CO-095

Molecular investigation of Rift Valley Fever outbreak in Mayotte, 2018

KWASIBORSKI Aurélia (1), COLLET Louis (2), HOURDEL Véronique (1), VANDENBOGAERT Mathias (1), BATÉJAT Christophe (1), MANUGUERRA Jean-Claude (1), VANHOMWEGEN Jessica (1), **CARO Valerie (1)**

(1) Institut Pasteur, Paris, FRANCE; (2) Mayotte Hospital, Mamoudzou, Mayotte, FRANCE

Objectif - Introduction
Mayotte Island is facing a severe Rift Valley Fever (RVF) outbreak with around 143 human cases since November 2018. RVF is an emerging zoonotic arboviral disease affecting humans and livestock, mainly in Sub-Saharan Africa. In Mayotte, RVF virus (RVFV) was detected for the first time in 2007 in humans, and seems to have been circulating at low level in livestock since 2011, without causing epidemics. To decipher the origin of this new emergence and help define appropriate public health measures, we performed a phylogeographic analysis of these circulating RVFV, by using next-generation sequencing approaches (NGS) on the earliest patient samples

Matériels (ou Patients) et méthodes
Plasma samples collected from the first five RT-PCR-confirmed cases were subjected to second (MiSeq, Illumina) and third (MinION, ONT) NGS. RNA extracts were depleted and used for cDNA synthesis and whole-transcription amplification. Nextera XT V2 (Illumina) multiplexed librairies were prepared and all samples were sequenced on a 2x150 bp-paired end MiSeq run. MinION multiplexed librairies were prepared with a rapid PCR barcoding kit, and run on FLO-MIN106 flow-cell during 24h. To reconstruct the full genomic sequences, Illumina data were de novo assembled using the SPAdes assembly tool and MinION data were analyzed using ONT dedicated softwares. Phylogeographic analysis was performed with BEAST (Bayesian Evolutionary Analysis Sampling Trees) tool

Résultats
By combining Illumina and MinION approaches, partial viral sequences of the three single-stranded RVFV genome segments (large, medium, and small) were obtained for 4 of the 5 plasma samples, and complete genome sequences were generated for the 2 samples with highest viral loads. Phylogenetic analysis indicated that RVFV belonged to lineage H and Kenya-2 clade, therefore not directly linked with the previous ones circulating in 2007 (clade Kenya-1). Moreover, RVFV showed high similarity with isolates recently spreading in humans and livestock in southwestern Uganda

Conclusion
The NGS approach is a useful tool to decipher the origin of the pathogen, and to track virus introduction and transmission networks. In this context, our study performed on the first patients provided epidemiological data on this new RVFV epidemic, and phylogenetic analysis also pointed to new introduction from Eastern African mainland

Mots Clés
Rift Valley Fever, Mayotte, Next generation sequencing, Phylogenetics