

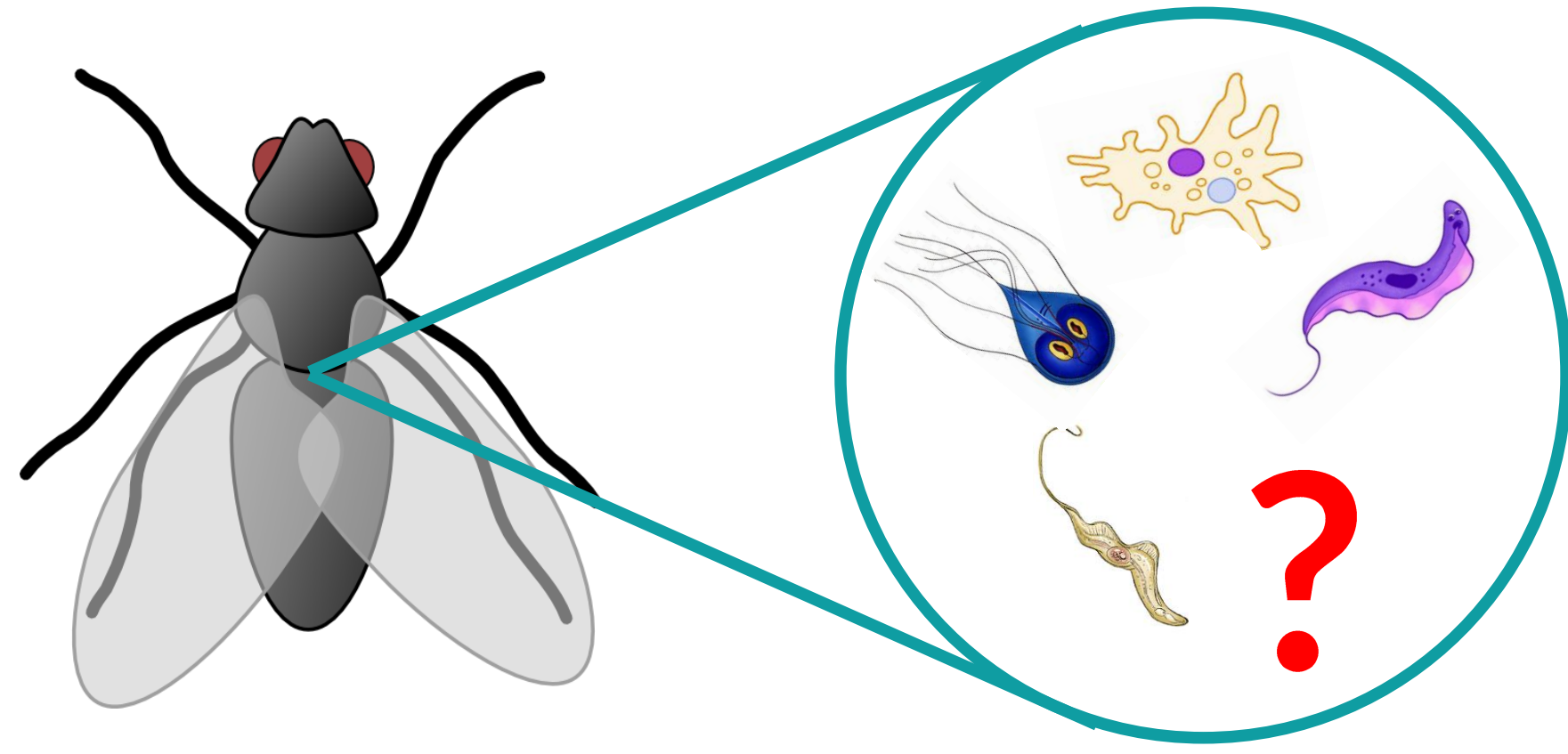
GENOMIC ANALYSIS OF PROTISTS FROM BLOOD-FEEDING ARTHROPODS



