Review article Casp. J. Vet. Sci., 2024; 1(1): 41-47

Amol University of Special Modern Technologies

Caspian Journal of Veterinary Science

doi: 10.22034/cjvs.2024.198849

Journal homepage: https://cjvs.ausmt.ac.ir/

Morbillivirus cell entry: by focusing on canine distemper and measles virus fusion machinery

Mojtaba Khosravi[1*], Sedigheh Mohammadzadeh[2]

[1] Department of Pathobiology, Faculty of Veterinary Medicine, Amol University of Special Modern Technologies, Amol, Iran.
[2] Department of Pathobiology, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran.
(*) Corresponding author: m.khosravi@ausmt.ac.ir

Article Info

Article history:

Received: 1 May 2024

Accepted: 16 June 2024

Keywords:

Fusion protein

Hemagglutinin

Membrane fusion

Morbilliviruses

Abstract

Morbilliviruses contain infectious pathogens causing important economic and health impact in livestock and wild animal as well as human, respectively. Membrane fusion is critical step to determine the fate of virus (virus cell entry and spread, and finally disease outcome). It is mediated by concerted action of two surface glycoproteins, including the hemagglutinin (H) and fusion protein (F). Initially, the H protein binds to the host cell receptor via its cuboidal head domain and then it leads to conformational changes resulting in F-triggering. In addition, the F-protein experiences a series of irreversible structural rearrangements that induces the merging of the viral envelope with the host cell plasma membrane and forming fusion pore. Morbilliviruses uses signalling lymphocyte activation molecule (SLAM/CD150) and Nectin4 as cellular receptors in immune and epithelial cells, respectively. Prior studies have shown the H protein adopts unique and overlapping receptor binding sites. Blades (β4-β6 or β4-β5) serve as receptor binding sites on H protein. Furthermore, Blades β4 and β5 form a hydrophobic pocket that engage in Nectin4 interaction with H, whereas SLAM does not directly bind into this hydrophobic pocket and bind mostly laterally. Recent studies were confirmed that the central domain of H protein carries short range interaction of F protein. Our knowledge about *morbillivirus* membrane fusion has greatly increased. It could be useful to obtain a fundamental understanding into the basic mechanisms supporting "receptor-based" host-pathogen interaction and introduces inhibitory molecules that impede this process by targeting attachment glycoprotein.

Introduction

The Paramyxoviridae family contains of non-segmented, negative-strand, enveloped RNA viruses. Four sub-families; Avulavirinae, Metaparamyxovirinae, Orthoparamyxovirinae, and Rubulavirinae are classified in this family. The Orthoparamyxovirinae sub-family involves eight genera, including *Aquaparamyxovirus, Ferlavirus, Henipavirus, Jeilongvirus, Morbillivirus, Narmovirus, Respirovirus,* and *Salemivirus* (ICTV, 2022).

Viruses belonging to this family can cause highly contagious and severe diseases in animal and human population. For example, canine distemper virus (CDV), sendai virus (SeV), parainfluenza virus type 5 (PIV5), as well as both newcastle disease virus (NDV) and rinderpest (RPV) are infecting animal, whereas respiratory syncytial virus (RSV), human parainfluenza viruses (hPIV), measles virus (MeV) and mumps virus (MuV) are human pathogens. Furthermore, hendra virus (HeV) and nipah virus (NiV) are bat -borne and recognized as zoonotic pathogens. They initially develop a disease in horses and pigs, respectively, which can also lead to respiratory and neurological disorders in humans (Lee and Ataman, 2011; Amaya and Broder, 2020).

The helical nucleocapsid core of *morbillivirus* is located in the viral particle, which is covered by a lipid bilayer envelope. Its RNA genome has roughly 15 to 16 kbp length and contains protein-encoding and non-coding sequences (Sidhu *et al*., 1993; Plattet *et al*.,

2004; Rendon-Marin *et al*., 2019).

The genome encodes six structural proteins (nucleocapsid protein (N), phosphoprotein (P), matrix protein (M), fusion protein (F), hemagglutinin protein (H) and the large protein (L)) and two non-structural (C and V) components. The tetrameric hemagglutinin (H) protein and the trimeric fusion (F) protein (virus surface glycoproteins) are anchored the viral envelope, which together form "spike" structures extending from the viral envelope. They form fusion machinery of virus that is required for cell entry (Kolakofsky *et al*., 2005; Lamb and Parks, 2007).

Recently, in order to clarify the putative role of H and F proteins in process of cell entry, many structural and biochemical studies have been performed. This data confirmed that the collaboration of these proteins is important for first step of cell entry process (referred as membrane fusion) (Lamb and Parks, 2007).

By considering the presence of severe human and animal pathogens in this family, it seems, increasing our understandings about attachment and fusion proteins oligomerization and their structural rearrangement before and after virus cell entry are important. Additionally, this information can lead to design new inhibitory molecules or/and drug that can abort virus-cell entry process.

Virus cell entry: virus- to- cell and cell- to- cell transmission by using viral membrane fusion machinery

The *morbillivirus* mode of infection was elucidated through the utilization of recombinant MeV and CDV particles. Virus uses its membrane fusion machinery for cell entry. It is a hetero-oligomeric complex containing tetrameric attachment (H) and trimeric fusion (F) glycoproteins. Briefly, after virus entry in the host, virus use this machinery to infect its primarily victims. It is assumed that upon H interaction with a specific host cell receptor using its cuboidal head domain; it may undergo a series of sequential cascade of conformational rearrangements, resulting to the transformation of F protein from a metastable prefusion state into a significantly stable postfusion state. Finally, these rearrangements cause virus–cell membrane fusion and develop pore formation and facilitate virus ribonucleocapsid complex injection in to host cytosol. Recent evidences also showed that virus also use this machinery for spread in the infected organs. This mode of transmission is called cell- to- cell spread and induces giant cell (also referred to as syncytia) (Lamb and Parks, 2007). In addition, virus uses another mode of transmission. It is called non-cytolytic cell- to- cell transmission. During brain infection, virus shows this phenotype of infection. In this case, virus dissemination does not induce syncytia formation (large multinucleated cells) (Zurbriggen *et al*., 1995; Alves *et al*., 2015).

Virus cellular receptors

In contrast of other *paramyxovirus* that use carbohydrate receptor (sialic acid), both morbilliviruses and henipaviruses adopt to use proteinaceous receptors. Before describing *morbillivirus* receptor, many biochemical studies suggested the presence of two discriminated receptors for virus in lymphatic and epithelial tissue. Initially, signaling lymphocyte activation molecule (SLAM/CD150) was discovered that support of the first phase of virus amplification in lymphatic organ. Latter, epithelial receptor (EpR/Nectin-4) was described. Henipaviruses also use ephrin B2 and B3 as entry receptors (Tatsuo *et al*., 2001; Bonaparte *et al*., 2005; Muhlebach *et al*., 2011; Noyce *et al*., 2011; Pratakpiriya *et al*., 2012). Both SLAM and Nectin-4 belong to the type-I transmembrane protein of immunoglobulin superfamily (Ig superfamily). The extracellular domain composed of C and V domains harboring via single-pass transmembrane domain. Structural and X-ray crystallography analysis showed that receptor activities of these receptors are related to the amino acid residues locating in their N- terminal V domains (Kwong *et al*., 1998; Khosravi *et al*., 2015).

***Morbillivirus* attachment protein (H protein)**

General properties of attachment protein:

All Paramyxoviridae members encode an attachment protein. *Morbillivirus* genus attachment protein is known by its hemagglutinin activity, whereas attachment protein of *Respirovirus, Metaavulavirus* and *OrthoRubulavirus* genera have additional activity that is called neuraminidase activity (HN protein). In addition, the *Henipavirus* attachment protein don't have both hemagglutinin and neuraminidase activities (referred to as G proteins). As mentioned, Attachment protein is multifunctional protein and it not only involves in receptor binding, but it also has tightly physical interaction via its stalk domain with large globular head domain of metastable F protein (Lamb and Parks, 2007; Avila *et al*., 2014).

Structural information of H protein:

H protein is a type II transmembrane protein. Its extracellular domain composes of a straight four helical

bundle stalk domain (aa 59 to 154) and a distal cuboidal receptor-recognition head module (aa 188 to 604 or 607) which are linked via a connecting region (neck domain (aa 155 to 187)). In addition, the ectodomain links to cytosolic part through a short single-spanning transmembrane region (Lamb and Parks, 2007; Ader-Ebert *et al*., 2015; Kalbermatter *et al*., 2023).

H protein oligomerization shows a unique type of homo dimer-of-dimers assembling via non-covalently dimer-to-dimer interaction. Furthermore, H dimerization facilitates through disulphide bridges formation. Naturally, two cysteine residues are existed at the neck domain (Cys-139 and Cys-154) that are involved in H dimerization (Plemper *et al*., 2000; Brindley and Plemper, 2010).

Structure of H-head:

Crystal structure studies illustrated that *paramyxovirus* monomeric H head shared a conserved tertiary folding, and organized as a pair of dimeric heads in H-tetramer oligomerization. Each head domain composes of a conserved six-bladed β-propeller structure (β1-β6). These propellers define receptor binding sites. The crystal structure of MeV H-head in dimeric oligomerization showed that both heads are extended from each other in titled manner. Strikingly, tetrameric MeV H- head crystal structure revealed two distinctive conformations, including planner and staggered structures in before and after receptor engagement (Hashiguchi *et al*., 2011). Recent data have shown that the spatial orientation of CDV-H neck domain in relation to the stalk domain, forming an asymmetric architecture. It bends almost 90° with respect to the stalk domain, causing the two head domain dimers to tilt to one side of the stalk in pre-receptor bound conformation (Kalbermatter *et al*., 2023).

Receptor binding site on H-head:

HN and G protein interact with receptor via a large pocket at top of the propeller structure, whereas MeV H and CDV-H protein binds laterally (sideway). Recently, evidences described an overlapping receptor binding sites that located in the blades (β4-β6 or β4-β5) and contain critical residues that mediate virus–cell surface receptors interaction. Blades β4 and β5 create a hydrophobic pocket supporting Nectin4 direct interaction. In contrast, SLAM adopts another way for binding and fully covering this pocket (Santiago *et al*., 2010; Hashiguchi *et al*., 2011; Mateo *et al*., 2013).

H-stalk domain support F binding site and trigger F activation:

Evidences were derived from site-directed alanine-based mutagenesis analyses confirmed that the residues from 111-118 of MeV and CDV H-stalk could be involved in H and F interaction (Lamb and Parks, 2007). In addition, structural studies using cysteine-based mutagenesis proposed four-helix bundle (4HB) conformation for the central domain of H-stalk (aa 85-115) (like as HN-stalk of hPIV5 and NDV) and functional activity to trigger F protein (Paal *et al*., 2009).

***Paramyxovirus* attachment protein structures**

Recent crystallographic analyses of the HN protein from NDV and PIV5 have revealed two unforeseen and innovative configurations of the attachment protein. Significantly, the crystal structure of the NDV HN protein employ a distinctive arrangement where one of the head domains in each dimeric unit of the HN protein withdraws and forms a direct contact with the stalk domain, while the other head domain adopts an upward orientation, known as the 'four-heads-down' conformation (Yuan *et al*., 2011; Jardetzky and Lamb, 2014).

In respect to the PIV5 HN protein, only one dimeric unite fold back and induce interaction with stalk domain, resembling the pattern observed in the NDV-HN protein and other assuming adopt an upward configuration. (Thus, referred to as the "2-heads-down and 2-heads-up" conformation) (Bose *et al*., 2011). As mentioned above, in co-crystal structure of MeV H and Hu SLAM, two monomeric MeV H- heads are organized very similarly in dimeric unite, whereas two dimeric units adopt two different configurations, including planner and staggered structures in before and after receptor binding (Hashiguchi *et al*., 2011).

***Morbillivirus* fusion protein (F)**

General properties of fusion protein:

F protein of *morbillivirus* is classified as the class I transmembrane surface glycoproteins. Tertiary protein is folded as a homo trimeric. Initially, F gene translates into functionally inactive precursor protein (called F0) and then it bears post translational modification including glycosylation and proteolytic cleavage in cell internal comportment. Finally, F protein converts into two disulphide-linked subunits (F1 + F2) (Yin *et al*., 2006). *Morbillivirus* F protein appears at the virus envelop and cell infected virus in close contact with H

protein. Before F trigging, like as other class I fusion protein it folds as high intrinsic energy configuration (referred as perfusion structure or metastable structure) and upon receptor binding and H activation, F undergoes irreversible conformation modifications and adopts highly stable postfusion structure (Lamb and Parks, 2007).

Structural properties and F remodeling:

F protein adopts two completely distinctive configurations in its pre and post fusion states. Atomic structure of prefusion (metastable) state of PIV5 F protein revealed a "tree"-like structure with a short stalk and a large globular head domain. The stalk domain is created by the three heptad repeat B (HRB) regions folding in a three-helix bundle (3HB) configuration of F1 and three distinctive subdomains; DI, DII and DIII, where forming the globular head domain. The heptad repeat region A (HRA) is located on the DIII domain and contained eleven segments (Fig. 1) (Yin *et al*., 2006; Welch *et al*., 2012; Philippe *et al*., 2016). Within the *morbillivirus* F protein, there is a third heptad repeat region, referred to as the HRC, which is present in the F2 subunit. This region plays a role as a modulator of fusogenicity (Plemper *et al*., 2003).

F activation is accompanied by heptad repeat region A (HRA) reorganization and it forms straight there - helical bundle (3HB) leading to injection of fusion peptide (FP) into cell plasma membrane (refereed as prehairpin structure). Latter, the heptad repeat region B (HRB) folds up and binds to the HRA forming 6HB structure (is known as classic structure of postfusion structure of class I fusion protein) (Fig. 2) (Russell and Luque, 2006; Yin *et al*., 2006; Lamb and Parks, 2007; Welch *et al*., 2012). The consequences of the alterations in structure following the activation of the F protein involve the virus and cell membrane moving closer together as a result of the presence of the transmembrane (TM) region in the virus membrane and FP in the target cell membrane, ultimately leading to membrane fusion and pore formation (Fig. 2) (Philippe *et al*., 2016).

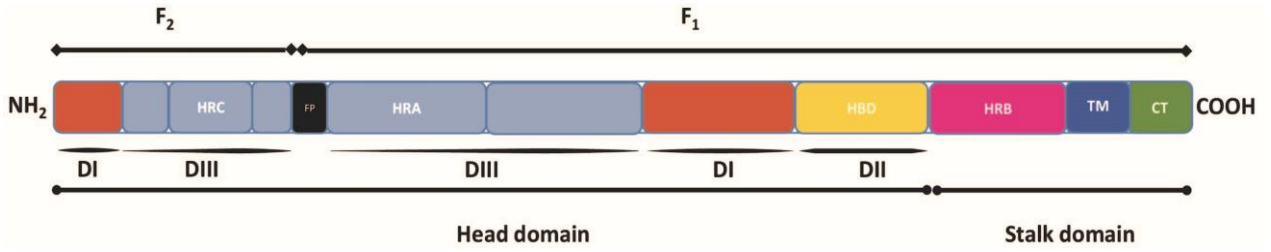

Fig. 1. Schematic representation of the CDV F protein.

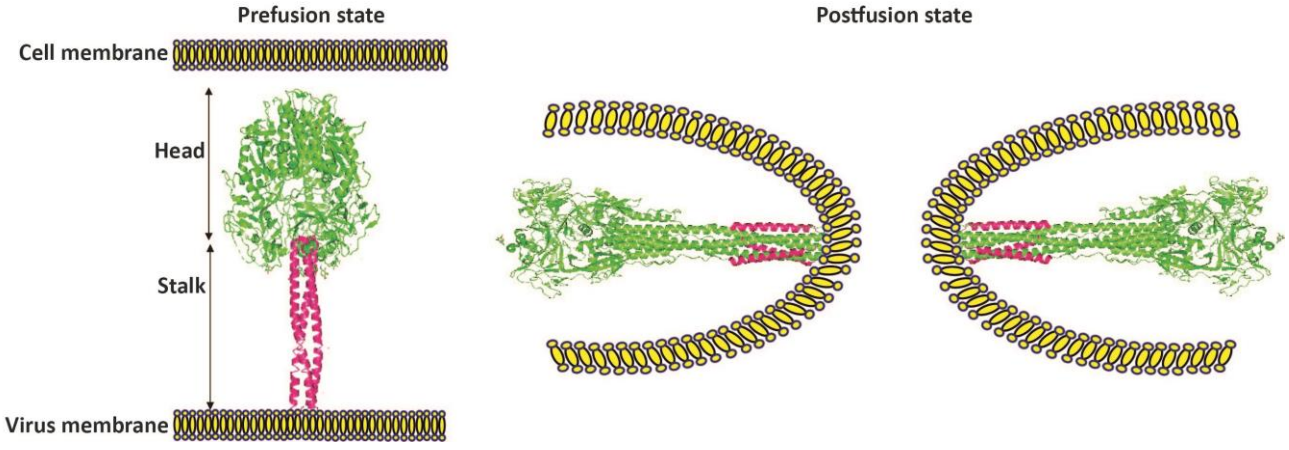

Fig. 2. F protein functional structure, during membrane fusion: F protein adopts two completely different configurations has been known as pre and postfusion state.

Modes of H protein/F protein interaction

Prior biochemical and functional studies suggested a homologues region of *paramyxovirus* attachment protein stalk domain as required for physical interaction with F protein. In addition, biochemical evidences, such as co-immunoprecipitation between attachment and F protein of morbilliviruses confirmed an intracellular assembly of virus glycoproteins. While, extracellular association is proposed for HN and F for NDV and PIV5. So, it leads to introduce to two models of vial glycoproteins assembly, including clamp and provocateur models.

In clamp model, as seen in CDV, the head domain dimer units of H protein just cover one side of stalk and the other side of stalk will be exposed, then necessary interface for supporting the short range interaction with F protein will be provided. Therefore, the auto-repressed state has been assumed by the H protein to impede the activation of high intrinsic energy configuration of F protein and also confirmed the supporting role of H protein to keep F protein in its metastable state.

In provocateur model, as for NDV and PIV5 HN and G protein of NiV, the head domain mask the F ineraction portion on stalk. Following the recpotre binding, this fuctuonal portion would be exposed and the glycoproteins interaction will be occurred (Paterson *et al*., 1997; Plemper *et al*., 2001; Connolly *et al*., 2009; Whitman *et al*., 2009; Plattet and Plemper, 2013).

Latest models of F activation (how H tetramers conduct actively F trimers triggering)

In regards to *morbillivirus* F protein trigging, mechanistic and structural studies proposed two new models such as sliding and safety-catch Model (Fig. 3).

The sliding Model

Two distinctive MeV H configurations in before and after receptor engagement lead to propose this model. Base of this model, dimeric head domains of MeV H protein adopt fairly planar configuration and stalks being held closely together (referred as conformation I). Upon, receptor engagement of H protein, the head domains undergo a change in their arrangement, resulting in a relatively staggered configuration with respect to each other, while the stalks become disassociated (referred to as conformation II), Which in turn, leads to the destabilization of the metastable F protein and triggers F activation (Hashiguchi *et al*., 2011).

The safety-catch mode

As mentioned above, in case of *morbillivirus* like CDV, H protein has physical interaction with F protein prior receptor engagement of H protein and allows auto-repressed state to trigging F protein activation. The recent asymmetric organization of the CDV H structure provides supporting evidences for this model. Briefly, the presence of unmasked portion at one side of stalk provides this interaction. Receptor binding is accompanied by structural rearrangement of the proximal C-terminal region of the protein H protein (neck domain). Subsequently, this molecular signal is transmitted to the functional part of the stalk that is interacted to the F protein, and resulting in alterations in the middle portion of the stalk (decomposing). This leads to the inactivation of the auto-silencing mechanism and the activation of the F protein (Philippe *et al*., 2016; Kalbermatter *et al*., 2023).

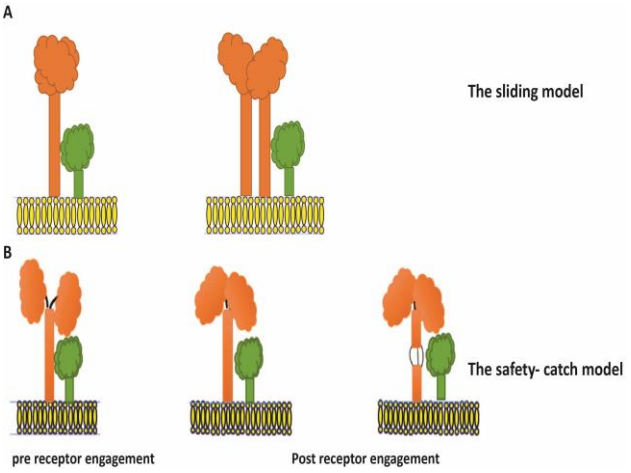

Fig. 3. *Morbillivirus* fusion protein activation. A and B: sliding and safety-catch models.

Conclusions and perspectives

Several hazardous human and animal pathogens are classified in this genus. Membrane fusion is critical and first step of virus-cell entry that it determines the virus pathogenicity and cell tropism. Among, *Paramyxovirus*, new biochemical findings proposed some variation in this process. But it seems the overall strategy that is adopted by them is similar. Prior structural and biochemical findings illustrated roughly a comprehensive knowledge about how *morbillivirus* fusion machinery does its duty. The ultimate target of these researches are determination steps that

potentially ablate H or/and F protein activation. Thus, many researches are conducted to draw or discover F and H inhibition molecules and drug. Actually, in this review, author tried to gather and describe new findings about viral glycoproteins and fundamental understanding into the basic mechanisms supporting membrane fusion.

Acknowledgment

This research has been financially supported by a grant from the Amol University of Special Modern Technologies, Amol, Iran.

Conflict of Interest

The authors do not have any potential conflict of interest to declare.

References

Ader-Ebert, N; Khosravi, M; Herren, M; Avila, M; Alves, L; Bringolf, F; ¨Orvell, C; Langedijk, JP; Zurbriggen, A; Plemper, RK and Plattet, P (2015). Sequential conformational changes in the *Morbillivirus* attachment protein initiate the membrane fusion process. PLOS Pathog., 11: e1004880.

Alves, L; Khosravi, M; Avila, M; Ader-Ebert, N; Bringolf, F; Zurbriggen, A; Vandevelde, M and Plattet, P (2015). Slam- and nectin-4-independent noncytolytic spread of canine distemper virus in astrocytes. J. Virol., 89: 5724–5733.

Amaya, M and Broder, CC (2020). Vaccines to emerging viruses: *Nipah* and *Hendra*. Ann. Rev. Virol., 7: 447-473.

Avila, M; Alves, L; Khosravi, M; Ader-Ebert, N; Origgi, F; Schneider-Schaulies, J; Zurbriggen, A; Plemper, RK and Plattet, P (2014). Molecular determinants defining the triggering range of prefusion F complexes of canine distemper virus. J. Virol., 88: 2951-2966.

Bonaparte, MI; Dimitrov, AS; Bossart, KN; Crameri, G; Mungall, BA; Bishop, KA; Choudhry, V; Dimitrov, DS; Wang, LF and Eaton, BT (2005). Ephrin-B2 ligand is a functional receptor for *Hendra* virus and *Nipah* virus. Proc. Nat. Acad. Sci., 102: 10652-10657.

Bose, S; Welch; BD; Kors, CA; Yuan, P; Jardetzky, TS and Lamb, RA (2011). Structure and mutagenesis of the *Parainfluenza* virus 5 hemagglutinin-neuraminidase stalk domain reveals a four-helix bundle and the role of the stalk in fusion promotion. J. Virol., 85: 12855-12866.

Brindley, MA and Plemper, RK (2010). Blue native PAGE and biomolecular complementation reveal a tetrameric or higher-order oligomer organization of the physiological measles virus attachment protein H. J. Virol., 84: 12174-12184.

Brindley, MA; Takeda, M; Plattet, P and Plemper, RK (2012). Triggering the measles virus membrane fusion machinery. Proc. Nat. Acad. Sci., 109: E3018-E3027.

Chua, KB; Bellini, WJ; Rota, PA; Harcourt, BH; Tamin, A; Lam, SK; Ksiazek, TG; Rollin, PE; Zaki, SR and Shieh, W (2000). *Nipah* virus: a recently emergent deadly *paramyxovirus*. Sci., 288: 1432-1435

Connolly, SA; Leser, GP; Jardetzky, TS and Lamb, RA (2009). Bimolecular complementation of *paramyxovirus* fusion and hemagglutinin-neuraminidase proteins enhances fusion: implications for the mechanism of fusion triggering. J. Virol., 83: 10857-10868.

Hashiguchi, T; Ose, T; Kubota, M; Maita, N; Kamishikiryo, J; Maenaka, K and Yanagi, Y (2011). Structure of the measles virus hemagglutinin bound to its cellular receptor SLAM. Nat. Struct. Mol. Biol., 18: 135-141

International Committee on Taxonomy of Viruses: ICTV. Virus taxonomy: the classification and nomenclature of viruses. The Online Report of the ICTV. https://talk.ictvonline.org/taxonomy/. Accessed July 15, 2022.

Jardetzky, TS and Lamb, RA (2014). Activation of *paramyxovirus* membrane fusion and virus entry. Curr. Opin. Virol., 5C: 24-33.

Kalbermatter, D; Jeckelmann, JM; Wyss, M; Shrestha, N; Pliatsika, D; Riedl, R; Lemmin, T; Plattet, P and Fotiadis, D (2023). Structure and supramolecular organization of the canine distemper virus attachment glycoprotein. Proc. Nat. Acad. Sci., 120: e2208866120.

Khosravi, M; Bringolf, F; Röthlisberger, S; Bieringer, M; Schneider-Schaulies, J; Zurbriggen, A; Origgi, F and Plattet, P (2015). Canine distemper virus fusion activation: critical role of residue E123 of CD150/SLAM. J. Virol., 90: 1622-37.

Kolakofsky, D; Roux, L; Garcin, D and Ruigrok, RW (2005). *Paramyxovirus* mRNA editing, the "rule of six" and error catastrophe: a hypothesis. J. Gen. Virol., 86: 1869-1877.

Kwong, PD; Wyatt, R; Robinson, J; Sweet, RW; Sodroski, J and Hendrickson, WA (1998). Structure of an HIV gp120 envelope glycoprotein in complex with the CD4 receptor and a neutralizing human antibody. Nat., 393: 648-659.

Lamb, RA and Parks, GD (2007). Paramyxoviridae: The viruses and their replication. In Fields' Virology, D.M. Knipe, and P.M. Howley, eds. 5th ed, (Philadelphia: Lippincott Williams & Wilkins). PP: 1449-1496.

Lee, B and Ataman, ZA (2011). Modes of *paramyxovirus* fusion: a *Henipa* virus perspective. Trends Microbiol., 19: 389-399.

Mateo, M; Navaratnarajah, CK; Syed, S and Cattaneo, R (2013). The measles virus hemagglutinin beta-propeller head beta4-beta5 hydrophobic groove governs functional interactions with nectin-4 and CD46 but not those with the signaling lymphocytic activation molecule. J. Virol., 87: 9208-9216.

Muhlebach, MD; Mateo, M; Sinn, PL; Prufer, S; Uhlig, KM; Leonard, VH; Navaratnarajah, CK; Frenzke, M; Wong, XX and Sawatsky, B (2011). Adherents junction protein nectin-4 is the epithelial receptor for measles virus. Nat., 480: 530-533.

Navaratnarajah, CK; Negi, S; Braun, W and Cattaneo, R (2012). Membrane fusion triggering: three modules with different structure and function in the u.pper half of the measles virus attachment protein stalk. J Biol. Chem., 287: 38543-38551.

Noyce, RS; Bondre, DG; Ha, MN; Lin, LT; Sisson, G; Tsao, MS and Richardson, CD (2011). Tumor cell marker PVRL4 (nectin 4) is an epithelial cell receptor for measles virus. PLoS Pathog., 7: e1002240.

Paal, T; Brindley, MA; St, CC; Prussia, A; Gaus, D; Krumm, SA; Snyder, JP and Plemper, RK (2009). Probing the spatial organization of measles virus fusion complexes. J. Virol., 83: 10480-10493.

Paterson, RG; Johnson, ML and Lamb, RA (1997). *Paramyxovirus* fusion (F) protein and hemagglutinin-neuraminidase (HN) protein interactions: intracellular retention of F and HN does not affect transport of the homotypic HN or F protein. Virol.. 237: 1-9.

Philippe, P; Lisa, A; Michael, H and Hector, CA (2016). Measles virus fusion protein: structure, function and inhibition. Viruses., 8: 112-130.

Plattet, P and Plemper, RK (2013). Envelope protein dynamics in *paramyxovirus* entry. mBio. 4: e00413-13

Plattet, P; Zweifel, C; Wiederkehr, C; Belloy, L; Cherpillod, P; Zurbriggen, A and Wittek, R (2004). Recovery of a persistent canine distemper virus expressing the enhanced green fluorescent protein from cloned cDNA. Virus Res., 101: 147-153.

Plemper, RK and Compans, RW (2003). Mutations in the putative HR-C region of the measles virus F2 glycoprotein modulate syncytium formation. J. Virol., 77: 4181–4190.

Plemper, RK; Hammond, AL and Cattaneo, R (2001). Measles virus envelope glycoproteins hetero-oligomerize in the endoplasmic reticulum. J. Biol. Chem., 276: 44239-44246.

Plemper, RK; Hammond, AL and Cattaneo, R (2000). Characterization of a region of the measles virus hemagglutinin sufficient for its dimerization. J. Virol., 74: 6485-6493.

Pratakpiriya, W; Seki, F; Otsuki, N; Sakai, K; Fukuhara, H; Katamoto, H; Hirai, T; Maenaka, K; Techangamsuwan, S and Lan, NT (2012). Nectin4 is an epithelial cell receptor for canine distemper virus and involved in neurovirulence. J. Virol., 86: 10207-10210.

Rendon-Marin, S; Budaszewski, RDF; Canal, CW and Ruiz-Saenz, J (2019). Tropism and molecular pathogenesis of canine distemper virus. Virol. J., 16: 30.

Russell, CJ and Luque, LE (2006). The structural basis of *paramyxovirus* invasion. Trends Microbiol., 14: 243-246.

Santiago, C; Celma, ML; Stehle, T and Casasnovas, JM (2010). Structure of the measles virus hemagglutinin bound to the CD46 receptor. Nat. Struct. Mol. Biol., 17: 124-129.

Sidhu, MS; Husar, W; Cook, SD; Dowling, PC and Udem, SA (1993). Canine distemper terminal and intergenic non-protein coding nucleotide sequences: completion of the entire CDV genome sequence. Virol., 193: 66-72.

Tatsuo, H; Ono, N and Yanagi, Y (2001). Morbilliviruses use signaling lymphocyte activation molecules (CD150) as cellular receptors. J. Virol., 75: 5842-5850.

Welch, BD; Liu, Y; Kors, CA; Leser, GP; Jardetzky, TS; Lamb, RA (2012). Structure of the cleavage-activated prefusion form of the *parainfluenza* virus 5 fusion protein. Proc. Nat. Acad. Sci., 109: 16672–16677.

Whitman, SD; Smith, EC and Dutch, RE (2009). Differential rates of protein folding and cellular trafficking for the *Hendra* virus F and G proteins: implications for F-G complex formation. J. Virol., 83: 8998-9001.

Yin, HS; Wen, X; Paterson, RG; Lamb, RA and Jardetzky, TS (2006). Structure of the *parainfluenza* virus 5 F protein in its metastable, prefusion conformation. Nat., 439: 38-44.

Yuan, P; Swanson, KA; Leser, GP; Paterson, RG; Lamb, RA and Jardetzky, TS (2011). Structure of the Newcastle disease virus hemagglutinin-neuraminidase (HN) ectodomain reveals a four-helix bundle stalk. Proc. Nat. Acad. Sci., 108: 14920-14925.

Zurbriggen, A; Graber, HU and Vandevelde, M (1995). Selective spread and reduced virus release leads to canine distemper virus persistence in the nervous system. Vet. Microbiol., 44: 281-288.