

Targeted Project / AY 2023 -2024

## Discovering host factors required for the replication and spread of Oropouche virus

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**Department/Institute:** Pathology

**Research area:** Virology, insect-bourn viruses

### Project outline:

Arbovirus spread is increasing dramatically across the globe and represent a major public health issue, particularly in tropical areas of the world. Oropouche virus (OROV) is one of the most common arboviruses that infects humans in South America. Over half million people have been infected by OROV in 30 outbreaks in South America over the past 60 years, although this is likely an underestimate due to a resemblance of Oropouche fever with the symptoms of other arboviruses (Dengue, Zika and Chikungunya). There are no therapeutics available for the treatment of OROV infections and so understanding the molecular mechanisms underlying OROV replication is crucial for development of antiviral drugs.

OROV belongs to the Peribunyaviridae family, one of the largest families of RNA viruses. The broader Bunyavirales order includes many important human and animal pathogens such as Hantavirus, Rift Valley fever virus and Crimean-Congo haemorrhagic fever virus. In a newly established collaboration with São Paulo University in Brazil we are investigating host factors involved in the replication of OROV. The aim of this PhD project will be to employ cutting-edge proteomics techniques and CRISPR/Cas9-based genome-wide screens to identify cellular pathways and specific druggable host factors that are crucial for the replication and spread of OROV and other bunyaviruses. The roles played by the identified host factors during bunyavirus replication will be investigated using advanced microscopy techniques (e.g. super-resolution) as well as a range of biochemical and cell biological techniques. This project will also provide the opportunity for collaborative research trips to Brazil.

**BBSRC DTP main strategic theme:** Bioscience for an integrated understanding of health