

Publication List

Book Chapters (4)

- Rodriguez-R, L. M.**, Harvey, W., Rossello-Mora, R., Tiedje, J., Cole, J., & Konstantinidis, K. (In Press). Classifying Prokaryotic Genomes Using the Microbial Genomes Atlas (MiGA) Webserver. In *Bergey's Manual of Systematics of Archaea and Bacteria*. Wiley.
- Rodriguez-R, L. M.**, Rossello-Mora, R., & Konstantinidis, K. T. (In Press). Chapter 13: Identification and Classification of Prokaryotes Using Whole Genome Sequences. In E. Stackebrandt, P. Bridge, & D. Smith (Eds.), *Reconciling microbial systematics*. CABI.
- Kostka, J. E., Overholt, W. A., **Rodriguez-R, L. M.**, Huettel, M., & Konstantinidis, K. (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.
- Luo, C.*, **Rodriguez-R, L. M.***, & Konstantinidis, K. T. (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).

Popular Science and Non-Peer-Reviewed Articles (4)

- Rodriguez-R, L. M.**, & Konstantinidis, K. T. (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, L. M.**, & Konstantinidis, K. T. (2014). Bypassing Cultivation To Identify Bacterial Species. *Microbe*, 9(3), 111–118.
- Benavides, N. A. M., Borrero, A. A., Ortiz, M. L. A., **Rodriguez-R, L. M.**, Rozo, D. O. B., Mosos, L. F. C., Beltran, C. T., Restrepo, S. R., Bernal, A., & others. (2020). The Type VI Secretion System of *Xanthomonas Phaseoli* pv. *Manihotis* is Involved in Virulence and in vitro Motility. Research Square. DOI: 10.21203/rs.3.rs-48039/v1.

Suttner, B., Johnston, E. R., Orellana, L. H., **Rodriguez-R, L. M.**, Hatt, J., Carychao, D., Carter, M. Q., Cooley, M. B., & Konstantinidis, K. T. (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, L. M.**, Kim, M., Hatt, J., Overholt, W., Kostka, J. E., Huettel, M. H., & Kostas, K. (2020). Oil Disturbance Selects for Generalists, not Specialists, in a Beach Sand Microbial Community. *Ocean Sciences Meeting 2020*.

Karthikeyan, S., **Rodriguez-R, L. M.**, Heritier-Robbins, P., Huettel, M. H., Kostka, J. E., & 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, L. M.**, Forero Serna, N., Zhao, S., Rafii, M., Verdier, V., & others. (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, L. M.**, Gagnevin, L., Pruvost, O., & Koebnik, R. (2013). *CRISPR systems in plant pathogens: A new tool for epidemiological surveillance*. DOI: 10.1094/PHYTO-103-6-S2.1.

Peer-Reviewed Articles (47)

* Denotes equal contribution (first co-authorship).

2020

Rodriguez-R, L. M., Tsementzi, D., Luo, C., & Konstantinidis, K. T. (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, L. M.**, Heritier-Robbins, P., Hatt, J. K., Huettel, M., Kostka, J. E., & Konstantinidis, K. T. (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, L. M.**, Luo, C., Hatt, J., Tsementzi, D., Konstantinidis, K. T., & Voit, E. O. (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, L. M.**, Kovalovszki, A., Ziels, R. M., Maus, I., Zhu, X., Kougias, P. G., 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, E. R., Orellana, L. H., **Rodriguez-R, L. M.**, Hatt, J. K., Carychao, D., Carter, M. Q., Cooley, M. B., & Konstantinidis, K. T. (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.

2019

- Karthikeyan, S., **Rodriguez-R, L. M.**, Heritier-Robbins, P., Kim, M., Overholt, W. A., Gaby, J. C., Hatt, J. K., Spain, J. C., 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, L. M.**, Ruiz-Perez, C. A., Meziti, A., Hatt, J. K., & Konstantinidis, K. T. (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, L. M.**, Hatt, J. K., Karayanni, H., Kormas, K. A., & Konstantinidis, K. T. (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, Kwanho, Muñoz-Bodnar, A., Rojas, N. A., Poulin, L., **Rodriguez-R, L. M.**, 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, L. M.**, Castro, J. C., Kyrpides, N. C., Cole, J. R., Tiedje, J. M., & Konstantinidis, K. T. (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, L. M.**, Gunturu, S., Harvey, W. T., Rosselló-Mora, R., Tiedje, J. M., Cole, J. R., & Konstantinidis, K. T. (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.
- Rodriguez-R, L. M.***, Gunturu, S.*, Tiedje, J. M., Cole, J. R., & Konstantinidis, K. T. (2018). Nonpareil 3: Fast estimation of metagenomic coverage and sequence diversity. *mSystems*, 3(3). DOI: 10.1128/mSystems.00039-18.
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- Castro, J. C., **Rodriguez-R, L. M.**, Harvey, W. T., Weigand, M. R., Hatt, J. K., Carter, M. Q., & Konstantinidis, K. T. (2018). imGLAD: accurate detection and quantification of target organisms in metagenomes. *PeerJ*, 6, e5882. DOI: 10.7717/peerj.5882.
- Pena-Gonzalez, A., **Rodriguez-R, L. M.**, Marston, C. K., Gee, J. E., Gulvik, C. A., Kolton, C. B., Saile, E., Frace, M., Hoffmaster, A. R., & Konstantinidis, K. T. (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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Orellana, L. H., **Rodriguez-R, L. M.**, & Konstantinidis, K. T. (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.

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Johnston, E. R., **Rodriguez-R, L. M.**, Luo, C., Yuan, M. M., Wu, L., He, Z., Schuur, E. A., Luo, Y., Tiedje, J. M., Zhou, J., & others. (2016). Metagenomics reveals pervasive bacterial populations and reduced community diversity across the Alaska tundra ecosystem. *Frontiers in Microbiology*, 7, 579. DOI: 10.3389/fmicb.2016.00579.

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