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Future Perspectives

As present, too little is known about ascoviruses to assess whether they are or will turn out to be of economic importance. Their poor infectivity per os makes it highly unlikely they will ever be developed as viral insecticides, especially given the successful advent of insect-resistant transgenic crops. However, as more entomologists become familiar with the disease caused by ascoviruses, it may be shown that in habitats rarely treated with chemical insecticides, such as transgenic crops, these viruses are responsible for significant levels of natural pest suppression, particularly where parasitic wasps are abundant. Such findings would encourage even greater emphasis on the development of biological control and other more environmentally sound methods of pest control. With respect to the cell biology of viral vesicle formation, ascoviruses provide an interesting model for how apoptosis can be manipulated at the molecular level. Additionally, study of the unusual process by which ascoviruses rescue the developing apoptotic bodies to form viral vesicles could lead to insights into how cells manipulate the cytoskeleton and mitochondria. Finally, it is possible that viral vesicles will provide a unique anucleate cellular system for studying the replication of a complex type of enveloped DNA virus in vitro.

See also: Baculoviruses: Apoptosis Inhibitors; Baculoviruses: General Features; Entomopoxviruses; Phycodnaviruses; Polydnaviruses: General Features.

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maturation step often involves the proteolytic cleavage of a precursor protein.

**Nucleocapsid core (NC)** Capsid protein packages the nucleic acid genome to form a stable protein–nucleic acid complex which is then enveloped with a lipid bilayer.

### Introduction

Viruses have long been distinguished by their physical features, usually visualized by electron microscopy or analyzed biochemically. One feature that has been frequently used to categorize viruses is the presence or absence of a lipid bilayer. Many animal viruses are surrounded by a lipid bilayer that is acquired when the nucleocapsid buds through cell membranes, usually at a late stage of virus assembly. While the protein coat of nonenveloped viruses plays a crucial role in protecting the genome from the environment, enveloped viruses acquire their lipid membrane partially fulfills this role. The lipid membranes are decorated with virus-encoded envelope proteins that are important for the subsequent infectivity of the virus, although some viruses also incorporate cellular proteins in their membrane. Virus envelopment can take place after the assembly of an intact nucleocapsid structure (betaretroviruses) or capsid assembly and envelopment can occur concomitantly (orthomyxovirus). Specific or nonspecific interactions between the viral envelope glycoproteins and the proteins that make up the nucleocapsid mediate the envelopment of the core or nucleoprotein–nucleic acid complex. Enveloped viruses acquire their lipid bilayer from a variety of locations within the cell, but a given virus will usually bud from one specific cellular membrane (Table 1). Enveloped viruses can take advantage of the cellular secretory pathway in order to assemble and bud out of the cell. In contrast, nonenveloped viruses usually exit infected cells by disrupting the plasma membrane. Thus, budding provides enveloped viruses with a nonlytic method of exiting infected cells, and they must do so while the cell is still alive.

### Viral Envelope

The main component of the viral envelope is the host-derived lipid bilayer. The precise composition of this lipid membrane varies, as different viruses acquire their envelopes from different cellular membranes. The choice of membrane from which the virus buds is often determined by the specific targeting and accumulation of the envelope proteins at a particular site in the secretory pathway (Table 1). There are examples of viruses that bud from the plasma membrane (Togaviridae, Rhabdoviridae, Paramyxoviridae, Orthomyxoviridae, and Retroviridae), endoplasmic reticulum (ER) (coronaviruses and flaviviruses) and the Golgi complex (bunyaviruses). There are also examples of viruses that undergo transient envelopment and reenvelopment (herpesvirus).

Viral proteins are found embedded in the lipid membrane. The majority of these proteins are transmembrane glycoproteins. The viral envelope glycoproteins mediate the interaction of the virus with cell receptors and promote the fusion of the viral and cellular membranes during infection of susceptible cells. Viral glycoproteins are also crucial for the assembly of the virion. They can make important lateral contacts with each other, thus driving oligomerization and also capturing other viral components such as the capsid or matrix protein. The majority of enveloped viruses contain one or more glycoproteins that are usually found as oligomers embedded within the lipid membrane. High-resolution structural information is available for many glycoproteins such as the hemagglutinin and neuraminidase proteins of influenza A virus, the gp120 of HIV, and the E protein of dengue virus. Based on these structural and biochemical studies, it has been shown that most glycoproteins are primed for the conformational changes that are required in order to gain entry to the host cell during an infection.

