

Publication List – Luis M Rodriguez-R

Non-Peer-Reviewed Articles, Preprints, and Other Media (7)

- Rodriguez-R LM** (2021). Behind the paper: Generalists thrive after a catastrophe. *Nature Portfolio Microbiology Community*.
<https://microbiologycommunity.nature.com/posts/generalists-thrive-after-a-catastrophe>.
- Rodriguez-R LM**, Konstantinidis KT (2016). The enveomics collection: A toolbox for specialized analyses of microbial genomes and metagenomes. *PeerJ Preprints* 4:e1900v1. DOI: 10.7287/peerj.preprints.1900v1.
- Rodriguez-R LM**, Konstantinidis KT (2014). Bypassing cultivation to identify bacterial species. *Microbe*, 9(3), 111–118.
- Rodriguez-R LM** (2022). Register list proposing *Elulimicrobium humile* sp. nov. gen. nov. and their lineage. *The SeqCode Registry* r:abw4_f8a. DOI: 10.57973/seqcode.r:abw4_f8a.
- Rodriguez-R LM** (2022). *Macondimonas diazotrophica* sp. nov. gen. nov. *The SeqCode Registry* r:6ns_rdob. DOI: 10.57973/seqcode.r:6ns_rdob.
- Simon SA, Aschmann V, Behrendt A, Hügler M, Engl LM, ..., **Rodriguez-R LM**, et al. Earth's most needed uncultivated aquatic prokaryotes. *OSF Preprints*. DOI: 10.31219/osf.io/qa5c9.
- Zhao J, Brandt G, Wang Z, Hunt DE, **Rodriguez-R LM**, et al (2024). Microbial Response to Natural Disturbances: Rare Biosphere Often Plays a Role. *bioRxiv*. DOI: 10.1101/2024.03.06.583742.

Non-Peer-Reviewed Conference Papers (5)

- Heritier-Robbins P, Karthikeyan S, **Rodriguez-R LM**, Kim M, Hatt J, Overholt W, Kostka JE, Huettel MH, Konstantinidis K (2020). Oil Disturbance Selects for Generalists, not Specialists, in a Beach Sand Microbial Community. *Ocean Sciences Meeting 2020*.
- Karthikeyan S, **Rodriguez-R LM**, Heritier-Robbins P, Huettel MH, Kostka JE, Konstantinidis K (2020). The Crude-Oil Microbiome Webserver: An interactive,

- searchable (meta-) genome repository that expands the catalogued diversity of crude-oil-associated microbes. *Ocean Sciences Meeting 2020*.
- Poulin L, Grygiel P, Magne M, Gagnevin L, Vernière C, **Rodríguez-R LM**, Forero Serna N, Zhao S, Rafii M, Verdier V, Koebnik R (2014). A VNTR tool for diagnostic and epidemiological surveillance of the plant pathogen *Xanthomonas oryzae* and its application to the newly reported Malagasy BLS epidemics. *Session 5-Dynamique, épidémiologie et génétique des populations bactériennes*.
- Jeong K, Munoz Bodnar A, Poulin L, Arias Rojas N, **Rodríguez-R LM**, Gagnevin L, Pruvost O, Koebnik R (2013). CRISPR systems in plant pathogens: A new tool for epidemiological surveillance. *APS-MSA Joint Meeting*. DOI: 10.1094/PHYTO-103-6-S2.1.
- Gutierrez S, **Rodriguez LM**, Pardo C, Pinzon D, Morales N, Restrepo S, Bernal A (2008). Identification of effector genes in *Xanthomonas axonopodis* pv. *Manihotis* using bioinformatics and a forward genetics screen. *2008 APS Centennial Meeting, Phytopathology*, 98(6), S64–S64. DOI: 10.1094/PHYTO.2008.98.6.S9.

Peer-Reviewed Book Chapters (4)

- Rodriguez-R LM**, Rossello-Mora R, Konstantinidis KT (2021). Chapter 13: Identification and Classification of Prokaryotes Using Whole Genome Sequences. In Stackebrandt E, Bridge P, Smith D (Eds.), *Reconciling microbial systematics*. CABI. DOI: 10.1079/9781789244984.0217.
- Rodriguez-R LM**, Harvey W, Rossello-Mora R, Tiedje JM, Cole JR, Konstantinidis KT (2020). Classifying Prokaryotic Genomes Using the Microbial Genomes Atlas (MiGA) Webserver. In *Bergey's Manual of Systematics of Archaea and Bacteria*. Wiley. DOI: 10.1002/9781118960608.bm00042.
- Luo C*, **Rodriguez-R LM***, Konstantinidis KT (2013). Chapter 23: A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. In *Methods in enzymology*, 531, 525–547. DOI: 10.1016/B978-0-12-407863-5.00023-X. * Equal contribution (first co-authorship).
- Kostka JE, Overholt WA, **Rodriguez-R LM**, Huettel M, Konstantinidis KT (2020). Toward a predictive understanding of the benthic microbial community response to oiling on the northern Gulf of Mexico coast. In *Scenarios and Responses to Future*

Deep Oil Spills (pp. 182–202). Springer, Cham. DOI: 10.1007/978-3-030-12963-7.

