

Polydnaviriformidae

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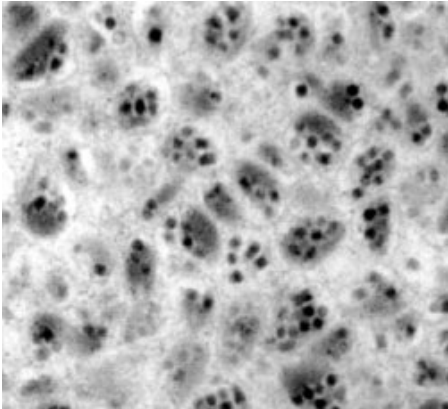
Polydnaviriformidae (/pɒˈlɪdnəvɪrəˌfɔːmidɛ/ **PDV**)^[1] is a family of insect viriforms; members are known as **polydnaviruses**. There are two genera in the family: *Bracoviriform* and *Ichnoviriform*. Polydnaviruses form a mutualitic relationship with parasitoid wasps. Ichnoviriforms (IV) occur in Ichneumonid wasps and Bracoviriforms (BV) in Braconid wasps. The larvae of wasps in both of those groups are themselves parasitic on Lepidoptera (moths and butterflies), and the polydnaviruses are important in circumventing the immune response of their parasitized hosts.^{[2][3]} Little or no sequence homology exists between BV and IV, suggesting that the two genera have been evolving independently for a long time.

Taxonomy [\[edit \]](#)

Bracoviriform

- Bracoviriform altitudinis*
- Bracoviriform argentifrontis*
- Bracoviriform blackburni*
- Bracoviriform canadense*
- Bracoviriform congregatae*
- Bracoviriform crassicornis*
- Bracoviriform croceipedis*
- Bracoviriform curvimaculati*
- Bracoviriform demolitoris*
- Bracoviriform ectdytolophae*
- Bracoviriform facetosae*
- Bracoviriform flavicoxis*
- Bracoviriform flavipedis*
- Bracoviriform flavitestaceae*
- Bracoviriform fumiferanae*
- Bracoviriform glomeratae*
- Bracoviriform hyphantriae*
- Bracoviriform inaniti*
- Bracoviriform indiense*
- Bracoviriform insularis*
- Bracoviriform kariyai*
- Bracoviriform liparidis*
- Bracoviriform marginiventris*

Polydnavirus



Electron micrograph of a bracovirus

Virus classification

Informal group: [Subviral agents](#)

Informal group: [Viriforms](#)

Family: ***Polydnaviriformidae***
Genera

- [Bracoviriform](#)
- [Ichnoviriform](#)

Synonyms

- Polydnaviriformidae* ICTV 2021
- Polydnaviridae* ICTV 1984

- *Bracoviriform melanoscelae*
 - *Bracoviriform nigricipitis*
 - *Bracoviriform ornigis*
 - *Bracoviriform paleacritae*
- *Bracoviriform quadridentatae*
 - *Bracoviriform rubeculae*
 - *Bracoviriform schaeferi*
 - *Bracoviriform texani*

Ichnoviriform

- *Ichnoviriform acronyctae*
 - *Ichnoviriform annulipedis*
 - *Ichnoviriform aprilis*
 - *Ichnoviriform arjunae*
 - *Ichnoviriform benefactoris*
 - *Ichnoviriform eribori*
 - *Ichnoviriform exiguae*
 - *Ichnoviriform flavicinctae*
 - *Ichnoviriform forcipatae*
 - *Ichnoviriform fugitivi*
 - *Ichnoviriform fumiferanae*
- *Ichnoviriform geniculatae*
 - *Ichnoviriform infestae*
 - *Ichnoviriform interrupti*
 - *Ichnoviriform lymantriae*
 - *Ichnoviriform montani*
 - *Ichnoviriform pilosuli*
 - *Ichnoviriform rivalis*
 - *Ichnoviriform rostralis*
 - *Ichnoviriform sonorensis*
 - *Ichnoviriform tenuifemoris*
 - *Ichnoviriform terebrantis*

