

The diagnosis of these cases showed the surveillance system of Senegal's capacity to quickly detect, isolate, and investigate those cases to take adequate control measures. Our findings indicate that the earliest cases in Senegal or sub-Saharan Africa were imported from Europe, implying that the particularly high volume of direct flights from Europe was a key factor in the spread of the virus in West Africa. However, we cannot exclude the possibility that a few COVID-19 cases were missed at that time in Senegal, including paucisymptomatic or asymptomatic cases (4,5). Our study emphasizes the imperative need for efficient epidemiologic investigations to identify the cases and characterize the transmission modes to prevent, control, and stop the spread of COVID-19.

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References

1. World Health Organization Regional Office for the Eastern Mediterranean. Update on COVID-19 in the Eastern Mediterranean Region, 16 February 2020 [cited 2020 Sep 8]. <http://www.emro.who.int/media/news/update-on-covid-19-in-the-eastern-mediterranean-region.html>
2. World Health Organization Regional Office for Africa. COVID-19 situation update for WHO African region, 4 March 2020 [cited 2020 Sep 8]. https://apps.who.int/iris/bitstream/handle/10665/331330/SITREP_COVID-19_WHOAFRO_20200304-eng.pdf
3. World Health Organization. Global surveillance for human infection with novel coronavirus (2019-nCoV): interim guidance, 21 January 2020 [cited 2020 Sep 16]. <https://www.who.gov.et/images/20200121-global-surveillance-for-2019-ncov.pdf>
4. Rothe C, Schunk M, Sothmann P, Bretzel G, Froeschl G, Wallrauch C, et al. Transmission of 2019-nCoV infection from an asymptomatic contact in Germany. *N Engl J Med*. 2020;382:970-1. <https://doi.org/10.1056/NEJMc2001468>
5. Spiteri G, Fielding J, Diercke M, Campese C, Enouf V, Gaymard A, et al. First cases of coronavirus disease 2019 (COVID-19) in the WHO European Region, 24 January to 21 February 2020. *Euro Surveill*. 2020;25. <https://doi.org/10.2807/1560-7917.ES.2020.25.9.2000178>

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Burkholderia pseudomallei in Soil, US Virgin Islands, 2019

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The distribution of *Burkholderia pseudomallei* in the Caribbean is poorly understood. We isolated *B. pseudomallei* from US Virgin Islands soil. The soil isolate was genetically similar to other isolates from the Caribbean, suggesting that *B. pseudomallei* might have been introduced to the islands multiple times through severe weather events.

Burkholderia pseudomallei is a gram-negative soil-dwelling bacterium and the causative agent of melioidosis (1). *B. pseudomallei* is endemic to tropical regions around the world (1), but its environmental distribution in the Caribbean remains poorly understood. Although it is rare but ecologically established in Puerto Rico (2,3), it has not been isolated from the environment in the neighboring US Virgin Islands (USVI). After the 2017 Caribbean hurricane season, melioidosis developed in 3 persons in the USVI (4), 2 in St. Thomas and 1 in St. John. We aimed to determine whether, as this cluster suggests, *B. pseudomallei* might be endemic to the USVI.

We collected 480 soil and 100 freshwater samples from 29 sites (24 terrestrial and 5 freshwater) on the 3 main USVI islands (i.e., St. Thomas, St. John, and St. Croix) during January 20–April 17, 2019. We selected study sites to maximize geographic distribution across the islands and epidemiologic connection to melioidosis cases in humans (Appendix Figure 1, <https://wwwnc.cdc.gov/EID/article/26/11/19-1577-App1.pdf>). These efforts followed consensus guidelines for environmental sampling of *B. pseudomallei* (5) and

methods previously reported (2) with 4 modifications: we collected 20 samples per site; we collected soil samples in 2 linear transects of 10 samples each; we collected 150 mL water per sample; and we used half of each sample for our analysis (the other half was archived). Although we strove for a sampling depth of 30 cm in soil, this was impossible at some sites because of rocks and debris (Appendix Table 1). We placed environmental samples in Ashdown’s liquid media for *Burkholderia* spp. enrichment (2). After enrichment, we extracted DNA using QiaAmp kits (QIAGEN, <https://www.qiagen.com>) and screened it using a *B. pseudomallei*-specific TaqMan assay (ThermoFisher Scientific, <https://www.thermofisher.com>)

(6,7). We cultured samples to isolate pure *B. pseudomallei* and generate whole-genome sequences (WGSs). We conducted a phylogenetic analysis as previously described (2) and conducted genetic typing on these WGSs, WGSs from the 3 patients with melioidosis from USVI in 2017, and 43 additional *B. pseudomallei* WGSs available in GenBank from the Caribbean, the Americas, and Africa (Appendix Table 2).

