

Publication List

Non-Peer-Reviewed Articles, Preprints, and Other Media (6)

- 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.
- Lindner BG, Suttner B, Conrad RE, **Rodriguez-R LM**, Hatt JK, Zhu KJ, Brown J, Konstantinidis KT (2021). Novel municipal sewage-associated bacterial genomes and their potential in source tracking. *bioRxiv*. DOI: 10.1101/2021.07.15.452399.
- Suttner B, Kim M, Johnston ER, Orellana L, Ruiz-Perez CA, **Rodriguez-R LM**, Hatt J, Brown J, Santo Domingo JW, Konstantinidis KT (2021). Transcriptomic and rRNA:rDNA signatures of environmental vs. enteric *Enterococcus faecalis* isolates under oligotrophic freshwater conditions. *bioRxiv*. DOI: 10.1101/2021.05.04.442698.
- Suttner B, Johnston ER, Orellana LH, **Rodriguez-R LM**, Hatt J, Carychao D, Carter MQ, Cooley MB & Konstantinidis KT (2019). Metagenomic characterization of creek sediment microbial communities from a major agricultural region in Salinas, California. *bioRxiv*, 737759. DOI: 10.1101/737759.

Non-Peer-Reviewed Conference Papers (4)

- 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, **Rodríguez-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.

Peer-Reviewed Book Chapters (4)

- Rodríguez-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.
- Rodríguez-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*, **Rodríguez-R LM*** & Konstantinidis KT (2013). Chapter 23: A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. In *Methods in enzymology* (Vol. 531, pp. 525–547). DOI: 10.1016/B978-0-12-407863-5.00023-X. * Equal contribution (first co-authorship).
- Kostka JE, Overholt WA, **Rodríguez-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 (53)

* Denotes equal contribution (first co-authorship).

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.

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.

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Heritier-Robbins P, Karthikeyan S, Hatt JK, Kim M, Huettel M, Kostka JE, Konstantinidis KT & **Rodriguez-R LM** (2021). Beach sand oil spills select for generalist microbial populations. *The ISME Journal*. DOI: 10.1038/s41396-021-01017-6.

Rodriguez-R LM, Jain C, Conrad RE, Aluru S & Konstantinidis KT (2021). 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 (2021). 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 (2021). 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 (2021). 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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Rodriguez-R LM, Tsementzi D, Luo C & Konstantinidis KT (2020). 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.

Karthikeyan S, **Rodriguez-R LM**, Heritier-Robbins P, Hatt JK, Huettel M, Kostka JE & Konstantinidis KT (2020). 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.

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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 & others (2020). 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 (2020). 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 & others. (2019). “*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 (2019). 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 (2019). 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 (2018). How much do rRNA gene surveys underestimate extant bacterial diversity? *Applied and Environmental Microbiology*, 84(6). DOI: 10.1128/AEM.00014-18.
- Rodriguez-R LM**, Gunturu S, Harvey WT, Rosselló-Mora R, Tiedje JM, Cole JR & Konstantinidis KT (2018). The Microbial Genomes Atlas (MiGA) webserver: Taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level. *Nucleic Acids Research*, 46(W1), W282–W288. DOI: 10.1093/nar/gky467.
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- Jain C, **Rodriguez-R LM**, Phillippy AM, Konstantinidis KT & Aluru S (2018). 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 (2018). 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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