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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

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.ebi.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/NEJMoa2001468
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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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),

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**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
1. 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
2. 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
3. Dokter 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
4. 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
5. Limmathurosaksul 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
6. 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/s41575-017-0085-z
7. 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
8. US Department of Agriculture. Web Soil Survey. 2018 [cited 2019 Sept 16]. https://websoilsurvey.sc.egov.usda.gov
9. 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
10. 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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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
| 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 |
|--------|-------------|-----------------------|-----------------|--------|--------------|------------|------------------------|------------------|----------------------|--------------|
| 106    | Soil        | 20                    | 2019 Jan 20     | St. Thomas | 143.60       | 5.82       | 6.30                   | 5.30             | Sandy loam, clay     | Dry          |
| 107    | Soil        | 20                    | 2019 Jan 21     | St. Thomas | 21.04        | 7.70       | 9.80                   | 6.30             | Sandy clay loam      | Dry          |
| 108    | Soil        | 20                    | 2019 Jan 21     | St. Thomas | 10.06        | 8.47       | 9.10                   | 6.70             | Silt loam            | Moist/wet/soaked |
| 109    | Soil        | 20                    | 2019 Jan 22     | St. Thomas | 14.63        | 8.78       | 9.70                   | 7.30             | Sandy clay loam      | Dry          |
| 110    | Soil        | 20                    | 2019 Jan 22     | St. Thomas | 10.06        | 8.72       | 9.10                   | 8.20             | Very gravelly loam   | Moist        |
| 111    | Soil        | 20                    | 2019 Jan 22     | St. Thomas | 10.06        | 8.66       | 9.40                   | 8.20             | Very gravelly loam   | Moist        |
| 112    | Soil        | 20                    | 2019 Jan 23     | St. Thomas | 12.80        | 8.48       | 9.10                   | 7.20             | Sandy loam, clay     | Moist        |
| 113    | Freshwater  | 20                    | 2019 Jan 21     | St. Thomas | 26.52        | 8.72       | 8.80                   | 8.50             | Sandy loam           | Moderately moist |
| 114    | Freshwater  | 20                    | 2019 Jan 21     | St. Thomas | 10.37        | 7.80       | 7.80                   | 7.70             | Sandy loam           | NA           |
| 115    | Soil        | 20                    | 2019 Jan 23     | St. Thomas | 12.50        | 9.19       | 9.50                   | 8.60             | Sandy loam, clay     | Moist        |
| 116    | Soil        | 20                    | 2019 Jan 24     | St. Thomas | 30.79        | 7.39       | 8.50                   | 6.30             | Very gravelly loam   | Dry/moderately moist |
| 117    | Soil        | 20                    | 2019 Jan 28     | St. John   | 10.37        | 8.22       | 9.20                   | 7.10             | Very gravelly loam   | Moderately moist |
| 118    | Soil        | 20                    | 2019 Jan 28     | St. John   | 7.93         | 9.42       | 9.90                   | 8.60             | Sandy loam           | Dry/moderately moist |
| 119    | Soil        | 20                    | 2019 Jan 28     | St. John   | 12.20        | 7.23       | 9.80                   | 6.60             | Gravelly clay loam   | Moderately moist |
| 120    | Soil        | 20                    | 2019 Jan 29     | St. John   | 37.20        | 8.49       | 9.50                   | 5.60             | Very gravelly loam   | Dry/moderately moist |
| 121    | Freshwater  | 20                    | 2019 Jan 28     | St. John   | 11.28        | 7.93       | 8.20                   | 7.90             | Sandy loam           | NA           |
| 122    | Soil        | 20                    | 2019 Jan 29     | St. John   | 75.91        | 7.8        | 8.7                    | 6.7              | Very gravelly loam   | NA           |
| 123    | Soil        | 20                    | 2019 Jan 30     | St. John   | 9.76         | 8.09       | 8.80                   | 7.30             | Clay loam            | Moist        |
| 124    | Soil        | 20                    | 2019 Jan 30     | St. John   | 9.76         | 7.76       | 9.20                   | 6.40             | Very gravelly loam   | Moist        |
Appendix Table 2. *Burkholderia pseudomallei* genomes from GenBank*

| Strain    | Country       | Year | Isolate source | GenBank accession no. | Multilocus sequence type | IT5 type (2) | Presence of YLF and BTFC gene clusters (3) | LPS type† (4) | Observed variant of *bimA‡ (5) | Bio sample no. |
|-----------|---------------|------|----------------|------------------------|-------------------------|-------------|--------------------------------------------|--------------|---------------------------------|---------------|
| MSHR6969  | Chad          | 1956 | NA             | ERR298347              | ST82                    | C           | YLF                                        | A            | *bimA-Bm*                       | SAMEA1920075  |
| H101180656 | Nigeria       | 2010 | NA             | ERR298772              | ST707                   | C           | YLF                                        | A            | *bimA-Bm*                       | SAMEA1920046  |
| BF103     | Burkina Faso  | 2012 | Human          | SRR3145394             | ST1121                  | G           | YLF                                        | A            | *bimA-Bm*                       | SAMN04376904  |
| BF111     | Burkina Faso  | 2012 | Human          | SRR3145395             | ST1122                  | C           | YLF                                        | A            | *bimA-Bm*                       | SAMN04376905  |
| 2014002816 | Africa        | 2013 | Human          | GCA_002113945          | ST1053                  | C           | YLF                                        | A            | *bimA-Bm*                       | SAMN06007575  |
| IS42705   | Kenya         | 2010 | NA             | ERR351984              | ST1540                  | E           | YLF                                        | A            | *bimA-Bm*                       | SAMEA2163737  |
| BEL2013   | Madagascar    | 2013 | Human          | SRR3145396             | ST1043                  | E           | YLF                                        | A            | *bimA-Bm*                       | SAMN04376903  |
| 11–1617   | Madagascar    | 2012 | Human          | SRR3145392             | ST1054                  | C           | Negative                                   | A            | *bimA-Bm*                       | SAMN04376901  |
| 11–1696   | Madagascar    | 2012 | Human          | SRR3145393             | ST1053                  | C           | YLF                                        | Negative      | *bimA-Bm*                       | SAMN04376902  |
| 3000015237 | Mexico        | 2014 | Human          | GCA_002111045          | ST951                   | G           | YLF                                        | A            | neither                         | SAMN06007576  |
| 3000015486 | Mexico        | 2015 | Human          | GCA_002111385          | ST92                    | G           | YLF                                        | A            | *bimA-Bm*                       | SAMN06007577  |
| 2013746776 | Mexico        | 2013 | Human          | GCA_002111185          | ST297                   | G           | YLF                                        | A            | neither                         | SAMN06007568  |
| VB976100  | Czech Republic| 2014 | Iguna          | GCA_001885195          | ST436                   | G           | YLF                                        | A            | *bimA-Bm*                       | SAMN05930279  |
| 3000465972 | Panama/Peru   | 2015 | Human          | GCF_00211305           | ST436                   | G           | YLF                                        | A            | *bimA-Bm*                       | 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            | *bimA-Bm*                       | SAMEA1920028  |
| 4900CFPatient | Brazil   | 2007 | Human          | GCA_000648355          | ST92                    | G           | YLF                                        | A            | *bimA-Bm*                       | SAMN02044373  |
| 2002734728 | USA           | 2007 | Iguna          | GCA_002111105          | ST518                   | G           | YLF                                        | A            | *bimA-Bm*                       | SAMN06007559  |
| 2013746777 | USA           | 2007 | Iguna          | GCA_002111205          | ST518                   | G           | YLF                                        | A            | *bimA-Bm*                       | SAMN06007569  |

*NA, not applicable; NL, not listed; min, minimum; max, maximum; USDA, US Department of Agriculture (f).
| Strain        | Country          | Year | Isolate source | GenBank accession no. | Multilocus sequence type | ITS type | Presence of YLF and BTFC gene clusters | LPS type† | Observed variant of bimA‡ | Biosample no. |
|--------------|------------------|------|----------------|-----------------------|--------------------------|---------|----------------------------------------|-----------|--------------------------|---------------|
| 2002721684   | USA              | 2004 | Human          | GCA_002110925         | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007558  |
| 3000047530   | Mexico           | 2014 | Human          | GCA_002111285         | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007578  |
| SID1615      | Brazil           | 2003 | NA             | ERR298753              | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMEA1920029  |
| BCC215       | Brazil           | NA   | NA             | GCA_000170595          | ST1355                   | G       | YLF                                    | A         | bimA-Bm                  | SAMN02470671  |
| 2002721183   | Unknown          | 2009 | NA             | GCA_001976195          | ST11                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN02408558  |
| 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_0021115385         | ST698                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007560  |
| 2010007509   | Costa Rica       | 2009 | Human          | GCA_002111145          | ST518                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007564  |
| 2002721171   | Venezuela        | 1976 | Human          | GCA_002111345          | ST12                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007556  |
| 3001161892   | St. John, US Virgin Islands | 2017 | Human          | GCA_003584055          | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN09941299  |
|              |                  |      |                |                       |                          |         |                                        |           |                          |               |
| MSHR7398     | Martinique       | 2010 | Human          | ERR298357              | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMEA1920085  |
| MSHR7400     | Martinique       | 2010 | Human          | ERR298359              | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMEA1920088  |
| 2011756189   | Martinique       | 2010 | Human          | GCA_002111165          | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMEA1920088  |
| 3001546678   | St. Thomas, US Virgin Islands | 2018 | Human          | GCA_007995115         | ST1492                   | G       | YLF                                    | A         | bimA-Bm                  | SAMN12500044  |
|              |                  |      |                |                       |                          |         |                                        |           |                          |               |
| 3001161891   | St. Thomas, US Virgin Islands | 2017 | Human          | GCA_003584065          | ST951                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN09941298  |
| BpOH2018     | British Virgin Islands | 2018 | Human          | SRS5472236            | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN12905775  |
| Bp9801       | British Virgin Islands | 2019 | Soil           | SRR10148518            | ST1492                   | G       | YLF                                    | A         | bimA-Bm                  | SAMN12784135  |
| H065460522   | British Virgin Islands | 2007 | Human          | ERR298778             | ST1492                   | G       | YLF                                    | A         | bimA-Bm                  | SAMEA1920053  |
| 2011756296   | Puerto Rico      | 2012 | Human          | GCA_002110985          | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007567  |
| 2013833055   | Puerto Rico      | 2013 | Soil           | GCA_002111025          | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007573  |
| 2013833057   | Puerto Rico      | 2013 | Soil           | GCA_002111265          | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007574  |
| 2011756295   | Trinidad         | 2012 | Human          | GCA_002110965          | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007566  |
| 2002721123   | Puerto Rico      | 1996 | Human          | GCA_002111325          | ST92                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007555  |
| 2002721100   | Puerto Rico      | 1982 | Human          | GCA_002111065          | ST95                     | G       | YLF                                    | A         | bimA-Bm                  | SAMN06007554  |
| Bp9039       | Puerto Rico      | 2017 | Soil           | SRR7457394            | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | SAMN09073295  |
| Bp9110       | Puerto Rico      | 2017 | Soil           | SRR7457423            | ST297                    | G       | YLF                                    | A         | bimA-Bm                  | 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, *Vernonia*-like fimbral. 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 (B11920).

‡GenBank gene references: *bimA*-Bp (BURPS668_A2119), *bimA*-Bm (BPS81492).
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.