

Skin microbes, volatiles, and vector behaviour: A strain-level perspective

Yulisa Moreno Patiño¹, Niels O. Verhulst¹, Dani Lucas-Barbosa^{1,2}, Mitchel E. Bourne¹

¹National Centre for Vector Entomology, Institute of Parasitology, One Health Institute, Vetsuisse and Medical Faculty, University of Zürich, Switzerland

²Department of Crop Sciences, Research Institute of Organic Agriculture FiBL, Frick, Switzerland

yulisa.morenopatino@uzh.ch

Mosquitoes depend strongly on volatile organic compounds (VOCs) emitted in body odours to locate suitable blood-hosts. These VOCs allow them to discriminate between host species and even between individuals at a distance. Most VOCs in human body odours are produced by microorganisms present on the skin. Previous work has identified correlations between mosquito attraction and skin bacterial communities. Several bacterial species have been implicated as enhancers or suppressors of mosquito attraction. However, behavioural validation studies typically test only a single representative strain per bacterial species, assuming species-level uniformity. Different strains of the same bacterial species typically share 80%–90% of their genes. Still, genomic differences between strains are known to include important biological functions, and recent studies have shown that strains belonging to the same species can emit different VOCs when grown under identical conditions. This is known to have consequences for the degree of attractiveness or repellence towards insects [1].

In this project, we systematically assess mosquito attraction across a diverse panel of human-associated bacterial strains to disentangle species- and strain-level contributions to host attractiveness. Using isolates obtained from the DSMZ biobank, we assemble a panel maximising intraspecific diversity across eight skin-associated bacterial species previously linked to mosquito behaviour. Bacteria are cultured under standardised conditions and presented to mosquitoes in a custom two-choice video-tracking arena, enabling quantification of behavioural attraction metrics. In parallel, headspace VOCs from all strains are collected for chemical profiling (GC–MS). Together, the outcomes will provide systematic evidence of how much intraspecific bacterial variation contributes to host odours, attractiveness and will clarify whether studies focusing only on species-level comparisons risk overlooking critical strain-level effects.

In addition, we are developing tools to decrease human and animal attractiveness to mosquitoes by altering the composition of the bacteria on our skin. We use an innovative methodology (bacteriophage-derived endolysins) to selectively kill bacteria that increase human attractiveness to mosquitoes, thereby reducing pathogen transmission and disease.

[1] Goelen, T., Sobhy, I. S., Vanderaa, C., Wäckers, F., Rediers, H., Wenseleers, T., ... & Lievens, B. (2020). Bacterial phylogeny predicts volatile organic compound composition and olfactory response of an aphid parasitoid. *Oikos*, 129(9), 1415-1428.