BIOGRAPHICAL SKETCH

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NAME: Gharaibeh, Raad

eRA COMMONS USER NAME (credential, e.g., agency login): rgharaib

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Baghdad University	B. Sc.	09/1998	Biology
Jordan University of Science and Technology	M. Sc.	09/2001	Applied Biology
Virginia Polytechnic and State University	Graduate Studies	05/2005	Bioinformatics
University of North Carolina at Charlotte	Ph. D.	09/2009	Bioinformatics
University of North Carolina at Charlotte	Postdoctoral	05/2010	Bioinformatics

A. Personal Statement

I have been involved in many genomics projects that utilize high-throughput technologies to answer complex biological questions. I have experience and publications in microbial genome and transcriptome assembly and annotation, microbial RNA-seq analysis, 16S amplicon sequencing analysis, metagenome and metatranscriptome analyses from both humans and model organisms. My research interest focuses on understanding how alterations in the microbiome can lead to promotion of gastrointestinal ailments using computational approaches, integrative approaches that examine microbiome and host response and understanding the functional capacities of gut microbiota.

1. Arthur JC, **Gharaibeh RZ**, Muhlbauer M, Perez-Chanona E, Uronis JM, McCafferty J, Fodor AA, Jobin C (2014) Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. Nat. Commun. 5:4724 doi: 10.1038/ncomms5724
2. Sun X, Winglee K, **Gharaibeh RZ**, Gauthier J, He Z, Tripathi P, Avram D, Bruner S, Fodor A, Jobin C. (2018) Microbiota-Derived Metabolic Factors Reduce Campylobacteriosis in Mice. Gastroenterology 154:1751-1763
3. He Z*, **Gharaibeh RZ***, Newsome RC, Pope JL, Dougherty MW, Tomkovich S, Pons B, Mirey G, Vignard J, Hendrixson DR, Jobin C. (2019) Campylobacter jejuni promotes colorectal tumorigenesis through the action of cytolethal distending toxin. Gut 68:289-300. *Co-first authors.
4. **Gharaibeh RZ** and Jobin C. (2019) Microbiota and cancer immunotherapy: in search of microbial signals. Gut. doi: 10.1136/gutjnl-2018-317220.

B. Positions and Honors

Positions and Employment

2001-2003	Part-time lecturer, Department of Biotechnology and Genetic Engineering and Department of Applied Biological Sciences, Jordan University of Science and Technology, Irbid, Jordan.
2001-2003	Part-time research assistant, Department of Biology, Yarmouk University, Irbid, Jordan.
2009-2010	Postdoctoral fellow, Department of Bioinformatics and Genomics, University of North Carolina at Charlotte. Charlotte, NC.
2010-2017	Bioinformatics Research Associate, Bioinformatics Services Division, UNC Charlotte, North Carolina Research Campus, Kannapolis, NC.
2017-present	Assistant Professor, Director microbiome genomics, Department of Medicine, University of Florida, Gainesville, FL.

Honors

1992	El Hassan Youth Award (the Jordanian version of duke of Edinburgh's Award). Award level: Bronze.
1998	Jordan University of Science and Technology Master Students Assistantship award.
2001	Jordan University of Science and Technology (JUST) graduate student award (first place).
2003	Virginia Tech Graduate Assistantship Award.
2004	Graduate Research and Development Award, Virginia Tech.
2006-2009	UNC Charlotte Graduate Assistant Support Plan (GASP) Award.

C. Contributions to Science

1. My early work focused on microbial genomics, specifically the detection and identification of medically and industrially important species. I was part of a team that developed a working identification system for the antibiotic producing bacterium *Streptomyces* were I computationally identified and experimentally verified specific 16S sequences that proved to be a strong predictor of *Streptomyces* presence and its antibiotic production ability. The system reduced the time required for such identification and subsequently, this reduction in time reduced the efforts and expenses needed to reach a reliable detection and identification. The system was applied to discovering several important isolates. I later adopted the same approach for the detection of *Salmonella* in food product.
    a. Saadoun, I. and **Gharaibeh, R.** (2003) The Streptomyces flora of Badia region of Jordan and its' potential as a source of antibiotics active against antibiotic-resistant bacteria. *Journal of Arid Environments*, 53:365-371.
    b. **Gharaibeh, R.**, Saadoun, I. and Mahasneh, A. (2003) Evaluation of combined 16S rDNA and strb1 gene targeted PCR to identify and detect streptomycin-producing Streptomyces. *Journal of Basic Microbiology*, 43: 301-311.
    c. Malkawi, H. and **Gharaibeh, R**. (2003) Multiplex PCR for the direct detection of Salmonella enterica from chicken, lamb and beef food products. Journal of Basic Microbiology, 43: 328-336.

