

# Research Scholars Program in Insect Biology: Bibliography of student peer-reviewed publications

## 2011 Cohort

- Atallah, J., G. Vurens, S. Mavong, A. Mutti, **D. Hoang**, and A. Kopp. 2014. Sex-specific repression of *dachshund* is required for *Drosophila* sex comb development. *Developmental Biology* 386:440-447.
- Campbell, R.**, T. C. Thiemann, D. Lemanager, and W. K. Reisen. 2013. Host-selection patterns of *Culex tarsalis* (Diptera: Culicidae) determine the spatial heterogeneity of West Nile Virus enzootic activity in Northern California. *Journal of Medical Entomology* 50:1303-1309.
- Carlson, J. S., E. Walther, R. TroutFryxell, **S. Staley**, L. A. Tell, R. N. M. Sehgal, C. M. Barker, and A. J. Cornel. 2015. Identifying avian malaria vectors: sampling methods influence outcomes. *Parasites & Vectors* DOI 10.1186/s13071-015-0969-0
- Fu, J., **K. A. Murphy**, M. Zhou, Y. H. Li, V. H. Lam, C. A. Tabuloc, J. C. Chiu, and Y. Liu. 2016. Codon usage affects the structure and function of the *Drosophila* circadian clock protein PERIOD. *Genes & Development* 30:1761-1775.
- Hoang, D.**, A. Kopp, and J. A. Chandler. 2015. Interactions between *Drosophila* and its natural yeast symbionts – Is *Saccharomyces cerevisiae* a good model for studying the fly-yeast relationship? *PeerJ* DOI 10.7717/peerj.1116.
- Jasper, W. C., T. A. Kinksvayer, J. Atallah, **D. Friedman**, J. C. Chiu, and B. R. Johnson. 2014. Large-scale coding sequence change underlies the evolution of postdevelopmental novelty in honey bees. *Molecular Biology and Evolution* 32:334-346.
- Morisseau, C., A. T. Wecksler, **C. Deng**, H. Dong, J. Yang, K. S. S. Lee, S. D. Kodani, and B. D. Hammock. 2014. Effect of soluble epoxide hydrolase polymorphism on substrate and inhibitor selectivity and dimer formation. *Journal of Lipid Research* 55:1131-1138.
- Murphy, K. A.**, T. R. Unruh, L. M. Zhou, F. G. Zalom, P. W. Shearer, E. H. Beers, V. M. Walton, B. Miller, and J. C. Chiu. 2015. Using comparative genomics to develop a molecular diagnostic for the identification of an emerging pest *Drosophila suzukii*. *Bulletin of Entomological Research* 105:364-372.
- Murphy, K. A., J. D. West**, R. S. Kwok, and J. C. Chiu. 2016. Accelerating research on spotted wing *Drosophila* management using genomic technologies. *Journal of Pest Science* 89:631-641.

**Murphy, K. A.**, C. A. Tabuloc, K. R. Cervantes, and J. C. Chiu. 2016. Ingestion of genetically modified yeast symbiont reduces fitness of an insect pest via RNA interference. *Scientific Reports* 6:22587. DOI 10.1038/srep22587

Neafsey, D. E., and 119 others, including **K. A. Murphy** and J. C. Chiu. 2015. Highly evolvable malaria vectors: the genomes of 16 *Anopheles* mosquitoes. *Science* 347:43.

Wang, B., N. Pakpour, E. Napoli, A. Drexler, E. K. K. Glennon, W. Surachetpong, K. Cheung, **A. Aguirre**, J. M. Klyver, E. E. Lewis, R. Eigenheer, B. S. Phinney, C. Giulivi, and S. Luckhart. 2015. *Anopheles stephensi* p38 MAPK signaling regulates innate immunity and bioenergetics during *Plasmodium falciparum* infection. *Parasites & Vectors* 8:424. DOI 10.1186/s13071-015-1016-x.

Zaragoza, J., Z. Bendiks, C. Tyler, M. E. Kable, T. R. Williams, **Y. Luchkovska**, E. Chow, K. Boundy-Mills, and M. L. Marco. 2017. Effects of exogenous yeast and bacteria on the microbial population dynamics and outcomes of olive fermentations. *mSphere* 2:e00315-16. <https://doi.org/10.1128/mSphere.00315-16>.