZ_CP009537.1
<i>B. pseudomallei</i> BPC006	BpBPC006	China	2008	Clinical (Human)	70	NZ_CP003781.1; NZ_CP003782.1
<i>B. pseudomallei</i> 1106a	Bp1106a	Thailand	2008	Clinical (Human)	70	NZ_CP008758.1; NZ_CP008759.1
<i>B. pseudomallei</i> MSHR1713	BpMSHR1713	Australia	2003	Clinical (Human)	131	NZ_CP111138.1; NZ_CP111139.1
<i>B. pseudomallei</i> MSHR1046	BpMSHR1046	Australia	2000	Clinical (Human)	131	NZ_CP111140.1; NZ_CP111141.1

Isolate	Abbreviation	Origin	Year	Source	MLST	GenBank accession no.
<i>B. mallei</i> ATCC23344	BmATCC23344	USA	1942	Clinical (Human)	40	NZ_CP124608.1; NZ_CP124607.1
<i>B. singularis</i> LMG 28154	BsLMG 28154	Canada	2003	Clinical (Human)	166	NZ_FXAN01000000
<i>B. oklahomensis</i> AU44776	BoAU44776	USA	2022	Clinical (Human)	1772	NZ_JAUJRD000000000.1
<i>B. cepacia</i> b124	Bcb124	Bangladesh	2017	Clinical (Human)	140	NZ_SNSI01000000
<i>B. cenocepacia</i> 548_BMUL	Bc548_BMUL	USA	2016	Clinical (Human)	162	NZ_JVCQ01000000
<i>B. multivorans</i> AU42639	BmAU42639	USA	2020	Clinical (Human)	79	NZ_JAHPLO010000000
<i>B. cocovenenans</i> ATCC25417	BcATCC25417	USA	2012	Environmental (leaves)	101	NZ_JPGG000000000.1
<i>B. mallei</i> FDAARGOS_587	BmFDAARGOS_587	USA	1961	Environmental (Horse)	40	NZ_RKJX000000000.1
<i>B. humptydoensis</i> MSMB43	BhMSMB43	Australia	1995	Environmental (Water)	318	NZ_AJXB000000000.1



Appendix Figure 1. Morphologic features of left-foot diabetic foot infection caused by *B. thailandensis* 2022DZh in a patient in Dazhu, Sichuan, China. A) Result of surgical debridement

of a wound in the 61-year-old male patient. B) Colony morphology of *B. thailandensis* 2022DZh from the patient on a Columbia blood plate.



Appendix Figure 2. The biochemical profiles of the API 20NE system, including arabinose assimilation, identified isolate 2022DZh as *B. thailandensis*.