Structure [\[edit \]](#)

Viruses in *Polydnaviridae* are [enveloped](#), with [prolate ellipsoid](#) and cylindrical geometries. [Genomes](#) are circular and segmented, composed of multiple segments of double-stranded, [superhelical DNA](#) packaged in [capsid proteins](#). They are around 2.0–31kb in length.^{[\[2\]](#)}

Genus	Structure	Symmetry	Capsid	Genomic arrangement	Genomic segmentation
<i>Ichnoviriform</i>	Prolate ellipsoid		Enveloped	Circular	Segmented
<i>Bracoviriform</i>	Prolate ellipsoid		Enveloped	Circular	Segmented

Life cycle [\[edit \]](#)

Viral replication is nuclear. DNA-templated [transcription](#) is the method of transcription. The virus exits the host cell by [nuclear pore export](#).

Parasitoid wasps serve as hosts for the virus, and Lepidoptera serve as hosts for these wasps. The female wasp injects one or more eggs into its host along with a quantity of virus. The virus and wasp are in a [mutualistic symbiotic](#) relationship: expression of viral genes prevents the wasp's host's immune system from killing the wasp's injected egg and causes other physiological alterations that ultimately cause the parasitized host to die. Transmission routes are parental.^{[\[2\]](#)}

Genus	Host details	Tissue tropism	Entry details	Release details	Replication site	Assembly site	Transmission
<i>Ichnoviriform</i>	Parasitoid wasps (Ichneumonidae)	Hemocytes; fat bodies	Unknown	Budding through cell membrane ^{[2][4]}	Nucleus	Nucleus	Unknown
<i>Bracoviriform</i>	Parasitoid wasps (Braconidae)	Hemocytes; fat bodies	Unknown	Lysis ^{[2]}	Nucleus	Nucleus	Unknown

These viruses are part of a unique biological system consisting of an endoparasitic wasp ([parasitoid](#)), a host (usually [lepidopteran](#)) larva, and the virus. The full [genome](#) of the virus is [endogenous](#), dispersed among the genome of the wasp. The virus only replicates in a particular part of the ovary, called the [calyx](#), of pupal and adult female wasps. The virus is injected along with the wasp egg into the body cavity of a lepidopteran host caterpillar and infects cells of the caterpillar. The infection does not lead to replication of new viruses; rather, it affects the caterpillar's [immune system](#), as the virion carries virulence genes instead of viral replication genes.^[5] It can be considered a type of [viral vector](#).^[6]

Without the virus infection, [phagocytic hemocytes](#) (blood cells) will encapsulate and kill the wasp egg and larvae, but the immune suppression caused by the virus allows survival of the wasp egg and larvae, leading to hatching and complete development of the immature wasp in the caterpillar. Additionally, genes expressed from the polydnavirus in the parasitised host alter host development and metabolism to be beneficial for the growth and survival of the parasitoid larva.^{[4][7]}

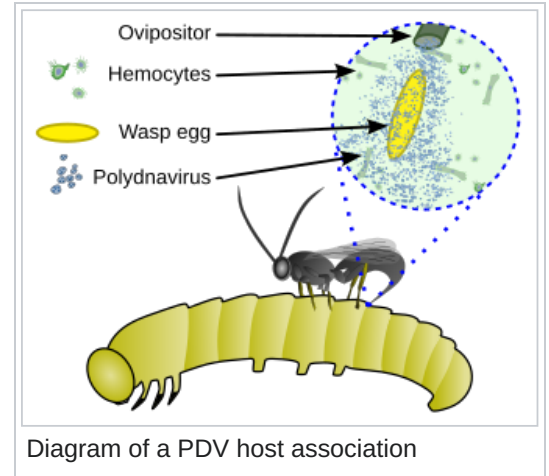
Potential carrier subfamilies [\[edit \]](#)

- [Ichneumonoidea](#)
 - [Braconidae](#)
 - [Microgastrinae](#)^{[4][8]}
 - [Miracinae](#)
 - [Cheloninae](#)^[4]
 - [Cardiochilinae](#)^[4]
 - [Mendeselinae](#)
 - [Khoikhoiinae](#)
 - [Ichneumonidae](#)
 - [Campopleginae](#)^[4]
 - [Banchinae](#)^{[4][6]}