Peer-Reviewed Articles (70)

* Denotes equal contribution (first co-authorship).

2025

Simon SA, Aschmann V, Behrendt A, Hügler M, Engl LM, ..., **Rodriguez-R LM**, ..., Probst AJ. Earth's most needed uncultivated aquatic prokaryotes. *Water Research* 273, 122928. DOI: 10.1016/j.watres.2024.122928.

2024

Rodriguez-R LM, Conrad RE, Viver T, Feistel DJ, Lindner BG, Venter SN, Orellana LH, Amann R, Rossello-Mora R, Konstantinidis KT. An ANI gap within bacterial species that advances the definitions of intra-species units. *mBio* 15(1). DOI: 10.1128/mbio.02696-23.

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Venter SN, **Rodriguez-R LM**, Chuvochina M, Palmer M, Hugenholtz P, Steenkamp ET. Options and considerations for validation of prokaryotic names under the SeqCode. *Systematic and Applied Microbiology* 47(6), 126554. DOI: 10.1016/j.syapm.2024.126554.

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Sutcliffe I, **Rodriguez-R LM**, Venter SN, Whitman WB. Quis custodiet ipsos custodes? A call for community participation in the governance of the SeqCode. *SAM* 47(2-3), 126498. DOI: 10.1016/j.syapm.2024.126498.

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- Díaz-García L, Chuvochina M, Feuerriegel G, Bunk B, Spröer C, Streit WR, **Rodriguez-R LM**, Overmann J, Jiménez DJ. Andean soil-derived lignocellulolytic bacterial consortium as a source of novel taxa and putative plastic-active enzymes. *Systematic and Applied Microbiology*, 47(1), 126485. DOI: 10.1016/j.syapm.2023.126485.
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- Lindner BG, Gerhardt K, Feistel DJ, **Rodriguez-R LM**, Hatt JK, Konstantinidis KT. A user's guide to the bioinformatic analysis of shotgun metagenomic sequence data for bacterial pathogen detection. *International Journal of Food Microbiology*, 410, 110488. DOI: 10.1016/j.ijfoodmicro.2023.110488.

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- Perez-Quintero AL*, **Rodriguez-R LM***, Cuesta-Morondo S, Hakalová E, Betancurt-Anzola D, *et al.* Comparative genomics identifies conserved and variable TAL effectors in African strains of the cotton pathogen *Xanthomonas citri* pv. *malvacearum*. *Phytopathology*, 113(8). DOI: 10.1094/PHYTO-12-22-0477-SC.
- Embacher J, Zeilinger S, Kirchmair M, **Rodriguez-R LM**, Neuhauser S. Wood decay fungi and their bacterial interaction partners in the built environment—A systematic review on fungal bacteria interactions in dead wood and timber. *Fungal Biology Reviews*, 45, 100305. DOI: 10.1016/j.fbr.2022.100305.

