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Glossary

Arp — A cellular complex of up to 7 proteins called the Arp2/3 complex is comprised of two actin related proteins (Arp) that resemble the structure of monomeric actin and 5 additional proteins.

Bacmid — Bacmids are baculovirus genomes that contain a bacterial origin of replication so that they can replicate in bacteria as a plasmid (1). The term is derived from a contraction of baculovirus and plasmid (Luckow, pers. comm.). The original construct contained the AcMNPV genome, a bacterial origin of replication, the target site for the bacterial transposon Tn7, and a selectable kanamycin resistance marker gene, and the lacZ gene all in the polyhedrin locus. This construct allowed for the manipulation and recombination via transposition of the viral genome in bacteria; however, the construct is viable upon transfection into insect cells.

Baculoviridae — A family of occluded viruses pathogenic for insects and possibly other invertebrates. They have large circular, supercoiled, double-stranded DNA genomes and replicate in nuclei.

Basal lamina — This is a fibrous structure that separates the insect midgut epithelium from the hemocele. It is a barrier that baculoviruses might have to cross to cause a systemic infection.

BmN, (BmN 1, 4, 5) — Variants of a cell line derived from *Bombyx mori* that are permissive for infection of BmNPV. The original cell line was isolated by Dr. T. D. Grace. The derivation of the different subclonal lines is ambiguous and is discussed in (2).

Burst Sequence — This is an A/T-rich regulatory sequence between the promoter and translational start site of the very late hyperexpressed genes, polyhedrin and p10. Evidence suggests that it binds VLF-1 (3).

Budded virus (BV) — A type of baculovirus that buds out of infected cells and spreads the infection within an insect and within cell culture. The BVs derive their envelope from modified cell membranes.

Caspase — A category of proteases activated in the apoptotic pathway. There are two types: initiator and effector. Initiator caspases are regulatory and cleave and thereby activate effector caspases. Effector caspases carry out the apoptotic program.

CIDE Domain Protein — Cell death-inducing DFF45-like effector (CIDE) domain is usually present near the N-terminus of a DNAse that is activated by caspase cleavage and is associated with the degradation of DNA during apoptosis and lipid homeostasis (4).

E (expect) value — The E-value is an indication of the statistical significance of a specific pairwise sequence alignment and reflects a combination of the number of sequences in a database and the scoring system employed. The lower the E-value, the more significant the relatedness. An alignment with an E-value of 0.001 indicates that this amount of relatedness has a 1 in 1000 probability of occurring by chance alone. Although E-

values often indicate convincing relatedness, they can be distorted by repeated amino acids and a variety of other factors.

Encapsulation — Encapsulation is a defense response in insects that is directed against objects that are too large to be phagocytose. It involves the accumulation of hemocytes that form a capsule around the object and often is accompanied with melanin deposition.

Enhancin — See Metalloproteinases

Errantivirus — Errantiviruses are insect retroelements that encode an env gene and their name is derived from Latin *errans*, to wander. Although similar to retroviruses, they have not been included within the Retroviridae because they are a distinct lineage, and evidence that they are infectious is indirect (see Chapter 11). Their env gene is related to the baculovirus F protein (4) (5).

ESCRT — Endosomal sorting complexes required for transport (ESCRT) are involved in a diverse set of processes used in budded virus production including endosomal sorting, vesicular trafficking, and virus budding

F protein — This protein is thought to be the fusion protein of most baculoviruses with the exception of Group I, which use gp64 and hymenopteran viruses that do not encode homologs of either gp64 or F. F protein homologs are present, as env proteins in insect retroviruses, also called errantiviruses. Homologs are also present in some insect lineages.

Few Polyhedra (FP) mutants — Few polyhedra (FP) mutants are a readily observable baculovirus phenotype that result in reduced numbers of polyhedra and an elevated titer of budded virus. Such mutants often contain an insert in the *fp* gene (ac61), although the phenotype can result from mutations elsewhere in the genome.

GP64 — The envelope fusion protein used by Group I NPVs. It is related to the envelope fusion protein of a group of arthropod-borne orthomyxoviruses, the thogotoviruses.

Granulosis viruses; granuloviruses (GV) — A lineage of baculoviruses pathogenic for Lepidoptera, which normally have a single virion per ovoid-shaped occlusion body.

Group I — One of two major lineages of lepidopteran NPVs; it is distinguished from other baculoviruses by using a different envelope fusion protein, gp64. Several other genes are also unique to this lineage.

