OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

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NAME: Chia, Nicholas Lee-Ping

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

POSITION TITLE: Associate Professor of Surgery

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
Georgetown University, Washington DC	B.S.	06/2001	Physics
The Ohio State University, Columbus, OH	Ph.D.	06/2006	Physics
Institute for Genomic Biology, University of Illinois, Urbana-Champaign, IL	Post-Doctoral Fellowship	06/2011	Biophysics

A. Personal Statement

My role in the proposed project is that of Co-PI. I have a broad background in biophysics and theoretical biology, with specific training in the systems and computational biology approaches needed to make this project successful. I have always believed that the most interesting subject a physicist can study is life. From my undergraduate days in microscopy, when I developed a glass-only total internal reflection microscope from spare parts, to my present focus on understanding how we can model the microbial-host interface to create better tools for diagnosis and prevention, biology has been a constant. As PI of an R01 on the role of the microbiome in causing colon cancer, I have demonstrated my ability to manage a large, interdisciplinary project involving metabolic modeling, metagenomic sequencing, and human samples. In addition, in my position as Co-Director of the Microbiome Program at Mayo Clinic, I am ideally placed to ensure that this project receives the clinical, bioinformatics, and statistical support required. This work builds logically on my prior experience and interests, and the direction of Principal Investigator Dr. Leigh Greathouse will provide complementary expertise in using MBRA models to study the effects of dietary prebiotics on the microbiome; we have published and presented work on the microbiome together in the past. Below, I list publications that exemplify my work in building and strengthening computational pipelines for clinical and basic research at Mayo Clinic; many recent publications from Mayo Clinic in the areas of Microbiology and Microbiome research have made use of these pipelines to generate novel findings. Of course, this proposal also requires expertise in microbiome bioinformatics, and representative publications in this area can be found in section C.

B. Positions and Honors

Positions and Employment

2006-2008 Postdoctoral Researcher under Nigel Goldenfeld and Carl Woese, University of Illinois at Urbana-Champaign, Champaign, IL
2011-2012 Senior Research Scientist, Institute for Systems Biology, Seattle, WA
2012-2014 Associate Consultant, Department of Surgery, Joint appointment in Health Sciences Research, Mayo Clinic, MN
2012-2018 Associate Director, Microbiome Program, Center for Individualized Medicine, Mayo Clinic, MN
2015-Present Senior Associate Consultant, Department of Surgery, Mayo Clinic, MN
2015-2018 Assistant Professor, Department of Surgery, Mayo Clinic, MN
2018-Present Associate Professor, Department of Surgery, Mayo Clinic, MN

Honors

2001 Awarded Fowler Fellowship by the Ohio State University Department of Physics
2006 Awarded the Alexander von Humboldt Fellowship for work in the area of Bioinformatics

C. Contribution to Science

My research career contains three key ingredients that relate to the success of this proposal, namely (1) creating new bioinformatics tools; (2) improving the accuracy of metabolic modeling, especially as regards the microbiome; and (3) designing theoretical models that predict biological reality. *Selected publications:

1. Jeraldo P, Kalari K, Chen X, Bhavsar J, Mangalum A, White BA, Nelson H, Kocher JP, **Chia N**. IM-TORNADO: A tool for comparison of 16S reads from paired-end libraries. PLOS One. 2014 Dec 15;9(12):e114804. PMCID: PMC4266640.
2. Sipos M, Jeraldo P, **Chia N**, Qu A, Dhillon AS, Konkel ME, Nelson KE, White BA, Goldenfeld N. Robust computational analysis of rRNA hypervariable tag datasets. PLoS One. 2010 Dec 31; 5(12):e15220. PMCID: PMC3013109.
3. Jeraldo P, **Chia N**, Goldenfeld N. On the suitability of short reads of 16S rRNA for phylogeny-based analyses in environmental surveys. Environ Microbiol. 2011 Nov; 13(11):3000-9.
4. Jeraldo P, Sipos M, **Chia N**, Brulc JM, Dhillon AS, Konkel ME, Larson CL, Nelson KE, Qu A, Schook LB, Yang F, Goldenfeld N, and White BA. Quantifying the role of neutral and niche processes in evolution, Proc Natl Acad Sci U S A.. 109, 9692-9698 (2012) PMCID: PMC3382495.
5. Jeraldo, P., Sipos, M., Chia, N., Brulc, J. M., Dhillon, A. S., Konkel, M. E., ... & Yang, F. (2012). Quantification of the relative roles of niche and neutral processes in structuring gastrointestinal microbiomes. *Proceedings of the National Academy of Sciences*, *109*(25), 9692-9698.
6. Sinha, R., Chen, J., Amir, A., Vogtmann, E., Shi, J., Inman, K. S., ... & Chia, N. (2016). Collecting fecal samples for microbiome analyses in epidemiology studies. *Cancer Epidemiology and Prevention Biomarkers*, *25*(2), 407-416.
7. Sipos M, Jeraldo P, Chia N, Qu A, Dhillon AS, Konkel ME, Nelson KE, White BA, Goldenfeld N. Robust Computational Analysis of rRNA Hypervariable Tag Datasets. PLoS One. 2010 Dec 31; 5(12):e15220. PMCID: PMC3013109
8. Multinu, F., Harrington, S. C., Chen, J., Jeraldo, P. R., Johnson, S., Chia, N., & Walther-Antonio, M. R. (2018). Systematic Bias Introduced by Genomic DNA Template Dilution in 16S rRNA Gene-Targeted Microbiota Profiling in Human Stool Homogenates. *mSphere*, *3*(2), e00560-17.

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/nicholas.chia.1/bibliography/47744991/public/?sort=date&direction=descending

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

Ongoing Research Support

R01 CA179243 (PI - N Chia) 06/05/2014 – 05/31/2019
Microbial Metabolic Toxicity Drives Colon Cancer. The aims of this application are to 1) build metabolic models reflective of the microbial production and consumption of potential toxins with special focus on the role of sulfate-reducing bacteria, methanogens, and microbial community structure, and 2) understand the role of microbially-produced metabolites in carcinogenesis in deficient and proficient mismatch repair colorectal cancer.

R01 AR56647 (R Patel) 09/01/14 – 08/31/19
Metagenomic Analysis of Arthroplasty Failure
The goals of this application is to understand the underlying microbial populations in prosthetic joint infections (PJIs) using next-generation sequencing methodologies to directly probe the environment in PJIs.
Role: Co-investigator

Mayo Clinic & University of Minnesota Cooperation Program
(K. Khazaie & R Blekhman) 02/01/18 – 01/31/20
Development of personalized microbiome-based treatment for colorectal cancer
Our objective in this application is to build a systems-level, mechanistic understanding of the functional interactions between tumor neoplastic mutations, standard of care treatments, and microbial factors (taxa, genes, and functions) in colorectal neoplasia.
Role: Co-investigator