

BIOGRAPHICAL SKETCH

NAME HongYuan (Rays) Jiang	POSITION TITLE Assistant Professor of Systems Biology		
eRA COMMONS USER NAME (credential, e.g., agency login) RAYSJIANG			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	MM/YY	FIELD OF STUDY
Wageningen University, the Netherlands	Ing	09/2000	Biotechnology
Wageningen University, the Netherlands	PhD	03/2006	Genomics
Virginia Bioinformatics Institute, the Broad Institute, Wageningen University	Internships	11/2007	Computational biology

A. Personal Statement

This project aims at studying hepatocyte generated merozoites in human malaria. Specifically, we will use genomics and bioengineering for in vitro late stage and early blood stage of *P. vivax*. I am highly motivated and have the required expertise to carry out the proposed project. I have a background in the area of infectious diseases and computational biology. I am familiar with infectious disease lab research settings. I have extensive research experience in high throughput data analysis and computational algorithm development – both are key areas of expertise for the proposed project. I also have collaborated with engineers to develop new single cell manipulation and imaging tools. When I worked as a computational biologist at the Broad Institute, I carried out analysis of diverse large data sets generated from cutting edge technologies. I also successfully coordinated a large collaborative genome project involving multiple research institutions across Europe and USA. This proposed project builds on and extends my research and administrative experiences. In summary, I have a track record of productive research projects highly relevant to innovated genomics technologies.

- a. Egan ES, Jiang RHY, Moechtar MA, Barteneva NS, et al. A forward genetic screen identifies erythrocyte CD55 as essential for Plasmodium falciparum invasion. **Science** 2015. 348(6235):711-4
- b. Cheemalapati SV, Winkas J, Wang H, Konnaiyan K, Zhdanov A, Roth A, Adapa SR, Deonarine A, Noble M, Das T, Gatenby R, Westerheide SD, Jiang RHY & Pyayt A. Subcellular and in-vivo Nano-Endoscopy. **Scientific Report**. 2016 Oct 3;6:34400

B. Positions and Honors

Title	Institution/Location	Dates
Post-doc Associate	Harvard University	2012-2013
Staff Computational Biologist	The Broad Institute of MIT and Harvard	2008-2013
Assistant Professor	University of South Florida	2014-current

Steering committee :

Oomycete molecular genetics network (OMGN) 2008-2011

Reading committee:

PhD thesis in theoretical biology department, Utrecht University, the Netherlands 2013.

Faculty recruiting committee

Genomics/Ethics Assistant/ Associated professor Position #5718, University of South Florida 2015

Disease biologist Assistant/Associated professor Position #8695, University of South Florida 2016

C. Contributions to Science (with selected publications)(*Co-Authorship; ^ Senior Authorship)

1. Innovative host-pathogen interaction genomics research

- a. Neafsey DE, Galinsky K, Jiang RHY, Young L, Sykes SM, et al. The malaria parasite *Plasmodium vivax* exhibits greater genetic diversity than *Plasmodium falciparum*. **Nature genetics** 2012. 44:1046
- b. Jiang RHY, Tyler BM. Mechanisms and evolution of virulence in oomycetes. **Annual Review of Phytopathology** 2012 50:295-318
- c. Jiang RHY, Stahelin RV, Bhattacharjee S, Haldar K. Eukaryotic virulence determinants utilize phosphoinositides at the ER and host cell surface. **Trends in Microbiology** 2013 (21:145-56)
- d. Jiang RHY, Marti M. A PIP Gets the plasmodium protein export pathway going. **Cell Host Microbe** 2012 11:99-100.
- e. Jiang RHY, de Bruijn I, Haas BJ, Belmonte R, et al. Distinctive expansion of potential virulence genes in the genome of the oomycete fish pathogen *Saprolegnia parasitica*. **PLoS Genetics** 2013. e1003272
- f. Coleman B, Skillman K, Jiang RHY, Childs L, et al. A *Plasmodium falciparum* Histone Deacetylase Regulates Antigenic Variation and Gametocyte Conversion. **Cell Host Microbe** 2014 Aug 13;16(2)
- g. Paul AS, Saha S, Engelberg K, Jiang RHY, Coleman BI, et al. Parasite Calcineurin Regulates Host Cell Recognition and Attachment by Apicomplexans. **Cell Host Microbe** 2015 June
- h. Merrick C, Jiang RHY, Skillman K, Samarakoon U, Howell D, et al. Functional analysis of sirtuin genes in multiple *Plasmodium falciparum* strains. **PLoS One**. 2015 10(3):e0118865
- i. Pellé KG*, Jiang RHY*, Mantel PY, Xiao YP, Hjelmqvist D, et al. Shared elements of host-targeting pathways among apicomplexan parasites of differing life styles. **Cell Microbiol** 2015
- j. Wang C, Adapa SR, Gibbons J, Sutton S, and Jiang RHY^. Punctuated chromatin states regulate *Plasmodium falciparum* antigenic variation at the intron and 2 kb upstream regions. **BMC Genomics**. 2016 Aug
- k. Thomas P, Sedillo J, Oberstaller J, Li S, Zhang M, Singh N, Wang C, Udenze K, Jiang RHY and Adams JHA. Phenotypic screens identify parasite genetic factors associated with malarial fever response in *Plasmodium falciparum* piggyBac mutants. **mSphere** in press

