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PROFESSIONAL EXPERIENCE**GEORGIA INSTITUTE OF TECHNOLOGY**

Postdoctoral fellow, Konstantinidis lab.

Atlanta, GA, USA, 2017

Graduate research assistant, Konstantinidis lab.

Atlanta, GA, USA, 2012-2016

Graduate teaching assistant, Biology 1510 (two terms).

Atlanta, GA, USA, 2011-2012

INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT (IRD)

Intern, Laboratory of Plant Resistance to Bio-aggressors (RPB).

Montpellier, France, 2011

Temporal researcher, Laboratory of Plant Genomics and Development (LGDP).

Montpellier, France, 2010

COLOMBIAN CENTER FOR GENOMICS AND BIOINFORMATICS OF EXTREME ENVIRONMENTS (GEBIX)

Researcher, Bioinformatics team.

Bogotá, Colombia, 2009-2010

UNIVERSIDAD DE LOS ANDES, DEPARTMENT OF BIOLOGICAL SCIENCES

Graduate teaching assistant, Cell Biology (2009, two terms).

Bogotá, Colombia, 2009-2010

Teacher, unofficial lecture on Perl programming for biological sciences (2010).

Researcher, Laboratory of Mycology and Plant Pathology (LAMFU).

Researcher, Laboratory of Mycology and Plant Pathology (LAMFU).

Bogotá, Colombia, 2008

UNIVERSIDAD NACIONAL DE COLOMBIA, BIOTECHNOLOGY INSTITUTE

Researcher, Centre for Bioinformatics of the Biotechnology Institute (CBIB).

Bogotá, Colombia, 2006-2008

Undergraduate teaching assistant, Bioinformatics.

Bogotá, Colombia, 2006

AWARDS AND DISTINCTIONS**SIGMA XI, GEORGIA TECH CHAPTER**

Sigma Xi Best Ph.D. Thesis Award.

Atlanta, GA, USA, 2017

INTERNATIONAL SOCIETY FOR MICROBIAL ECOLOGY – ISME

ISME Travel Award, ISME 16, Montréal, Canada.

Montréal, QC, Canada, 2016

GEORGIA INSTITUTE OF TECHNOLOGY, SCHOOL OF BIOLOGY

School of Biology Graduate Excellence Award 2015.

Atlanta, GA, USA, 2015

RÉGION LANGUEDOC ROUSSILLON, FRANCE

Fellowship granted by the region to outstanding international students.

France, 2010-2011

EVALUATION-ORIENTATION OF SCIENTIFIC COOPERATION (ECOS) PROGRAM

Scientific mission to the *Institut de Recherche pour le Développement* (IRD).

Montpellier, France, 2009

UNIVERSIDAD NACIONAL DE COLOMBIA, COLLEGE OF SCIENCE

Award *Matricula de Honor* for the first semester of 2004.

Bogotá, Colombia, 2004

PUBLICATIONS**CURRENTLY IN PREPARATION OR UNDER REVIEW**

Rodriguez-R LM, Tsementzi D, Luo C, Hatt JK, Konstantinidis KT. Biogeography and seasonal variation disentangled in microbial meta-communities of five connected lakes.

Rodriguez-R LM*, Gunturu S*, Guo J, Luo C, Tiedje JM, Cole J, Konstantinidis KT. Nonpareil 3: Fast estimation of metagenomic coverage and sequence diversity. *Equal contribution.

Rodriguez-R LM*, Castro JC*, Kyrpides NC, Cole JR, Tiedje JM, Konstantinidis KT. How much rRNA gene surveys underestimate extant microbial diversity? * Equal contribution.

Rodriguez-R LM, Dam P, Tsementzi D, Luo C, Voit E, Konstantinidis KT. Characterization of microbial interactions and detection of microbial guilds in a six-years freshwater metagenomic chronoseries.

Rodriguez-R LM, Gunturu S, Fall A, Luo C, Tiedje JM, Cole J, Konstantinidis KT. Microbial Genomes Atlas: Standardizing genomic and metagenomic analyses for *Archaea* and *Bacteria*.

Rodriguez-R LM, Pena-Gonzalez A, Gee JE, Marston CK, Hoffmaster A, Konstantinidis KT. Accurate typing of *Bacillus anthracis* in hundreds of genomes using Average Nucleotide Identity.

