Template for Taxonomic Proposal to the ICTV Executive Committee

To create a new Family

Code† 2005.004F.04 To create a new family* °

Code† 2005.005F.04 To name the new family* Mimiviridae

Code† To accommodate the new genus created:

Mimivirus

† Assigned by ICTV officers
° Leave blank is not appropriate
* repeat these lines and the corresponding arguments for each genus created in the family

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Old Taxonomic Order

Order
Family
Genus Mimivirus
Type Species Acanthamoeba polyphaga mimivirus
Species in the Genus Acanthamoeba polyphaga mimivirus
Tentative Species in the Genus
Unassigned Species in the family

New Taxonomic Order

Order
Family Mimiviridae
Genus Mimivirus
Type Species Acanthamoeba polyphaga mimivirus
Species in the Genus Acanthamoeba polyphaga mimivirus
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Unassigned Species in the family

ICTV-EC comments and response of the SG
Argumentation to create a new family:

Acanthamoeba polyphaga mimivirus (AY653733) is an emerging virus characterized in 2002-2004. It is a nucleocytoplasmic large DNA virus (NCLDV) (virions are 600 nm in diameter) the complete genome of which has been sequenced (Raoult et al., 2005, Science 306(5700):1344-50). The genome size is 1.2 Mb and contains 1261 ORFs (greater than 300 nt), including 911 very likely protein coding genes. The virus exhibits many original features such as numerous translation apparatus-related genes (e.g. 4 aminoacyl-tRNA synthetases, 4 translation factors, enzymes for all DNA repair mechanism, and 3 types of topoisomerase 1a, 1b, and 2). Phylogenetic trees derived from a concatenation of the sequences of 7 NCLDV conserved gene sequences indicate that it occupies an intermediate position between Iridoviridae, and Phycodnaviridae.

Origin of the proposed family name

Mimiviridae, mimi-for “microbe mimicking” because of its particle size that makes it visible under the light microscope, resembling to a small Gram-positive coccus on Gram staining (mimicking microbe).

References


Annexes:
A Giant Virus in Amoebae

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During a study following a pneumonia outbreak in 1992, a microorganism growing in amoebae and resembling a small Gram-positive coccus (Fig. 1A) was isolated from the water of a cooling tower in Bradford, England. Despite attempts with various extraction protocols and low-stringency PCR amplification, no amplification product was obtained with universal 16S rDNA bacterial primers (1).

Study of this microorganism within Acan-thamoeba polyphaga (2) revealed a characteristic viral morphology with mature particles of 400 nm in diameter and surrounded by an icosahedral capsid. This structure is consistent with the finding that Mimivirus is not filterable through 0.2-μm pore size filters. No envelope was observed, but 80-nm fibrils attached to the capsid were visible (Fig. S1). A typical virus development cycle, including an eclipse phase, was observed (Fig. S2). As it resembles a bacterium on Gram staining, it was named Mimivirus (for Mimicking microbe) (Fig. 1A). DNA digestion by Sal I and Sac II treatment of purified particles (2), followed by pulsed-field gel electrophoresis, demonstrated that Mimivirus has a double-stranded DNA circular genome of about 800 kilobase pairs (kbp). Its genome is thus larger than the sequenced genomes of several bacteria, including Mycoplasma genitalium (580 kbp), Pyrococcus woesei (752 kbp), Buchnera sp. (641 kbp), and Wolbachia wespaeaei (698 kbp) (3). Consistent with this large genome, Mimivirus particles have a size comparable to that of small bacteria such as U. urealyticum (Fig. 1B). The viruses with the largest genomes previously described are Phytophthora infestans, infecting Phytophthora infestans (860 kbp) and phage D of Bacillus megaterium (670 kbp) (4, 5).

Mimivirus is a macrocytoplasmic large DNA virus (NCLDV). This group of viruses shares many features with other large viruses, including the enveloped Poroviridae, which infect vertebrates (Chlamydomovirusae) and insects (Lentivirusae). The three others are also icosahedral. Iridoviridae and Phycodnaviridae are aquatic viruses, and Astroviridae infect vertebrates (6).

While genome shotgun sequencing is under way, two libraries (5-kb and 9-kb inserts) obtained by mechanical shearing, cloned in pBlu2.1 with Bst XI adapters were constructed. Plasmid inserts were sequenced from both ends with flanking vector sequences and dye terminator primers. The preliminary assembly using the Phred/Phrap/Consed software (7) of 6X coverage shotgun data confirmed that the Mimivirus genome is about 800 kbp (734 kbp of preliminary sequence data with phrap score ≥ 20 is available in the WGS section of GenBank, accession # AABV01000000). More than 900 open reading frames (ORFs) longer than 100 amino acids were identified, representing ~82.4% of the available genome, a coding fraction comparable to other NCLDV's. Comparisons to DNA and protein sequence databases (GenBank, Swissprot, and TrEMBL) did not reveal any sign of amoebal or other contamination.

Following lyr et al. (8), we compared Mimivirus ORF's with viral proteins only, allowing greater sensitivity in relating it to one of the established families of large eukaryotic DNA viruses (2). We identified 21 Mimivirus proteins with known functional attributes and clear homologies in at least one of these virus families, as follows: nine in Phycodnaviridae, five in Iridoviridae, and one in Bocavirusidae. Some of the genes also exhibited lower similarity to Bocavirusidae or Astroviridae homologs. These results suggest that Mimivirus occupies an interdomain position between Poroviridae, Iridoviridae, and Phycodnaviridae, with which Mimivirus appears to share the Vps54 capsid protein and a glucosamine synthetase unique to the Paramaecium bursaria Chlorella virus. Mimivirus appears as a deep branch in the phylogenetic tree (Fig. IC), suggesting early divergence from other virus families.

Although further characterization is needed, Mimivirus's icosahedral structure and the typical eclipse phase in its life cycle support its viral nature. Furthermore, Mimivirus lacks universal bacterial genes, such as those encoding ribosomal RNA or proteins, as well as other ubiquitous bacterial proteins involved in protein translation. The high fraction (80%), P value < 10^-6) of ORFs without significant similarity to other organisms is also typical of viruses. Finally, the Mimivirus genome has 21 genes encoding homologs to proteins highly conserved in most NCLDV's (8). We propose that Mimivirus is a member of a new family of giant viruses, the Mimiviridae, that represents a divergent taxon within the NCLDV group.

References and Notes
2. Materials and Methods are on Science Online.
3. See: vacciencb.univ-mrs.fr/Genome/Genomalab.g.txt.
7. E. Ewing et al., Genome Res. 8, 175 (1998).
9. Multiple alignment was done with T-COFFEE software (geneev.com/soft.html) and a JTT matrix computed on the EBI server (www.ebi.ac.uk/clustalw) with the default options, except for correcting distances and phylogeny tree. Accession numbers: Mimivirus, AJ262888; Coronavirus, NP 016828; Lyssavirus, NP 007457; Paramyxovirus virus hemorrhagic fever, NP 062496; and African encephalitis virus, NP 062478.
10. We thank T. Buchhammer for providing the isolate now identified as Mimivirus, W. F. Dittos for helpful discussion, and B. Cueni, A. Carlier, and L. Barnani for technical help. Supported by a grant from the Ministère de l’Éducation Nationale et de la Recherche (convention BHOC0013).

Supporting Online Material
www.sciencemag.org/cgi/content/full/299/5612/2039/DC1

Materials and Methods
Figs. S1 and S2

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