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Microbiota for life history analysis in mosquitoes

Insects are virtually omnipresent, effectively taking over a huge variety of different ecological niches on the planet. However, insects are themselves ecological niches, populated by many different microbes that form their microbiota. Fungi, bacteria, viruses, they all live on and in the host body, being affected by changes in the environment and by the habits and preferences of the host. Microbiota can today be considered, in insect as in humans, a detailed report of the life history of its host. However, despite microbial data being a huge source of information, still today this tool has not been exploited to its full potential, leaving space for the possibility of pioneering novel ways of addressing problems and answering questions through its analysis.

In our lab, we are now investigating how the microbiota of different insect species is influenced and shaped depending on their geographical location. It has been proven that, in some species, its composition strongly correlates with the location of collection. Shedding light on what drives this correlation and for which insect species this is true or not, is extremely important to find new applications for the analysis of microbiota and spatial distribution in insects.

This project aims to uncover the limits of some of the methodologies that are routinely used nowadays to investigate microbial data. With that in mind, the student will have to deal with 16S amplicon sequencing data and the processing of them, going from raw data to producing plots and conducting relevant statistical analyses, to draw conclusions and identify microbial patterns in the dataset.

This will be accomplished through the analysis of a dataset containing raw read data from whole mosquitoes, collected in Burkina Faso in different villages. We are interested in investigating whether sequencing depth influences the observed patterns, and if patterns will be conserved at lower depths.

The student undertaking the project will then learn both to use the current methodologies in the field (data handling, denoising of reads to infer ASVs, rarefaction, ordination plots and ecological diversity indexes, permutational analysis of variance), as well as how to interpret the results of these analyses to propose hypotheses and draw conclusions in autonomy.

If interested, please contact:

Lorenzo Assentato lorenzo.assentato@icm.uu.se

and/or Olle Terenius olle.terenius@isp.uu.se