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Giant Virus

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Abstract

Viruses are the most common infectious agents on Earth, found in virtually every environment. Most viruses possess only a small number of genes necessary for replication and capsid formation. In contrast, giant viruses-first discovered in the early 21st century-have genomes exceeding 1 Mbp and can encode up to 1,000 proteins. Since the initial discovery of Acanthamoeba polyphaga mimivirus, numerous strains belonging to different viral families have been identified. The complexity of giant viral proteomes includes features typically associated with cellular organisms. These include components of the translational machinery, DNA repair enzymes, and metabolic functions. Such discoveries have challenged traditional definitions of viruses and opened new avenues in evolutionary biology, microbiology, and virology.

Keywords: Giant virus; Nucleocytoplasmic large DNA viruses (NCLDV); Mimiviridae; Marseilleviridae; Pandoraviridae

Introduction to Giant Viruses and its discovery:

Giant viruses are also known as Girus, are double standard DNA viruses. The name giant virus is given to these viruses because of their extremely large genome size compared to other traditional viruses. These viruses encode hundreds of genes encoding proteins and can be visualized under light microscope unlike other viruses. They are classified under Nucleocytoplasmic Large DNA Viruses (NCLDV) [1]. Acanthamoeba polyphaga mimivirus (APMV), the first gigantic virus, was identified in 2003 [2]. Its size, which was comparable to microscopic bacteria or archaea, was

unprecedented. APMV was visible under a light microscope, unlike any other virus that had previously been discovered [3]. Only ten years after its isolation was it identified as a virus after first being thought to be a bacterium [4]. Numerous other large viral species have been discovered following the initial discovery of APMV [5] (Figure 1). Although there are now many more representatives of giant viruses, the proportion of uncharacterized proteins in their proteomes is still remarkably high. Many of these uncharacterized proteins were also categorised as orphan genes (ORFans), meaning that no substantial sequence match was found.



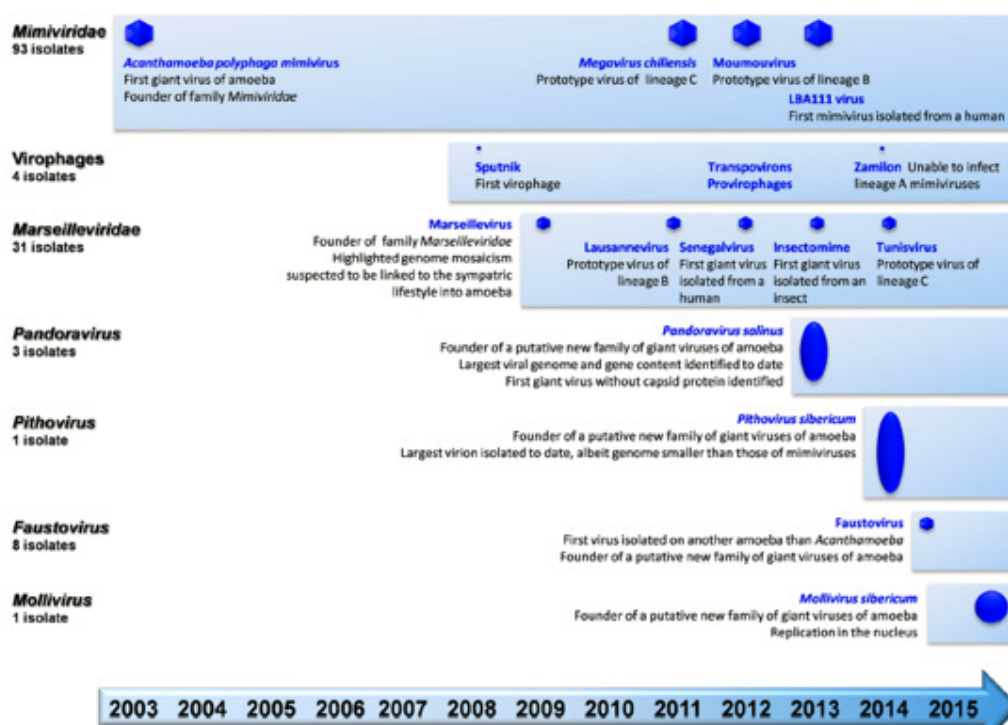


Figure 1: Discovery of major representatives of giant viruses [6].

Giant virus vs traditional viruses:

Size: Since a long time ago, viruses have only been strictly understood as microscopic infectious particles that can pass through 0.2 mm-pore filters and cannot be seen under a light microscope. In contrast, Megavirales virions (giant virus) range in size from 0.2 to 1.5 μm. As a result, for a very long time, Mimivirus and Pandoravirus virions were regarded as Gram-positive bacteria and parasitic endosymbionts, respectively. They also have giant genome structure.

