



# Draft Genomic Sequences of *Chromobacterium* sp. nov. Strains MWU13-2610 and MWU14-2602, Isolated from Wild Cranberry Bogs in Massachusetts

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**ABSTRACT** *Chromobacterium* sp. nov. strains MWU13-2610 and MWU14-2602 were isolated from cranberry bogs in the Cape Cod National Seashore. These nonpigmented bacteria represent two new presumptive species of the rapidly growing genus *Chromobacterium*. Gene homologs are present for multiple antibiotic resistance, virulence functions, and prophages.

*Chromobacterium* sp. nov. strain MWU13-2610 and *Chromobacterium* sp. nov. strain MWU14-2602 were isolated from native cranberry bogs at Race Point and High Head at the Cape Cod National Seashore in Massachusetts. These bacteria represent two new presumptive species of the rapidly growing genus *Chromobacterium* (1–9). The genomes were sequenced at the Arizona State University College of Liberal Arts and Sciences (CLAS) Genomics Core facility using an Illumina MiSeq platform. Genomic DNA was sheared to approximately 600-bp fragments using the Covaris M220 ultrasonicator, and Illumina libraries were generated on an Apollo 384 liquid handler (Wafergen) using the Kapa Biosystems library preparation kit (catalog number KK8201). DNA fragments were end repaired and A tailed, as described in the Kapa protocol. Combined indexes/adapters (catalog number 520999; Bioo) were ligated onto each sample and multiplexed into one lane. Adapter-ligated molecules were cleaned using AMPure beads (catalog number A63883; Agencourt Bioscience/Beckman Coulter) and amplified with a Kapa HiFi enzyme. Libraries were analyzed on an Agilent Bioanalyzer and quantified by quantitative PCR (qPCR) (catalog number KK4835; Kapa library quantification kit) before multiplex pooling and sequencing in a 2 × 300-bp paired-end (PE) flow cell on the MiSeq platform (Illumina). Adapters were computationally segregated and trimmed in the Illumina BaseSpace pipeline and then partially assembled using the Velvet assembly tool (10). The *Chromobacterium* sp. nov. MWU13-2610 genome has 62.4% GC content and consists of 4,387,023 bp distributed over 130 scaffolds, 77 of which are larger than 1 kbp. The largest contig is 445,097 bp, the  $N_{50}$  value is 105,364 bp, and the  $N_{75}$  value is 76,063 bp, with a sequence coverage of 51.4×. The *Chromobacterium* sp. nov. MWU14-2602 genome has 63.36% GC content and consists of 4,532,842 bp distributed over 233 scaffolds, 149 of which are larger than 1 kbp. The largest contig is 401,085 bp, the  $N_{50}$  value is 69,582 bp, and the  $N_{75}$  value is 32,238 bp, with a sequence coverage of 60.3×. These two genome sequences were compared using the Genome-to-Genome Distance Calculator (GGDC) provided online by the DSMZ (11). *Chromobacterium* sp. nov. MWU13-2610 and *Chromobacterium* sp. nov. MWU14-2602 were 30.2% homologous, indicating that they belong to different species.

*Ab initio* gene prediction was performed on the assembly using PATRIC (<https://www.patricbrc.org>) (12). The genome of MWU13-2610 contains 4,360 predicted genes, of which 3,055 were predicted to have functional assignments. The genome has multiple

Received 16 March 2018 Accepted 20 March 2018 Published 12 April 2018

**Citation** O'Hara-Hanley K, Harrison A, Soby SD. 2018. Draft genomic sequences of *Chromobacterium* sp. nov. strains MWU13-2610 and MWU14-2602, isolated from wild cranberry bogs in Massachusetts. *Genome Announc* 6: e00332-18. <https://doi.org/10.1128/genomeA.00332-18>.

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potential antibiotic resistance genes, including those for  $\beta$ -lactamases, catalase (*katG*), drug efflux pumps, and aminoglycoside transferases. Although there is no indication that MWU13-2610 is pathogenic, it may contain virulence genes that encode type III secretion systems and the chaperone protein SicA. The genome of MWU14-2602 contains 4,448 predicted genes, of which 3,139 have predicted functions. It contains multiple potential antibiotic resistance genes, including those encoding catalases, drug efflux pumps, and aminoglycoside transferases. Both genomes were scanned for prophages using PHAST (13), and both contain prophage genes. MWU13-2610 has three complete prophages, and MWU14-2602 has one complete prophage genome.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers [PPTF00000000](https://doi.org/10.1093/nar/gkz485) (MWU13-2610) and [PQWB00000000](https://doi.org/10.1093/nar/gkz485) (MWU14-2602). The versions described in this paper are PPTF01000000 and PQWB01000000, respectively.