We isolated *B. pseudomallei* from only 1 (≈4%) of 24 soil sites, a prevalence resembling that of nearby Puerto Rico (2), where another study isolated *B. pseudomallei* from 2 soil samples collected at only 1 (2%) of 50 sampled sites. We obtained the *B. pseudomallei*-positive sample from site 122 (Appendix Figure 1),

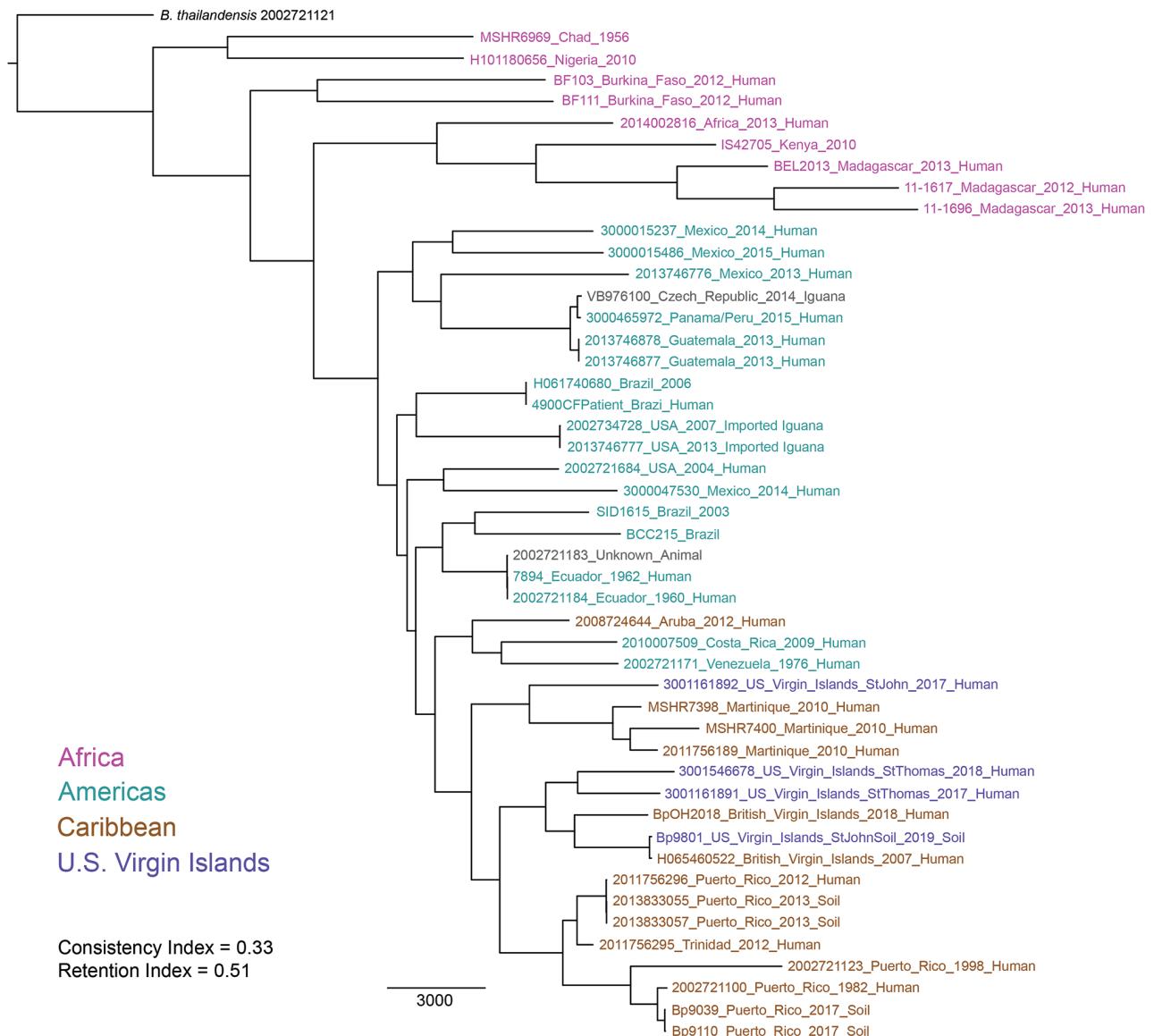


Figure. Maximum-likelihood phylogeny of *Burkholderia pseudomallei* isolates from patients and the environment in the US Virgin Islands and reference isolates available in GenBank from other countries in the Americas, Africa, and the Caribbean.

which was adjacent to a paved roadway 76 meters above sea level on eastern St. John. We collected the soil sample, which was composed of dry gravelly loam and had a pH of 6.9, from a depth of 30 cm (8) (Appendix; Appendix Table 1, Figure 2).

