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Complete Genome Sequence of *Ochrobactrum haematophilum* FI11154, Isolated from Kunu-Zaki, a Nigerian Millet-Based Fermented Food

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ABSTRACT *Ochrobactrum haematophilum* FI11154 was isolated from kunu-zaki, a Nigerian traditional fermented millet-based food. Here, we present the first complete genome sequence of this species. The genome consists of five replicons and contains genes related to iron uptake and phosphatase activities.

Here, we report the first complete genome sequence of *Ochrobactrum haematophilum*, a Gram-negative, nonmotile, rod-shaped, oxidase-positive bacterium from the *Alphaproteobacteria* class. This species was first isolated from human blood (1) but is frequently associated with plants (2) and the rhizosphere (3, 4). *O. haematophilum* has been reported to promote plant growth through the solubilization of phosphates and the production of siderophores (3, 4) and to produce fungicidal substances (4).

O. haematophilum FI11154 was isolated from kunu-zaki, a traditional Nigerian fermented food produced through the spontaneous fermentation of millet. Genomic DNA was extracted from a pure culture grown in Luria broth (5) using the cetyltrimethylammonium bromide-based extraction protocol (6), including RNase treatment. The genome was sequenced using the Pacific Biosciences (PacBio) RS II sequencing platform (Centre for Genomic Research, University of Liverpool, Liverpool, UK). *De novo* assembly of the read sequences was performed using the Canu 1.6 assembler (7), resulting in five contigs. PCR confirmed that the contigs correspond to five circular molecules. Annotation was performed using the Rapid Annotations using Subsystems Technology server version 2.0 (8).

Based on the definition of Harrison et al. (9), the genome of *O. haematophilum* FI11154 comprises one chromosome of 2,602,474 bp, with an average GC content of 57.51%, one chromid of 1,396,538 bp, with an average GC content of 57.5%, one megaplasmid of 1,035,251 bp, with an average GC content of 55.69%, and two plasmids of 266,969 and 181,071 bp with average GC contents of 55.78 and 55.59%, respectively. A total of 5,539 protein-coding sequences were identified, along with with 62 tRNA genes and 12 rRNA operons. Species identification was carried out by comparison of the 16S rRNA gene using the Seqmatch tool from the Ribosomal Database Project (10).

Several genes and gene clusters related to the uptake of iron were identified in the genome. Among them are the gene cluster *efeUOB,* putatively encoding an elemental ferrous iron transporter (11), the *fepC*, *fepG, fepD*, and *fepB* genes, putatively encoding a ferric enterobactin transport system, a gene cluster putatively encoding the vitamin B_{12} transport system BtuCDF (12), and several genes putatively encoding TonB-dependent transporters, which bind and transport ferric chelates, as well as vitamin B_{12},

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nickel complexes, and carbohydrates (13). The capacity of this microorganism to chelate iron can promote plant growth (3, 4); however, it could be detrimental to the nutritional value of the fermented foods from which it was isolated. The presence of two genes encoding putative exopolyphosphatases could be related to the phosphate solubilization activity described for this species (2, 4). Interestingly, a gene expected to encode an antilisterial bacteriocin (linocin M18 [14]) was predicted using antiSMASH 3.0 (15). The complete genome sequence of *O. haematophilum* FI11154 will contribute to a better understanding of the microbial diversity and dynamics of cereal-based fermented foods.

Accession number (s). The genome sequence has been deposited at the European Nucleotide Archive under the accession no. OOFM01000000.

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REFERENCES

1. Kämpfer P, Scholz HC, Huber B, Falsen E, Busse H-J. 2007. *Ochrobactrum haematophilum* sp. nov. and *Ochrobactrum pseudogrignonense* sp. nov., isolated from human clinical specimens. Int J Syst Evol Microbiol 57:2513–2518. https://doi.org/10.1099/ijs.0.65066-0.
2. Pereira SI, Castro PM. 2014. Diversity and characterization of culturable bacterial endophytes from *Zea mays* and their potential as plant growth-promoting agents in metal-degraded soils. Environ Sci Pollut Res Int 21:14110–14123. https://doi.org/10.1007/s11356-014-3309-6.
3. Gao L, Kong F, Feng C, Wang J, Gao J, Shen G, Zhang C. 2016. Isolation, characterization, and growth promotion of phosphate-solubilizing bacteria associated with *Nicotiana tabacum* (tobacco). Pol J Environ Stud 25:993–1003. https://doi.org/10.15244/pjoes/61820.
4. Zhao L, Teng S, Liu Y. 2012. Characterization of a versatile rhizospheric organism from cucumber identified as *Ochrobactrum haematophilum*. J Basic Microbiol 52:232–244. https://doi.org/10.1002/jobm.201000491.
5. Bertani G. 1951. Studies on lysogenesis I. The mode of phage liberation by lysogenic *Escherichia coli*. J Bacteriol 62:293–300.
6. Wilson K. 2001. Preparation of genomic DNA from bacteria. Curr Protoc Mol Biol Chapter 2:Unit 2.4.
7. Koren S, Walenz BP, Berlin K, Miller JR, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive *k*-mer weighting and repeat separation. Genome Res 27:722–736. https://doi.org/10.1101/gr.215087.116.
8. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res 42:D206–D214. https://doi.org/10.1093/nar/gkt1226.
9. Harrison PW, Lower RP, Kim NK, Young JP. 2010. Introducing the bacterial "chromid": not a chromosome, not a plasmid. Trends Microbiol 18:141–148. https://doi.org/10.1016/j.tim.2009.12.010.
10. Cole JR, Wang Q, Fish JA, Chai B, McGarrell DM, Sun Y, Brown CT, Porras-Alfaro A, Kuske CR, Tiedje JM. 2014. Ribosomal Database Project: data and tools for high throughput rRNA analysis. Nucleic Acids Res 42:D633–D642. https://doi.org/10.1093/nar/gkt1244.
11. Cao J, Woodhall MR, Alvarez J, Cartron ML, Andrews SC. 2007. EfeUOB (YcdNOB) is a tripartite, acid-induced and CpxAR-regulated, low-pH Fe^{2+} transporter that is cryptic in *Escherichia coli* K-12 but functional in *E. coli* O157:H7. Mol Microbiol 65:857–875. https://doi.org/10.1111/j.1365-2958.2007.05802.x.
12. de Veaux LC, Clevenson DS, Bradbeer C, Kadner RJ. 1986. Identification of the *btuCED* polypeptides and evidence for their role in vitamin B_{12} transport in *Escherichia coli*. J Bacteriol 167:920–927.
13. Noinaj N, Guillier M, Barnard TJ, Buchanan SK. 2010. TonB-dependent transporters: regulation, structure, and function. Annu Rev Microbiol 64:43–60. https://doi.org/10.1146/annurev.micro.112408.134247.
14. Valdes-Stauber N, Scherer S. 1996. Nucleotide sequence and taxonomical distribution of the bacteriocin gene *lin* cloned from *Brevibacterium linens* M18. Appl Environ Microbiol 62:1283–1286.
15. Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Res 43:W237–W243. https://doi.org/10.1093/nar/gkv437.