

THESE

Mardi 19 Janvier 2021 à 13h30

Visioconférence

Institut de biologie structurale - 71 avenue des Martyrs CS 10090 38044 Grenoble Cedex 9 - T.+33 (0)4 57 42 85 00

www.ibs.fr

par **Amélie Donchet**

Institut de Biologie Structurale

Groupe Machines de Réplication Virale

Interaction between the influenza replication machineries and the nuclear import system

Thèse de Doctorat de l'Université de Grenoble

In 2014, American and Chinese studies have identified the influenza D virus (IDV). This new member of the *Orthomyxoviridae* family shares only 50% sequence identity with the already well characterized influenza C virus and less than 30% sequence identity with influenza A and B viruses. IDV has been detected in pigs and cattle, and has been shown to replicate in the ferret, the main animal model for influenza virus studies in humans, suggesting a possible transmission. In 2018, a new study identified the first influenza viruses infecting cold-blooded animals. A phylogenetic comparison highlighted that these viruses, and more particularly a toad-infecting virus (ToadV), were closer to influenza B viruses than influenza A viruses. This relationship is surprising, taking into account the influenza B restricted host spectrum in comparison to the influenza A one.

After the work on influenza A and B viruses and in line with it, the team collaborates now with Mariette Ducatez (INRA - ENV Toulouse) to detail the IDV replication, but also the replication machinery of ToadV. The replication machinery comprises various proteins, including the RNA polymerase (RdRp) and the nucleoprotein (NP). The RdRp is composed of three subunits (PA, PB1 and PB2), binds both the highly conserved 3'- and 5'-ends of the vRNA segment which is covered by multiple copies of NP. This macromolecular complex replicates the viral genome in the nucleus of infected cells and makes many contacts with cellular partners for its assembly. We have gained evidences that IDV NP uses the importins- α system, similar to influenza A and B nucleoproteins. By using advanced techniques of modern biology and physics (X-ray, electron microscopy, surface plasmon resonance, fluorescence anisotropy, ...), the aims of this project are 1/ to provide structural and functional data on IDV and ToadV nucleoproteins and also on their interactions with host partners, and 2/ to highlight both the common and specific features of all types of influenza NPs, giving precious insights on the evolution processes occurring within this growing family of viruses.

Lien pour suivre par visioconférence : <https://testbbbibs.isbg.fr/b/odi-lqv-hhf>