Soutenance

THESE

Lundi 01 Juillet 2019 à 14h

Salle des séminaires

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

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Investigating the role of conformational disorder in mumps virus proteins

Thèse de Doctorat de l'Université de Grenoble

Mumps is a highly contagious disease caused by the mumps virus. The prevention treatment (vaccine) against it is already in the routine use. However, recent outbreaks still remain uncontrollable. Therefore, it is important to understand the molecular mechanism of the mumps virus life cycle. This virus belongs to the family of *Paramyxoviridae*. Its genome, negative strand non-segmented RNA is protected by the nucleoprotein (N) by forming filamentous structures called nucleocapsids. N plays an important role in viral genome synthesis. Together with the polymerase and its cofactor phosphoprotein (P) they constitute the transcription-replication machinery. Both N and P contain folded and unfolded regions. Despite mumps virus common morphology with other paramyxovirus, there are some differences. It has been proposed that P is an antiparallel oligomer with two extremities on the one side being in interaction with the structural part of N (Ncore). The function of the disordered domain (Ntail) remains unclear, as it does not seem to bind to the C-terminal part of P, as is the case for other paramyxoviruses. The role of the disordered domains of P is also not known. In this project we revealed mechanisms of interaction between different regions of N and P and we explain how disordered regions of N and P are implicated in the regulation of the complex machinery of viral replication. We used the nuclear magnetic resonance which is the most powerful method to determine structure, dynamics and potential interaction partners, and therefore, function of disordered viral proteins.