BIOGRAPHICAL SKETCH

NAME: **Jessica Tingsan Lin**

eRA COMMONS USER NAME: Jessica_Lin

POSITION TITLE: **Assistant Professor of Medicine**

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	DATES	FIELD OF STUDY
Yale University, New Haven, CT	BS	1997-2001	Molecular Biophysics & Biochemistry
Baylor College of Medicine, Houston, TX	MD	2001-2005	International Health Track Underserved Care Pathway
University of California, San Diego Medical Center	Residency	2005-2008	Internal Medicine
University of North Carolina, Chapel Hill, NC	Fellowship	2009-2012	Infectious Diseases
UNC Gillings School of Global Public Health, NC	MSCR	2012-2016	Clinical Research, Translational Track

A. Personal Statement

I am an infectious disease physician-scientist working at the interface of clinical and molecular studies on malaria. I began my career as a clinical trial investigator conducting malaria studies on the Thai-Cambodian border. I then trained in molecular epidemiology and next generation sequencing during my infectious disease fellowship training at the University of North Carolina, where I am now faculty on the tenure track. Over the past ten years, my research has focused on 1) the emergence and spread of highly drug-resistant *Plasmodium falciparum* in western Cambodia, 2) the ability of *Plasmodium vivax* to resist control efforts through relapses from the liver, and 3) the role of gametocytes in defining the human infectious reservoir and as targets for interrupting malaria transmission.

B. Positions and Honors

Positions and Employment

2008-2009 Medical Research Scientist, Armed Forces Research Institute of Medical Sciences, Bangkok
2008-2009 Volunteer Physician, Kwai River Christian Hospital, Sangklaburi, Thailand
2009-2011 Clinical Fellow, Division of Infectious Diseases, University of North Carolina, Chapel Hill
2011-2012 Clinical Instructor, Division of Infectious Diseases, University of North Carolina, Chapel Hill
2013-present Assistant Professor, Division of Infectious Diseases, University of North Carolina, Chapel Hill

Certifications and Boards

2008/2018 American Board of Internal Medicine certification in Internal Medicine
2009-present North Carolina Medical License
2009 ASTMH Certificate of Knowledge in Clinical Tropical Medicine and Traveler's Health
2011 American Board of Internal Medicine certification in Infectious Diseases
2011 Advanced Course in Clinical Tropical Medicine, Gorgas Memorial Institute, Peru

Other Experience and Professional Memberships

2006-present Member, American Society of Tropical Medicine and Hygiene

2009-present Member, Infectious Disease Society of America
2011-present Adhoc Reviewer for Nature Communications, Journal of Infectious Diseases, Emerging Infectious Diseases, PLoS Neglected Tropical Diseases, Scientific Reports, Antimicrobial Agents & Chemotherapy, PLoS ONE, American Journal of Tropical Medicine & Hygiene, Genome Medicine, Genome Biology and Evolution, BMC Genomics, Malaria Journal, Experimental Parasitology, Tropical Medicine & International Health
2016-2017 Malaria Pre-Review Panel, DoD Congressionally Directed Medical Research Program
2016-present Member, Antimicrobial Stewardship Team, UNC
2017-present Member, Safety IRB Committee, UNC
2018 Adhoc Reviewer for Medical Research Council, UK
2018-2019 Member, Safety Monitoring Committee, Phase I study of DM1157
2018-present Scientific Program Committee, American Society of Tropical Medicine & Hygiene
2019 Adhoc Reviewer for European Science Foundation

Honors & Awards

2000 Richard U. Light Fellowship for study abroad in China, Yale University
2000 East Asia Study Grant, Yale University
2001 Charles Kao Fellowship, Yale University
2004 IDSA Summer Research Scholarship, Infectious Disease Society of America
2005 CDC Foundation O.C. Hubert Fellowship in International Health
2005 Baylor Department of International Medicine Fellowship
2008 ASTMH/Pfizer Centennial Travel Award in Basic Science Tropical Disease Research
2012 Burroughs Wellcome Fund-ASTMH Postdoctoral Fellowship in Tropical Infectious Diseases
2012 UNC University Council Research Grant
2012 NIH Loan Repayment Award
2014 NIH Loan Repayment Award
2015 UNC Explorations in Global Health Grant
2016 UNC Department of Medicine Junior Faculty Development Award
2016 NIH Loan Repayment Award

C. Contribution to Science

1. Malaria drug resistance. I started my malaria research career as a study physician on a 2008-9 artemisinin resistance clinical trial in Cambodia. I combined this clinical background with molecular epidemiology techniques to help describe the genetic basis of rapidly emerging resistance in Southeast Asia. We were the first to link clinical failure after artemisinin-based combination therapy (ACT) with the predominant *kelch13* mutant now found in western Cambodia. We used population genetics tools to show that selection pressure from different ACT partner drugs have contributed to parasite population fracturing and clonal expansion. These studies have provided evidence to directly guide drug policy in the region.

