

METATROPICS

metagenomics for tropical fevers

Problem

Tropical undifferentiated febrile illness (i.e., without organ-specific symptoms) is caused by a broad range of pathogens including (ARBO)viruses.

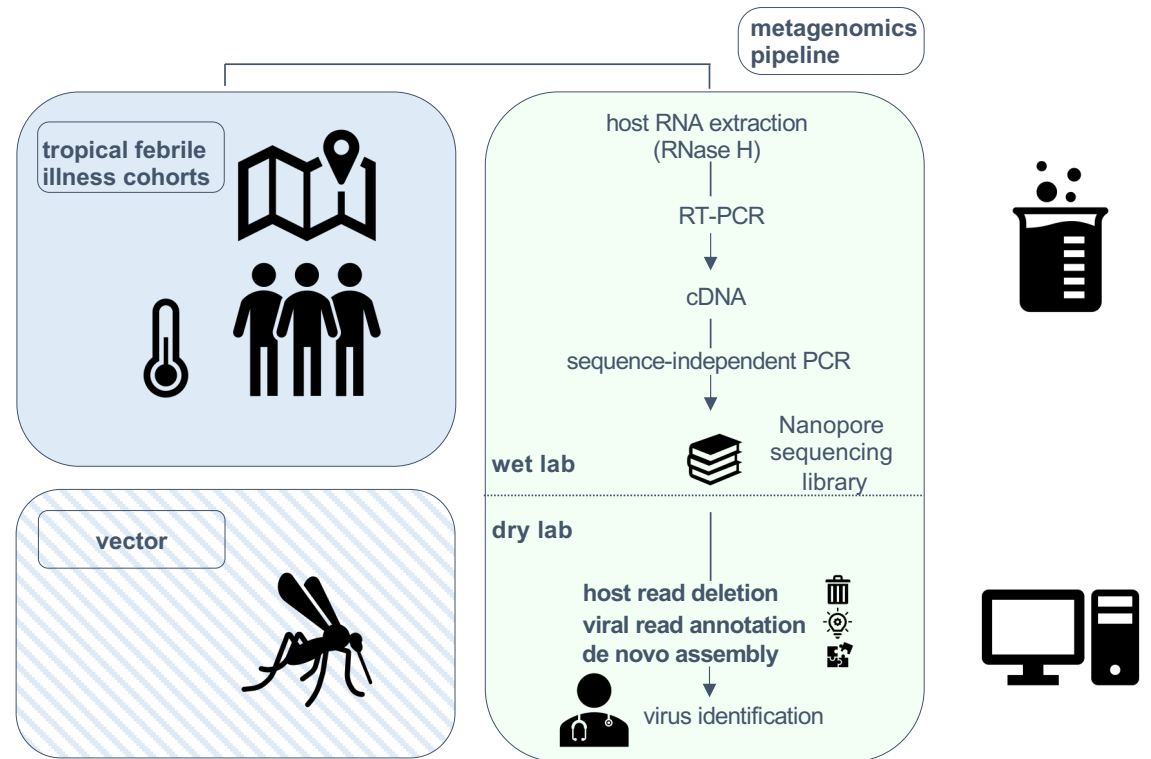
Clinical management in low-income countries is empiric (antibiotics and antimalarials) based on limited regional pathogenic knowledge (since lack of routine diagnostic tests).

Regionally circulating pathogens can be mapped in studies that investigate febrile illness patient cohorts, but typically only test for a narrow panel of preselected pathogens. Even if gold-standard molecular tests are employed -PCR- the risk exists of missing (newly emerging) viruses not present in the panel or those that mutated. Most tropical febrile patients indeed remain undiagnosed within such studies.

Hypothesis

metagenomic sequencing could increase viral knowledge generated in febrile illness studies to better inform on regionally circulating viral pathogens.

Potential impact on clinical management (antibiotics and antimalarials overconsumption), public health (awareness) and epidemiology (outbreak-prone virus alert)



Kvercauteren@itg.be, Pselhorst@itg.be
and Karien@itg.be

We are recruiting a talented Master student applying for ITM's master in tropical medicine programme with molecular laboratory expertise to:

- develop advanced sequencing laboratory skills
- apply those skills on available samples collected by the applicant ('s network)