

## ESR 14 – SINGLE CELL GENOMIC ANALYSIS OF EUKARYOTIC MICROBES ASSOCIATED WITH BLOODFEEDING ARTHROPODS

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| <p><b>Research project</b></p>    | <p>Many eukaryotic microbes associated with insects and other arthropods are important parasites such as Plasmodium, Trypanosoma and Thelazia species. However many, probably most, have evolved with their invertebrate hosts from millions of years before they became associated with vertebrate hosts. There are also many eukaryotic microbes that are known to have symbiotic associations with insects, such as the trichomonads that associate with termites to break down cellulose. Understanding the evolution of commensal or symbiotic eukaryotic microbiota and their association with arthropods will inform us about pathogen biology, as these organisms will have evolved to circumvent the host innate immunity and may share common ancestry with vectored pathogens. However, the diversity of the eukaryotic microbes associated with arthropods has not yet been deeply and systematically investigated. As these organisms are often uncultivable, studies have generally employed barcoding or metagenomic approaches but not sequencing from single cells. The objective of this study is to obtain an understanding of the diversity of eukaryotic microbes associated with bloodfeeding arthropods at the genomic level. We would sample guts from a small number of individuals from Isopoda and Diptera blood feeders using micromanipulation cell sorting to isolate single cells for whole genome sequencing. Comparative genomic analysis of these organisms will be employed to identify shared and unique characters to provide insights into host adaptation. The distribution of these organisms can then be investigated using PCR assays designed using the genomic information gained.</p> |
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| <p><b>Host institution</b></p>    | <p>University of Liverpool (UoL)<br/>Liverpool, UK</p>   |
| <p><b>PhD program</b></p>         | <p>Biological Sciences</p>   |
| <p><b>Expected results</b></p>    | <p>A single cell study of arthropod microeukaryotic biodiversity. Identification of gene repertoires related to host adaptation in different host environments. Identification and quantification of the level of horizontal gene transfer between microbiota and eukaryotes that could promote host colonisation.</p>   |
| <p><b>Planned secondments</b></p> | <p>LU - Month 18 (3 m) - Overview of population genetics for environmental studies<br/>UNEXE - Month 26 (4 m) - Gene annotation and functions derived from genome analyses<br/>ASC - Month 40 (2 m) - SAG databases and tools for genome screening</p>   |
| <p><b>Required profile</b></p>    | <p>Graduate in Biology, Bioinformatics, or Molecular Biology</p>   |