Our phylogenetic analysis assigned the 4 isolates (3 from patients, 1 from the environment) from the USVI to a monophyletic clade with all other *B. pseudomallei* isolates from the Caribbean (except 1 from Aruba) (Figure). However, none of the 4 isolates from the USVI were close genomic matches. These isolates differed by 6,355–10,115 single-nucleotide polymorphisms (SNPs) in the core genome, exhibiting more genomic diversity than *B. pseudomallei* isolates within Puerto Rico and Martinique (Figure). The 2019 soil and 2017 human isolates from St. John were not closely related (differing by 10,115 core genome SNPs), suggesting multiple introductions of *B. pseudomallei* to this island. The closest genomic match to the St. John soil isolate (differing by 170 core genome SNPs) was a 2007 isolate from Road Town, Tortola, British Virgin Islands (9). Although the dispersal mechanism of *B. pseudomallei* to this region is unknown, a dispersal event between these 2 locations (≈ 11 km) might have been caused by aerosolization of *B. pseudomallei* during an extreme weather event, such as a hurricane (10). This mechanism of long-distance dispersal might also explain why the 2017 isolate from St. John is more closely related to isolates from Martinique than to the other isolates from USVI; this patient from the USVI was infected shortly after hurricane Maria (4). We placed the 2 isolates, despite differing by 6,355 core genome SNPs, from patients on St. Thomas in a single subclade; this pattern might suggest long-term endemicity on this island. However, these scenarios are based on an analysis of a relatively small number of *B. pseudomallei* WGSs from the Caribbean.

Our findings demonstrate that *B. pseudomallei* is rare in the environment in the USVI. The 2017 cases of melioidosis and the soil isolate from St. John indicate this bacterium might be ecologically established in the USVI. Additional environmental sampling will determine the environmental distribution of *B. pseudomallei* in the USVI, aiding the development of public health strategies to mitigate the risk for melioidosis.

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References

- Currie BJ. Melioidosis: evolving concepts in epidemiology, pathogenesis, and treatment. *Semin Respir Crit Care Med*. 2015;36:111–25. <https://doi.org/10.1055/s-0034-1398389>
- Hall CM, Jaramillo S, Jimenez R, Stone NE, Centner H, Busch JD, et al. *Burkholderia pseudomallei*, the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. *PLoS Negl Trop Dis*. 2019;13:e0007727. <https://doi.org/10.1371/journal.pntd.0007727>
- Doker TJ, Sharp TM, Rivera-Garcia B, Perez-Padilla J, Benoit TJ, Ellis EM, et al. Contact investigation of melioidosis cases reveals regional endemicity in Puerto Rico. *Clin Infect Dis*. 2015;60:243–50. <https://doi.org/10.1093/cid/ciu764>
- Guendel I, Ekpo LL, Hinkle MK, Harrison CJ, Blaney DD, Gee JE, et al. Melioidosis after hurricanes Irma and Maria, St. Thomas/St. John District, US Virgin Islands, October 2017. *Emerg Infect Dis*. 2019;25:1952–5. <https://doi.org/10.3201/eid2510.180959>
- Limmathurotsakul D, Dance DA, Wuthiekanun V, Kaestli M, Mayo M, Warner J, et al. Systematic review and consensus guidelines for environmental sampling of *Burkholderia pseudomallei*. *PLoS Negl Trop Dis*. 2013;7:e2105. <https://doi.org/10.1371/journal.pntd.0002105>
- Wiersinga WJ, Virk HS, Torres AG, Currie BJ, Peacock SJ, Dance DAB, et al. Melioidosis. *Nat Rev Dis Primers*. 2018;4:17107. <https://doi.org/10.1038/nrdp.2017.107>
- Novak RT, Glass MB, Gee JE, Gal D, Mayo MJ, Currie BJ, et al. Development and evaluation of a real-time PCR assay targeting the type III secretion system of *Burkholderia pseudomallei*. *J Clin Microbiol*. 2006;44:85–90. <https://doi.org/10.1128/JCM.44.1.85-90.2006>
- US Department of Agriculture. Web Soil Survey. 2018 [cited 2019 Sept 16]. <https://websoilsurvey.sc.egov.usda.gov>
- Corral DM, Coates AL, Yau YC, Tellier R, Glass M, Jones SM, et al. *Burkholderia pseudomallei* infection in a cystic fibrosis patient from the Caribbean: a case report. *Can Respir J*. 2008;15:237–9. <https://doi.org/10.1155/2008/290412>
- Cheng AC, Jacups SP, Gal D, Mayo M, Currie BJ. Extreme weather events and environmental contamination are associated with case-clusters of melioidosis in the Northern Territory of Australia. *Int J Epidemiol*. 2006;35:323–9. <https://doi.org/10.1093/ije/dyi271>