Complexity: In terms of their nucleic acid and protein composition, giant viruses are more complex than “conventional” viruses. As a result, unlike the majority of other viruses, Megaviruses include both DNA and RNA, including messenger RNAs and transfer RNAs. Additionally, proteomics found dozens or perhaps hundreds of proteins inside giant virions, many of which are hypothetical proteins and some of which are involved in transcription and translation. These messenger RNAs and proteins could speed up the first stages of the replicative cycle, reducing the dependence of giant viruses on their hosts for replication compared to other viruses [6].

Translation components: A peptide chain release factor, a GTP-binding elongation factor, translation initiation factors, and four aminoacyl-tRNA synthetases, some of which were proved to be functional and expressed, were discovered as a result of the discovery of Mimivirus [7]. Only one gene for a translation elongation factor

had previously been discovered in Phycodnaviruses. Six transfer RNAs were also discovered. Then, genes for translational proteins and tRNA were found. This is a highly characteristic trait of these viruses [8].

Mobilome: Genetic components that can travel both within and between genomes are referred to as the mobilome. While they are uncommon in traditional viruses, group I and II introns were frequently found in the conserved genes of giant viruses [2]. Additionally, transpovirons, a new type of transposable elements, were found in Mimiviruses; they are related to virus-associated plasmids seen in bacteria and archaea and depend on these large viruses for reproduction and spread. DNA transposable elements were also found in the genome of some giant viruses eg: P. salinus [9].

Broad host spectrum: Giant virus such as Megaviruses infect a wide variety of cellular hosts, including invertebrates, mammals, amoebozoa, green algae and chromalveolates, which are phylogenetically very distant from them. This is in contrast to viruses from other orders or families [10]. Various protists, insects, and mammals, including humans, have been found to harbour Mimiviruses and Marseilleviruses. It has also been demonstrated that Mimivirus enters macrophages through a mechanism similar to phagocytosis, operating like bacteria. Giant viruses that infect amoebas also enter their host through phagocytosis [2,11]. This differs with “conventional” virus entry processes, which require particular interactions with cell receptors [12].

Classification:

• Superfamily: Nucleocytoplasmic large DNA viruses (NCLDV).

- Family: Mimiviridae
- Family: Marseilleviridae
- Family: Pandoraviridae
- Genus: Pithovirus, Mollivirus and Faustovirus

Family- Mimiviridae: *Acanthamoeba polyphaga mimivirus* (APMV) is the first representative of this family with a capsid size of ~400nm capsid size. They have fibrils that are ~120–140 nm long 1.4 nm thick and genome length of 1.2 Mb containing 979 genes encoding proteins. They have aminoacyl tRNA synthetases and their genome encodes four different tRNAs and >75% ORFan genes. They were identified as viral particles by electron microscopy, then named Mimivirus for “Mimicking microbes [13].

Family- Marseilleviridae: In 2007, Marseillevirus was isolated in Marseille, France. *Acanthamoeba polyphaga marseillevirus* (APMaV), its first member, was discovered in 2007 after being cultured on amoebae from water taken from a cooling tower in Paris, France. APMaV has a diameter of 250 nm and an icosahedral symmetry. Marseillevirus have dsDNA (350–380 kbp large) encoding 457 genes [14].

Family- Pandoraviridae: The virions are irregular ovoid. It has the largest viral genome size i.e., 2500 kbp with 2556 predicted proteins by its genome. More than 85% of its genome has no detectable sequence similarity to any other sequence in the public databases [15].

Genus- Pithovirus: Pithovirus has circular, dsDNA and are also called as Zombie virus with 1500 nm by 500 nm in size and 610 kbp genome. The name Pithovirus, refers to big storage containers of ancient Greece known as pithoi. From a from a >30,000-year-old dated Siberian permafrost sample, Pithovirus sibericum was isolated [6]. It encodes 467 ORFs and translating to 467 proteins. It is the largest virus in terms of size found yet. Internally, its structure resembles a honeycomb. Recent isolation of Pithovirus massiliensis from sewage.

Genus- Mollivirus: The virion has an original spherical shape, a diameter of 500-600 nm. The ds DNA genome of *M. sibericum* is linear, 651 kb in length. Host encodes 523 proteins & histone homologs and HMG-like chromatin-associated proteins and has 65% are ORFans [6].

Genus- Faustovirus: Faustovirus virions have an icosahedral capsid with a diameter of 200 nm. It was the first giant virus isolated on another free-living amoeba than *Acanthamoeba*. Its genome is a 461 kb long circular dsDNA with 451 proteins predicted. It also has genes encoding a ribosomal protein acetyl transferase, a bacteriophage tail fiber protein and two polyproteins shared with Asfarvirus [16].