### Table 1

| Virus family | Membrane |
|--------------|----------|
| Arenaviridae  | Plasma membrane |
| Arteriviridae | Endoplasmic reticulum |
| Asfarviridae  | Endoplasmic reticulum and plasma membrane |
| Bunyaviridae  | Plasma membrane |
| Coronaviridae | ER Golgi intermediate compartment |
| Cystoviridae  | Plasma membrane |
| Delthavirus   | Endoplasmic reticulum |
| Filoviridae   | Plasma membrane |
| Flaviviridae  | Endoplasmic reticulum |
| Fuselloviridae| Plasma membrane |
| Hepadnaviridae| Endoplasmic reticulum |
| Herpesviridae | Nuclear envelope |
| Hypoviridae   | Plasma membrane |
| Iridoviridae  | Plasma membrane |
| Lipothrixviridae| Plasma membrane |
| Orthomyxoviridae| Plasma membrane |
| Paramyxoviridae| Plasma membrane |
| Plasmaviridae | Plasma membrane |
| Polydnaviridae| Plasma membrane |
| Poxviridae    | ER Golgi intermediate compartment |
| Retroviridae  | Plasma membrane |
| Rhabdoviridae | Plasma membrane |
| Togaviridae   | Plasma membrane |

**a**Animal viruses unless otherwise noted.  
**b**This group also includes plant viruses.  
**c**Bacteriophage.  
**d**Archaea.
Some enveloped viruses contain integral membrane proteins that have multiple membrane-spanning regions that oligomerize to form channels in the membrane. The influenza A virus M2 protein forms an ion channel and plays an important role in the assembly and entry of the virus particle. Some viruses such as the retroviruses also incorporate cellular membrane proteins into the viral envelope. In a majority of the cases the host proteins that are present at the sites of assembly or budding are incorporated in a passive, nonselective manner. However, there are examples where the virus actively recruits specific host proteins that may help in evading the defenses of the immune system or enhance infectivity.

### Icosahedral Enveloped Viruses: Alphaviruses and Flaviviruses

Alphaviruses, and more recently, flaviviruses have served as model systems to study the assembly and budding of simple enveloped viruses. These positive-strand RNA viruses consist of a single RNA genome that is encapsidated by multiple copies of a capsid protein to form the nucleocapsid core (NC). The envelopment of the NC is mediated by the interaction between the envelope glycoproteins and this core. The assembly and budding of these two simple enveloped viruses will be described in detail in order to present common themes in the assembly of icosahedral enveloped viruses.

### Alphavirus Assembly

#### Alphavirus life cycle

Alphaviruses are members of the family *Togaviridae*, which also includes the genus *Rubivirus*. Alphaviruses enter the host cell by receptor-mediated endocytosis via the clathrin-coated endocytic pathway. Following fusion at low pH with the endosomal membrane, the NC is released into the cytoplasm. The NC has been proposed to uncoat by transfer of capsid proteins (CPs) to ribosomes. This releases the genome RNA into the cytoplasm which is translated to produce the nonstructural proteins. The nonstructural proteins transcribe a negative-sense RNA which is translated to produce the nonstructural proteins. The genomic RNA, codes for the structural proteins of the virus. CP is found at the N-terminus of the structural polyprotein, followed by proteins PE2 (E3+E2), 6K, and E1. Two hundred and forty copies of CP, E2, and E1 assemble to form the alphavirus virion (Figure 1(a)). The transmembrane E1 glycoprotein functions during entry to mediate the fusion of the viral membrane with that of the endosomal membrane, while the transmembrane E2 glycoprotein is responsible for cell receptor binding. E1 and PE2, a precursor of E2 and E3, are processed together as a heterodimer in the ER and Golgi, and are transported to the cell surface in the form of spikes that are each composed of three heterodimers of E1/E2. E3 serves as a chaperone to promote the correct folding of E2, as well as to prevent the premature fusion of E1 in the acidic environment of the late Golgi. The maturation cleavage of PE2 to generate E3 and E2 by a furin-like protease in a late Golgi compartment primes the glycoprotein spike complex for subsequent fusion during virus entry. The function of 6K is unclear but it does promote infectivity of the particle. A single copy of the genome RNA is packaged by 240 copies of the CP to form an icosahedral NC in the cytoplasm of infected cells. The NC interaction with the E1/E2 trimeric spikes at the plasma membrane results in the budding of the mature virus from the cell membrane.

