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Mimivirus is a circular double-stranded virus that grows within amoebae. The virus was studied within *Acanthamoeba polyphaga* as its host and was revealed through electronic microscopy to possess a characteristic viral morphology with virions of 400 nm surrounded by an icosahedral capsid. This viral size was confirmed by testing the filterability of a suspension of Mimivirus through a 0.2 μ (200 nm) filter which determined it was unable to pass through. Further investigation of the morphology using electron microscopy showed the virus lacked an envelope but had fibrils attached to the capsid. Gram-staining of the virus illustrated its resemblance to a small gram-positive coccus bacterium. Through DNA digestion by Sal I and Sal II treatment of particles and pulsed-field gel electrophoresis, the genome was determined to be 800 kbp, larger than several bacteria. Confirmation of the size of the Mimivirus genome was achieved through whole genome shotgun sequencing. Mimivirus is a nucleocytoplasmic large DNA virus (NCLDV), which contains four other families of viruses, such as *Poxviridae*, *Iridoviridae*, *Phycodnaviridae*, and *Asfarviridae*. 82.4% of the genome was determined to be ORFs of more than 100 amino acids, a comparable ratio to other NCLDV. No sign of amoebal genome contamination was revealed through GenBank analysis. A local protein database of whole genomes from members of NCLDV was established. Mimivirus ORFs were compared with viral proteins and 21 proteins with known functions were identified encoding homologs to proteins conserved in NCLDVs. A phylogenetic position between *Poxviridae*, *Iridoviridae*, and *Phycodnaviridae* is suggested. The icosahedral structure, typical eclipse phase (through confocal microscopy), and lack of bacterial genes supports its viral nature. This work suggests Mimivirus as a new family of giant virus, *Mimiviridae*, that represents a divergent taxon within NCLDV. Further studies may reveal more viruses sharing the *Mimiviridae* classification in the future.