Characteristics [\[edit \]](#)

Both genera of PDV share certain characteristics:

- the virus particles of each contain multiple segments of dsDNA (double-strand, or "normal" DNA, as contrasted with positive- or negative-sense single-strand DNA or RNA, as found in some other viruses) with each segment containing only part of the full genome (much like chromosomes in [eukaryotic organisms](#))
- the genome of the virus has eukaryotic characteristics such as the presence of [introns](#) (common for insect genes but rare for viruses) and a low coding density^[9]
- the genome of each virus is integrated into the host wasp genome^[10]
- the genome is organized in several multiple-member genes families (which differ between Bracoviruses and Ichnoviruses)
- the virus particles are only produced in specific cell types in the female wasp's reproductive organs



The morphologies of the two genera are different when observed by electron microscopy. Ichnoviruses tend to be ovoid while bracoviruses are short rods. The virions of Bracoviruses are released by [cell lysis](#); the virions of Ichnoviruses are released by budding.

Evolution [\[edit \]](#)

Nucleic acid analysis suggests a very long association of the viruses with the wasps (estimated 73.7 million years $\pm$ 10 million).^[11]

Older wasp-derived theory [\[edit \]](#)

Two proposals have been advanced for how the wasp/virus association developed. The first suggests that the virus is derived from wasp genes. Many parasitoids that do not use PDVs inject proteins that provide many of the same functions, that is, a suppression of the immune response to the parasite egg. In this model, the braconid and ichneumonid wasps packaged genes for these functions into the viruses—essentially creating a gene-transfer system that results in the caterpillar producing the immune-suppressing factors. In this scenario, the PDV structural proteins (capsids) were probably "borrowed" from existing viruses.^[12]

Current endogenous virus theory [\[edit \]](#)

See also: *[Endogenous viral element](#)*

The alternative proposal suggests that ancestral wasps developed a beneficial association with an existing virus that eventually led to an [endogenization](#) of the virus into the wasp's genome. Following integration, the genes responsible for virus replication and the capsids were (eventually) no longer included in the PDV genome. This hypothesis is supported by the distinct morphology differences between IV and BV, suggesting different ancestral viruses for the two genera. BV has likely evolved from a [nudivirus](#), specifically a betanudivirus,^[13] ~100 million years ago.^[14] IV has a less clear origin: although earlier reports found a protein p44/p53 with structural similarities to [ascovirus](#), the link was not confirmed in later studies.^[15] As a result, the current opinion is that IV originated from a yet-unidentified novel viral family,^[13] with a weak link to the [NCLDVs](#).^[16] In either case, both genera were formed through a single integration event in their respective wasp lineages.^[5]

The two groups of viruses in the family are not in fact phylogenetically related suggesting that this taxon may need revision.^[17]

Effect on host immunity [\[edit \]](#)

In the host, several mechanisms of the insect immune system can be triggered when the wasp lays its eggs and when the parasitic wasp is developing. When a large body (wasp egg or small particle used experimentally) is introduced into an insect's body, the classic immune reaction is the encapsulation by hematocytes. An encapsulated body can also be melanised in order to asphyxiate it, thanks to another type of hemocyte, which uses the [phenoloxidase](#) pathway to produce melanin. Small particles can be phagocytosed, and macrophage cells can then be also melanised in a nodule. Finally, insects can also respond with production of [antiviral peptides](#).^[18]

PolyDNAvirus protect the hymenopteran larvae from the host immune system, acting at different levels.