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Burkholderia pseudomallei in Soil, US Virgin Islands, 2019

Appendix

Description of *Burkholderia pseudomallei*-Positive Soil Sample

The soil type and soil profile for this sample were very gravelly loam (Appendix Figure 2) and southgate-rock outcrop complex, respectively (Appendix Table 1). Southgate has a typical geologic profile of 0–5 inches: gravelly loam; 5–10 inches: very gravelly loam; 10–17 inches: weathered bedrock; and 17–60 inches: unweathered bedrock. The southgate landform is hillsides, mountain slopes, or ridges, and it is well drained with no flooding. Rock outcrop has a typical profile of 0–60 inches: unweathered bedrock, and a landform of ridges. These soil characteristics and landform information were obtained from the USDA National Resource Conservation Service's Web Soil Survey (1).

References:

1. US Department of Agriculture. Web Soil Survey [cited 2019 Sep 16].
<https://websoilsurvey.sc.egov.usda.gov/>
2. Liguori AP, Warrington SD, Ginther JL, Pearson T, Bowers J, Glass MB, et al. Diversity of 16S-23S rDNA internal transcribed spacer (ITS) reveals phylogenetic relationships in *Burkholderia pseudomallei* and its near-neighbors. PLoS One. 2011;6:e29323. [PubMed](#)
<https://doi.org/10.1371/journal.pone.0029323>
3. Tuanyok A, Auerbach RK, Brettin TS, Bruce DC, Munk AC, Detter JC, et al. A horizontal gene transfer event defines two distinct groups within *Burkholderia pseudomallei* that have dissimilar geographic distributions. J Bacteriol. 2007;189:9044–9. [PubMed](#)
<https://doi.org/10.1128/JB.01264-07>
4. Tuanyok A, Stone JK, Mayo M, Kaestli M, Gruendike J, Georgia S, et al. The genetic and molecular basis of O-antigenic diversity in *Burkholderia pseudomallei* lipopolysaccharide. PLoS Negl Trop Dis. 2012;6:e1453. [PubMed](#) <https://doi.org/10.1371/journal.pntd.0001453>

5. Sitthidet C, Stevens JM, Chantratita N, Currie BJ, Peacock SJ, Korbsrisate S, et al. Prevalence and sequence diversity of a factor required for actin-based motility in natural populations of *Burkholderia* species. *J Clin Microbiol.* 2008;46:2418–22. [PubMed](#)
<https://doi.org/10.1128/JCM.00368-08>
6. Sahl JW, Caporaso JG, Rasko DA, Keim P. The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. *PeerJ.* 2014;2:e332.
[PubMed](#) <https://doi.org/10.7717/peerj.332>
7. Rasko DA, Myers GS, Ravel J. Visualization of comparative genomic analyses by BLAST score ratio. *BMC Bioinformatics.* 2005;6:2. [PubMed](#) <https://doi.org/10.1186/1471-2105-6-2>

Appendix Table 1. Sampling sites for *Burkholderia pseudomallei*, US Virgin Islands, 2019*

