



## MMI 291 Seminar Series

Winter Quarter 2023 – CRN 33700 - Zoom

### “Genetic strategies to control mosquito-borne arbovirus transmission in the field”

The research work in my laboratory focuses on the molecular interactions of arthropod-borne (arbo)viruses such as dengue, chikungunya, and Zika viruses with the mosquitoes *Aedes aegypti* and *Ae. albopictus*. These mosquito-borne viruses are important human pathogens, some of which have been responsible for recent explosive disease outbreaks throughout the tropical regions of the world. Our goal is to understand the molecular basis of mosquito vector competence for arboviruses to develop novel strategies aiming at interrupting the viral disease cycle in the insect. One research effort has focused on the mosquito's innate RNA interference (RNAi) pathway and its manipulation to block arbovirus replication in relevant mosquito tissues. An important tool for this research is the germline transformation of mosquitoes. As a result, we generated transgenic *Ae. aegypti* lines that are inheritably refractory to either dengue 2 virus or Zika virus. We are also exploring other antiviral effector designs based on modified catalytic RNAs and, in collaboration with the Rothenburg laboratory at UC Davis School of Medicine, Recombinant Enhanced Antiviral Restrictors (REAVRs). In addition, we are developing and optimizing single-component and split gene drive systems for *Ae. aegypti* based on CRISPR/Cas9 technology to potentially drive antiviral effectors through mosquito populations. Another research effort addresses a long-standing question in arbovirology/vector biology: how do arboviruses traverse the tissue (organ) barriers in their insect vectors? Specifically, we are looking at the mechanism(s) underlying the dissemination of arboviruses from the midgut of *Ae. aegypti*.

#### Publications

Reid W, Williams AE, Sanchez-Vargas I, Lin J, Juncu R, Olson KE, Franz AWE. Assessing single-locus CRISPR/Cas9-based gene drive variants in the mosquito *Aedes aegypti* via single-generation crosses and modeling. *G3* (Bethesda). 2022 Dec 1;12(12):jkac280. doi: 10.1093/g3journal/jkac280. PMID: 36250791; PMCID: PMC9713460.

Kantor AM, Grant DG, Balaraman V, White TA, Franz AWE. Ultrastructural Analysis of Chikungunya Virus Dissemination from the Midgut of the Yellow Fever Mosquito, *Aedes aegypti*. *Viruses*. 2018 Oct 18;10(10):571. doi: 10.3390/v10100571. PMID: 30340365; PMCID: PMC6213114.

Franz AW, Sanchez-Vargas I, Raban RR, Black WC 4th, James AA, Olson KE. Fitness impact and stability of a transgene conferring resistance to dengue-2 virus following introgression into a genetically diverse *Aedes aegypti* strain. *PLoS Negl Trop Dis*. 2014 May 8;8(5):e2833. doi: 10.1371/journal.pntd.0002833. PMID: 24810399; PMCID: PMC4014415.

# February 24



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February 24, 2023  
12:10 – 1 p.m.

Medical Microbiology  
& Immunology  
School of Medicine

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We hope to see you there!