- First they can disable or destroy hematocytes. The polyDNAvirus associated with *Cotesia rubecula*, code for a protein CrV1 that denatures actin filaments in hematocytes, so those cells become less able to move and adhere to the larvae.^[18] *Microplitis demolitor* Bracovirus (MdBV) induce apoptosis of hematocytes, thanks to its gene PTP-H2.^[18] It

also decreases the adhesion capacity of hematocytes, thanks to its gene Glc1.8. The gene also inhibits phagocytosis.^[19]

- PolyDNAvirus can also act on melanisation, MdBV interferes with the production of [phenoloxidase](#).^[20]
- Finally, polyDNAvirus can also produce viral [ankyrins](#), that interfere with production of antiviral peptides.^[21] In some Ichnoviruses, Vankyrin can also prevent apoptosis, the extreme reaction of a cell to block viral propagation.^{[22][23]}
- The Ichnoviruses produce some proteins called vinnexins which have been recognized as homologous to the [innexins](#) of insects. They are responsible for the encoding of the structural units of the gap-junctions. These proteins may alter the intercellular communication which could explain the disruption of the [encapsidation](#) process.^[24]

Virus-like particles [\[edit \]](#)

Another strategy used by parasitoid [Hymenoptera](#) to protect their offspring is production of [virus-like particles](#). VLPs are similar to viruses in their structure, but they don't carry any nucleic acid. For example, *Venturia canescens* ([Ichneumonidea](#)) and *Leptopilina* sp. ([Figitidae](#)) produce VLPs.

VLPs can be compared to PolyDNAvirus because they are secreted in the same way, and they both act to protect the larvae against the host's immune system. *V. canescens*-VLPs (VcVLP1, VcVLP2, VcNEP ...) are produced in the calyx cells before they go to the oviducts. Work in 2006 did not find their link to any viruses and assumed a cellular origin.^[12] More recent comparison links them to highly reshuffled domesticated [Nudivirus](#) sequences. This link produces the name *Venturia canescens endogenous nudivirus* (VcENV), an alphanudivirus closely related to NIENV found in *Nilaparvata lugens*.^[25]

VLPs protect the Hymenoptera larvae locally, whereas polyDNAvirus can have a more global effect. VLPs allow the larvae to escape the immune system: the larva is not recognised as harmful by its host, or the immune cells can't interact with it thanks to the VLPs.^[12] *Venturia canescens* uses these instead of polydnaviruses because its ichnovirus has been deactivated.^[25]

The wasp *Leptopilina heterotoma* secrete VLPs that are able to penetrate into the [lamellocytes](#), thanks to specific receptors, and then modify the shape and surface properties of the lamellocytes so they become inefficient and the larvae are safe from encapsulation.^[26] The *Leptopilina* VLPs or mixed-strategy extracellular vesicles (MSEVs) contain some secretion systems. Their evolutionary picture is less clear,^[27] but a recently reported virus, *L. boulardi* Filamentous Virus (LbFV), shows significant similarities.^[28]

Micro-RNA [\[edit \]](#)

MicroRNA are small RNA fragments produced in the host cells thanks to a specific enzymatic mechanism. They promote viral RNA destruction. MicroRNA attach to viral-RNA because they are complementary. Then the complex is recognised by an enzyme that destroys it. This phenomenon is known as [PTGS](#) (for post transcriptional gene silencing)^[29] or RNAi ([RNA interference](#).)

It is interesting to consider the microRNA phenomenon in the polyDNAvirus context. Many hypotheses can be formulated:

- Braconidae carry [nudivirus](#)-related genes in their genome,^[30] so they may be able to produce microRNA against nudivirus, as an innate immunity.
- Wasps perhaps use microRNA to control the viral genes they carry.
- PolyDNAvirus can also use PTGS to interfere with the host's gene expression.
- PTGS is also used for organisms' development, using the same enzymes as antiviral gene silencing, so we can imagine that if the host uses PTGS against polyDNAvirus, perhaps it also affects its development.

