Identification and characterization of Cysteine-rich proteins from giant viruses

Keywords: iron-sulfur clusters, giant virus, structural biology, EPR spectroscopy, cysteine-rich proteins

Summary

The discovery of Mimivirus in 2003 was revolutionary for the field of virology. Giant viruses revived old debates about the concept of virus, their position in the tree of life, their biology, and the role they played in the emergence of life on Earth(1). Seven distinct families of giant viruses have since been discovered by a handful of research teams, including the IGS. The giant double-stranded DNA viruses have viral particles easily visible under a regular light microscope. In addition, these families all bring unexpected characteristics that have extended the interest of the scientific community from virology all the way to evolutionary biology: (i) their genome sizes, encoding for 500-2500 proteins, rival with most bacterial ones; (ii) they do not rely entirely on the host for transcription or translation of their genomes, contrary to "classical" viruses; (iii) ~2/3 of their genomes encode for ORFan proteins without cellular or viral homolog. Genomic and transcriptomic studies of Acanthamoeba cells infected by giant viruses allowed identification of a large number of cysteine-rich proteins whose function is unknown(2). These proteins may present unique iron-sulfur coordination patterns, participate in novel metabolic pathways, and may help us elucidate the origins of all viruses. Characterizing new metabolic pathways in these viruses may therefore provide new clues about chemical and biological processes at the origin of life. For this project, interdisciplinary approaches including bioinformatics, cell biology, biochemistry, spectroscopy and biophysics will be used to elucidate the role of these proteins in the physiology of giant viruses. The elucidation of new cellular and metabolic pathways in giant viruses will be of outstanding interest for the fields of virology, evolutionary biology, and biology in general. The discovery of proteins with novel function and chemistry may provide a new source for biotechnology tools, similar to what bacterial restriction enzymes provided for the development of molecular biology as we know it today, or the CrispR/cas system for genetic studies.

1. Claverie, J.-M., and Abergel, C. (2018) Mimiviridae: An Expanding Family of Highly Diverse Large dsDNA Viruses Infecting a Wide Phylogenetic Range of Aquatic Eukaryotes. Viruses. 10, 506
2. Legendre, M., et al. (2010) mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. Genome Res. 20, 664–674

The co-supervisors

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Location

IGS, Luminy Campus, Marseille, France
BIP, 31 chemin Joseph Aiguier Marseille, France

Doctoral school

Life and Health Sciences (ED 62) or Chemical Sciences (ED 250), Aix-Marseille Université

Expected profile of the candidate

The candidate should have an education background in Biochemistry, Structural Biology and/or Chemistry for Biological Sciences, with strong knowledge on protein expression/purification, molecular and structural biology. The PhD student will carry experimental characterization of targeted cysteine-rich proteins including protein cloning, expression, purification, biochemical, structural and biophysical experiments, under the joined supervision of S1 and S2.