Master's thesis (+IRT3) projects available in the Evolutionary and Pathogen Genomics Group

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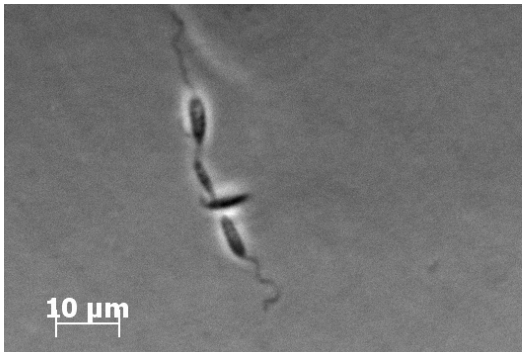
In my group, we use whole genome sequencing and computational approaches to understand the evolution from short time scales (population level) to longer time periods (between species). Our focal genus is ***Leishmania***, is a unicellular eukaryotic parasite (protist), that is transmitted by sandflies to humans and other mammalian hosts. Parasite infection causes the neglected tropical disease leishmaniasis in humans.
(see https://www.evol.bio.lmu.de/research/franssen/index.html for more information)
All projects described below are initially planned as purely computational. Please contact me if you are interested or have any questions about the projects.

Project overview:

I. **Phylogenetics and comparative genomics** of the *Leishmania* genus
II. Evaluation of **single cell sequencing** technologies for **aneuploidy** estimation in *Leishmania*
III. Role of **mosaic aneuploidy** for short term adaptation in *Leishmania*

I. Phylogenetics and comparative genomics of the *Leishmania* genus

The *Leishmania* genus comprises more than 20 species causing human infections. Different species are associated with different geographic origins and are a large determinant of disease phenotypes that can range from local cutaneous lesions (LCL), mucocutaneous disease infecting and destroying mucosal tissues (MCL) and visceral disease infecting internal organs (VL) and being fatal without treatment. Additionally, parasite species are restricted to different sand fly vectors and other mammalian hosts they can infect.

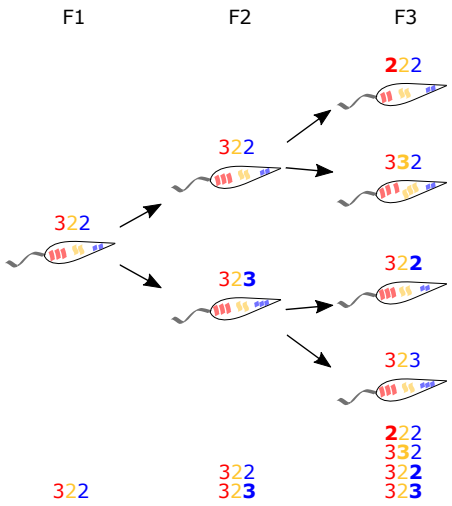


Leishmania mexicana in cell culture.

In order to understand the evolution and genetics that influence these parasite species specific traits, we will use comparative genomics approaches across *Leishmania* species. This will initially comprise building robust species phylogenies based on whole genome data. In the next steps, we want to characterize genome content, understand selection pressures, gene family evolution and structural rearrangements across *Leishmania*. This analysis is expected to provide an important resource for future studies of the genetic basis of several *Leishmania* traits such as host specificity, vector compatibility and disease phenotypes.

II. Evaluation of single cell sequencing technologies for aneuploidy estimation in *Leishmania*

Leishmania have an unusual genetic feature termed mosaic aneuploidy. Aneuploidy alone means that each chromosome can occur in different copy numbers in contrast to for example humans that have diploid genomes meaning two copies are present of each chromosome. In *Leishmania* the genome cannot only be aneuploid but copy numbers of individual chromosomes can change relatively frequently between mother and daughter cells. This phenomenon is termed mosaic aneuploidy because in a cell population of clonal origin there can be a mosaic of different aneuploidy profiles between different unicellular parasites.



Mosaic aneuploidy in a clonal *Leishmania* cell population.

In this project, we want to compare how well different single cell sequencing methods can estimate mosaic aneuploidy in *Leishmania*. The straight forward way is to whole genome sequence the genomic DNA of individual cells (scCNV) to estimate the copy number of each chromosome. However, also single cell gene expression methods (scRNA-seq) exists and initial studies show that the copy number of a chromosome relative to other chromosomes can also be estimated via the expression levels across all genes of each chromosome. We want to compare both approaches for aneuploidy estimation in *Leishmania*.

III. Role of mosaic aneuploidy for short term adaptation in *Leishmania*

This project is looking at mosaic aneuploidy, the phenomenon in *Leishmania*, where individual cells in a parasite population can have different chromosome copy number profiles (described also for project II.). Here, we want to apply single cell sequencing technology to estimate chromosome copy number profiles in a population of parasite cells. Next, we want to see how stable these are across culturing conditions and cryopreservation methods. We ultimately want to access the role that variation and changes in aneuploidy have during adaptation. This can be done in a follow-up project via assessing changes in aneuploidy during experimental evolution to different laboratory environments. For this project a background or interest in population genetics is beneficial.