The human body harbours a diverse microbial community belonging to the three domains of life: Bacteria, Archaea and Eukarya. Yet, most of the studies of the intestinal microbiota neglect the eukaryotes, which taxonomic and functional characterisation remains insufficient.

Intestinal eukaryotes include protists, fungi and helminths, some of which have purported associations to disease. However, the disease-association of some eukaryotes has been challenged due to its inconsistency across studies. Considering that functional differences have been established even at the intra-genus level, it is possible that some of the observed inconsistencies might trace back to this, mostly uncontrolled, diversity.

Eukaryotes appear to be a common component of the intestinal ecology, especially in non-industrialised societies. While some species, like Blastocystis, are common across the world, the largest diversity of gut eukaryotes is observed in rural communities.

Although the biological role of gut eukaryotes is unclear, their assumed pathogenic potential makes them a target for medical interventions. Eradication of alleged parasitic eukaryotes is standard of care, with unforeseen potential consequences to the gut homeostasis.

Continuous transition of human subsistence modes is associated with changes in the gut microbiota. Microbial diversity is reduced with industrialization raising questions about which are the microorganisms we are losing and, with them, what functions are disappearing or evolving within the human gut. Multiple studies have described consistent elements of the gut microbiota (a microbial core); however, to date no study has identified a multi-domain core microbiota.

The main aims of this doctoral thesis are: 1) To characterize the (understudied) taxonomic diversity and distribution of eukaryotes in the faecal microbiota, and 2) To characterise the multi-domain gut microbiota across a gradient of urbanisation.