Sandfly adaptation to anthropogenic environmental change

1. Introduction:

Throughout history, parasites have emerged from natural environments to exploit humans, our livestock, and our crops[1]. While much of this adaptation happened too long ago to study in detail, our recent genomic surveillance of *Leishmania* parasites discovered more recent example of parasite adaptation. In the region of Manaus in the Amazon rainforest, we studied *Leishmania guyanensis*, which usually infects wild animals across the region Amazon region[2,3] but also infects people, particularly in the Manaus which has a population of 2 million [4,5,6]. We identified two distinct populations of this parasite: an ancestral population in forested areas further from the city, and a newer, periurban population, closer to Manaus. Satellite data analysis showed that the periurban locations have earlier and more severe deforestation. Genomic data suggest these two populations diverged about 300 years ago—around the time Europeans settled in Manaus (unpub. data). Our current hypothesis is that the sandflies that transmit the *Leishmania* parasites are adapting to biological and physical aspects of the disturbed environment, establishing a novel parasite transmission cycle. This is an example of a parasite emerging from the natural environments to exploit humans.

2. Objectives: To work towards testing this hypothesis the student will work with an MSc student, York staff and entomologists in Manaus to examine sandflies that have been collected in i) three densely forested locations where we find the ancestral population, and ii) three periurban deforested sites where we find the new (derived) *Leishmania* population. The student will work within an international collaboration in both English and Portuguese (via translation apps) to examine aspects of sandfly biotic interactions and their microbiomes (which we expect to be very labile to environmental change).

3. Summary of proposed experimental work and time line

Weeks 1-2; Learn and optimise DNA extraction protocols for single sandflies (which are very small) to enable downstream work, including genomic sequencing of individual sandflies

Weeks 2-4; Single sandfly PCR and sequencing experiments to; a) determine blood meal sources via a mammalian mitochondrial marker PCR, b) determine plant sugar feeding sources via a plant chloroplast marker, and c) produce sand fly microbiome data via the commonly used 16S ribosomal DNA marker.

Weeks 4-7; Analyse sequence data as it becomes available, using simple methods such as phylogenies and BLAST.

Weeks 7-8; Data archiving and report writing

Research training for the student: Working with the MSc student and interacting with staff at York and in Manaus, the student will gain experience in laboratory techniques (DNA extraction, PCR, sequencing), bioinformatics (sequence analysis, environmental data processing), ecoepidemiology (understanding disease systems in complex changing environments**,** international collaborative research and regulatory awareness such as SISBio (Brazilian system to authorizes research in protected areas) and The Nagoya Protocol on Access and Benefit-sharing.

References

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