- [Mutualism](#)

References [\[edit\]](#)

- ↑ "[Taxon Details: Polydnvirifformidae](#)" . *ictv.global*. "Proposal: 2021.006D.R.Polydnvirifformidae_1renfam_3rensp"
- ↑ ***a b c d e*** "Viral Zone" . ExpASy. Retrieved 15 June 2015.
- ↑ "[Virus Taxonomy: 2020 Release](#)" . International Committee on Taxonomy of Viruses (ICTV). March 2021. Retrieved 24 May 2021.
- ↑ ***a b c d e f g*** Webb, B. A. (1998). *Polydnvirus biology, genome structure, and evolution*. In Miller, L.K., Ball, L.A., Eds. *The Insect Viruses*. Plenum Publishing Corporation. pp. 105–139.
- ↑ ***a b*** Strand, MR; Burke, GR (May 2015). "[Polydnviruses: From discovery to current insights](#)" . *Virology*. 479–480: 393–402. doi:10.1016/j.virol.2015.01.018 . PMC 4424053 . PMID 25670535 .
- ↑ ***a b*** Burke, Gaelen R.; Strand, Michael R. (31 January 2012). "[Polydnviruses of Parasitic Wasps: Domestication of Viruses To Act as Gene Delivery Vectors](#)" . *Insects*. **3** (1): 91–119. doi:10.3390/insects3010091 . PMC 4553618 . PMID 26467950 .
- ↑ Roossinck, M. J. (2011). "[Changes in population dynamics in mutualistic versus pathogenic viruses](#)" . *Viruses*. **3** (1): 12–19. doi:10.3390/v3010012 . PMC 3187592 . PMID 21994724 .
- ↑ Murphy, Nicholas; Banks, Jonathan C.; Whitfield, James B.; Austin, Andrew D. (1 April 2008). "Phylogeny of the parasitic microgastroid subfamilies (Hymenoptera: Braconidae) based on sequence data from seven genes, with an improved time estimate of the origin of the lineage". *Molecular Phylogenetics and Evolution*. **47** (1): 378–395. doi:10.1016/j.ympev.2008.01.022 . PMID 18325792 .
- ↑ Webb, B. A.; Strand, M. R.; Dickey, S. E.; Beck, M. H.; Hilgarth, R. S.; Barney, W. E.; Kadash, K.; Kroemer, J. A.; Lindstrom, K. G.; Rattanadechakul, W.; Shelby, K. S.; Thoetkiattikul, H.; Turnbull, M. W.; Witherell, R. A.; et al. (2006). "[Polydnvirus genomes reflect their dual roles as mutualists and pathogens](#)" . *Virology*. **347** (1): 160–174. doi:10.1016/j.virol.2005.11.010 . PMID 16380146 .
- ↑ Fleming, J.-A. G. W. & Summers, M. D. (1991). "[Polydnvirus DNA is integrated in the DNA of its parasitoid wasp host](#)" . *Proceedings of the National Academy of Sciences*. **88** (21): 9770–9774. Bibcode:1991PNAS...88.9770F . doi:10.1073/pnas.88.21.9770 . PMC 52802 . PMID 1946402 .
- ↑ Whitfield, J. B. (2002). "[Estimating the age of the polydnvirus-braconid wasp symbiosis](#)" . *Proceedings of the National Academy of Sciences*. **99** (11): 7508–7513. Bibcode:2002PNAS...99.7508W . doi:10.1073/pnas.112067199 . PMC 124262 . PMID 12032313 .
- ↑ ***a b c*** Annette Reineke; Sassan Asgari & Otto Schmidt (2006). "Evolutionary Origin of Venturia canescens Virus-Like Particles". *Archives of Insect Biochemistry and Physiology*. **61** (3): 123–133. doi:10.1002/arch.20113 . PMID 16482583 .
- ↑ ***a b*** Drezen, JM; Leobold, M; Bézier, A; Huguet, E; Volkoff, AN; Herniou, EA (August 2017). "Endogenous viruses of parasitic wasps: variations on a common theme". *Current Opinion in Virology*. **25**: 41–48. doi:10.1016/j.coviro.2017.07.002 . PMID 28728099 .
- ↑ Herniou EA, Huguet E, Thézé J, Bézier A, Periquet G, Drezen JM (2013). "[When parasitic wasps hijacked viruses: genomic and functional evolution of polydnviruses](#)" . *Philos Trans R Soc Lond B Biol Sci*. **368** (1626) 20130051. doi:10.1098/rstb.2013.0051 . PMC 3758193 . PMID 23938758 .
- ↑ Volkoff, AN; Jouan, V; Urbach, S; Samain, S; Bergoin, M; Wincker, P; Demettre, E; Cousserans, F; Provost, B; Coulibaly, F; Legeai, F; Béliveau, C; Cusson, M; Gyapay, G; Drezen, JM (27 May 2010). "[Analysis of virion structural components reveals vestiges of the ancestral ichnovirus genome](#)" . *PLOS Pathogens*. **6** (5) e1000923. doi:10.1371/journal.ppat.1000923 . PMC 2877734 . PMID 20523890 .
- ↑ Béliveau, C; Cohen, A; Stewart, D; Periquet, G; Djoumad, A; Kuhn, L; Stoltz, D; Boyle, B; Volkoff, AN; Herniou, EA; Drezen, JM; Cusson, M (September 2015). "[Genomic and Proteomic Analyses Indicate that Banchine and Campoplegine Polydnviruses Have Similar, if Not Identical, Viral Ancestors](#)" . *Journal of Virology*. **89** (17): 8909–8921. doi:10.1128/JVI.01001-15 . PMC 4524098 . PMID 26085165 .
- ↑ Dupuy C, Huguet E, Drezen JM (2006). "Unfolding the evolutionary story of polydnviruses". *Virus Res*. **117** (1): 81–89. doi:10.1016/j.virusres.2006.01.001 . PMID 16460826 .

