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# Publication List

## NON-PEER-REVIEWED ARTICLES, PREPRINTS, AND OTHER MEDIA (6)

Rodriguez-Gijon A, Pacheco-Valenciana A, Milke F, Dharamshi JE, Hampel JJ, …, **Rodriguez-R LM**, Garcia SL (2025). The ecological success of freshwater microorganisms is mediated by streamlining and biotic interactions. *bioRxiv*. DOI: 10.1101/2025.03.24.644981.

**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.

**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.

## 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.

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* Denotes equal contribution (first co-authorship).

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Ernster NM, **Rodriguez-R LM**. A practical guide on environmental genomics for prokaryotic systematics. *Systematic and Applied Microbiology* 48(5): 126643. DOI: 10.1016/j.syapm.2025.126643.

Gerhard K*, Ruiz-Perez CA*, **Rodriguez-R LM***, Jain C, Tiedje JM, Cole JR, Konstantinidis KT. FastAAI: efficient estimation of genome average amino acid identity and phylum-level relationships using tetramers of universal proteins. *Nucleic Acids Research* 53, gkaf348. DOI: 10.1093/nar/gkaf348.

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

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Zohar M, Shaheen N, Goyal SM, Mor SK, **Rodriguez-R LM**, Imran M. Probiotic potential of yeast, mold, and intermediate morphotypes of *Geotrichum candidum* in modulating gut microbiota and body physiology in mice. *Probiotics and Antimicrobial Proteins*. DOI: 10.1007/s12602-025-10497-3.

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Zhao J, Pachiadaki M, Conrad RE, Jannet JK, Bristow LA, **Rodriguez-R LM**, Rossello-Mora R, Stewart FJ, Konstantinidis KT. Promiscuous and genome-wide recombination underlies the sequence-discrete species of the SAR11 lineage in the deep ocean Promiscuous and genome-wide recombination underlies the sequence-discrete species of the SAR11 lineage in the deep ocean. *The ISME Journal*, wraf072. DOI: 10.1093/ismejo/wraf072.

### 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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Perez-Quintero AL*, **Rodriguez-R LM***, Cuesta-Morrondo 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.

## 2022

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.

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**Rodriguez-R LM**, Tsementzi D, Luo C, Konstantinidis KT. Iterative subtractive binning of freshwater chronoseries metagenomes identifies over 400 novel species and their ecologic preferences. *Environmental Microbiology* 22(8), 3394–3412. DOI: 10.1111/1462-2920.15112.

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### **2015 and Before** (23)

**Rodriguez-R LM**, Overholt WA, Hagan C, Huettel M, Kostka JE, Konstantinidis KT (2015). Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. *The ISME Journal* 9(9), 1928–1940. DOI: 10.1038/ismej.2015.5.

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