

Coccolithovirus

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Virion

Morphology	Icosahedral
Envelope	Yes
Diameter (nm)	170-190
Structural Components	Core, capsid, envelope
Buoyant Density (g/ml)	1.2
Buoyant Density Method	CsCl
Lipid Composition	Envelope lipids appear to be derived directly from the membrane of the host cell.
Additional Information	Virion is composed of at least 25 proteins, 23 of which are predicted to membrane proteins. Besides the major capsid protein, putative function can be assigned to four other components: two lectin proteins, a thioredoxin and a S/T protein kinase.

Genome

Nucleic Acid	DNA
Strandedness	Double-stranded
Polarity	Ambisense
Configuration	Circular
Segments	1
Size (kb)	410
G+C Content (%)	40.2
mRNA Transcripts	>255

Additional Information

Microarray analysis has shown a biphasic transcriptional profile.

Replication

Entry Mechanism	Unknown
Site of Transcription	Cytoplasm and possibly nucleus
Transcriptase	Viral encoded RNA polymerase (holozyme composed of 6 subunits)
Site of Genome Replication	Cytoplasm
Replicase	Virus-encoded DNA-dependent DNA polymerase
Replication Intermediate	Unknown
Site of Virion Assembly	Cytoplasm
Egress Mechanism	Budding at membrane
Additional Information	Most probable hypothesis is that early transcription occurs in the nucleus using the host's RNA polymerase, followed by cytoplasmic transcription using the virus own RNA polymerase.

History

Year	Event	Reference
1974	First observation of virus-like particles in dead and moribund <i>E. huxleyi</i> cells.	Manton J, Leadbeater BSC (1974) Det Kongelige Danske Videnskabernes Selskab Biologiske Skrifter 20:1-26
2002	First isolation and characterization of an <i>E. huxleyi</i> virus (EhV).	Castberg T, Larsen A, Sandaa R, Heldal M, Van Etten J, Bratbak G (2002) J Phycology 38:767-774
2002	First characterisation of a large scale number of strains of the virus that infects <i>Emiliana huxleyi</i> .	DC Schroeder, J Oke, G Malin, WH Wilson (2002) Arch Virol 147:1685-1698
2005	Complete genome sequence and lytic phase transcription profile of EhV-86.	Wilson WH et al (2005) Science 309:1090-1092
2006	Distinctive biphasic transcriptional profile identified.	Allen et al (2006) J Virol (2006) 80(15):7699-705
2007	EhV strain wide genomic diversity using DNA sequence, host-range, and microarray data.	Allen MJ et al (2007) Environ Microbiol 9(4):971-982

2008 EhV virion profiled for protein content

[Allen et al \(2008\) Proteome Sci 17:6-11](#)

2009 Description of the entry and exit stages of a coccolithovirus

[Mackinder LCM, Worthy CA, Biggi G, Hall M, Ryan KP, Varsani A, Harper G, Wilson WH, Brownlee C, Schroeder DC \(2009\) J Gen Virol 90:2306-23](#)

Genus Members

Species (Abbreviation) - Synonyms (Abbreviation)	ICTV Status	Host Range
Emiliana huxleyi virus 86 (EhV-86)	type species	
Emiliana huxleyi virus 163 (EhV163)	tentative	
Emiliana huxleyi virus 201 (EhV201)	tentative	
Emiliana huxleyi virus 202 (EhV202)	tentative	
Emiliana huxleyi virus 203 (EhV203)	tentative	
Emiliana huxleyi virus 205 (EhV205)	tentative	
Emiliana huxleyi virus 207 (EhV207)	tentative	
Emiliana huxleyi virus 208 (EhV208)	tentative	
Emiliana huxleyi virus 2KB1 (EhV-2KB1)	tentative	
Emiliana huxleyi virus 2KB2 (EhV-2KB2)	tentative	
Emiliana huxleyi virus 84 (EhV84)	tentative	
Emiliana huxleyi virus 88 (EhV88)	tentative	
Emiliana huxleyi virus 99B1 (EhV-99B1)	tentative	