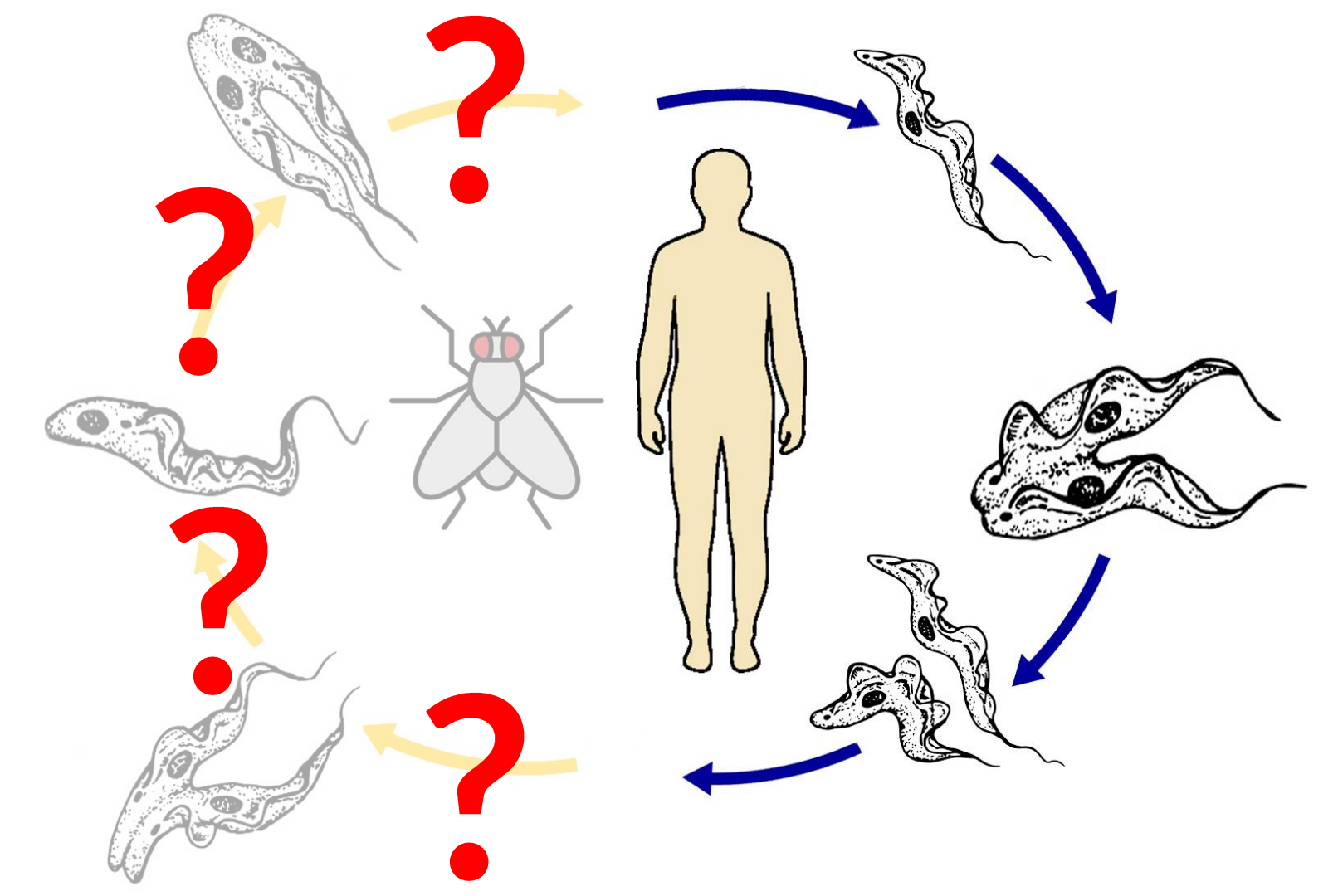
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WHO?