2. I studied the relationship between DNA microarray probe sequence properties and the resulting hybridization signal intensity. The work focused mainly on probe properties (secondary structure, mismatch number and location) and their effects on probe hybridization behavior. Those properties were later integrated in probe signal interpretation and probe design and selection. This resulted in enhanced background noise correction for microarray analysis, accurate estimation of target concentration on microarrays and the design and development of biophysically-sound microarrays.
    a. **Gharaibeh, R.Z.**, Fodor, A.A. and Gibas, C.J. (2007) Using probe secondary structure information to enhance Affymetrix GeneChip background estimates. *Computational biology and chemistry*, 31, 92-98.
    b. **Gharaibeh, R.Z.**, Fodor, A.A. and Gibas, C.J. (2008) Background correction using dinucleotide affinities improves the performance of GCRMA. *BMC Bioinformatics*, 9, 452.

c. Zahn LM, Ma X, Altman NS, Zhang Q, Wall PK, Tian D, Gibas CJ, **Gharaibeh R**, Leebens-Mack JH, Depamphilis CW, Ma H. (2010) Comparative transcriptomics among floral organs of the basal eudicot *Eschscholzia californica* as reference for floral evolutionary developmental studies. *Genome Biology*, 11(10):R101.
d. **Gharaibeh, R.Z.,** Newton, J.S., Weller, J.W. and Gibas, C.J. (2010) Application of equilibrium models of solution hybridization to microarray design and analysis. *PLoS One*, 2010 5(6):e11048.

3. With a team of collaborators, I did extensive work on analyzing and modeling complex genomic sequences from host-microbe interaction experiments. Special emphasis was placed on detecting, addressing and correcting confounding factors that arise from experimental setups in metagenomics studies. This work successfully modeled the effect of confounding factors like housing conditions thus allowing for more accurate measurement of changes in the host microbiome therefore providing a clearer picture of its impact on the host phenotype. Moreover, I was able to assemble a near complete genome of *pks*$^{+}$ E. coli (a bacterium that promote tumor genesis in animal models and may drive cancer risk in human cohorts) and demonstrated that a handful of its genes are influenced by the state of inflammation/cancer.
    a. McCafferty J, Muhlbauer M, **Gharaibeh RZ**, Arthur JC, Perez-Chanona E, Sha W, Jobin C, Fodor AA. (2013) Stochastic changes over time and not founder effects drive cage effects in microbial community assembly in a mouse model. ISME-J, 7(11):2116-25
    b. Arthur JC, **Gharaibeh RZ**, Uronis JM, Perez-Chanona E, Sha W, Tomkovich S, Muhlbauer M, Fodor AA, Jobin C. (2013) VSL#3 probiotic modifies mucosal microbial composition but does not reduce colitis-associated colorectal cancer. Sci. Rep. 3:2868. doi: 10.1038/srep02868
    c. Arthur JC*****, **Gharaibeh RZ***, Muhlbauer M, Perez-Chanona E, Uronis JM, McCafferty J, Fodor AA, Jobin C (2014) Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. Nat. Commun. 5:4724 doi: 10.1038/ncomms5724 (***** equal contribution)

Complete list of published work

http://www.ncbi.nlm.nih.gov/pubmed/?term=Raad+Gharaibeh

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

- **R21AI131205 NIH R21** 07/01/17-06/30/2019

Transcriptional control of genes implicated in suppression function of Treg cells

The goal of this proposal is to examine the role of bcl11b in regulating genes critical for suppression mediated pAde and IL10 at steady state and inflammatory conditions

Role: Co-Investigator

- **R01DK073338 NIH R01** 07/01/2018–03/31/2023

Role of Bacteria in Colitis-Associated Colon Cancer

The goal of this proposal is to understand how microbes contribute to the development of intestinal inflammation and colorectal cancer through production of toxins.

Role: Co-Investigator

- **R01CA214005A1 NIH R01** 12/15/2017–11/30/2022

Role of the microbiota in DNA methylation and CRC development

The goal of this proposal is to define the microbiome across the spectrum of CIMP+ tumors, investigate the impact of CIMP+ associated bacteria on tumorigenesis and DNA methylation in mice and study metabolites by which bacteria influence DNA methylation profile.

Role: Co-Investigator

- **MRSG-17-228-01-TBG American Cancer Society - Norma and Rich DiMarco Mentored Research Scholar Grant** 12/1/2017-30/11/2022

The role of the microbiome on pancreatic carcinogenesis in a murine model

The goal of this grant is to investigate the elements of the host microbiome that accentuate the initiationand progression of pancreatic carcinogenesis

Role: Co-Investigator

- **Florida Academic Cancer Center Alliance (FACCA)** 07/01/2018–06/30/2019

Role of intestinal microbiota in lung cancer therapy
Role: Co-Investigator

- **FCBTR/ABC^2** 07/1/2017-06/30/2019

The Florida Center for Brain Tumor Research (FCBTR) and Accelerate Brain Cancer Cure (ABC^2)
Pilot study of commensal gut microbiome as a modifier of checkpoint inhibitor efficacy in glioblastoma
Role: Microbiome Analyst