Rodriguez-R LM*, Tsementzi D*, Konstantinidis KT. A novel method for the quantification of *in situ* intra-population genetic diversity from metagenomes. * Equal contribution.

Castro JC*, **Rodriguez-R LM***, Hatt J, Carter M, Konstantinidis KT. Development of a metagenomics-based method for detection of foodborne pathogens on fresh produce. * Equal contribution.

Soto-Giron J, **Rodriguez-R LM**, Castro JC, Konstantinidis KT. Comparative genomic analysis of recombination rates among bacterial species.

PUBLISHED WORKS

Wang Y, Hatt JK, Tsementzi D, **Rodriguez-R LM**, Ruiz-Pérez CA, Weigand MR, Kizer H, Maresca G, Krishnan R, Poretsky R, Spain JC, Konstantinidis KT. 2017. *Applied and Environmental Microbiology*, In press.

Orellana LH*, **Rodriguez-R LM***, Konstantinidis KT. 2017. ROCKr: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. *Nucleic Acids Research* 45(3): e14. * Equal contribution.

Tsementzi D, Wu J, Deutsch S, Nath S, **Rodriguez-R LM**, Burns AS, Ranjan P, Sarode N, Malmstrom RR, Padilla CC, Stone BK, Bristow LA, Larsen M, Glass JB, Thamdrup B, Woyke T, Konstantinidis KT, Stewart FJ. 2016. SAR11 bacteria linked to ocean anoxia and nitrogen loss. *Nature* 536(7615): 179-183.

Soto-Giron MJ, **Rodriguez-R LM**, Luo C, Elk M, Ryu H, Hoelle J, Santo Domingo J, Konstantinidis KT. 2016. Biofilms on hospital shower hoses: Characterization and implications for nosocomial infections. *Applied and Environmental Microbiology* 82(9): 2872-2883.

Rodriguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a toolbox for specialized analyses of microbial genomes and metagenomes. *PeerJ Preprints*: e1900v1.

Johnston ER, **Rodriguez-R LM**, Luo C, Yuan MM, Wu L, He Z, Schuur EAG, Luo Y, Tiedje JM, Zhou J, Konstantinidis KT. 2016. Metagenomics reveals pervasive bacterial populations and reduced community diversity across the Alaska tundra ecosystem. *Frontiers in Microbiology* 7:579.

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.

Poulin L, Grygiel P, Magne M, Gagnevin L, **Rodriguez-R LM**, Forero Serna N, Zhao S, El Rafii M, Dao S, Tekete C, Wonni I, Koita O, Pruvost O, Verdier V, Vernière C, Koebnik R. 2015. 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.

Tsementzi D, Poretsky R, **Rodriguez-R LM**, Luo C, Konstantinidis KT. 2014. Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. *Environmental Microbiology Reports* 6(6): 640-655.

Rodriguez-R LM, Konstantinidis KT. 2014. Estimating coverage in metagenomic data sets and why it matters. *The ISME Journal* 8: 2349-2351.

Rodriguez-R LM, Konstantinidis KT. 2014. Bypassing cultivation to identify bacterial species. *Microbe* 9(3): 111-118.

Luo C, **Rodriguez-R LM**, Konstantinidis KT. 2014. MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. *Nucleic Acids Research* 42(8): e73.

Rodriguez-R LM, Konstantinidis KT. 2014. Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. *Bioinformatics* 30(5): 629-635.

Luo C, **Rodriguez-R LM**, Johnston ER, Wu L, Cheng L, Xue K, Tu Q, Deng Y, He Z, Zhou Shi J, Yuan MM, Sherry RA, Li D, Luo Y, Schuur EAG, Chain P, Tiedje JM, Zhou J, Konstantinidis KT. 2014. Soil microbial community re-

sponses to a decade of warming as revealed by comparative metagenomics. *Applied and Environmental Microbiology* 80(5): 1777-1786.

Orellana LH, **Rodriguez-R LM**, Higgins S, Chee-Sanford JC, Sanford RA, Ritalahti KM, Löffler FE, Konstantinidis KT. 2014. Detecting nitrous oxide reductase (*nosZ*) genes in soil metagenomes: method development and implications for the nitrogen cycle. *mBio* 5(3): e01193-14.

Poretsky R, **Rodriguez-R LM**, Luo C, Tsementzi D, Konstantinidis KT. 2014. Strengths and limitations of 16S rRNA gene amplicon sequencing in revealing temporal microbial community dynamics. *PLoS ONE* 9(4): e93827.