WHY?

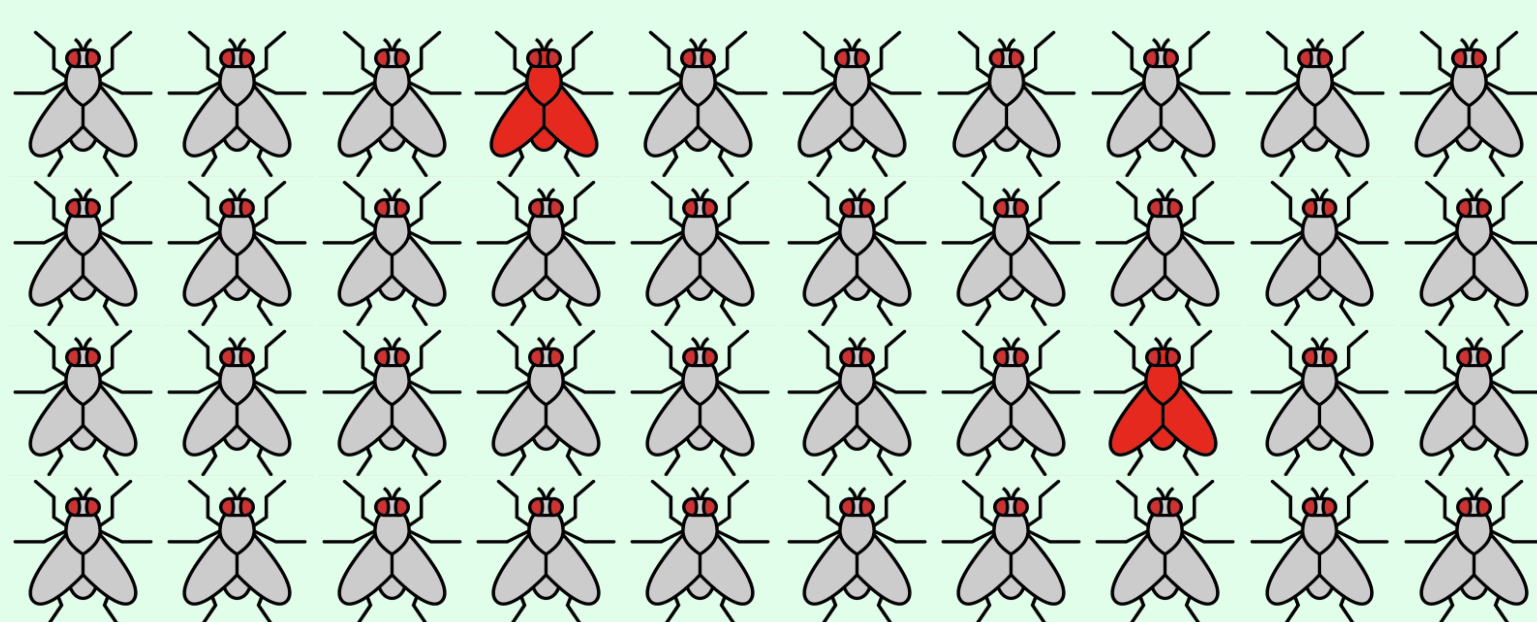


Symbiotic protistan diversity of Arthropoda is hugely underinvestigated. The focus of the current work is the development of methodological approaches to comprehensively characterize eukaryotic microbiome of blood feeding arthropods.