    a. Spring MD, **Lin JT**, Manning JE, Vanachayangkul P, Somethy S, Bun R, Se Y, Chann S, Ittiverakul M, Sia-Ngam P, Kuntawunginn W, Arsanok M, Buathong N, Chaorattanakawee S, Gosi P, Ta-Aksorn W, Chanarat N, Sundrakes S, Kong N, Heng TK, Nou S, Teja-Isavadharm P, Pichyangkul S, Phann ST, Balasubramanian S, Juliano JJ, Meshnick SR, Chour CM, Prom S, Lanteri CA, Lon C, Saunders DL (2015). Dihydroartemisinin-piperaquine failure associated with a triple mutant including kelch13 C580Y in Cambodia: an observational cohort study. Lancet Infect Diseases. 15(6): 683-91.

    b. Parobek CP, Parr JB, Lon Chanthap, Balasubramanian S, Chaorattanakawee S, Gosi P, Barnett E, Brazeau N, Meshnick SR, Spring MD, LAnteri CA, Saunders DL, **Lin JT***, Juliano JJ* (2017). Partner-drug resistance and

population substructuring of artemisinin-resistant *Plasmodium falciparum* in Cambodia. Genome Biology and Evolution. 9(6): 1673-1686. *joint senior authors.

c. **Lin JT**, Patel JC, Levitz L, Wojnarski M, Chaorattanakawee S, Gosi P, Buathong N, Chann S, Rekol H, Thay K, Sea D, Nou S, Takala-Harrison S, Fukuda M, Smith P, Spring M, Saunders D, Lon C (2018). Gametocyte Carriage, Antimalarial Use, and Drug Resistance in Cambodia, 2008-2014. American Journal of Tropical Medicine and Hygiene. 99(5):1145-1149.

d. Wojnarski M, Lon C, Vanachayangkul P, Gosi P, Sok S, Rachmat A, Harrison D, Berjohn CM, Spring M, Chaoratanakawee S, Ittiverakul M, Buathong N, Chann S, Wongarunkochakorn S, Waltmann A, Kuntawunginn W, Fukuda MM, Burkly H, Heang V, Heng TK, Kong N, Boonchan T, Chum B, Smith P, Vaugn A, Prom S, **Lin JT**, Lek D, Saunders D (2019). Atovaquone-proguanil in combination with artesunate to treat multidrug-resistant (MDR) *P. falciparum* malaria in Cambodia: an open-label, randomized trial. Open Forum Infectious Diseases. In press.

2. Relapsing vivax malaria. *P. vivax* is the most widely distributed malaria species with its eradication made difficult due to its ability to cause relapse. I have used unique vivax cohorts to study genotypic signatures of relapse. My initial work on cohorts in Cambodia showed that vivax in the region is incredibly polyclonal, with persons harboring many different strains at once. We used amplicon deep sequencing to exploit this polyclonality to identify recurrences in individuals as probable relapses rather than re-infections. We are now using whole genome sequencing to better understand whether parasites in successive relapses showed relatedness via identity by descent analyses.

   a. **Lin JT**, Bethell D, Tyner ST, Lon C, Shah NK, Saunders DL, Sriwichai S, Khemawoot P, Kuntawunggin W, Smith BL, Noedl H, Schaecher K, Socheat D, Se Y, Meshnick SR, Fukuda MM (2011). *Plasmodium falciparum* gametocyte carriage is associated with subsequent *Plasmodium vivax* relapse after treatment. PLoS One. 6(4): e18716.

   b. **Lin JT**, Juliano JJ, Kharabora O, Sem R, Lin F, Muth S, Ménard D, Wongsrichanalai C, Rogers WO, Meshnick SR (2012). Individual *Pvmsp1* variants within polyclonal *Plasmodium vivax* infections display different propensities for relapse. Journal of Clinical Microbiology. 50(4): 1449-51.

   c. Andrianaranjaka V, **Lin JT**, Golden C, Juliano JJ, Randrianarivelojosia M (2013). Activation of minority-variant Plasmodium vivax hypnozoites following artesunate + amodiaquine treatment in a 23-year old man with relapsing malaria in Antananarivo, Madagascar. *Malar J*. 12(1):177.

   d. **Lin JT**, Hathaway NJ, Saunders DL, Lon C, Balasubramanian S, Kharabora O, Gosi P, Sriwichai S, Kartchner L, Chuor CM, Satharath P, Lanteri C, Bailey JA, Juliano JJ. (2015) Using Amplicon Deep Sequencing to Detect Genetic Signatures of Plasmodium vivax Relapse. Journal of Infectious Diseases. 212(6): 999-1008.