Group II — One of two major lineages of lepidopteran NPVs; members are thought to use a fusion protein (F) to initiate infection

HOAR — A predicted open reading frame described in (6). According to Prof. David Tribe the name is derived as follows: 'H refers to *Heliothis*, O for open reading frame and Hoar sounds like the given second name of the student Hoa (T.H. Le) who determined the sequence.' It is found in many group II Alphabaculoviruses and has sequence similarity to ubiquitin ligase.

Homolog (homologous protein; ortholog, paralog) — Homolog is an inclusive term that indicates that two proteins are evolutionarily related. Homologs are divided into orthologs and paralogs. **Orthologs** (ortho = exact) have homology resulting from speciation and are directly related evolutionarily to one another from a common ancestor via vertical descent, whereas **paralogs** (para = parallel) show relatedness that results from gene duplication. Often, this leads to one copy evolving a different function. Due to the presence of more than one lineage and the possible loss of one duplicate in some lineages, the phylogeny of paralogous proteins may not reflect a direct phylogenetic relationship via a common ancestor.

***Hrs,* homologous repeated sequences** — These are often located at several sites in a baculovirus genome, which have been implicated as origins of DNA replication and transcriptional enhancers.

Hytrosavirus. — Hytrosaviruses are also known as the salivary gland hypertrophy viruses and have been characterized from several of Diptera including the tsetse fly, the vector for sleeping sickness. They are non-occluded and contain large, circular, double stranded DNA genomes within enveloped rod-shaped nucleocapsids. They appear to infect the salivary gland and although not particularly virulent, they can result in a significant reduction in reproductive fitness. They encode several per os infectivity factor proteins related to those of baculoviruses and nudiviruses. The name is derived from the symptoms (hypertrophy of the salivary gland)(7).

Inhibitor of apoptosis (IAP) — The IAP gene family was originally discovered in baculoviruses (8). Subsequently homologs have been found in almost all baculovirus and also entomopox and irridoviruses, and they are also widely distributed in eukaryotes, from yeast to mammals. IAP sequences have a number of distinguishing domains. These include baculovirus IAP repeat (BIR) domains of about 70 amino acids. BIR domains are often present in multiple copies with two copies present in many baculovirus IAPs and up to three copies in some cellular IAPs. A zinc (RING) finger domain is also often present near the C-terminus of the protein. For more information see Chapter 7.

LEF, late expression factor — In AcMNPV, these are factors that are involved in transient DNA replication or late transcription.

Melanization — In insects, melanization involves the synthesis and deposition of melanin at the site of injury. It is regulated by a cascade of serine proteases that cleave and activate prophenoloxidase (to phenoloxidase) that is then able to catalyze the oxidation of phenols (e.g., tyrosine) to quinones (nonaromatic ring compounds), which then polymerize and form melanin (9).

Metalloproteinases — Metalloproteinases are peptidases that contain divalent cations as integral components of their structure (10). Baculoviruses encode a several members of this group of enzymes. They include enhancin, which is thought to enhance infectivity of some viruses by digesting the peritrophic membrane. Enhancin is found in a few lepidopteran NPVs (e.g., Ld-, Cf-, and MacoNPV) and GVs (e.g., Ag-, As-, Tn-, XcGVs). Another group consists of stromelysin1-like metalloproteinases. Orthologs of this family are found in all sequenced GV genomes. The third metalloproteinase is cathepsin, which is found in most lepidopteran group I and II viruses, but is only present in three GVs genomes. It is not present in the genomes of the hymenopteran and dipteran viruses.

Midgut — The site of that baculovirus occlusion bodies are dissolved and infection is initiated. It is where food digestion takes place in lepidopteran larvae.

MNPV/SNPV, Multiple (M) or singly (S) enveloped nucleocapsids — The morphology of nucleocapsids, in which multiple or single nucleocapsids are present within an envelope. MNPVs are found in Group I and II lepidopteran NPVs and are normally not present in GVs, or hymenopteran, or dipteran NPVs. Although characteristic of viral lineages, it does not appear to be a phylogenetic trait.

NSF — See SNARES.

Nimaviridae — See Whispovirus.

Nuclear polyhedrosis virus; nucleopolyhedrovirus (NPV) — The most widely distributed type of baculovirus. NPVs replicate in the nucleus and usually produce polyhedron-shaped occlusion bodies containing more than one virion.

Nudiviruses — A group of viruses pathogenic for invertebrates and related to baculoviruses. They have enveloped, rod-shaped nucleocapsids with large circular DNA genomes and share about 15 core genes with baculoviruses. However, they are not occluded and therefore are not included in the Baculoviridae.

Occlusion-derived virus (ODV) — Viruses that are derived from occlusion bodies. They obtain their envelope within the nucleus. Also called OV.