Site ID	Sample type	No. samples collected	Collection date	Island	Elevation, m	pH at site			Soil sampling depth, cm	USDA soil profile	Observed soil profile	Soil moisture
						Average	Max	Min				
106	Soil	20	2019 Jan 20	St. Thomas	143.60	5.82	6.30	5.30	30	Very gravelly clay loam	Sandy loam, clay	Dry
107	Soil	20	2019 Jan 21	St. Thomas	21.04	7.70	9.80	6.30	30	Very gravelly loam	Sandy clay loam	Dry
108	Soil	20	2019 Jan 21	St. Thomas	10.06	8.47	9.10	6.70	20–30	Silt loam	Sandy clay loam	Moist/wet/soaked
109	Soil	20	2019 Jan 22	St. Thomas	14.63	8.78	9.70	7.30	30	Very gravelly loam	Sandy clay	Dry
110	Soil	20	2019 Jan 22	St. Thomas	10.06	8.72	9.10	8.20	15–30	NL	Sandy loam, loam	Dry/moderately moist/moist
111	Soil	20	2019 Jan 22	St. Thomas	10.06	8.66	9.40	8.20	15–20	Very gravelly clay loam	Sand, sandy loam	Moist
112	Soil	20	2019 Jan 23	St. Thomas	12.80	8.48	9.10	7.20	30	Clay loam	Sandy loam	Moderately moist
113	Freshwater	20	2019 Jan 21	St. Thomas	26.52	8.72	8.80	8.50	NA	NA	NA	NA
114	Freshwater	20	2019 Jan 21	St. Thomas	10.37	7.80	7.80	7.70	NA	NA	NA	NA
115	Soil	20	2019 Jan 23	St. Thomas	12.50	9.19	9.50	8.60	30	Gravelly fine sandy loam	Sandy loam	Moist
116	Soil	20	2019 Jan 24	St. Thomas	30.79	7.39	8.50	6.30	20–30	Very gravelly loam	Loam, sandy clay loam	Dry/moderately moist
117	Soil	20	2019 Jan 28	St. John	10.37	8.22	9.20	7.10	30	Very gravelly loam	Clay, sandy clay loam, sandy loam	Moderately moist
118	Soil	20	2019 Jan 28	St. John	7.93	9.42	9.90	8.60	30	NL	Loam, sandy clay loam	Dry/moderately moist/moist
119	Soil	20	2019 Jan 28	St. John	12.20	7.23	9.80	6.60	30	Gravelly clay loam	Loam	Moderately moist
120	Soil	20	2019 Jan 29	St. John	37.20	8.49	9.50	5.60	30	Very gravelly clay loam	Loam	Dry/moderately moist
121	Freshwater	20	2019 Jan 28	St. John	11.28	7.93	8.20	7.90	NA	NA	NA	NA
122	Soil	20	2019 Jan 29	St. John	75.91	7.8	8.7	6.7	20–30	Very gravelly loam	Sandy loam	Dry/moderately moist
123	Soil	20	2019 Jan 30	St. John	9.76	8.09	8.80	7.30	30	Clay loam	Clay loam	Moist
124	Soil	20	2019 Jan 30	St. John	9.76	7.76	9.20	6.40	30	Very gravelly loam	Clay	Moist

Site ID	Sample type	No. samples collected	Collection date	Island	Elevation, m	pH at site			Soil sampling depth, cm	USDA soil profile	Observed soil profile	Soil moisture
						Average	Max	Min				
149	Freshwater	20	2019 Apr 16	St. Croix	31.10	8.04	8.20	7.80	NA	NA	NA	NA
150	Soil	20	2019 Apr 15	St. Croix	16.16	8.61	9.20	7.90	30	Clay	Loam	Dry
151	Freshwater	20	2019 Apr 16	St. Croix	73.17	8.30	8.40	8.10	NA	NA	NA	NA
152	Soil	20	2019 Apr 15	St. Croix	25.30	9.03	9.40	8.50	30	Clay	Loam	Dry
153	Soil	20	2019 Apr 15	St. Croix	43.90	9.29	9.70	7.70	30	Clay loam	Clay loam	Dry
154	Soil	20	2019 Apr 16	St. Croix	11.89	9.15	9.80	8.10	30	Clay	Clay loam	Dry
155	Soil	20	2019 Apr 16	St. Croix	28.96	8.73	9.50	7.80	30	Very gravelly clay	Gravels	Dry
156	Soil	20	2019 Apr 17	St. Croix	18.60	8.99	9.70	7.00	30	Very gravelly loam	Gravels	Dry
157	Soil	20	2019 Apr 17	St. Croix	30.49	8.87	9.50	7.80	30	Very gravelly clay	Clay	Dry
158	Soil	20	2019 Apr 17	St. Croix	22.26	7.47	8.90	6.60	30	Very gravelly clay	Gravels	Dry

*NA, not applicable; NL, not listed; min, minimum; max, maximum; USDA, US Department of Agriculture (1).