DeLeon-Rodriguez N, Lathem TL, **Rodriguez-R LM**, Barazesh JM, Anderson BE, Beyersdorf AJ, Ziemba LD, Bergin M, Nenes A, Konstantinidis KT. 2013. *PNAS* 110(7): 2575-2580.

Luo C*, **Rodriguez-R LM***, Konstantinidis KT. 2013. Chapter 23: A user's guide to quantitative and comparative analysis of metagenomic datasets. In: DeLong EF (ed.). 2013. Microbial metagenomics, metatranscriptomics, and metaproteomics. *Methods in enzymology* 531. * Equal contribution.

Pérez-Quintero AL, **Rodriguez-R LM**, Dereeper A, López C, Koebnik R, Szurek B. 2013. An improved method for TAL effectors DNA-binding sites prediction reveals functional convergence in TAL repertoires of *Xanthomonas oryzae* strains. *PLoS ONE* 8(7): e68464.

Arrieta-Ortiz ML, **Rodriguez-R LM**, Pérez-Quintero AL, Poulin L, Díaz AC, Arias Rojas N, [...], Koebnik R, Bernal A. Genomic survey of pathogenicity determinants and VNTR markers in the cassava bacterial pathogen *Xanthomonas axonopodis* pv. *manihotis* strain CIO151. *PLoS ONE* 8(11): e79704.

Zhao S, Poulin L, **Rodriguez-R LM**, Forero Serna N, Liu S-Y, Wonni I, Szurek B, Verdier V, Leach JE, He Y-Q, Feng J-X, Koebnik R. 2012. Development of a Variable Number of Tandem Repeats typing scheme for the bacterial rice pathogen *Xanthomonas oryzae* pv. *oryzicola*. *Phytopathology* 102(10): 948-956.

Cárdenas A, **Rodriguez-R LM**, Pizarro V, Cadavid LF, Arévalo-Ferro C. 2012. Shifts in bacterial communities of two caribbean reef-building coral species affected by white plague disease. *The ISME Journal* 6: 502-512.

Rodriguez-R LM, Grajales A, Arrieta-Ortiz ML, Salazar C, Restrepo S, Bernal A. 2012. Genomes-based phylogeny of the genus *Xanthomonas*. *BMC Microbiology* 12:43.

Pinzón A, **Rodriguez-R LM**, González A, Bernal A, Restrepo S. 2011. Targeted Metabolic Reconstruction: a novel approach for the characterization of plant pathogen interactions. *Briefings in Bioinformatics* 12(2): 151-62.

Gorrón E, Rodríguez F, Bernal D, **Rodríguez-Rojas LM**, Bernal A, Restrepo S, Tohme J. 2010. A new method for designing degenerate primers and its use in the identification of sequences in *Brachiaria* showing similarity to apomixis-associated genes. *Bioinformatics* 26(16): 2053-2054.

Méndez-Ortega MC, Restrepo S, **Rodríguez-R LM**, Pérez I, Mendoza JC, Martínez AP, Sierra R, Rey-Benito GJ. 2010. An RNAi *in silico* approach to find an optimal shRNA cocktail against HIV-1. *Journal of Virology* 7:369.

Sierra R*, **Rodriguez-R LM***, Chaves D, Pinzon A, Grajales A, Rojas A, Mutis G, Cárdenas M, Burbano D, Jiménez P, Bernal A, Restrepo S. 2010. Discovery of *Phytophthora infestans* genes expressed in planta through mining of cDNA libraries. *PLoS ONE* 5(3): e9847. * Equal contribution.

Cháves D, Sandoval A, **Rodríguez L**, Garcia JC, Restrepo S, Zambrano MM. 2010. Análisis comparativo de seis genomas del complejo *Mycobacterium tuberculosis* [Comparative analysis of six genomes of the complex *Mycobacterium tuberculosis*]. *Biomédica* 30(1).

Burbano Sefair DA, Castro Barrera HE, Pérez Cabarcas MA, Restrepo Restrepo S, **Rodríguez LM**. 2009. Grid-enabled HMMER (G-HMMER): A Uniandes contribution to the biology community. In: Mayo R, Hoeger H, Ciuffo LN, Barrera R, Dutra I, Gavillet P, Marechal B (eds.). 2009. Proceedings of the second EELA-2 Conference. Ed. CIEMAT. Madrid. ISBN: 978-84-7834-627-1.