Nucleotide Sequences

Genomic Region	Virus Species / Strain	Nucleotides	Accession Number	Reference
Complete genome	EhV, 86	407,339	AJ890364	Wilson WH et al (2005) Science 309:1090-1092
Incomplete genome	EhV, 163		DQ127552:DQ12781	Allen et al (2006) Genome comparison of two Coccolithoviruses. Virol J 3:15

Proteins

Protein Name	Abbreviation	Amino Acids	Molecular Weight (kDa)	Time of Expression	Accession Number	Additional Information
ATP-dependent protease	ehv133	738	26.6	2 h post-	VD 002886	

ATP-dependent protease proteolytic subunit	ehv133	238	20.0	2 h post-infection	YP_293880
Deoxycytidylate deaminase	ehv023	173	19.5	4 h post-infection	YP_293777
Deoxyuridine 5'-triphosphate nucleotidohydrolase	ehv397	148	15.9	2 h post-infection	YP_294155
Dihydrofolate reductase/thymidylate synthase	ehv113	480	54.4	2 h post-infection	YP_293867
DNA binding protein	ehv184	438	49.7	2 h post-infection	YP_293937
Dna J domain-containing protein	ehv393	336	39.3	4 h post-infection	YP_294151
DNA ligase	ehv158	622	69.0	2 h post-infection	YP_293911
DNA polymerase delta catalytic subunit	ehv030	1012	114.8	2 h post-infection	YP_293784
DNA topoisomerase	ehv444	1,103	123.7	Unknown	YP_294202
DNA-binding protein	ehv072	293	34.0	Unknown	YP_293826
DNA-dependent RNA polymerase II largest subunit	ehv064	1,493	162.9	2 h post-infection	YP_293818
DNA-directed RNA polymerase II subunit	ehv434	1,156	128.3	2 h post-infection	YP_294182
DNA-directed RNA polymerase subunit	ehv399	229	25.5	2 h post-infection	YP_294157
Endonuclease	ehv230	128	15.2	2 h post-infection	YP_293985
ERV1/ALR family protein	ehv128	169	18.5	Unknown	YP_293881
Esterase	ehv363	263	30.4	Unknown	YP_294121
Fatty acid desaturase	ehv061	320	37.7	2 h post-infection	YP_293815
Helicase	ehv430	902	102.5	4 h post-infection	YP_294188
HNH endonuclease family protein	ehv093	126	15.1	Unknown	YP_293847
Hydrolase	ehv101	268	30.5	4 h post-infection	YP_293853
Hypothetical protein	ehv141	420	45.9	2 h post-infection	YP_293894
Lectin protein	ehv346	254	19.1	2 h post-	YP_294104

				infection	
Lipase	ehv028	263	29.6	2 h post-infection	YP_293782
Lipid Phosphate phosphatase	ehv079	243	26.7	2 h post-infection	YP_293833
Longevity-assurance (LAG1) family protein	ehv014	288	33.0	2 h post-infection	YP_293768
Major capsid protein	ehv085	533	55.1	4 h post-infection	YP_293839
Major facilitator superfamily protein	ehv179	541	58.7	2 h post-infection	YP_293932
MRNA capping enzyme	ehv453	375	43.1	2 h post-infection	YP_294211
Nucleic acid binding protein	ehv136	202	22.4	2 h post-infection	YP_293889
Nucleic acid independent nucleoside triphosphatase	ehv459	699	78.4	2 h post-infection	YP_294217
OTU-like cysteine protease	ehv109	175	19.7	unknown	YP_293863
Phosphate permease	ehv117	534	57.1	Unknown	YP_293871
Phosphoglycerate mutase family protein	ehv022	429	48.8	2 h post-infection	YP_293776
Proliferating cell nuclear antigen protein	ehv440	288	32.3	2 h post-infection	YP_294198
Protease	ehv349	234	26.7	1 h post-infection	YP_294107
Protein kinase	ehv451	271	30.8	2 h post-infection	YP_294209
Putative fatty acid desaturase	ehv415	258	30.1	Unknown	YP_294173
Putative helicase	ehv104	527	60.1	2 h post-infection	YP_293858
Putative proliferating cell nuclear antigen	ehv020	259	29.0	2 h post-infection	YP_293774
Putative thioredoxin protein	ehv465	196	22.1	2 h post-infection	YP_294223
Ribonuclease	ehv401	209	23.2	2 h post-infection	YP_294159
Ribonucleoside-diphosphate reductase protein	ehv428	746	84.3	2 h post-infection	YP_294186