P35 — P35 is an inhibitor of apoptosis encoded by AcMNPV. Closely related orthologs are only found in a few Group I baculoviruses closely related to AcMNPV. A homolog has also been reported in a GV of *Choristoneura occidentalis* (ChocGV) (11) and a variant (p49) is found in a Group II NPV (SpliNPV) (12). In addition, a p35 ortholog was identified in an entomopox virus. P35 is a substrate for an effector caspase, caspase 1, but in the process of its cleavage it irreversibly binds to and inactivates caspase 1 (13). Subsequently p35 was found to block other categories of caspases in a similar manner - reviewed in (14). For more information see Chapter 7.

Peritrophic matrix (PM) — A tube-like structure that separates food from the midgut epithelium. It is composed of chitin and protein.

per os (per mouth) — This refers to the route of infection of insects by ingestion.

PIB, Polyhedral inclusion bodies — This refers to NPV occlusion bodies.

PIF; per os infectivity factors — Factors that are required for oral infection by ODV. An abbreviation that preceded this refers to yeast 'petite integration frequency' mutants (15).

Polydnaviruses — Polydnaviruses are not true viruses because they do not contain genetic material for their own replication. They are produced in the ovaries of parasitic wasps and the virus-like particles contain genetic material from the wasp and are injected into host lepidopteran larvae along with the wasp eggs. They are named because they contain multiple circular double-stranded DNA molecules (polydispersed DNA) encompassing up to 560 kb that encode gene products that compromise the target host immune system and other processes and are essential for the successful development of the wasp egg. There are two lineages of parasitic wasps that employ these elements; the braconid and ichneumonids and they produce bracovirus and ichnovirus polydnavirus elements, respectively. Evidence indicates that the structural proteins of the virus-like particles of the braconid lineage are related to per os infectivity factors and are derived from an integrated nudivirus-like virus (16).

Ring zone — The ring zone is a less electron dense region near the margins of nuclei and surrounding the virogenic stroma of NPV infected cells. Polyhedra initially form in this zone, but they eventually can fill the whole nucleus.

Sf-9, Sf-21 — Sf-21 is a cell line that was derived from ovarian tissue from *Spodoptera frugiperda* pupae (17). Sf-9 cells are a clonal isolate derived from Sf21 cells. Both cell lines are permissive for AcMNPV infection.

TED — In the process of characterizing AcMNPV FP mutants produced after 25 passages in *Trichoplusia ni* cells, an isolate, (FP-D), was found to contain an integrated retrotransposon that originated from the host genome. It was called transposable element D or TED (18). This element had features of a retrovirus including long terminal repeats and was demonstrated to express gag, pol, and env-like genes that are capable of being incorporated into virus-like particles (19-21).

SNARES and NSF — SNAREs and NSF (soluble N-ethylmaleimide-sensitive factor (NSF) attachment protein receptor) proteins are the minimal machinery involved in the fusion of transport vesicles with membranes and are critical for the initiation of infection by enveloped virions.

Tn-368. — A cell line derived from *Trichoplusia ni* that is permissive for AcMNPV infection. It was derived from ovarian tissue of a virgin adult (22).

Virogenic stroma — This is an electron dense chromatin-like structure in nuclei of baculovirus infected insects. A molecular scaffold that is believed to be produced for the replication of viral genomes and the assembly of nucleocapsids.

WASP — Wiskott-Aldrich syndrome protein (WASP). The Arp complex is involved in nucleating the formation of F-actin filaments. Activators are required for this process and they bind both monomeric G actin and the Arp2/3 complex. One category of such activators is called Wiskott-Aldrich syndrome protein (WASP), and an ortholog of WASP (PP78/83) (AcMNPV orf9) is encoded by all lepidopteran NPV genomes. The Wiskott-Aldrich syndrome is a rare, inherited, X-linked, recessive disease caused by mutations in the WASp gene. It is associated with immune dysregulation.

White spot syndrome virus — See Whispovirus.

Whispovirus — *Whispovirus* is the only genus in the family Nimaviridae and contain a single species, white spot syndrome virus (WSSV) that causes disease in a wide variety of crustaceans. Severe disease outbreaks of the disease are a major problem in cultured penaeid shrimp, particularly in Asia. WSSV is a non-occluded, enveloped, rod-shaped virus with a double stranded DNA genome of about 300 kb. It is highly virulent and causes major tissue damage and the infection results in white spots of calcium deposited in the shell (23). The name *Whispovirus* is from *wh*ite *spo*t syndrome virus. Nimaviridae is from Latin nima "thread", that refers to a flagellum-like structure protruding from the nucleocapid.

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