Buitrago F, Sierra R, Grajales A, **Rodríguez-R LM**, Jiménez P, Bernal A, Restrepo S. 2009. Comparative study of Chalcone synthase promoters across plant families. *Revista Colombiana de Biotecnología*, 11(2):136-142.

Restrepo S, Pinzón A, **Rodríguez-R LM**, Sierra R, Grajales A, Bernal A, Barreto E, Moreno P, Zambrano MM, Cristancho M, González A, Castro H. 2009. Computational Biology in Colombia. *PLoS Computational Biology* 5(10): e1000535.

Rodríguez LM., Reguero Reza MT. 2007. Toxicómica: una aproximación racional para ensayos toxicológicos [Toxicomics: a rational approach for toxicologic assays]. *Revista Colombiana de Biotecnología* ISSN 1909-8758, 9(2):79-81.

PARTICIPATION IN CONFERENCES AND OTHER SELECT ACTIVITIES

16TH INTERNATIONAL SYMPOSIUM ON MICROBIAL ECOLOGY; MONTRÉAL, QC, CANADA – 2016

Rodriguez-R LM, Tsementzi D, Luo C, Hatt JK, Konstantinidis KT. Biogeography and seasonal variation disentangled in microbial meta-communities of five connected lakes. Oral presentation.

Rodriguez-R LM, Gunturu S, Luo C, Tiedje JM, Cole JR, Konstantinidis KT. Microbial Genomes Atlas (MiGA): Standardized diversity and taxonomic analyses of archaeal and bacterial genomes and metagenomes at the whole-genome level. Poster.

10TH INTERNATIONAL CONFERENCE IN BIOINFORMATICS; ATLANTA, GA, USA – 2015

Rodriguez-R LM, Tsementzi D, Konstantinidis KT. A novel method to measure genetic diversity within natural bacterial populations. Poster.

Rodriguez-R LM, Pena-Gonzalez A, Marston CK, Gee JE, Beesley CA, Saile E, Frace M, Weigand MR, Konstantinidis KT, Hoffmaster A. A bioinformatics pipeline for the comparative analysis of 100s of *Bacillus anthracis* genome sequences. Poster.

Rodriguez-R LM, Luo C, Konstantinidis KT. Expanding the bioinformatics toolbox for the analysis of genomes and metagenomes. Poster.

CENTER FOR DISEASE CONTROL AND PREVENTION, DIVISION OF HIGH-CONSEQUENCE PATHOGENS AND PATHOLOGY SCIENCE SEMINAR; ATLANTA, GA, USA – 2015

Rodriguez-R LM, Pena-Gonzalez A, Gee J, Konstantinidis K, Hoffmaster A. Increased utilization of WGS for molecular epidemiology investigations of anthrax and melioidosis. Invited talk.

AMERICAN SOCIETY FOR MICROBIOLOGY GENERAL MEETING; NEW ORLEANS, LA, USA – 2015

Rodriguez-R LM, Orellana LH, Konstantinidis KT. Accurate detection and quantification of functional genes in complex short-read metagenomic datasets: methods development and application to nitrogen cycle genes. Poster.

Tsementzi D, Meziti A, **Rodriguez-R LM**, Konstantinidis KT. Metagenomic insights into the adaptations of microbial life in the deep Gulf of Mexico Sea. Poster.

INTERNATIONAL UNION OF MICROBIOLOGICAL SOCIETIES (IUMS) - XIV INTERNATIONAL CONGRESS OF BACTERIOLOGY AND APPLIED MICROBIOLOGY; MONTRÉAL, QC, CANADA – 2014

Rodriguez-R LM, Luo C, Konstantinidis KT. Expanding the bioinformatics toolbox for the analysis of genomes and metagenomes. Oral presentation.

15TH INTERNATIONAL SYMPOSIUM ON MICROBIAL ECOLOGY; SEOUL, SOUTH-KOREA – 2014

Rodriguez-R LM, Luo C, Konstantinidis KT. Expanding the bioinformatics toolbox for the analysis of genomes and metagenomes. Poster.

