

Cellular receptors for viruses: links to tropism and pathogenesis

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Introduction

The interaction of a virus with its cellular receptor initiates a chain of dynamic events that will enable entry of the virus into the cell. In addition to the fact that the virus–receptor interaction is a multistep process in itself, multiple attachment receptors may be used sequentially, or in a cell-type-specific manner, and co-receptors may also be involved (for a review, see Haywood, 1994). It is beyond the scope of this article to give a complete review of cellular receptors for viruses. The data presented here, therefore, have been selected to focus attention on those virus–receptor interactions that provide links to virus tropism and pathogenesis.

For most viruses, the receptor distribution in an individual is wider than the observed tissue tropism. Also, many virus–receptor interactions determine the host range and therefore constitute an interspecies barrier. Although mutations can accumulate rapidly, especially in RNA viruses, tolerable changes in the viral envelope proteins are constrained by the need to interact with a certain receptor. However, eventually, such changes may drastically alter the tropism and virulence of a virus. Furthermore, even in non-infected cells, the virus–receptor interaction may induce signal transduction, resulting in cytokine secretion, apoptosis, stimulation of the immune response, or, conversely, immunosuppression.

Virus tropism and pathogenicity are multifactorial

The term ‘entry’ for the first step of a virus life-cycle describes the various ways a virus can get into a cell and can be taken to mean pH-independent fusion at the cell surface, pH-dependent fusion in acidic endosomes, uptake of non-enveloped virions by endocytosis or the conformational changes leading to the uncoating of the viral genome (Fig. 1). The general concept of a ‘spring-loaded’ metastable state and conformational changes induced by low pH or binding of a virus to its receptor has been developed using influenza virus haemagglutinin (HA) and seems to be valid for a variety of viruses (for reviews, see Skehel *et al.*, 1994; Steinhauer *et al.*, 1992; White *et al.*, 1994). Thus, HA switches from a native

non-fusogenic to a fusogenic conformation, which is induced by exposure to acidic pH in the endosome. This conformational change can also be achieved by exposing HA to heat or denaturing agents such as urea, suggesting that the native structure of the molecule is trapped in a metastable state and that the fusogenic conformation is released by destabilization of the native structure. Coupling the energetically expensive process of membrane fusion to an energetically favourable conformational change drives the reaction (Carr *et al.*, 1997). Similar fusion (F)-protein structures have been found in the influenza virus HA, simian parainfluenza virus 5 F, human immunodeficiency virus (HIV) gp41, mouse moloney leukaemia virus envelope transmembrane protein, and Ebola virus gp2 protein (Baker *et al.*, 1999 and references therein). Although structurally different, the tick-borne encephalitis virus (TBEV) E protein is also functionally analogous (Rey *et al.*, 1995; Stiasny *et al.*, 1996).

Although the virus–receptor interaction is needed to initiate infection, pathogenesis is a multistep process and the development of disease is influenced by the intracellular milieu, induced cell functions such as the capacity of the host to develop a proper immune response, the velocity of virus replication, cytopathogenicity and the spread of infection within and between organs, which again may or may not depend on the presence of specific cellular receptors. Even when infection does not proceed, virus–receptor-mediated signal transduction may induce the secretion of cytokines, such as interferons, which can have a great impact on the development of a disease. For example, enveloped viruses such as HIV and herpes simplex virus (HSV) can induce interferon- α via the mannose receptor on dendritic cells or monocytes (Milone & Fitzgerald-Bocarsly, 1998). This interaction induces signals in cells important for the immune system, but it does not lead to the uptake of viruses.

The budding and the release of viruses can also have a decisive impact on pathogenesis by determining the parameters of virus spread. This is obvious for pantropic viruses such as influenza or Sendai. The uptake and release of these viruses in polarized epithelial cells of the respiratory tract is restricted to the apical side. This is an important factor in preventing systemic infection. In contrast, viruses that are released basolaterally may spread systemically (for a review, see Compans, 1995).