Appendix Table 2. *Burkholderia pseudomallei* genomes from GenBank*

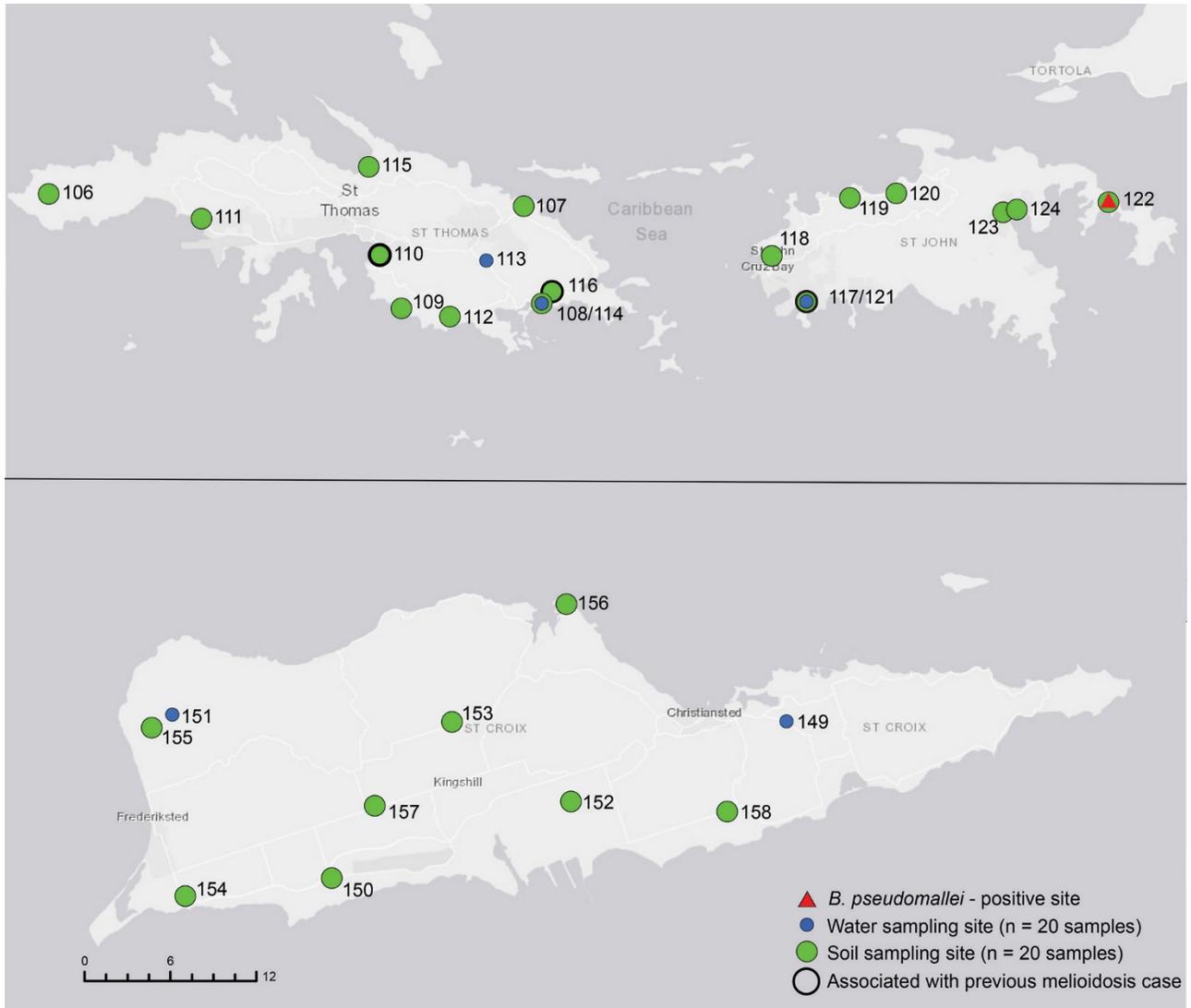
Strain	Country	Year	Isolate source	GenBank accession no.	Multilocus sequence type	ITS type (2)	Presence of YLF and BTFC gene clusters (3)	LPS type† (4)	Observed variant of <i>bimA</i> ‡ (5)	Biosample no.
MSHR6969	Chad	1956	NA	ERR298347	ST82	C	YLF	A	<i>bimA-Bm</i>	SAMEA1920075
H101180656	Nigeria	2010	NA	ERR298772	ST707	C	YLF	A	<i>bimA-Bm</i>	SAMEA1920046
BF103	Burkina Faso	2012	Human	SRR3145394	ST1121	G	YLF	A	<i>bimA-Bm</i>	SAMN04376904
BF111	Burkina Faso	2012	Human	SRR3145395	ST1122	C	YLF	A	<i>bimA-Bm</i>	SAMN04376905
2014002816	Africa	2013	Human	GCA_002113945	ST1053	C	YLF	A	<i>bimA-Bm</i>	SAMN06007575
IS42705	Kenya	2010	NA	ERR351984	ST1540	E	YLF	A	<i>bimA-Bm</i>	SAMEA2163737
BEL2013	Madagascar	2013	Human	SRR3145396	ST1043	E	YLF	A	<i>bimA-Bm</i>	SAMN04376903
11-1617	Madagascar	2012	Human	SRR3145392	ST1054	C	YLF	Negative	<i>bimA-Bm</i>	SAMN04376901
11-1696	Madagascar	2012	Human	SRR3145393	ST1053	C	YLF	Negative	<i>bimA-Bm</i>	SAMN04376902
3000015237	Mexico	2014	Human	GCA_002111045	ST951	G	YLF	A	neither	SAMN06007576
3000015486	Mexico	2015	Human	GCA_002111385	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMN06007577
2013746776	Mexico	2013	Human	GCA_002111185	ST297	G	YLF	A	neither	SAMN06007568
VB976100	Czech Republic	2014	Iguana	GCA_001885195	ST436	G	YLF	A	<i>bimA-Bm</i>	SAMN05930279
3000465972	Panama/Peru	2015	Human	GCF_002111305	ST436	G	YLF	A	<i>bimA-Bm</i>	SAMN06007579
2013746878	Guatemala	2013	Human	GCA_002111005	ST1038	G	YLF	A	neither	SAMN06007572
2013746877	Guatemala	2013	Human	GCA_002111245	ST1038	G	YLF	A	neither	SAMN06007571
H061740680	Brazil	2006	NA	ERR298754	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMEA1920028
4900CFPatient	Brazil	NA	Human	GCA_000648355	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMN02044373
2002734728	USA	2007	Iguana	GCA_002111105	ST518	G	YLF	A	<i>bimA-Bm</i>	SAMN06007559
2013746777	USA	2007	Iguana	GCA_002111205	ST518	G	YLF	A	<i>bimA-Bm</i>	SAMN06007569