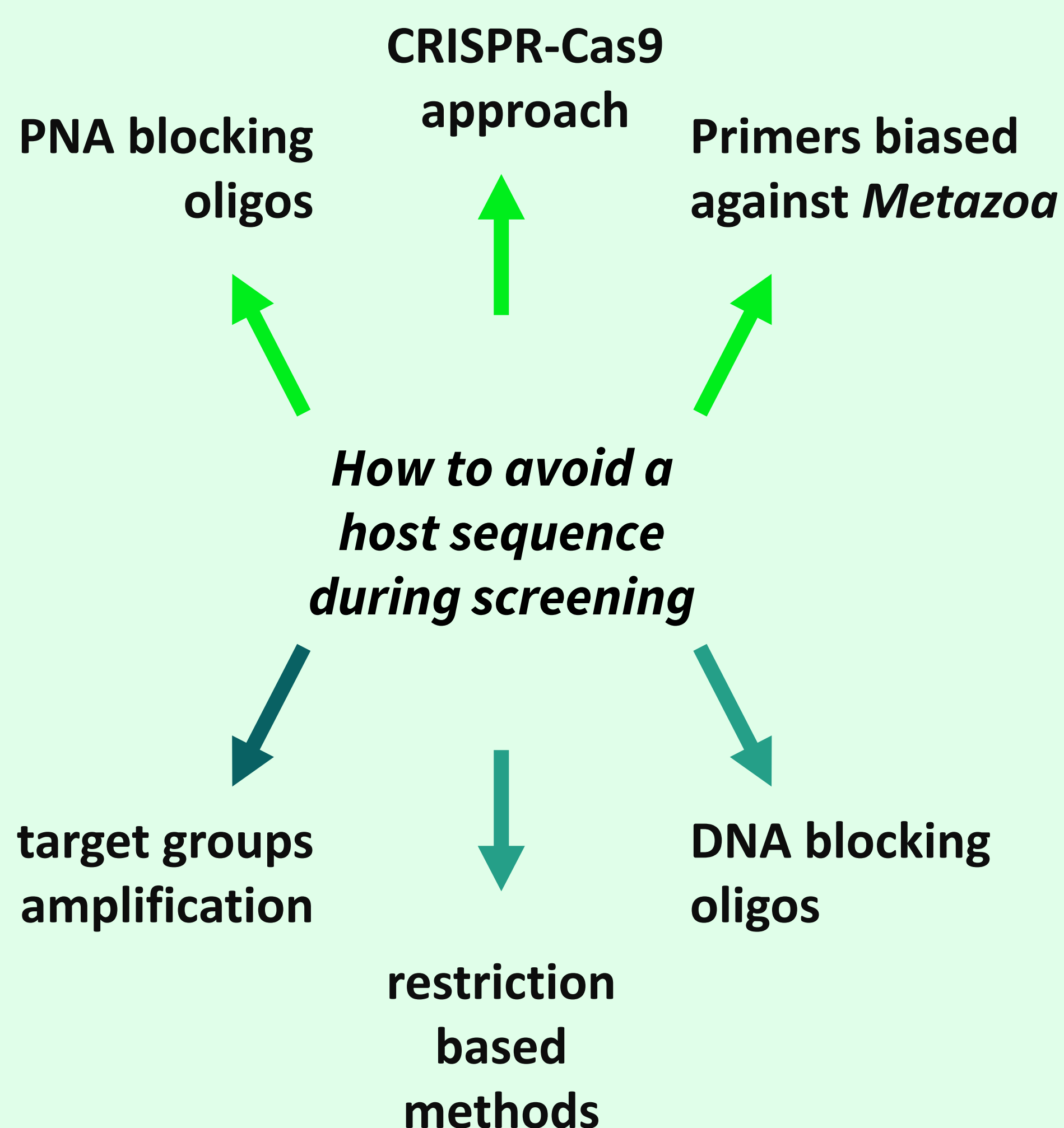
While we are interested in novel eukaryotic symbionts there're also gaps in our knowledge about life cycle of well known parasites. Studying parasites is focused on the right part of the figure, while host/pathogen interactions mostly remain unknown.

I SCREENING

A small percent of arthropods has eukaryotic symbionts, so before we can explore symbionts at the single cell level, we have to develop a method for populational survey.