#### Alphavirus virion structure

Cryo-electron microscopy (cryo-EM) and image reconstruction techniques have revolutionized the understanding of the molecular architecture of alphaviruses (Figure 1(a)). Studies with Ross River, Semliki Forest, Venezuelan equine encephalitis, Aura, and Sindbis have shown that these viruses consist of an outer protein layer made up of the glycoproteins E1 and E2 (Figures 1(a) and 1(c)). The membrane spanning regions of these glycoproteins traverse a host-derived lipid bilayer that surrounds the NC of the virus. The CP and glycoprotein layers interact with one another and are arranged symmetrically in a T=4 icosahedral configuration. Fitting of the atomic coordinates of the crystal structures of the ectodomain of E1 and amino acids 106–264 of the CP into the cryo-EM density of Sindbis virus allowed a pseudo-atomic model of the virus to be generated. The fitting of the E1 structure into the cryo-EM density reveals that E1 forms an icosahedral scaffold on the surface of the viral membrane. E1 is positioned almost tangential to the lipid bilayer, whereas E2 has a more radial arrangement. The bulk of E2 lies on top of E1 and caps the fusion peptide, thereby preventing premature fusion with cell membranes. This arrangement of the glycoproteins is in agreement with the function of each protein, where the surface-exposed E2 interacts with cellular receptors and protects E1 until it is required for fusion. The fusion peptide is only exposed when the E1–E2 heterodimer dissociates in the presence of low pH in the endosome. Fitting of amino acids 106–264 of the CP into the cryo-EM density of Sindbis virus showed that each subunit of the projecting pentamers and hexamers (known as capsomeres) observed in the NC layer is made up of the CP protease domain consisting of amino acids 114–264. There is very little interaction between amino acids 114–264 of the CP either within the capsomere or in between capsomeres. Thus, the major contributors to the stability of the NC in the absence of glycoproteins are
CP–RNA and RNA–RNA interactions that take place in the RNA–protein layer below the projecting capsomeres.

**Alphavirus assembly and budding**

Alphavirus virions always contain an NC and it is likely that this promotes and is required for budding through direct interactions with the glycoproteins. Thus, the first step in assembly is for the alphavirus CP to specifically recognize and encapsidate the genome RNA to form NCs in the cytoplasm of infected cells (Figure 2). The N-terminus of the CP (amino acids 1–80, SINV numbering) is largely basic and thought to be involved in charge neutralization of the genome RNA. Amino acids 38–55 are conserved uncharged residues that form a coiled-coil alpha-helix (helix I) important in dimerization of the CP during the assembly process.

While the process of virus assembly is difficult to study in the complex cellular environment, the development of an *in vitro* assembly system based on bacterial expression of CP has led to advances in understanding NC assembly. These studies suggest that the initial event of NC assembly is the binding of CP amino acids 81–112 to the encapsidation signal on the genome RNA corresponding to nucleotides 945–1076 (SINV numbering) (Figure 2). This interaction exposes a second site on the encapsidation signal where another molecule of CP binds and forms a dimer with the first CP molecule. Amino acids 114–264 constitute the previously mentioned chymotrypsin-like serine protease that autoproteolytically cleaves CP from the nascent structural polyprotein. This region is involved in binding residues from the cytoplasmic domain of E2, thus linking the outer icosahedral glycoprotein shell with the NC across the lipid bilayer (Figure 1(a)).

Other lines of evidence support the dimer model of NC assembly. Helix I of CP, which is required for core accumulation in infected cells, may be functionally substituted by a GCN4 helix that forms dimeric coiled-coil interactions but not by a GCN4 helix that has a propensity to form trimeric coiled-coil interactions. In addition, helix I acts as a checkpoint in NC assembly whereby incompatible helices
prevent the formation of core-like particles (CLPs) in vitro. Furthermore, a portion of CPs in either NCs or CLPs may be cross-linked into dimers by DMS, a lysine specific cross-linker with a 12 Å cross-linking distance. Cross-linking enabled an assembly deficient helix mutation of CP to assemble into NCs, suggesting that the cross-link can functionally replace the helix interaction.