Strain	Country	Year	Isolate source	GenBank accession no.	Multilocus sequence type	ITS type (2)	Presence of YLF and BTFC gene clusters (3)	LPS type† (4)	Observed variant of <i>bimA</i> ‡ (5)	Biosample no.
2002721684	USA	2004	Human	GCA_002110925	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN06007558
3000047530	Mexico	2014	Human	GCA_002111285	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMN06007578
SID1615	Brazil	2003	NA	ERR298753	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMEA1920029
BCC215	Brazil	NA	NA	GCA_000170595	ST1355	G	YLF	A	<i>bimA-Bm</i>	SAMN02470671
2002721183	Unknown	NA	Animal	GCA_001976195	ST11	G	YLF	A	neither	SAMN04208558
7894	Ecuador	1962	Human	GCA_000959265	ST11	G	YLF	A	neither	SAMN03075630
2002721184	Ecuador	1960	Human	GCA_002111085	ST11	G	YLF	A	neither	SAMN06007557
2008724644	Aruba	2012	Human	GCA_002115385	ST698	G	YLF	A	<i>bimA-Bm</i>	SAMN06007560
2010007509	Costa Rica	2009	Human	GCA_002111145	ST518	G	YLF	A	<i>bimA-Bm</i>	SAMN06007564
2002721171	Venezuela	1976	Human	GCA_002111345	ST12	G	YLF	A	<i>bimA-Bm</i>	SAMN06007556
3001161892	St. John, US Virgin Islands	2017	Human	GCA_003584055	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMN09941299
MShR7398	Martinique	2010	Human	ERR298357	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMEA1920085
MShR7400	Martinique	2010	Human	ERR298359	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMEA1920088
2011756189	Martinique	2010	Human	GCA_002111165	ST92	G	YLF	A	neither	SAMN06007574
3001546678	St. Thomas, US Virgin Islands	2018	Human	GCA_007995115	ST1492	G	YLF	A	<i>bimA-Bm</i>	SAMN12500044
3001161891	St. Thomas, US Virgin Islands	2017	Human	GCA_003584065	ST951	G	YLF	A	<i>bimA-Bm</i>	SAMN09941298
BpOH2018	British Virgin Islands	2018	Human	SRS5472236	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMN12905775
Bp9801	St. John, US Virgin Islands	2019	Soil	SRR10148518	ST1492	G	YLF	A	<i>bimA-Bm</i>	SAMN12784135
H065460522	British Virgin Islands	2007	Human	ERR298778	ST1492	G	YLF	A	<i>bimA-Bm</i>	SAMEA1920053
2011756296	Puerto Rico	2012	Human	GCA_002110985	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN06007567
2013833055	Puerto Rico	2013	Soil	GCA_002111025	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN06007573
2013833057	Puerto Rico	2013	Soil	GCA_002111265	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN06007574
2011756295	Trinidad	2012	Human	GCA_002110965	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN06007566
2002721123	Puerto Rico	1998	Human	GCA_002111325	ST92	G	YLF	A	<i>bimA-Bm</i>	SAMN06007555
2002721100	Puerto Rico	1982	Human	GCA_002111065	ST95	G	YLF	A	<i>bimA-Bm</i>	SAMN06007554
Bp9039	Puerto Rico	2017	Soil	SRR7457394	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN09073285
Bp9110	Puerto Rico	2017	Soil	SRR7457423	ST297	G	YLF	A	<i>bimA-Bm</i>	SAMN09073352