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- Gerhardt K*, Ruiz-Perez CA*, **Rodriguez-R LM***, Conrad RE, Konstantinidis KT. RecruitPlotEasy: An advanced read recruitment plot tool for assessing metagenomic population abundance and genetic diversity. *Frontiers in Bioinformatics*, 1, 826701. DOI: 10.3389/fbinf.2021.826701.
- Zhang SY*, Suttner B*, **Rodriguez-R LM***, Orellana LH, Conrad RE, Liu F, Rowell JL, Webb HE, Williams-Newkirk AJ, Huang A, Konstantinidis KT. ROcker models for reliable detection and typing of short-read sequences carrying β -lactamase genes. *mSystems*, 7(3). DOI: 10.1128/msystems.01281-21.
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- prokaryotes described from sequence data. *Nature Microbiology*, 7, 1702-1708. DOI: 10.1038/s41564-022-01214-9.
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- Kim M, **Rodriguez-R LM**, Hatt JK, Kayali O, Nalá R, Dunlop AL, Brennan PA, Corwin E, Smith AK, Brown J, Konstantinidis KT. Higher pathogen load in children from Mozambique vs USA revealed by comparative fecal microbiome profiling. *ISME Communications*, 2, 74. DOI: 10.1038/s43705-022-00154-z.
- Díaz Rodríguez CA, Díaz-García L, Bunk B, Spröer C, Herrera K, Taraona NA, **Rodriguez-R LM**, Overmann J, Jiménez DJ. Novel bacterial taxa in a minimal lignocellulolytic consortium and their potential for lignin and plastics transformation. *ISME Communications*, 2, 89. DOI: 10.1038/s43705-022-00176-7.
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- Heritier-Robbins P, Karthikeyan S, Hatt JK, Kim M, Huettel M, Kostka JE, Konstantinidis KT, **Rodriguez-R LM**. Beach sand oil spills select for generalist microbial populations. *The ISME Journal*, 15, 3418-3422. DOI: 10.1038/s41396-021-01017-6.
- Rodriguez-R LM**, Jain C, Conrad RE, Aluru S, Konstantinidis KT. Reply to: “Re-evaluating the evidence for a universal genetic boundary among microbial species”. *Nature Communications*, 12, 4060. DOI: 10.1038/s41467-021-24129-1.
- Meziti A*, **Rodriguez-R LM***, Hatt JK, Peña-Gonzalez A, Levy K, Konstantinidis KT. The reliability of metagenome-assembled genomes (MAGs) in representing natural

- populations: insights from comparing MAGs against isolate genomes derived from the same fecal sample. *Applied and Environmental Microbiology*, 87(6). DOI: 10.1128/AEM.02593-20.
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- Suttner B, Kim M, Johnston ER, Orellana LH, Ruiz-Perez CA, **Rodriguez-R LM**, Hatt JK, Brown J, Santo Doming JW, Konstantinidis KT. Transcriptomic and rRNA:rDNA signatures of environmental versus enteric *Enterococcus faecalis* isolates under oligotrophic freshwater conditions. *Microbiology Spectrum*, 9(2): e00817-21. DOI: 10.1128/Spectrum.00817-21.
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- Campanaro S, Treu L, **Rodriguez-R LM**, Kovalovszki A, Ziels RM, Maus I, Zhu X, Kougias PG, Basile A, Luo G, *et al.* New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. *Biotechnology for Biofuels*, 13(1), 1–18. DOI: 10.1186/s13068-020-01679-y.
- Suttner B, Johnston ER, Orellana LH, **Rodriguez-R LM**, Hatt JK, Carychao D, Carter MQ, Cooley MB, Konstantinidis KT. Metagenomics as a public health risk

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Karthikeyan S, **Rodriguez-R LM**, Heritier-Robbins P, Kim M, Overholt WA, Gaby JC, Hatt JK, Spain JC, Rosselló-Móra R, Huettel M, *et al.* “*Candidatus* Macondimonas diazotrophica”, a novel gammaproteobacterial genus dominating crude-oil-contaminated coastal sediments. *The ISME Journal*, 13(8), 2129–2134. DOI: 10.1038/s41396-019-0400-5.

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Meziti A, Tsementzi D, **Rodriguez-R LM**, Hatt JK, Karayanni H, Kormas KA, Konstantinidis KT. Quantifying the changes in genetic diversity within sequence-discrete bacterial populations across a spatial and temporal riverine gradient. *The ISME Journal*, 13(3), 767–779. DOI: 10.1038/s41396-018-0307-6.

Jeong K, Muñoz-Bodnar A, Rojas NA, Poulin L, **Rodriguez-R LM**, Gagnevin L, Vernière C, Pruvost O, Koebnik R. CRISPR elements provide a new framework for the genealogy of the citrus canker pathogen *Xanthomonas citri* pv. *citri*. *BMC Genomics*, 20(1), 917. DOI: 10.1186/s12864-019-6267-z.

2018

Rodriguez-R LM, Castro JC, Kyrpides NC, Cole JR, Tiedje JM, Konstantinidis, KT. How much do rRNA gene surveys underestimate extant bacterial diversity? *Applied and Environmental Microbiology*, 84(6). DOI: 10.1128/AEM.00014-18.

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2016

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2015

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- Luo C, **Rodriguez-R LM**, Johnston ER, Wu L, Cheng L, Xue K, Tu Q, Deng Y, He Z, Shi JZ, *et al.* Soil microbial community responses to a decade of warming as revealed by comparative metagenomics. *Applied and Environmental Microbiology*, 80(5), 1777–1786. DOI: 10.1128/AEM.03712-13.
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