18. ^{a b c} JM. Drezen; S. Savary; M. Poirier; G. Periquet (1999). "Polydnaviruses, viral entities domesticated by the parasitoid wasps". *Virologie*. **3** (1): 11–21.
 19. [^] Markus Beck & Michael R. Strand (February 2005). "Glc1.8 from *Microplitis demolitor* Bracovirus Induces a Loss of Adhesion and Phagocytosis in Insect High Five and S2 Cells" . *Journal of Virology*. **79** (3): 1861–1870. doi:10.1128/jvi.79.3.1861-1870.2005 . PMC 544146 . PMID 15650210 .
 20. [^] Lu Zhiqiang; Beck Markus H.; Wang Yang; Jiang Haobo; Strand Michael R (August 2008). "The Viral Protein Egf1.0 Is a Dual Activity Inhibitor of Prophenoloxidase-activating Proteinases 1 and 3 from *Manduca sexta*" . *Journal of Biological Chemistry*. **283** (31): 21325–21333. doi:10.1074/jbc.M801593200 . PMC 2490783 . PMID 18519564 .
 21. [^] Bae Sungwoo; Kim Yonggyun (1 September 2009). "Ikb genes encoded in Cotesia plutellae bracovirus suppress an antiviral response and enhance baculovirus pathogenicity against the diamondback moth, *Plutella xylostella*". *Journal of Invertebrate Pathology*. **102** (1): 79–87. doi:10.1016/j.jip.2009.06.007 . ISSN 0022-2011 . PMID 19559708 .
 22. [^] Fath-Goodin A.; Kroemer J. A.; Webb B. A (August 2009). "The Campoletis sonorensis ichnovirus vankyrin protein P-vank-1 inhibits apoptosis in insect Sf9 cells". *Insect Molecular Biology*. **18** (4): 497–506. doi:10.1111/j.1365-2583.2009.00892.x . PMID 19453763 . S2CID 31146050 .
 23. [^] Clavijo G, Dorémus T, Ravallec M, Mannucci MA, Jouan V, Volkoff AN, Darboux I (2011). "Multigenic families in Ichnovirus: A tissue and host specificity study through expression analysis of vankyrins from *Hyposoter didymator* Ichnovirus" . *PLOS ONE*. **6** (11) e27522. Bibcode:2011PLoSO...627522C . doi:10.1371/journal.pone.0027522 . PMC 3210807 . PMID 22087334 .
 24. [^] Marziano N.K.; Hasegawa D.K.; Phelan P.; Turnbull M.W. (October 2011). "Functional Interactions between Polydnavirus and Host Cellular Innexins" . *Journal of Virology*. **85** (19): 10222–10229. doi:10.1128/jvi.00691-11 . PMC 3196458 . PMID 21813607 .
 25. ^{a b} Leobold, Matthieu; Bézier, Annie; Pichon, Apolline; Herniou, Elisabeth A; Volkoff, Anne-Nathalie; Drezen, Jean-Michel; Abergel, Chantal (July 2018). "The Domestication of a Large DNA Virus by the Wasp *Venturia canescens* Involves Targeted Genome Reduction through Pseudogenization" . *Genome Biology and Evolution*. **10** (7): 1745–1764. doi:10.1093/gbe/evy127 . PMC 6054256 . PMID 29931159 .