Ribonucleoside-diphosphate reductase small chain	ehv026	325	37.7	2 h post-infection	YP_293778
RING finger protein	ehv166	242	27.7	Unknown	YP_293919
Serine palmitoyltransferase	ehv050	870	96.2	2 h post-infection	YP_293804
Serine protease	ehv447	301	31.9	2 h post-infection	YP_294205
Sialidase	ehv455	373	41.9	4 h post-infection	YP_294213
Sterol desaturase	ehv031	328	37.9	2 h post-infection	YP_293785
Thioredoxin	ehv358	158	17.1	Unknown	YP_294116
Thymidylate kinase	ehv431	327	38.7	2 h post-infection	YP_294189
Transcription factor S-II (TFIIS) family protein	ehv105	164	17.2	2 h post-infection	YP_293859
Transmembrane fatty acid elongation protein	ehv077	322	33.3	2 h post-infection	YP_293831
Vesicle-associated membrane protein	ehv103	117	13.2	2 h post-infection	YP_293856

Key Literature

- [Allen MJ, Forster T, Schroeder DC, Hall M, Roy D, Ghazal P, Wilson WH \(2006\) Locus-specific gene expression pattern suggests a unique propagation strategy for a giant algal virus. J Virol 80:7699-7705](#)
- [Allen MJ, Howard JA, Lilley KS, Wilson WH \(2008\) Proteomic analysis of the EhV-86 virion. Proteome Sci 6:11](#)
- [Bidle KD, Haramaty L, Ramos JBE, Falkowski P \(2007\) Viral activation and recruitment of metacaspases in the unicellular coccolithophore, *Emiliana huxleyi*. Proc Natl Acad Sci USA 104:6049-6054](#)
- [Frada M, Probert I, Allen MJ, Wilson WH, de Vargas C \(2008\) The “Cheshire Cat” escape strategy of the coccolithophore *Emiliana huxleyi* in response to viral infection. Proc Natl Acad Sci USA 105:15944-15949](#)
- [Mackinder LCM, Worthy CA, Biggi G et al \(2009\) A unicellular algal virus, *Emiliana huxleyi* virus 86, exploits an animal-like infection strategy. J Gen Virol 90:2306-2316](#)
- [Monier A, Pagarete A, de Vargas C, Allen MJ, Read B, Claverie JM, Ogata H \(2009\) Horizontal gene transfer of an entire metabolic pathway between a eukaryotic alga and its DNA virus. Genome Res 19\(8\):1441-1449](#)
- [Pagarete A, Allen MJ, Wilson WH, Kimmance SA, de Vargas C \(2009\) Host-virus shift of the sphingolipid pathway along an *Emiliana huxleyi* bloom: survival of the fattest. Environ Microbiol 11\(11\):2840-2848](#)
- [Schroeder DC, Oke J, Malin G, Wilson WH \(2002\) Coccolithovirus \(Phycodnaviridae\): characterisation of a new large dsDNA algal virus that infects *Emiliana huxleyi*. Arch Virol 147:1685-1698](#)
- [Wilson WH, Schroeder DC, Allen MJ, Holden MTG, Parkhill J, Barrell BG et al \(2005\) Complete genome sequence and lytic phase transcription profile of a Coccolithovirus. Science 309:1090-1092](#)