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INVESTIGATION OF EMERGING ZOONOTIC VIRUSES IN EUROPE AND AFRICA

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Emerging viruses are in most cases of zoonotic origin. Current Covid-19 pandemic alarms on how the availability of innovative strategies for detecting and monitoring emerging viral agents represents one of the challenges for preparedness nowadays. In this presentation I will illustrate some examples of investigation of emerging zoonotic viruses under different circumstances of survey of chosen groups of study in endemic areas, by several methodological tools.

A The first part will concern the search for evidence of zoonotic transmission from animal to humans, such it was the case of works focused on the emergence of simian retroviruses in Central Africa. In a molecular epidemiology study, we demonstrated that a bite by a Non Human Primate (NHP) is a risk factor for Human T-Lymphotropic Virus type-1 (HTLV-1) infection, by comparing a group of ~250 individuals from rural Cameroun having reported a contact with NHPs with the same number of persons as controls.

A Then, I will present the implementation of a molecular high-throughput approach, based on resequencing microarray, for detecting zoonotic viruses and identifying new genetic variants that could potentially emerge. This technology allowed the genetic characterization of highly pathogenic viruses associated with hemorrhagic fevers, not only in cultured cell supernatants, but also in human samples during outbreaks in endemic areas, as observed for distinguishing the tick-borne Crimean-Congo Hemorrhagic Fever Virus in East Europe and Middle East.

Lastly, I will describe how the One Health concept has been applied to investigate hantavirus zoonoses in the Indian Ocean region. A new hantavirus, genetically related to the Thailand hantavirus, has been discovered in black rats (*Rattus rattus*) in Mayotte island, by using traditional RT-PCR up to next generation sequencing. Its variant Anjozorobe virus circulating in Madagascar made the object of deeper studies designed to better evaluate the dissemination and the zoonotic risk in the country, by both animal and human investigation at the national scale.

Specific molecular (Real-time RT-PCR) and serological (IgG Elisa) tools for the analysis of Anjozorobe virus were validated. Molecular testing in animal tissues has shown ~12% (111/897) of positivity. Serological testing in human indicated that the Malagasy population is exposed to hantavirus with a national prevalence of 2,7% (46/1680). The potential risk of zoonotic transmission being assessed, an additional investigation has been set up to establish the pathogenicity in the community and the impact of such zoonosis for human health in Madagascar. Altogether, these works aim to bring a contribution for a better comprehension in the field of viral emergence, a topic of growing concern worldwide.