 26. [^] R. M. Rizki; T. M. Rizki (November 1990). "Parasitoid virus-like particles destroy *Drosophila* cellular immunity" . *Proceedings of the National Academy of Sciences of the United States of America*. **87** (21): 8388–8392. Bibcode:1990PNAS...87.8388R . doi:10.1073/pnas.87.21.8388 . PMC 54961 . PMID 2122461 .
 27. [^] Heavner, ME; Ramroop, J; Gueguen, G; Ramrattan, G; Dolios, G; Scarpati, M; Kwiat, J; Bhattacharya, S; Wang, R; Singh, S; Govind, S (25 September 2017). "Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of *Drosophila*" . *Current Biology*. **27** (18): 2869–2877.e6. doi:10.1016/j.cub.2017.08.019 . PMC 5659752 . PMID 28889977 .
 28. [^] Di Giovanni, D; Lepetit, D; Guinet, B; Bennetot, B; Boulesteix, M; Couté, Y; Bouchez, O; Ravallec, M; Varaldi, J (1 October 2020). "A Behavior-Manipulating Virus Relative as a Source of Adaptive Genes for *Drosophila* Parasitoids" . *Molecular Biology and Evolution*. **37** (10): 2791–2807. bioRxiv 10.1101/342758 . doi:10.1093/molbev/msaa030 . PMID 32080746 .
 29. [^] Li, H.W. & Ding, S.W. (2005). "Antiviral silencing in animals" . *FEBS Lett*. **579** (26): 5965–5973. doi:10.1016/j.febslet.2005.08.034 . PMC 1350842 . PMID 16154568 .
 30. [^] Bézier A, Annaheim M, Herbinière J, Wetterwald C, Gyapay G, Bernard-Samain S, Wincker P, Roditi I, Heller M, Belghazi M, Pfister-Wilhem R, Periquet G, Dupuy C, Huguet E, Volkoff AN, Lanzrein B, Drezen JM (13 February 2009). "Polydnaviruses of braconid wasps derive from an ancestral nudivirus" . *Science*. **323** (5916): 926–930. Bibcode:2009Sci...323..926B . doi:10.1126/science.1166788 . PMID 19213916 . S2CID 6538583 .
- ICTVdB Management (2006). 00.055. Polydnaviridae. In: ICTVdB—The Universal Virus Database, version 4. Büchen-Osmond, C. (Ed), Columbia University, New York, USA
 - Espagne, E.; et al. (2004). "Genome Sequence of a Polydnavirus: Insights into Symbiotic Virus Evolution" . *Science*. **306** (5694): 286–289. Bibcode:2004Sci...306..286E . doi:10.1126/science.1103066 . PMID 15472078 . S2CID 12260572 .

External links ^{[[edit](#)]}

- <http://research.biology.arizona.edu/mosquito/willott/507/polydnaviruses.html>

- **Viralzone:** Polydnaviridae
- **ICTV**

V

T

E

Baltimore (virus classification)

[show]

Taxon identifiers

PolydnaviridaeWikidata: Q1892353 • Wikispecies: Polydnaviriformidae • CoL: 627KB • EoL: 8046 • GBIF (old): 1933 • IRMNG: 106550 • NCBI: 10482 • WoRMS: 600029

Categories: Polydnaviridae | Symbiosis

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