

Publication List – Luis M Rodriguez-R

Non-Peer-Reviewed Articles, Preprints, and Other Media (9)

- 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, Both JP, **Rodriguez-R** & Konstantinidis (2022). GSearch: Ultra-Fast and Scalable Microbial Genome Search by combining Kmer Hashing with Hierarchical Navigable Small World Graphs. *bioRxiv*. DOI: 10.1101/2022.10.21.513218.
- 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.
- Conrad RE, Brink CE, Viver T, **Rodriguez-R LM**, Aldeguer Riquelme B, *et al* (2024). Microbial species exist and are maintained by ecological cohesiveness coupled to high homologous recombination. *bioRxiv*. DOI: 10.1101/2024.05.25.595874.

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 (66)

* Denotes equal contribution (first co-authorship).

2024

Rodriguez-R LM, Conrad RE, Viver T, Feistel DJ, Lindner BG, *et al.* An ANI gap within bacterial species that advances the definitions of intra-species units. *mBio* 15(1). DOI: 10.1128/mbio.02696-23.

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.

Whitman WB, Chuvochina M, Hedlund BP, Konstantinidis KT, Palmer M, **Rodriguez-R LM**, Sutcliffe I, Wang F. Why and how to use the SeqCode. *mLife* 3(1), 1-13. DOI: 10.1002/mlf2.12092.

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.

Viver T, Conrad RE, **Rodriguez-R LM**, Ramírez AS, Venter SN, *et al.* Towards estimating the number of strains that make up a natural bacterial population. *Nature Communications*, 15, 544. DOI: 10.1038/s41467-023-44622-z.

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.

2023

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.

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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. ROCK models for reliable detection and typing of short-read sequences carrying β -lactamase genes. *mSystems*, 7(3). DOI: 10.1128/msystems.01281-21.

Hedlund BP, Chuvochina M, Hugenholtz P, ..., **Rodriguez-R LM**, Rossello-Mora R, Sutcliffe IC, Venter SN & Whitman WB. SeqCode: a nomenclatural code for prokaryotes described from sequence data. *Nature Microbiology*, 7, 1702-1708. DOI: 10.1038/s41564-022-01214-9.

Whitman WB, Chuvochina M, Hedlund BP, ..., **Rodriguez-R LM**, Rossello-Mora R, Sutcliffe I & Venter SN. Development of the SeqCode: a proposed nomenclatural code for uncultivated prokaryotes with DNA sequences as type. *Systematic and Applied Microbiology*, 45(5), 126405. DOI: 10.1016/j.syapm.2022.126305.

Pallen MJ, **Rodriguez-R LM** & Alikhan NF. Naming the unnamed: over 65,000 *Candidatus* names for unnamed *Archaea* and *Bacteria* in the Genome Taxonomy Database. *International Journal of Systematic and Evolutionary Microbiology*, 72(9). DOI: 10.1099/ijsem.0.005482.

- 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.
- Lindner BG, Suttner B, Zhu KJ, Conrad RE, **Rodriguez-R LM**, Hatt JK, Brown J & Konstantinidis KT. Toward shotgun metagenomic approaches for microbial source tracking sewage spills based on laboratory mesocosms. *Water Research*, 210, 117993. DOI: 10.1016/j.watres.2021.117993.

2021

- 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.
- Montenegro Benavides NA, Alvarez A, Arrieta-Ortiz ML., **Rodriguez-R LM**, Botero D, Tabima JF, Castiblanco L, Trujillo C, Restrepo S & Bernal A. The Type VI secretion system of *Xanthomonas phaseoli* pv. *manihotis* is involved in virulence and *in vitro* motility. *BMC Microbiology*, 21(14). DOI: 10.1186/s12866-020-02066-1.
- 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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Karthikeyan S, **Rodriguez-R LM**, Heritier-Robbins P, Hatt JK, Huettel M, Kostka JE & Konstantinidis KT. Genome repository of oil systems: An interactive and searchable database that expands the catalogued diversity of crude oil-associated microbes. *Environmental Microbiology*, 22(6), 2094–2106. DOI: 10.1111/1462-2920.14966.

Dam P, **Rodriguez-R LM**, Luo C, Hatt J, Tsementzi D, Konstantinidis KT & Voit EO. Model-based comparisons of the Abundance Dynamics of Bacterial communities in two Lakes. *Scientific Reports*, 10(1), 1–12. DOI: 10.1038/s41598-020-58769-y.

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 assessment tool in a study of natural creek sediments influenced by agricultural and livestock runoff: Potential and limitations. *Applied and Environmental Microbiology*, 86(6). DOI: 10.1128/AEM.02525-19.

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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.

- Tsementzi D, **Rodriguez-R LM**, Ruiz-Perez CA, Meziti A, Hatt JK & Konstantinidis KT. Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus “*Candidatus Fonsibacter*” and proposal of “*Ca. Fonsibacter lacus*” sp. nov. *Systematic and Applied Microbiology*, 42(4), 495–505. DOI: 10.1016/j.syapm.2019.03.007.
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- 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.

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- 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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- Rodriguez-R LM***, Gunturu S*, Tiedje JM, Cole JR & Konstantinidis KT. Nonpareil 3: Fast estimation of metagenomic coverage and sequence diversity. *mSystems*, 3(3). DOI: 10.1128/mSystems.00039-18.
- Jain C, **Rodriguez-R LM**, Phillippy AM, Konstantinidis KT & Aluru S. High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. *Nature Communications*, 9(1), 1–8. DOI: 10.1038/s41467-018-07641-9.
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- Pena-Gonzalez A, **Rodriguez-R LM**, Marston CK, Gee JE, Gulvik CA, Kolton CB, Saile E, Frace M, Hoffmaster AR & Konstantinidis KT. Genomic characterization and copy number variation of *Bacillus anthracis* plasmids pXO1 and pXO2 in a

historical collection of 412 strains. *mSystems*, 3(4). DOI: 10.1128/mSystems.00065-18.

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Poulin L, Grygiel P, Magne M, Gagnevin L, **Rodriguez-R LM**, Serna NF, Zhao S, El Rafii M, Dao S, Tekete C, *et al.* New multilocus variable-number tandem-repeat analysis tool for surveillance and local epidemiology of bacterial leaf blight and bacterial leaf streak of rice caused by *Xanthomonas oryzae*. *Applied and Environmental Microbiology*, 81(2), 688–698. DOI: 10.1128/AEM.02768-14.

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Orellana L, **Rodriguez-R L**, Higgins S, Chee-Sanford J, Sanford R, Ritalahti K, Löffler F & Konstantinidis K. Detecting nitrous oxide reductase (*nosZ*) genes in soil metagenomes: Method development and implications for the nitrogen cycle. *mBio*, 10(5), 01193–14. DOI: 10.1128/mBio.01193-14.

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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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