

Publication List

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* (Vol. 531, pp. 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.

Popular Science and Non-Peer-Reviewed Articles (5)

- 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.

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, **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.

Peer-Reviewed Articles (50)

* Denotes equal contribution (first co-authorship).

2021

- 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.

2020

- Rodriguez-R LM**, Tsementzi D, Luo C & Konstantinidis KT (2020). Iterative subtractive binning of freshwater chronoserries 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.
- Dam P, **Rodriguez-R LM**, Luo C, Hatt J, Tsementzi D, Konstantinidis KT & Voit EO (2020). 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 & 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.

Tsementzi D, **Rodriguez-R LM**, Ruiz-Perez CA, Meziti A, Hatt JK & Konstantinidis KT (2019). 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.

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.

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- Castro JC, **Rodriguez-R LM**, Harvey WT, Weigand MR, Hatt JK, Carter MQ & Konstantinidis KT (2018). imGLAD: accurate detection and quantification of target organisms in metagenomes. *PeerJ*, 6, e5882. DOI: 10.7717/peerj.5882.
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- Orellana LH, **Rodriguez-R LM** & Konstantinidis KT (2017). ROcKer: Accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. *Nucleic Acids Research*, 45(3), e14–e14. DOI: 10.1093/nar/gkw900.
- Wang Y, Hatt JK, Tsementzi D, **Rodriguez-R LM**, Ruiz-Pérez CA, Weigand MR, Kizer H, Maresca G, Krishnan R, Poretsky R & others. (2017). Quantifying the importance of the rare biosphere for microbial community response to organic

pollutants in a freshwater ecosystem. *Applied and Environmental Microbiology*, 83(8), e03321-16. DOI: 10.1128/AEM.03321-16.

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