#FEMSmicroBlog: Giant viruses between bacteria and eukaryotes - 19-04-2022

Giant viruses belonging to the Megavirinae subfamily have capsids with extending glycans. These hair-like structures play major roles in the infection process since amoeba recognize the “sweet taste” similar to saccharides on bacterial surfaces. The study Giant viruses of the Megavirinae subfamily possess biosynthetic pathways to produce rare bacterial-like sugars in a clade-specific manner in microLife reveals that the saccharide composition of these co-called fibrils is highly variable and depends on the clade the virus belongs to. Anna Notaro, Cristina De Castro and Chantal Abergel explain for the #FEMSmicroBlog how novel virally encoded machineries synthesize these saccharides. #FascinatingMicrobes

Giant viruses and glycans: a paradigm shift

Eukaryotic viruses decorate their capsid proteins with oligosaccharides of 6 to 12 monosaccharide units. For a long time, it was thought that these glycans are produced by the host cell machinery, thus echoing those of the host.

Yet, in the early 2000s, a study on Paramecium bursaria chlorella revealed that viruses can synthesize oligosaccharides with unique structures relying on their own glycosylation machineries. In 2021, Mimivirus was discovered as the prototype of the subfamily Megavirinae in the Mimiviridae family – an amoeba-infecting species. Interestingly, this giant virus decorates its viral capsid with hair-like fibrils made of huge polysaccharides.

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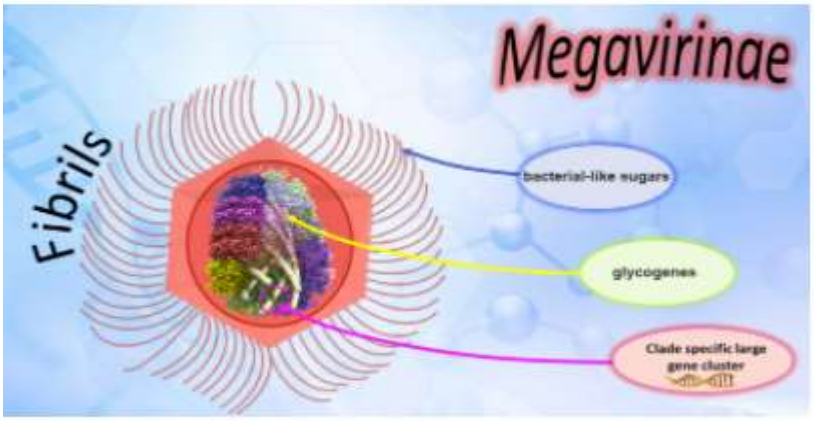
It then became clear that this is a hallmark of the entire subfamily – a highly glycosylated layer of fibrils giving their capsids a hairy appearance. The subfamily is currently composed of five clades and the fibril layer varies in length and thickness depending on the clade they belong to.

The research article “Giant viruses of the Megavirinae subfamily possess biosynthetic pathways to produce rare bacterial-like sugars in a clade-specific manner” in microLife identified the monosaccharide composition of fibrils for different members of the clades and linked them to the responsible viral genes.

Giant viruses make their own bacterial-like sugars

Generally, glycans on the surface of eukaryote-infecting viruses come from the host. However, this is not the case for giant viruses belonging to the Megavirinae subfamily. Within their complex genomes of up to 1.5 Mb encoding up to 1500 proteins, they contain atypical genes never encountered in common viruses. For example, they encode glycosylation machineries producing rare amino sugars only encountered in the bacterial world.



The capsids of giant viruses from the Megavirinae family.

The capsids of giant viruses Megaviriniae.

The study found that viruses in the Megavirinae subfamily possess biosynthetic pathways to produce these unique sugars. First activated as nucleotides, they then function as substrates for further sugar-modifying enzymes known as glycosyltransferases.

Additional enzymes then modify these sugars by adding decorations – small chemical groups such as pyruvic acid or sulfate. Finally, the glycosyltransferases assemble the sugars to make one or more complex glycans.

Interestingly, the genes for the glycan biosynthetic pathways are located within gene clusters. Similar to what is known from bacteria, these clusters contain six to thirty-three genes and are clade-specific.

What is the biological relevance of this high sugar variability?

Results from this study suggest that the gene clusters for glycan biosynthesis evolved through homologous recombination. Yet, each clade contains its own glycosylation machinery indicating clade-specific adaptation.

Interestingly, the study showed that Moumouvirus australiensis is an exception within the Megaviriniae. Its core genes are conserved in the subfamily showing that it clearly belongs to the B-clade. However, its glycan biosynthesis cluster appears to belong to either the D- or E-clades. This supports the idea that M. australiensis was just about to evolve a new glycosylation machinery.

The findings from this study reinforce the hypothesis that giant viruses evolved their own glycosylation machineries. Gene exchanges with other organisms associated with hosts such as aemoba most likely allowed for this genomic flexibility.

Giant viruses evolved their own versatile glycosylation toolboxes to adapt to their hosts.

The capability to diversify their glycan repertoire provides giant viruses with a versatile toolbox and allows them to adapt to the available host. This could give them an ecological advantage by enabling them to outcompete other amoeba-infecting organisms in the environment.

Read the paper “Giant viruses of the Megavirinae subfamily possess biosynthetic pathways to produce rare bacterial-like sugars in a clade-specific manner” by Notaro et al. (2022).

About the authors of this blog

Anna Notaro is a Post-doc in Carbohydrate Chemistry at the University of Naples Federico II. She holds a double PhD in Organic Chemistry and in Structural Biochemistry in the frame of the Italy-France Vinci program. During her PhD, she was awarded the STAR-2017 grant. Her research activity is focused on the study of the glycosylation machinery of giant viruses from different perspectives: glycans structures, identification of glycogenes, structural and functional characterization of glyco-enzymes. She is a member of Interdivisional Group of the Chemistry of Carbohydrates of the Italian Chemical Society.

Cristina De Castro is an Associate Professor of Organic Chemistry, University of Naples Federico II; she has always been working in the field of carbohydrate chemistry and biochemistry. Her research activity focuses on the study of the carbohydrate polymers from microbes (both Gram-positive and Gram-negative), and the glycobiology of giant viruses. Prof. De Castro is (co-)author of about 150 papers and is on the executive committee of the Interdivisional Group of the Chemistry of Carbohydrates of the Italian Chemical Society. She serves as Associate Editor of the Carbohydrate Polymers journal, and she is a member of the Editorial Board of Carbohydrate Research, Glycobiology and Polysaccharides journals.

Chantal Abergel is the Head of the Structural and Genomic Information Laboratory, CNRS-AMU, Marseille (France). Her research activity focuses on the isolation, experimental biology and genomic studies of giant viruses, including members of the Mimiviridae, Pandoraviridae, Pithocedratviridae, and Marseilleviridae families. Her research has been published in more than 110 papers and in about 60 3D structures in the Protein Structure Database, including 3cryoEM structures. She received several awards for her research in the field of giant viruses. She is a member of the Scientific CNRS Council, the European Academy of Microbiology (EAM) and the World Society of Virology.