## ACKNOWLEDGMENTS

This research was supported by the Office of Research and Sponsored Programs, College of Health Sciences, and Biomedical Sciences Program, Midwestern University.

Microbial samples were taken with the kind assistance of the University of Massachusetts Cranberry Station, East Wareham, MA, USA, and the Cape Cod National Seashore, U.S. National Parks Service.

## REFERENCES

- Young C-C, Arun AB, Lai W-A, Chen W-M, Chou J-H, Chao J-H, Shen F-T, Rekha PD, Kämpfer P. 2008. *Chromobacterium aquaticum* sp. nov., isolated from spring water samples. *Int J Syst Evol Microbiol* 58:877–880. <https://doi.org/10.1099/ijs.0.65573-0>.
- Zhou S, Guo X, Wang H, Kong D, Wang Y, Zhu J, Dong W, He M, Hu G, Zhao B, Zhao B, Ruan Z. 2016. *Chromobacterium rhizoryzae* sp. nov., isolated from rice roots. *Int J Syst Evol Microbiol* 66:3890–3896. <https://doi.org/10.1099/ijsem.0.001284>.
- Soby SD, Gadagkar SR, Contreras C, Caruso FL. 2013. *Chromobacterium vaccinii* sp. nov., isolated from native and cultivated cranberry (*Vaccinium macrocarpon* Ait.) bogs and irrigation ponds. *Int J Syst Evol Microbiol* 63:1840–1846. <https://doi.org/10.1099/ijs.0.045161-0>.
- Menezes CBA, Tonin MF, Corrêa DBA, Parma M, de Melo IS, Zucchi TD, Destéfano SAL, Fantinatti-Garbozzini F. 2015. *Chromobacterium amazonense* sp. nov. isolated from water samples from the Rio Negro, Amazon, Brazil. *Antonie Van Leeuwenhoek* 107:1057–1063. <https://doi.org/10.1007/s10482-015-0397-3>.
- Martin PAW, Gundersen-Rindal D, Blackburn M, Buyer J. 2007. *Chromobacterium subtsugae* sp. nov., a betaproteobacterium toxic to Colorado potato beetle and other insect pests. *Int J Syst Evol Microbiol* 57:993–999. <https://doi.org/10.1099/ijs.0.64611-0>.
- Han XY, Han FS, Segal J. 2008. *Chromobacterium haemolyticum* sp. nov., a strongly haemolytic species. *Int J Syst Evol Microbiol* 58:1398–1403. <https://doi.org/10.1099/ijs.0.64681-0>.
- Kämpfer P, Busse H-J, Scholz HC. 2009. *Chromobacterium piscinae* sp. nov. and *Chromobacterium pseudoviolaceum* sp. nov., from environmental samples. *Int J Syst Evol Microbiol* 59:2486–2490. <https://doi.org/10.1099/ijs.0.008888-0>.
- Blackburn MB, Farrar RR, Jr, Sparks ME, Kuhar D, Mitchell A, Gundersen-Rindal DE. 2017. *Chromobacterium sphagni* sp. nov., an insecticidal bacterium isolated from *Sphagnum* bogs. *Int J Syst Evol Microbiol* 67:3417–3422. <https://doi.org/10.1099/ijsem.0.002127>.
- Bajaj A, Kumar A, Yadav S, Kaur G, Bala M, Singh NK, Mathan Kumar R, Manickam N, Mayilraj S. 2016. Isolation and characterization of a novel Gram-negative bacterium *Chromobacterium alkanivorans* sp. nov., strain IITR-71<sup>T</sup> degrading halogenated alkanes. *Int J Syst Evol Microbiol* 66:5228–5235. <https://doi.org/10.1099/ijsem.0.001500>.
- Zerbino DR. 2010. Using the Velvet *de novo* assembler for short-read sequencing technologies. *Curr Protocols Bioinform* Chapter 15:Unit 11.15. <https://doi.org/10.1002/0471250953.bi1105s31>.
- Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M. 2013. Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics* 14:60. <https://doi.org/10.1186/1471-2105-14-60>.
- Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon 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 center. *Nucleic Acids Res* 45:D535–D542. <https://doi.org/10.1093/nar/gkw1017>.
- Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.