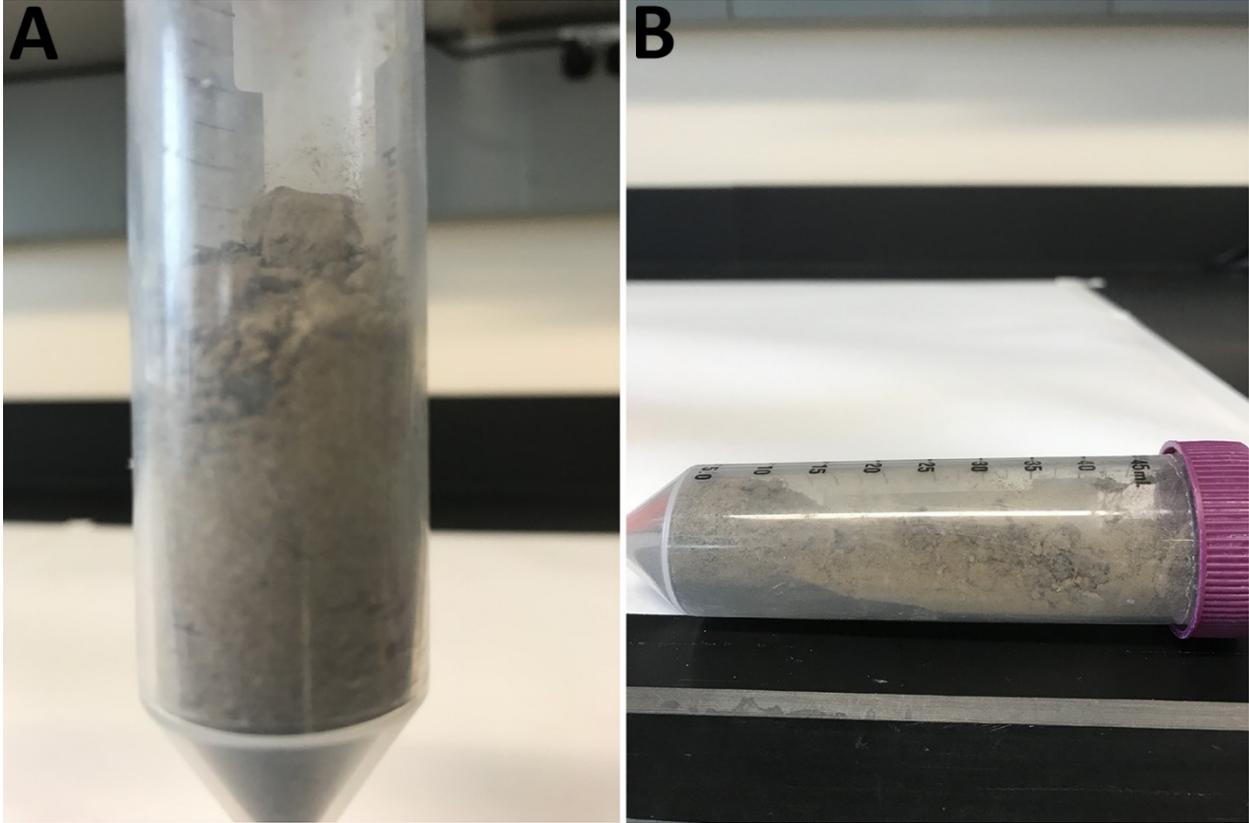
**bimA*, *Burkholderia* intracellular motility A gene; BTFC, *B. thailandensis*-like flagellum and chemotaxis; ITS, 16S–23S internal transcribed spacer; LPS, lipopolysaccharide; LS-BSR, large-scale Blast Score Ratio; NA, not available; YLF, *Yersinia*-like fimbrial. Genome assemblies were screened for genotypes by using the LS-BSR method (6) with a 0.95 BSR (7) threshold.

†GenBank gene references: LPS A (BPSL2676), LPS B (BBK_2267), and LPS B2 (BTI_920).

‡GenBank gene references: *bimA-Bp* (BURPS668_A2118), *bimA-Bm* (BPSS1492).



Appendix Figure 1. Sampling sites for *Burkholderia pseudomallei*, US Virgin Islands, 2019. Numbers indicated site IDs. Map created with ArcGIS software by Esri.



Appendix Figure 2. Photographs of *Burkholderia pseudomallei*-positive soil sample, US Virgin Islands, 2019.