We analysed, evaluated *in silico* and *in vitro* and improved several methods for eliminating host sequences in a mixture of DNA from a host and its symbionts.

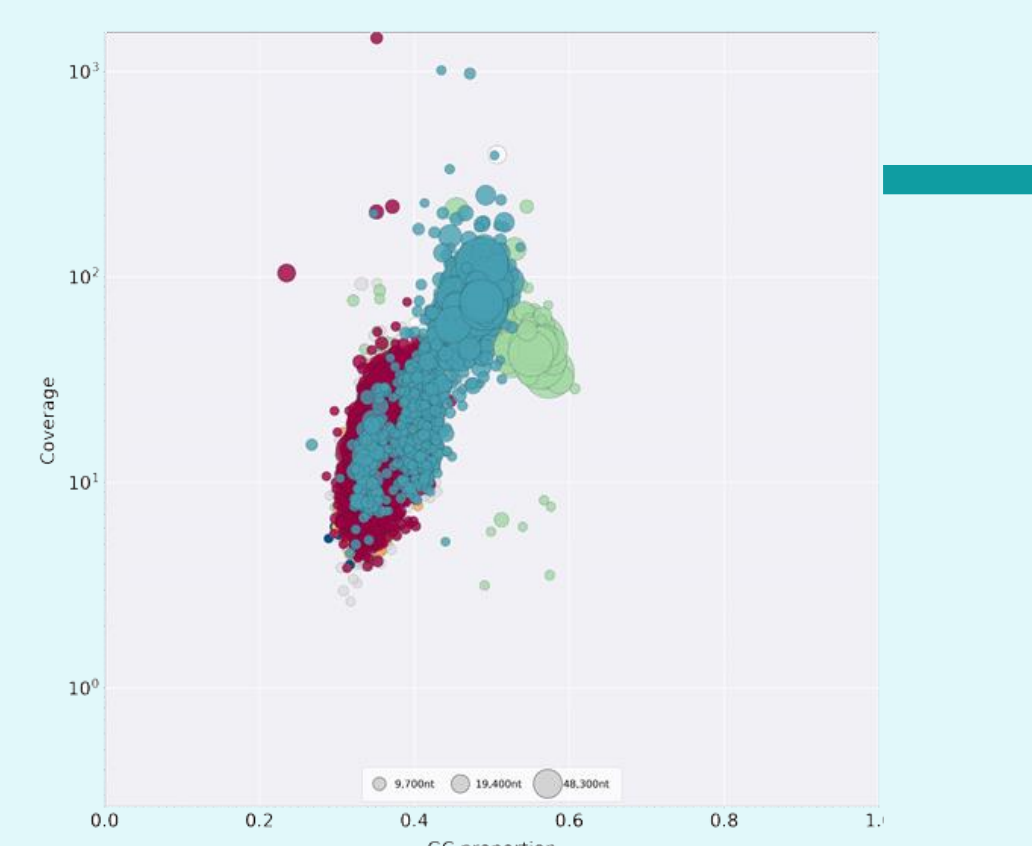


II REFERENCE

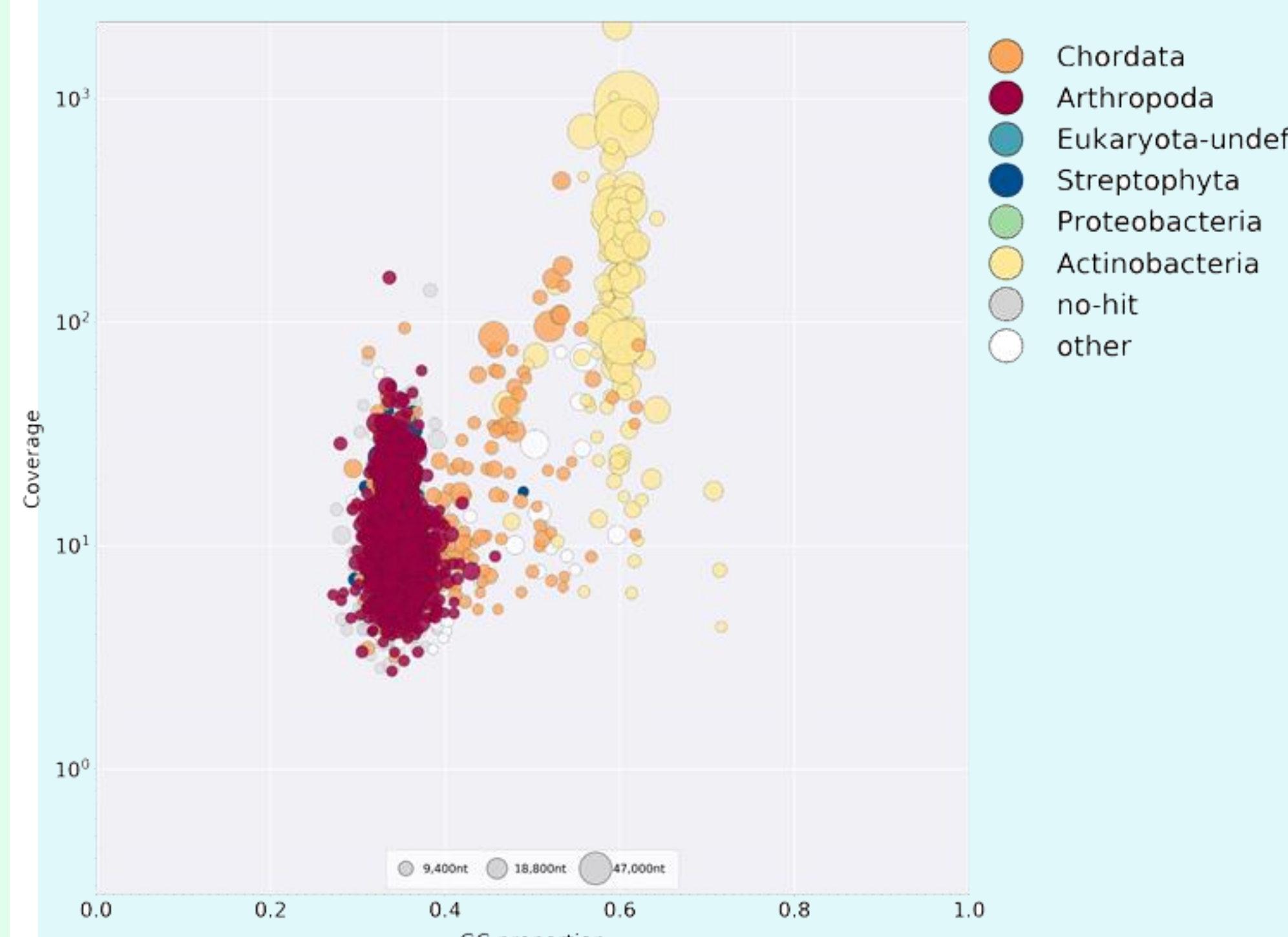
Existing arthropods' genome references are chunky and have numerous symbionts sequences within them. Bioinformatic approaches allow easily extract prokaryotic genomes, but protists' genomes remain hidden in host sequences. Combining short and long-read sequencing technologies we attempted to improve several genomes of blood-feeding insects.

illumina +

MinION



Microdissected symbiont of *G. morsitans*



III BIOLOGY

Single-cell methods allow unparalleled insights into host/symbiont interactions. Using a cell line from *Rhipicephalus microplus* infected with three pathogens and single cell RNA-seq we are going to address these questions:

- Are there several cell types in the cell line or just one?
- How these cell types are responding to pathogen invasion?
- Compare transcriptomic response on different stages of invasion

10X GENOMICS