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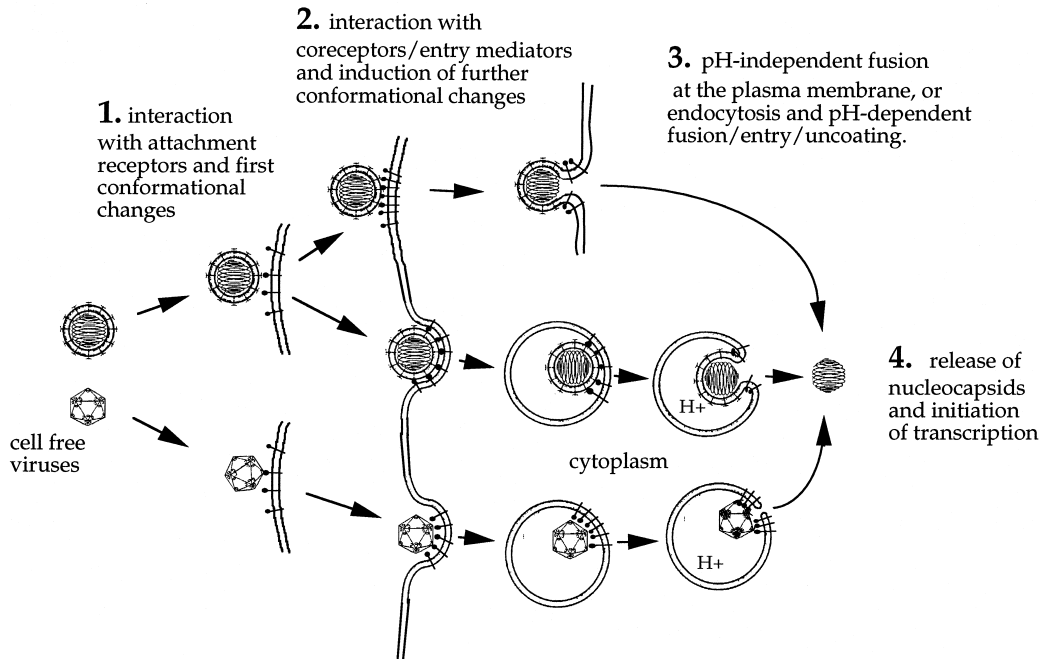


Fig. 1. Four steps of virus entry into target cells. The interaction of the virion with the attachment receptor leads to the first conformational changes in the viral envelope proteins (1). This step enables the interaction with co-receptors, or entry mediators, and further conformational changes at the plasma membrane (2), which may deliver the energy for membrane fusion (3). Several viruses require the low pH in acidic endosomes to induce this conformational change. These mechanisms lead to the release and possibly the uncoating of the virus genome, and the initiation of the virus replication cycle (4).

The primary infection usually involves a small initial dose of virus and leads to little impact for the host. Replication of virus within the initial site of infection will then lead to a substantial multiplication of virus particles and considerable damage in secondary target organs. For the spread of virus to different organs and cell types, the use of multiple receptors might be advantageous. Viruses may either have the intrinsic capacity to use more than one receptor, as found for complex viruses such as herpes viruses (Tufaro, 1997), or they may change their capacity to bind to receptors or co-receptors by mutation of their envelope proteins. Both mechanisms are observed during HIV infection.

Receptor usage and the pathogenesis of HIV

CD4 has been found to act as the primary receptor for HIV (Klatzmann *et al.*, 1984). In recent years, rapid progress has been made in identifying a set of chemokine receptors, which belong to a family of G-protein-coupled seven-transmembrane proteins, that represent co-receptors for HIV infection. Although not all factors are known yet, it appears that macrophage-tropic, T-cell-tropic and dual-tropic HIV strains use certain sets of co-receptors: macrophage-tropic strains primarily use CCR5, and T-cell-tropic strains primarily use CXCR4. In an infected individual, the co-receptor-determined tropism of the virus may change from macrophages or dendritic

cells in mucosal tissues to a tropism for T cells. This change is due to mutations emerging in the viral envelope genes during progression of the infection (for a review, see Berger *et al.*, 1999).

The concept of consecutive conformational changes is valid for HIV entry. The most favoured current model proposes that the initial binding of gp120 to CD4 induces a conformational change in gp120 which enables it to interact with a co-receptor. This interaction is supposed to induce a further conformational change in the viral envelope which results in the activation of gp41 and the positioning of its fusion active peptide in close proximity to the membrane and finally in the insertion of the fusion peptide into the membrane of the target cell. The dramatic conformational changes of gp120 have been confirmed by X-ray crystallographic studies (for a review, see Berger *et al.*, 1999). As with influenza virus HA, the native HIV envelope protein gp120/gp41 complex appears to be trapped in a metastable state until the receptor interaction induces the transition to an energetically more favourable state. This conclusion is also supported by the enhancement of the infection with low concentrations of soluble CD4 or neutralizing antibodies which can facilitate structural alterations (Allan *et al.*, 1990; Sullivan *et al.*, 1995), and the inhibition of infection or cell-cell fusion by short peptides interacting with transiently exposed structures of the envelope proteins (Eckert *et al.*, 1999 and references therein).

A major contribution to HIV pathogenesis (Fauci, 1993,

1996) is the presence of the attachment receptor, CD4, on cells central to the immune response, and its downregulation following infection (Aiken *et al.*, 1994; Jabbar *et al.*, 1990; