Draft Genome Sequence of a *Chryseobacterium indologenes* Strain Isolated from a Blood Culture of a Hospitalized Child in Antananarivo, Madagascar

Mamitina Alain Noah Rabenandrasana,a Lala Fanomezantsoa Rafetrarivony,a Lalainosa Odile Rivoarilala,a Vincent Enouf,a Annick Lalaina Robinson,d Ando Rakotozanany,d Jessica Vanhomwegen,b Valérie Caro,b Cassandre Von Platen,c Jean-Claude Manuguerra,b Jean-Marc Collard,e

8a Experimental Bacteriology Unit, Institut Pasteur de Madagascar, Antananarivo, Madagascar
8b Laboratory for Urgent Response to Biological Threats, Institut Pasteur, Paris, France
8c Center for Translational Science, Institut Pasteur, Paris, France
8d Centre Hospitalier Universitaire Mère-Enfant Tsaralalana (CHUMET), Antananarivo, Madagascar
8e Pasteur International Bioresources Network (PIBnet), Plateforme de Microbiologie Mutualisée (P2M), Institut Pasteur, Paris, France

**ABSTRACT** We report here the draft genome sequence of a *Chryseobacterium indologenes* strain, isolated from a blood culture of a 2.2-year-old child admitted to the hospital for vomiting and coughing. The genome was composed of 5,063,674 bp and had 37.04% GC content. We detected 4,796 genes with predicted protein-coding functions, including those associated with antibiotic resistance.

*Chryseobacterium* is a nonmotive, chemoorganotrophic, and glucose-nonfermentative Gram-negative rod-shaped bacteria. The most pathogenic species of the genus, *Chryseobacterium meningosepticum*, which causes numerous infections, was reclassified to the genus *Elizabethkingia* (1). *Chryseobacterium indologenes*, although ubiquitous in nature and found mainly in soil and water, is an uncommon human pathogen. However, in rare cases, it can cause serious infections, particularly among immunocompromised hospitalized patients with severe underlying diseases and/or with indwelling catheters (2). These include keratitis, bacteremia (2), pneumonia, cellulitis, and artificial shunt infection (3–6).

*Chryseobacterium indologenes* was isolated from a positive blood culture (time to positivity, 23 h) collected by venipuncture from a 2.2-year-old child hospitalized at the pediatric hospital of Tsaralalanà, Antananarivo, Madagascar. This child was admitted 1 day before blood sampling with fever, coughing, and vomiting. The study was approved by the Ministry of Health and the National Ethics Committee of Madagascar (number 140-MSANP/CE). Informed written consent was obtained from at least one child’s parent before sampling.

The strain forms on solid blood agar in typical yellow colonies due to a flexirubin-type pigment. After 24 h, the colonies were identified by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) as *C. indologenes*, with a score of >2.0. The antimicrobial susceptibility testing was performed according to the standard disc methods described in the CA-SFM guidelines (7), and susceptibility to chloramphenicol and tetracycline was also tested. The isolate was resistant to ticarcillin, piperacillin, ticarcillin plus clavulanate, tazobactam, ceftazidime, aztreonam, imipenem, gentamicin, tobramycin, amikacin, and ciprofloxacin, displayed an intermediate resistance to chloramphenicol, and remained susceptible to cefepime and tetracycline.

DNA extraction was done from an overnight culture using a DNA blood and tissue kit (Qiagen, France). A DNA sequencing library was prepared using a Nextera XT DNA sample prep kit (Illumina, Inc., San Diego, CA), according to the manufacturer’s instruc-
 Genome sequencing was performed using MiSeq Illumina technology (2 × 300 bp), generating 3,772,882 paired-end reads. FqCleaner version 3.0 was used to eliminate adapter sequences (8, 9), reduce redundant or overrepresented reads (10), correct sequencing errors (11), merge overlapping paired reads, and discard reads with a Phred score (measure of the quality of identification of nucleobases generated by automated DNA sequencing) of <20. Illumina read de novo assembly was performed using SPAdes version 3.10.0 (12, 13), with default parameters. Acquired resistance genes were detected using ResFinder version 3.0 (14). The genome was annotated using the PATRIC Web server version 3.5.39 (15). In total, 48 assembled contigs with an N50 value of 193,241 bp and an average coverage of 36.1×, which had 5,063,674 bp and 37.04% GC content, were annotated using the PATRIC Web server annotation pipeline (15–19). The genome harbors 64 tRNA genes, 3 rRNA genes, and 4,796 protein-coding sequences. The antimicrobial resistance (AMR) genes detected in this genome and the corresponding AMR mechanisms are provided in Table 1.

The extended-spectrum β-lactamase gene blaCIA was responsible for the resistance to ticarcillin, piperacillin, ticarcillin plus clavulanate, tazobactam, and ceftazidime but not to cefepime. A metallo-β-lactamase gene, blaIND-2a, was responsible for the resistance to imipenem. Our phenotypic results showed that the catB gene did not confer complete resistance to chloramphenicol and that the tet(X) gene was nonfunctional, like that originally found in Bacteroides spp. (20–23). The Tet(X) protein showed 62% identity with Tet(X) from the strain AF25-18 (GenBank accession number RJV36860) and 62% with Tet(X) from Chryseobacterium oncorhynchi (GenBank accession number PWN64762). Studies on hosted bacteriophages, secretion systems, mobility, and ability to form biofilms would allow us to understand the pathogenic potential of our C. indologenes isolate and its role in bacteremia.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number VCBR00000000. The version described in this paper is version VCBR01000000. Raw sequence data for this strain were deposited under SRA accession number PRJNA551338.

**ACKNOWLEDGMENTS**

We thank Norohasina Randriamanga, the field investigator, and the staff of pediatric hospital Tsaralalana, Antananarivo, Madagascar.

We thank the Programme Transversal de Recherche (PTR) Child’s Play number 471 funded by the Institut Pasteur (Paris, France), which supported this work, and the staff of the Plateforme de Microbiologie Mutualisée (P2M) at Institut Pasteur Paris, where the whole-genome sequencing was performed.

**REFERENCES**

1. Kim KK, Kim MK, Lim JH, Park HL. 2005. Transfer of Chryseobacterium meningosepticum and Chryseobacterium miricola to Elizabethkingia gen. nov. as Elizabethkingia meningoseptica comb. nov. and Elizabeth-
genes in four patients with leukemia. Transpl Infect Dis 17:583–587. https://doi.org/10.1111/tid.12400.
3. Lu PC, Chan JC. 1997. Flavobacterium indologenes keratitis. Ophthalmologica 211:98–100. https://doi.org/10.1111/003010769.
4. Kienzle N, Muller M, Pegg S. 2001. Chryseobacterium in burn wounds. Burns 27:179–182. https://doi.org/10.1016/S0305-4179(00)00087-5.
5. Doiz O, Llorente MT, Mateo A, Seral C, Garcia C, Rubio MC. 1999. Corneal abscess by Flavobacterium indologenes. A case report. Enferm Infecc Microbiol Clin 17:149–150. (In Spanish.)
6. Green BT, Nolan PE. 2001. Cellulitis and bacteremia due to Chryseobacterium indologenes. J Infect 42:219–220. https://doi.org/10.1053/jinf.2001.0822.
7. Société Française de Microbiologie. 2017. Communiqué 2017. Comité de l’antibiogramme de la Société Française de Microbiologie (CA-SFM)/European Committee on Antimicrobial Susceptibility Testing (EUCAST), Paris, France.
8. Criscuolo A, Brisse S. 2013. AlienTrimmer: a tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. Genomics 102:500–506. https://doi.org/10.1016/j.ygeno.2013.07.011.
9. Crusoee MR, Alamedinid HF, Awad S, Boucher E, Caldwell A, Cartwright R, Charbonneau A, Constantines B, Edvenson G, Fay S, Fenton J, Fenzl T, Fish J, Garcia-Gutierrez L, Garland P, Gluck J, Gonzalez I, Guermond S, Guo J, Gupta A, Herr JR, Howe A, Hyer A, Harper A, Irber L, Kidd R, Lin D, Lippi J, Mansour T, McNulty P, McDonald E, Mizzi J, Murray KD, Nahum JR, Nanlohy K, Nederbragt AJ, Ortiz-Zuazaga H, Orly J, Pell J, Pepe-Ranney C, Ross ZN, Schwarz E, Scott C, Seaman J, Sievert S, Simpson J, Skennerton CT, Spencer J, Srivinasan R, Standage D, et al. 2015. The khmer software package: enabling efficient nucleotide sequence analysis. F1000Res 4:900. https://doi.org/10.12688/f1000research.69241.1.
10. Liu Y, Schröder J, Schmidt B. 2013. Musket: a multistage k-mer spectrum-based error corrector for Illumina sequence data. Bioinformatics 29:308–315. https://doi.org/10.1093/bioinformatics/bts690.
11. Choi Y, Sims GE, Murphy S, Miller JR, Chan AP. 2012. Predicting the functional effect of amino acid substitutions and indels. PLoS One 7:e46688. https://doi.org/10.1371/journal.pone.0046688.
12. Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, Prijibelski AD, Pyszkin A, Siriotkin A, Siriotkin Y, Stepanauskas R, Clin- genepeel SR, Woyke T, McLean JS, Lasken R, Tesler G, Alekseyev MA, Pevzner PA. 2013. Assembling genomes and mini-metagenomes from highly chimeric reads, p 158–170. In Deng M, Jiang R, Sun F, Zhang X (ed), Research in computational molecular biology. Springer, Berlin, Germany.
13. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prijibelski AD, Pyszkin AV, Siriotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
14. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother 67:2640–2644. https://doi.org/10.1093/jac/dks261.
15. Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenenov RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 2017. Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource. Nucleic Acids Res 45:D535–D542. https://doi.org/10.1093/nar/gkw1017.
16. Kanehisa M, Sato Y, Kawashima M, Furumichi M, Tanabe M. 2016. KEGG as a reference resource for gene and protein annotation. Nucleic Acids Res 44:D545–D462. https://doi.org/10.1093/nar/gkv1070.
17. Davis JJ, Gerdes S, Olsen GJ, Olson R, Pusch GD, Shukla M, Vonstein V, Wattam AR, Yoo H. 2016. PATTyFams: protein families for the microbial genomes in the PATRIC database. Front Microbiol 7:118. https://doi.org/10.3389/fmicb.2016.00118.
18. Schomburg I, Chang A, Ebeling C, Gremse M, Heldt C, Huhn G, Schomburg D. 2004. BRENDA, the enzyme database: updates and major new developments. Nucleic Acids Res 32:D431–D433. https://doi.org/10.1093/nar/gkh081.
19. Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, Harris MA, Hill DP, Issel-Tarver L, Kasarskis A, Lewis S, Matese JC, Richardson JE, Ringwald M, Rubin GM, Sherlock G. 2000. Gene Ontology: tool for the unification of biology. Nat Genet 25:25–29. https://doi.org/10.1038/75556.
20. Markley JL, Wencewicz TA. 2018. Tetracycline-inactivating enzymes. Front Microbiol 9:1058. https://doi.org/10.3389/fmicb.2018.01058.
21. Leski TA, Baner S, Chandraa S, Chiu S, Chen KS, Converse M, Craig G, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenenov RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 2017. Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource. Nucleic Acids Res 45: D535–D542. https://doi.org/10.1093/nar/gkw1017.