Importance of Giant viruses in animals: Giant viruses, though initially discovered in amoebae, are increasingly recognized for their potential significance in animal health and biology. Recent studies have identified giant virus-like sequences in animal-associated microbiomes, suggesting that these viruses may play indirect roles in shaping host-pathogen interactions or influencing immune responses [4, 13]. The presence of genes in giant viruses related to translation, immune modulation, and stress responses further supports the idea that they could impact animal-associated microbial communities or even participate in horizontal gene transfer [10, 11]. While direct infections of animals by giant viruses have not been definitively confirmed, their detection in diverse environments-including aquatic and soil habitats shared with wildlife and livestock-raises concerns about their potential zoonotic relevance [5, 16]. Understanding the ecological and evolutionary roles of giant viruses may therefore offer new insights into viral biodiversity, host adaptation, and the broader dynamics of animal ecosystems.

Conclusion

The discovery of giant viruses has fundamentally reshaped our understanding of viral biology, genome complexity, and the evolutionary relationships between viruses and cellular life. Unlike conventional viruses, giant viruses possess remarkably large genomes, encode components of the translational machinery, and display a level of genetic and structural complexity previously thought to be exclusive to cellular organisms. Their classification within the Nucleocytoplasmic Large DNA Viruses (NCLDV) superfamily underscores their unique position in the viral world. Moreover, their presence in diverse environments and potential interactions with a broad range of hosts-including animals-suggests that they may play a more significant ecological and biomedical role than previously recognized. As research continues, giant viruses will likely remain at the forefront of discussions about the origins of life, the definition of viruses, and the boundaries between living and non-living entities.

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None.

Conflict of interest

No conflict of interest.

References

1. Brandes N, Linial M (2019) Giant viruses-Big surprises. *Viruses* 11: 404.
2. La Scola B, Audic S, Robert C, Jungang L, De Lamballerie X, et al. (2003) A giant virus in amoebae. *Science* 299: 2033.
3. Xiao C, Chipman PR, Battisti AJ, Bowman VD, Renesto P, et al. (2005) Cryo-electron microscopy of the giant Mimivirus. *J Mol Biol* 353: 493-496.
4. Abergel C, Legendre M, Claverie JM (2015) The rapidly expanding universe of giant viruses: Mimivirus, Pandoravirus, Pithovirus and Mollivirus. *FEMS Microbiol Rev* 39: 779-796.
5. Aherfi S, Colson P, La Scola B, Raoult D (2016) Giant viruses of amoebas: An update. *Front Microbiol* 7: 349

6. Legendre M, Lartigue A, Bertaux L, Jeudy S, Bartoli J, et al. (2015) In-depth study of Mollivirus sibericum, a new 30,000-y-old giant virus infecting Acanthamoeba. *Proc Natl Acad Sci USA* 112: E5327-E5335.
7. Raoult D, Audic S, Robert C, Abergel C, Renesto P, et al. (2004) The 1.2-megabase genome sequence of Mimivirus. *Science* 306: 1344-1350.
8. Claverie JM, Abergel C (2010) Mimivirus: the emerging paradox of quasi-autonomous viruses. *Trends Genet* 26: 431-437.
9. Desnues C, La Scola B, Yutin N, Fournous G, Robert C, et al. (2012) Provirophages and transpovirons as the diverse mobilome of giant viruses. *Proc Natl Acad Sci USA* 109: 18078-18083.
10. Koonin EV, Yutin N (2010) Origin and evolution of eukaryotic large nucleo-cytoplasmic DNA viruses. *Intervirology* 53: 284-292.
11. Philippe N, Legendre M, Doutre G, Coute Y, Poirot O, et al. (2013) Pandoraviruses: amoeba viruses with genomes up to 2.5 Mb reaching that of parasitic eukaryotes. *Science* 341: 281-286.
12. Ghigo E, Kartenbeck J, Lien P, Pelkmans L, Capo C, et al. (2008) Ameobal pathogen Mimivirus infects macrophages through phagocytosis. *PLoS Pathog* 4: e1000087.
13. Sharma V, Colson P, Pontarotti P, Raoult D (2016) Mimivirus inaugurated in the 21st century the beginning of a reclassification of viruses. *Curr Opin Microbiol* 31: 16-24.
14. Colson P, Pagnier I, Yoosuf N, Fournous G, La Scola B (2013) Marseilleviridae, a new family of giant viruses infecting amoebae. *Arch Virol* 158: 915-920.
15. Legendre M, Fabre E, Poirot O, Jeudy S, Lartigue A, et al. (2018) Diversity and evolution of the emerging Pandoraviridae family. *Nat Commun* 9: 2285.
16. Reteno DG, Benamar S, Khalil JB, Andreani J, Armstrong N, et al. (2015) Faustovirus, an Asfarvirus-related new lineage of giant viruses infecting amoebae. *J Virol* 89: 6585-6594.