AMERICAN SOCIETY FOR MICROBIOLOGY GENERAL MEETING; BOSTON, MA, USA – 2014

Rodriguez-R LM, Overholt WA, Lin X, Delgadito J, Huettel M, Kostka JE, Konstantinidis KT. Metagenomics insights into the effects of the Deepwater Horizon oil spill on indigenous communities in beach sands. Oral presentation.

AMERICAN SOCIETY FOR MICROBIOLOGY CONFERENCE FOR UNDERGRADUATE EDUCATORS (ASMCUE); DANVERS, MA, USA – 2014

Course Integrated Research by J Tiedje, KT Konstantinidis, J Cole, and **LM Rodriguez-R**. Hands-on bioinformatics exercises for the analysis of complex microbiomes in the classroom. Workshop.

SOUTHWESTERN BIOGEOCHEMISTRY SYMPOSIUM; ATLANTA, GA, USA – 2014

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. Dispersal and habitat limitations detected in a bacterial metacommunity from connected freshwater ecosystems. Poster.

9TH INTERNATIONAL CONFERENCE IN BIOINFORMATICS; ATLANTA, GA, USA – 2013

Rodriguez-R LM, Luo C, Konstantinidis KT. From theory to practice: new approaches and accompanying bioinformatics tools in environmental genomics. Poster.

14TH INTERNATIONAL SYMPOSIUM ON MICROBIAL ECOLOGY; COPENHAGEN, DENMARK – 2012

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. Spatial and temporal characterization of bacterial metapopulations reveal dispersal and habitat limitations in interconnected freshwater ecosystems. Poster.

8TH INTERNATIONAL CONFERENCE IN BIOINFORMATICS; ATLANTA, GA, USA – 2011

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. Microbial community diversity and shifts along a freshwater-to-marine gradient revealed by metagenomics. Poster.

FIRST COLOMBIAN MEETING IN COMPUTATIONAL BIOLOGY; BOGOTÁ, COLOMBIA – 2011

Rodriguez-R LM, Perlaza L, Grajales A, Arrieta M, Salazar C, Koebnik R, Restrepo S, Bernal A. Genomes-based phylogeny of the genus *Xanthomonas*. Oral presentation (Perlaza L).

EUROPEAN CONFERENCE IN COMPUTATIONAL BIOLOGY 2010, SATELLITE MEETING OF THE EUROPEAN STUDENTS COUNCIL; GHENT, BELGIUM – 2010

Rodriguez-R LM, Grajales A, Arrieta M, Salazar C, Szurek B, Verdier V, Koebnik R, Restrepo S, Bernal A. Bacterial phylogenomics revisited: A case study for the *Xanthomonas* genus. Poster.

SCIENTIFIC MISSION; MONTPELLIER, FRANCE – 2009

Scientific mission to the *Institut de Recherche pour le Développement* (IRD) in the frame of the program of cooperation and partnership ECOS-Nord.

3RD COLOMBIAN MEETING ON BIOTECHNOLOGY; BOGOTÁ, COLOMBIA – 2008

Rodríguez LM, Mantilla JR, Falquet L, Reguero Reza MT, Barreto-Hernández E. Diseño e implementación de un sistema bioinformático para el almacenamiento y clasificación de beta-lactamasas: BLA.id [Design and implementation of a bioinformatics system for the storage and classification of beta-lactamases: BLA.id]. Oral presentation.

EDUCATION

Ph.D. Bioinformatics (Minor: Biomedical Engineering)

Georgia Institute of Technology, Atlanta, GA – 2011 - 2016.

M.Sc. Applied Informatics (Skills Integration, Bioinformatics)

Université de Montpellier 2, Montpellier, France – 2010 - 2011.

M.Sc. Biological Sciences (Microbiology)

Universidad de Los Andes, Bogotá, Colombia – 2009 - 2011.

B.Sc. Biology (5 years program)

Universidad Nacional de Colombia, Bogotá, Colombia – 2004 - 2009.

OTHER STUDIES

Universidad Nacional de Colombia, Department of Philosophy, Bogotá, Colombia – Teoría de la Evolución [Evolution theory], 2005.

University of Maryland, School of Medicine, Institute for Genome Sciences, Baltimore, MD, USA – IGS Genomics Workshop, 2009.

LANGUAGES

Spanish Mother tongue; high proficiency.

English Reads, writes, speaks; high proficiency, six years immersion.

French Reads, speaks; intermediate proficiency, one year immersion.

Italian Reads, writes, speaks; intermediate proficiency.