3. Submicroscopic malaria and transmission. Efforts to eliminate malaria altogether hinge on the ability to prevent transmission. I co-authored a much-cited review that exposed the lack of evidence for the prevailing wisdom that submicroscopic parasitemia forms a hidden reservoir that drives malaria transmission. This set the stage for studies on which field deployable diagnostics are most suited to elimination efforts, characterizing the human infectious reservoir in low transmission settings, and the effect of transmission-blocking interventions on this reservoir.

   a. **Lin JT**, Saunders DL, Meshnick SR (2014). The role of submicroscopic parasitemia in malaria transmission: what is the evidence? Trends in Parasitology. 30(4): 183-90.

   b. **Lin JT**, Ubalee R, Lon C, Balasubramanian S, Kuntawunggin W, Rahman R, Saingam P, Heng TK, Vy D, San S, Nuom S, Burkly H, Chanarat N, Ponsa C, Levitz L, Parobek C, Chuor CM, Somethy S, Spring M, Lanteri C, Gosi P, Meshnick SR, Saunders DL (2016). Microscopic *Plasmodium falciparum* gametocytemia and infectivity to mosquitoes in Cambodia. Journal of Infectious Diseases. 213(9): 1491-4.

c. **Lin JT**, Lon C, Spring MD, Sok S, Chann S, Ittiverakul M, Kuntawunginn W, My M, Thay K, Rahman R, Balasubramanian S, Char M, Lanteri CA, Gosi P, Ubalee R, Meshnick SR, Saunders DL (2017). Single dose primaquine to reduce gametocyte carriage and Plasmodium falciparum transmission in Cambodia. PLoS One. 12(6):e0168702.

d. Balasubramanian S, Rahman R, Lon C, Parobek C, Ubalee R, Hathaway N, Kuntawunggin W, My M, Vy D, Saxe J, Lanteri C, Lin F, Spring M, Meshnick SR, Juliano JJ, Saunders DL, **Lin JT** (2019). Efficient transmission of mixed *Plasmodium falciparum/vivax* infections from humans to mosquitoes. Journal of Infectious Diseases. DOI: 10.1093/infdis/jiz388.

4. Malaria elimination strategies. What will it take to eliminate malaria? I am interested in how the biology of different parasite species drives their unique strategies to maintain transmission. I have contributed to discussions regarding how the submicroscopic reservoir in *P. falciparum* and the hypnozoite reservoir in *P. vivax* should inform the design of public health interventions designed to achieve malaria elimination.

a. Parobek CP, **Lin JT**, Saunders DL, Barnett EJ, Lon C, Lanteri CA, Balasubramanian S, Brazeau N, DeConti DK, Garba DL, Meshnick SR, Spring MD, Chuor CM, Bailey JA, Juliano JJ (2016). A selective sweep suggests transcriptional regulation may underlie *Plasmodium vivax* resilience to malaria control measures in Cambodia. Proceedings of the National Academy of Sciences USA. 113(50):E8096-E8105.

b. Bassat Q, Velarde M, Mueller I, **Lin J**, Leslie T, Wongsrichanalai, Baird JK (2016). Key knowledge gaps for Plasmodium vivax control and elimination. American Journal of Tropical Medicine and Hygiene. 95(6 Suppl):62-71.

c. Manning J, Lon C, Spring M, Wojnarski M, Somethy S, Chann S, Gosi P, Soveasna K, Sriwichai S, Kuntawunginn W, Fukuda MM, Smith PL, Rekol H, Sinoun M, So M, **Lin J**, Satharath P, Saunders D (2018). Cluster-randomized trial of monthly malaria prophylaxis versus focused screening and treatment: a study protocol to define malaria elimination strategies in Cambodia. Trials.19(1):558.

d. Meeting Report of the WHO Evidence Review Group on Low-Density Malaria Infections. May 2017, Geneva, Switzerland.

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/jessica.lin.1/bibliography/41175207/public/?sort=date&direction=descending

D. Research Support

Ongoing Research Support

R01 AI137395 Lin (PI) 7/01/18-6/30/23
Determinants of malaria transmission by submicroscopic gametocytemia
A field study in Tanzania that will determine which asymptomatic persons contribute to transmission and pilot a field test to target these infectious carriers for treatment, as an alternative to mass drug administration.

NSF R01 TW010870 (PI: Juliano) 07/01/17-06/30/22
Impacts of the African Origin of Plasmodium vivax on Contemporary Parasite Populations
To study the African origin of Plasmodium vivax and how genetic bottlenecking has impacted current vivax malaria populations.
Role: Co-I

Completed Research Support

1K08AI110651 Lin (PI) 02/01/14-1/31/19

Genetic determinants of *Plasmodium vivax* relapse
To use next generation sequencing techniques to improve our ability to identify relapsing parasites and establish tools for uncovering the genetic basis of relapse, with the ultimate goal of informing the design of better anti-relapse drugs for malaria caused by *P. vivax*.
Role: PI

IBM Junior Faculty Development Award, University of North Carolina 01/01/16-12/31/16
Field validation of a newly discovered molecular marker for chloroquine resistant *Plasmodium vivax* malaria
To validate a molecular marker for chloroquine resistance in vivax malaria using a set of Indonesia parasite isolates that have been phenotyped for resistance
Role: PI