

No evidence for ONNV or MAYV infections in returning travelers diagnosed in Belgium, from 2006-2023: a retrospective study

Jasmine Coppens¹, Alexandra Vujkovic¹, Dorien Van den Bossche¹, Koen Vercauteren¹, Marjan Van Esbroeck¹

¹ Institute of Tropical Medicine Antwerp

The rising prevalence of arboviroses in tropical regions poses a global health threat, compounded by the challenge of symptom-based differentiation. O'nyong-nyong (ONNV) and Mayaro virus (MAYV), both Alphaviruses in the *Togaviridae* family, genetically closely related to chikungunya virus (CHIKV) are endemic to Sub-Saharan Africa and Latin America, respectively, and have the potential for global dissemination (Esposito et al., 2017; Pezzi et al., 2019). This study investigated the presence of ONNV and MAYV in samples previously testing PCR positive for CHIKV at the Institute of Tropical Medicine in Antwerp, Belgium.

From 2006 to 2023, 54 samples from 52 patients tested positive with the CHIKV PCR adapted from (Panning et al., 2008), known to cross-detect ONNV and MAYV. Of the 49 patients with a known travel history, 16 travelled to Africa and nine to Latin America. In this study, we tested the leftover RNA extracts, mostly from serum samples, utilizing real-time PCRs targeting the ONNV and MAYV 5'UTR-nsP1 genes (Waggoner et al., 2017 and 2018) and re-analyzed them with the CHIKV PCR as a positive control. All 54 included samples tested positive using the CHIKV PCR setup, whereas none of the samples tested positive using the ONNV and MAYV specific setup. This retrospective study did not find evidence for of ONNV and MAYV infections in returning travelers in Belgium. From 2024 onwards, ONNV and MAYV PCR will be performed prospectively on all CHIKV PCR-positive samples for further differentiation.