While assembly of the CP into NCs proceeds in the cytoplasm, the processing and assembly of the glycoproteins occur in the ER and Golgi (Figures 1(c) and 2). The autocatalytic cleavage of the CP reveals a signal sequence on the N-terminus of the newly cleaved structural polyprotein that directs it to the ER (Figure 1(c)). PE2 is translocated into the ER until it reaches a 26-amino-acid stop transfer signal which anchors PE2 in the membrane. The C-terminal 33 residues of E2 then act as a second signal sequence to direct the next protein, 6K (55 amino acids), into the ER. 6K possesses a stop transfer sequence which anchors it in the membrane, and the C-terminus of 6K acts as signal sequence for the translocation of E1. E1 is anchored in the ER membrane by a final stop transfer sequence close to its C-terminus. The release of PE2 and E1 by cellular signalase cleavage allows the formation of PE2-E1 heterodimers in the ER (Figure 2). PE2 and E1 are each glycosylated in all alphaviruses, but the number and location of the modifications vary. In addition to glycosylation, the glycoproteins are palmitoylated in the Golgi apparatus. As the heterodimers are processed and transported through the ER and Golgi, they undergo a series of folding intermediates that are mediated by disulfide exchange and chaperones. Ultimately, they associate to form spikes which are composed of trimers of PE2-E1 dimers (Figure 2).

The final maturation event is the cleavage of PE2 into E3 and E2 by a furin-like protease (Figure 2). This cleavage occurs in a late Golgi or post-Golgi compartment and results in the destabilization of the heterodimer enabling the mature virus to fuse more readily with the target membrane. In most alphaviruses including Sindbis, E3 is released and not found in the mature virion. The final destination for the spike complexes is the plasma membrane, where the cytoplasmic domain of E2 (cdE2) recruits NCs assembled in the cytoplasm (Figure 2). Structural studies show that cdE2 residues Tyr400

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**Figure 2** Alphavirus assembly. Two capsid proteins (CPs) bind the encapsidation signal of the genome RNA to form a CP dimer-RNA complex in the cytoplasm. The CP dimer is stabilized by coiled–coil helix I interactions. The subsequent steps of nucleocapsid core assembly have not been elucidated but cores form and accumulate in the cytoplasm. The glycoproteins PE2 and E1 form heterodimers in the endoplasmic reticulum (ER). The glycoproteins are folded, glycosylated, and palmitoylated as they are transported through the ER and Golgi. The PE2-E1 heterodimers form spike complexes [PE2-E1]3 in the Golgi. E3 is cleaved from the spikes by a furin-like protease before they are transported to the plasma membrane. The NC interacts with the cytoplasmic domain of E2 in the spike complexes, driving the budding of the mature virus from the plasma membrane.
and Leu402 bind into a hydrophobic pocket of the CP. Mutation of Tyr400 negatively impacted virus budding, while protein translation and core accumulation were at wild-type levels. This interaction of cED2 with the hydrophobic pocket in the CP is thought to drive the budding of the mature virus at the cell membrane.

**Flavivirus Assembly**

**Flavivirus life cycle**

Flaviviruses belong to the family Flaviridae of positive-strand RNA viruses which also consist of the pestiviruses and the hepaciviruses. The flaviviruses comprise more than 70 members including important human pathogens such as yellow fever virus, dengue virus, and West Nile virus. Flaviviruses enter cells via receptor-mediated endocytosis. The low pH environment of the endosomal membrane triggers the conformational change of the envelope glycoprotein which results in the fusion of the viral and endosomal membranes releasing the genome into the cytoplasm. The viral proteins are translated from the RNA genome as a single polyprotein. Signal sequences and stop transfer sequences result in the translocation of the nascent polyprotein to the ER membrane. The polyprotein is processed by a combination of cellular and viral proteases to produce the mature structural and nonstructural proteins. Genome replication and virion assembly occur in ER membrane-bound vesicles. The structural proteins and the genome bud into the lumen of the ER to form the immature virion which is transported through the secretory pathway. Prior to secretion of the virion, a furin cleavage converts the immature virus into the mature, infectious form of the virus.

**Flavivirus virion structure**

The flavivirus virion is made up of three structural proteins: capsid (C), pre-membrane (prM), and envelope (E) that are translated from the 5′ one-third of the RNA genome (Figures 1(b) and 1(d)). Signal sequences at the C-terminus of the C protein and prM serve to translocate prM and E respectively into the ER (Figure 1(d)). The role of the highly basic C protein (12 kDa) is to encapsidate the viral genome during virion assembly. In contrast to the alphavirus CP which exhibits no membrane association, the flavivirus C protein is anchored to the membrane, at least transiently (Figure 1(d)). However, Rubella virus, the sole member of the genus Rubivirus within the family Togaviridae, has a membrane anchored CP, perhaps indicating a common origin for the Togaviridae and Flaviviridae. prM is a glycoprotein that associates with the E protein and serves as a chaperone to facilitate the proper folding of E. The immature virions that bud into the ER consist of prM-E heterodimers. prM prevents premature fusion from occurring in the acidic environment of the ER and Golgi. Thus, prM has several functions analogous to the E3 glycoprotein of the alphaviruses. Cleavage of prM into pr and M by a furin-like protease triggers the rearrangement of the prM-E heterodimers into E–E homodimers, resulting in a radical change in size and shape required for the formation of the mature virus particle. The E glycoprotein is responsible for host cell receptor binding and for fusion of the viral and cellular membranes. The E glycoprotein is also critical for the assembly of the virion. High-resolution structures of the ectodomains of several flavivirus E proteins are available. The ectodomain is divided into three domains. Domain II constitutes the dimerization domain as it contains most of the intradimeric contacts between E–E homodimers. Domain II also contains the fusion peptide, a glycan-rich hydrophobic sequence that initiates fusion by insertion into the target cell membrane. Domain III comprises the immunoglobulin-like domain responsible for receptor binding. In addition to the dramatic conformational and translational changes that the E protein undergoes during the virion maturation process, it also changes conformation during membrane fusion. The low pH of the endosome during infection triggers a conformational change which results in the formation of E homotrimers. In this arrangement, the fusion peptides are exposed and available to insert into cellular membranes. Interestingly, the structure of the E protein was found to be very similar to the structure of the Semliki Forest virus E1 protein, the fusion protein of the alphaviruses.

The structures of two flaviviruses, dengue and West Nile virus, have been solved by cryo-EM and image reconstruction techniques and have been shown to be similar (Figure 1(b)). The mature virion is ∼50 nm in diameter and exhibits a smooth outer surface in contrast to the alphaviruses which have distinctive spike structures (cf. Figures 1(a) and 1(b)). The E proteins are arranged parallel to the surface of the virus, with 90 E dimers arranged in groups of three to form a ‘herringbone’ pattern on the viral surface. This arrangement of the E proteins completely covers the surface of the virus, thus rendering the lipid bilayer inaccessible. Domain III of E protrudes slightly from the viral surface, allowing interaction with cell receptors. The membrane-spanning regions of E and M proteins form antiparallel helices while the stem regions are arranged parallel to the membrane.

The immature virus particle exhibits a dramatically different glycoprotein organization compared to the mature virion. Cryo-EM and image reconstruction of dengue and yellow fever virus immature virions have revealed that these particles are larger (∼60 nm) and have spikes that protrude from the surface of the virus. These spikes are composed of trimers of prM-E heterodimers. The pr peptide covers the fusion peptide of E in this arrangement, similar to E2 covering E1 in alphaviruses, thus protecting it from premature fusion as the immature particle is transported through the acidic environment of the secretory pathway.
The NC is found below the viral envelope and is composed of a single copy of the genome RNA and multiple copies of the C protein. Cryo-EM reconstructions of the virion have shown that in contrast to the alphaviruses, there is no apparent organization to the flavivirus NC. This may be because there is no direct interaction between the C proteins in the core and the glycoproteins in the viral envelope since the E and M proteins do not penetrate below the inner leaflet of the membrane. Furthermore, no NCs have been observed in the cytoplasm of infected cells and attempts to establish an in vitro assembly system analogous to the alphavirus in vitro assembly system have failed. The lack of coordination between the C protein and the viral envelope proteins suggests that the assembly of virions is driven by the lateral interactions of the E and M proteins in the viral envelope and not by the C protein. This is supported by the observation that flavivirus infections result in the production of noninfectious subviral particles which are composed of just the viral envelope (E and M) and the lipid bilayer. Thus, the flavivirus glycoproteins are sufficient to induce particle budding.

**Flavivirus assembly and budding**

Virus-induced membrane structures called vesicle packets, which are continuous with the ER membrane, are the sites of flavivirus replication and assembly (Figure 3). Within these structures the structural proteins are in intimate contact with the genome RNA. The C protein associates with the genome RNA via interactions between the positive charges distributed throughout the protein and the negatively charged phosphate backbone of the RNA. It is not yet clear how the C protein specifically recognizes the genome RNA; unlike for alphaviruses, a packaging signal has not been conclusively identified for flaviviruses. Coupling between genome replication and assembly within the vesicle packets has been proposed as a mechanism to ensure the specific encapsidation of the genome RNA. It has been shown that one or more nonstructural proteins (NS2A and NS3) are involved in genome packaging and NC assembly. The NC lacks a defined icosahedral structure as described above. Therefore, core formation is probably concomitant with the association of the C protein and RNA genome with the viral glycoproteins and budding into the ER lumen, thus giving rise to the immature particle (Figure 3). The immature virion is transported from the ER to the Golgi where the viral glycoproteins are post-translationally modified. The cleavage of the prM protein in the trans-Golgi network triggers the dramatic reorganization of the viral glycoproteins that results in the formation of the mature virion (Figure 3). The mature virion is then released from the host cell by exocytosis.

![Figure 3](image_url)  
*Figure 3  Flavivirus assembly. Flavivirus assembly occurs on ER-associated membranes known as vesicle packets. Assembly and genome replication are coupled and the sites of assembly consist of the capsid proteins (C), the glycoproteins prM and E, the RNA genome, and one or more nonstructural proteins and/or host factors. The immature virion buds into the ER and is transported to the Golgi and trans-Golgi network. The glycoproteins are post-translationally modified as the immature virus is transported through the secretory pathway. Furin cleavage of prM results in the formation of the mature virus which then exits the cell by exocytosis.*
Conclusion

Following from the discussion of alphavirus and flavivirus assembly, it is apparent that the assembly of even the simplest enveloped viruses requires the complex interaction of viral and host factors in order to produce a virus particle which is at once stable and at the same time primed for disassembly. The whole range of the cell’s machinery including the translation apparatus, polymerases, chaperones, and post-translational modification enzymes are co-opted by viruses in order to replicate the viral components necessary for assembly. Enveloped viruses have evolved to utilize different cellular membranes and cellular compartments for assembly and they take advantage of the secretory pathway to produce their viral glycoproteins. A majority of viruses bud from the plasma membrane (Table 1). This is the case with alphaviruses, where NC assembly occurs in the cytoplasm and the final assembly of the mature virion occurs at the plasma membrane. The high concentration of viral proteins, often concentrated at specific sites allows for the efficient interaction and assembly of virions. In contrast to alphaviruses, NC assembly and glycoprotein assembly is coupled in the flaviviruses and occurs in vesicle packets associated with the ER. Thus, the whole flavivirus virion is transported through the ER and Golgi while in the case of the alphaviruses only the glycoproteins are transported through the secretory pathway. These exit strategies are not unique and thus serve as model systems to study enveloped virus assembly and release.

Proteolytic cleavage of glycoproteins in order to convert them from stable oligomeric structures to metastable structures primed for fusion are common themes in enveloped virus structure and assembly. Cleavage of PE2 into E3 and E2 by a furin-like protease primes the alphavirus spike complex for fusion. A similar cleavage of prM triggers a dramatic conformational change of the flavivirus glycoproteins resulting in the formation of the mature virion which is now infectious.

Alphavirus budding requires the specific interaction of the NC with the E1–E2 spike complexes at the plasma membrane, thus ensuring that all virions have a genome packaged into them. However, the flaviviruses only require the interaction of the envelope proteins for budding, giving rise to subviral particles devoid of the C protein and genome RNA. Thus, the flavivirus envelope proteins alone are sufficient to drive budding of virus particles and the close coupling of genome replication and the C protein (perhaps mediated by replication proteins and host factors) is required to package the genome into virus particles. A third strategy for budding is exhibited by the retroviruses where capsid assembly has been shown to be sufficient to drive budding of the virus. In this case, targeting of the envelope proteins to these sites of CP assembly is essential to ensure the incorporation of the glycoproteins into the virion.

Although much has already been discovered about enveloped virus assembly, there are still many processes yet to be described. There is an increasing interest in the assembly pathway of viruses partly fueled by the potential to develop successful therapeutic agents targeting virus specific assembly processes. Advances in the field of structural biology will further help attempts to understand the assembly pathway of this important class of viruses.

See also: Assembly of Viruses: Nonenveloped Particles.

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