2. Uncovering human host genetics in important infectious diseases

- a. Egan ES, Jiang RHY, Moechtar MA, Barteneva NS, et al. A forward genetic screen identifies erythrocyte CD55 as essential for *Plasmodium falciparum* invasion. **Science** 2015. 348(6235):711-4
- b. Dankwa S, Lim C, Bei A, Jiang RHY, Abshire J, et al. Ancient human sialic acid variant restricts an emerging zoonotic malaria parasite. **Nature Communication** 2016
- c. MohanKumar K, Namachivayam K, Cheng F, Jiang RHY, Flores-Torres J, Torres BA, Maheshwari A. Trinitrobenzene Sulfonic Acid-induced Intestinal Injury in Neonatal Mice Activates Transcriptional Networks Similar to those seen in Human Necrotizing Enterocolitis. **Pediatr Res**. 2016 Sep

3. Developed novel machine learning data mining methods

- a. Jiang RHY, Weide R, van de Vondervoort PJ, Govers F. 2006. Amplification generates modular diversity at an avirulence locus in the pathogen *Phytophthora*. **Genome Research** 2006 16:827-40
- b. Jiang RHY, Tripathy S, Govers F, Tyler BM. RXLR effector reservoir in two *Phytophthora* species is dominated by a single rapidly evolving superfamily with more than 700 members. **PNAS** 2008 105:4874-9
- c. Tyler BM, Tripathy S, Zhang X, Dehal P, Jiang RHY, et al. 2006. *Phytophthora* genome sequences uncover evolutionary origins and mechanisms of pathogenesis. **Science** 2006. 313:1261-6
- d. Haas BJ, Kamoun S, Zody MC, Jiang RHY, Handsaker RE, et al. Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*. **Nature** 2009 461:393-8
- e. Baxter L, Tripathy S, Ishaque N, Boot N, Cabral A, ... Jiang RHY, et al. Signatures of adaptation to obligate biotrophy in the *Hyaloperonospora arabidopsidis* genome. **Science** 2010 330:1549-51
- f. Raffaele S, Farrer RA, Cano LM, Studholme DJ, MacLean D ... Jiang RHY et al. Genome evolution following host jumps in the Irish potato famine pathogen lineage. **Science** 2010 330:1540-3

4. Developing cross disciplinary methods in high-throughput biology and single cell biology

- a. Jiang RHY, Govers F. Nonneutral GC3 and retroelement codon mimicry in *Phytophthora*. **Journal of molecular evolution** 2006. 63:458-72
- b. Jiang RHY, Tyler BM, Whisson SC, Hardham AR, Govers F. Ancient origin of elicitor gene clusters in *Phytophthora* genomes. **Molecular Biology and Evolution**. 2006. 23:338-51
- c. Tripathy S, Jiang RHY. Massively parallel sequencing technology in pathogenic microbes. **Methods in molecular biology** 2012. 835:271-94
- d. Pradhan A, Siwo GH, Singh N, Martens B, Balu B, Button-Simons KA, Tan A, Zhang M, Udenze KO, Jiang RHY, Ferdig MT, Adams JH, Kyle DE. Chemogenomic profiling of *Plasmodium falciparum* as a tool to aid antimalarial drug discovery. *Sci Rep*. 2015
- e. NovBronner IF, Ottoa TD, Zhang M, Udenze K, Wang CC, Quail MA, Jiang RHY, Adams JH, Rayner JC. Quantitative Insertion-site Sequencing (QIseq) for high throughput phenotyping of transposon mutants. **Genome Research**. 2016 May 10.
- f. Malaria box consortium (Van Voorhis WC, ... Jiang RHY...). Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. **PLoS Pathog**. 2016 Jul
- g. Cheemalapati SV, Winkas J, Wang H, Konnaiyan K, Zhdanov A, Roth A, Adapa SR, Deonaraine A, Noble M, Das T, Gatenby R, Westerheide SD, Jiang RHY & Pyayt A. Subcellular and in-vivo Nano-Endoscopy. **Scientific Report**. 2016 Oct 3;6:34400

D. Research Support

On going research support

NIH R01 #AI117017-01 JH Adams(PI) RHY Jiang(Co-Investigator) 04/01/2015-04/01/2020
Chemogenomic Profiling of *Plasmodium falciparum* Drug Responses and Resistance

NIH R35 #R35CA197731 S Sebti(PI) RHY Jiang(Co-Investigator) 01/03/2016-31/12/2022
Targeting Mutant KRAs for Cancer Therapy

Gates Foundation Supplement DE Kyle(PI) RHY Jiang(Senior personnel) 01/11/2015-01/11/2017
3D Microfluidic Human Liver Models for Malaria Drugs

New investigator research award of USF RHY Jiang(PI) 01/05/2016 – 01/05-2017
Exploring third generation sequencing technology for malaria genomics