Sequences producing significant alignments Download Select columns Show 100

select all 100 sequences selected GenBank Graphics Distance tree of results MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Burkholderia thailandensis strain BPM chromosome 2, complete sequence	Burkholderia thailandensis	2542	2542	100%	0.0	100.00%	2875717	CP050021.1
Burkholderia thailandensis strain BPM chromosome 1, complete sequence	Burkholderia thailandensis	2542	7826	100%	0.0	100.00%	3725540	CP050020.1
Burkholderia thailandensis strain FDAARGOS_242 chromosome 1, complete sequence	Burkholderia thailandensis	2542	7808	100%	0.0	100.00%	3801254	CP022217.1
Burkholderia thailandensis strain FDAARGOS_242 chromosome 2, complete sequence	Burkholderia thailandensis	2542	2542	100%	0.0	100.00%	2852057	CP022218.1
Burkholderia thailandensis strain FDAARGOS_237 chromosome 1, complete sequence	Burkholderia thailandensis	2542	7818	100%	0.0	100.00%	3819771	CP020390.1
Burkholderia thailandensis strain MSMB59 chromosome 2, complete sequence	Burkholderia thailandensis	2542	2542	100%	0.0	100.00%	2822193	CP013408.1
Burkholderia thailandensis strain MSMB59 chromosome 1, complete sequence	Burkholderia thailandensis	2542	7826	100%	0.0	100.00%	3917337	CP013407.1
Burkholderia thailandensis 2002721643 chromosome II, complete sequence	Burkholderia thailandensis 2002721643	2542	2542	100%	0.0	100.00%	2914772	CP009802.1
Burkholderia thailandensis 2002721643 chromosome I, complete sequence	Burkholderia thailandensis 2002721643	2542	7826	100%	0.0	100.00%	3808029	CP009801.1
Burkholderia thailandensis E254 chromosome 2, complete sequence	Burkholderia thailandensis E254	2542	2542	100%	0.0	100.00%	2870750	CP004382.1
Burkholderia thailandensis E254 chromosome 1, complete sequence	Burkholderia thailandensis E254	2542	7820	100%	0.0	100.00%	3805680	CP004381.1
Burkholderia thailandensis MSMB59 chromosome 2, complete sequence	Burkholderia thailandensis MSMB59	2542	2542	100%	0.0	100.00%	2823178	CP004388.1
Burkholderia thailandensis MSMB59 chromosome 1, complete sequence	Burkholderia thailandensis MSMB59	2542	7820	100%	0.0	100.00%	3916324	CP004385.1
Burkholderia thailandensis E264 chromosome 2, complete sequence	Burkholderia thailandensis E264	2542	5078	100%	0.0	100.00%	2735759	CP008788.1
Burkholderia thailandensis E264 chromosome 1, complete sequence	Burkholderia thailandensis E264	2542	5078	100%	0.0	100.00%	3986340	CP008785.1
Burkholderia thailandensis USAMRU Malaysia #20 chromosome 2, complete sequence	Burkholderia thailandensis USAMRU...	2542	2542	100%	0.0	100.00%	2821713	CP004384.1
Burkholderia thailandensis USAMRU Malaysia #20 chromosome 1, complete sequence	Burkholderia thailandensis USAMRU...	2542	7815	100%	0.0	100.00%	3882848	CP004383.1
Burkholderia thailandensis E444 chromosome 2, complete sequence	Burkholderia thailandensis E444	2542	2542	100%	0.0	100.00%	2852101	CP004118.1
Burkholderia thailandensis E444 chromosome 1, complete sequence	Burkholderia thailandensis E444	2542	7818	100%	0.0	100.00%	3799595	CP004117.1
Burkholderia thailandensis 2002721723 chromosome 2, complete sequence	Burkholderia thailandensis 2002721723	2542	2542	100%	0.0	100.00%	2914718	CP004098.1
Burkholderia thailandensis 2002721723 chromosome 1, complete sequence	Burkholderia thailandensis 2002721723	2542	7826	100%	0.0	100.00%	3682415	CP004097.1
Burkholderia thailandensis strain AW34-19p chromosome 2, complete sequence	Burkholderia thailandensis	2542	2542	100%	0.0	100.00%	2826723	CP008710.1
Burkholderia thailandensis strain AW34-19p chromosome 1, complete sequence	Burkholderia thailandensis	2542	7484	100%	0.0	100.00%	3830943	CP008709.1
Burkholderia thailandensis E264 chromosome I, complete sequence	Burkholderia thailandensis E264	2542	7826	100%	0.0	100.00%	3809201	CP000088.1
Burkholderia thailandensis E264 16S ribosomal RNA, partial sequence	Burkholderia thailandensis E264	2538	2538	100%	0.0	99.93%	1529	NR_074312.2
Burkholderia thailandensis E264 chromosome II, complete sequence	Burkholderia thailandensis E264	2538	2538	100%	0.0	99.93%	2914771	CP000085.1
Burkholderia thailandensis strain FDAARGOS_241 chromosome 2, complete sequence	Burkholderia thailandensis	2534	2534	100%	0.0	99.93%	2821680	CP022215.1
Burkholderia thailandensis strain FDAARGOS_237 chromosome 2, complete sequence	Burkholderia thailandensis	2534	2534	100%	0.0	99.93%	2853041	CP020389.1
Burkholderia thailandensis strain BD10-00323 16S ribosomal RNA, partial sequence	Burkholderia thailandensis	2534	2534	99%	0.0	100.00%	1459	NR_118829.1
Burkholderia thailandensis strain BD11-00023 16S ribosomal RNA gene, partial sequ...	Burkholderia thailandensis	2534	2534	99%	0.0	100.00%	1485	KF444905.1
Burkholderia thailandensis strain BD11-00022 16S ribosomal RNA gene, partial sequ...	Burkholderia thailandensis	2534	2534	99%	0.0	100.00%	1457	KF444904.1
Burkholderia thailandensis E264 16S ribosomal RNA, partial sequence	Burkholderia thailandensis E264	2531	2531	99%	0.0	100.00%	1541	NR_118051.1
Burkholderia thailandensis strain 2002721627 16S ribosomal RNA gene, partial sequ...	Burkholderia thailandensis	2531	2531	99%	0.0	100.00%	1488	AY268182.1
Burkholderia thailandensis strain FDAARGOS_241 chromosome 1, complete sequence	Burkholderia thailandensis	2529	7554	100%	0.0	99.85%	3882584	CP022214.1

Appendix Figure 3. The 16S rRNA gene sequencing of strain 2022DZh using nucleotide BLAST.