THE UNIVERSITY OF CHICAGO | DEPARTMENT OF STATISTICS

Master's Thesis Presentation

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"Using Statistical Modeling to Identify Associations Between Mosquito Bloodmeal Consumption and the Functional Capabilities of Their Associated Bacteria"

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Abstract

Mosquito-associated bacteria play critical roles in vector competence and nutrient processing of mosquitoes. Although blood feeding alters the composition of the mosquito gut microbiota, how these shifts affect bacterial functional capabilities remains poorly understood. Leveraging the Mosquito-Associated Isolate Collection (MosAIC)—392 high-quality bacterial genome assemblies from a diverse set of mosquitoes contributed by laboratories worldwide—we compared the genetic profile of bacterial isolates from blood-fed and non-blood-fed female mosquitoes. We used eggNOG-mapper to annotate each genome with KEGG Orthology (KO) groups, then compiled presence–absence matrices at three levels—individual enzymes (KOs), KEGG modules, and their associated BRITE functional categories. Exact Fisher tests, corrected for multiple comparisons, identified 91 enzymes and 7 KEGG modules significantly enriched in blood-fed bacterial isolates, and 8 enzymes significantly enriched in non-blood-fed isolates. In blood-fed isolates, we observed significant enrichment of several metabolic pathways—aromatic-amino-acid catabolism, glutathione and heme biosynthesis, the glyoxylate shunt, purine metabolism, and nitrogen recycling—that together facilitate detoxification of heme-derived oxidative stress and exploitation of the protein-rich blood meal. We also detected enrichment of antibiotic-resistance modules and the Type II secretion system, underscoring a functional overlap between blood-fed mosquito bacteria and known pathogens. Bootstrap analyses of KEGG BRITE categories confirmed the Fisher test findings for enzymes and modules. Stratified Fisher tests indicate that feeding-status associations remain strong after accounting for both the collecting laboratory and field-versus-colony origin of the mosquito isolates. By contrast, the strong gut vs. whole-body imbalance could bias results; future work should either analyze gut

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and whole-body isolates separately or use bootstrapping to equalise tissue representation in both feeding groups. Collectively, these findings show that a blood meal selects for bacterial functions that mitigate oxidative stress, recycle nitrogen, and exploit protein-rich substrates, offering new insights into microbe–host interactions and suggesting targets for paratransgenic vector-control strategies.
This work was conducted under the supervision of Dr. Sarah Short and Dr. Nikos Ignatiadis.
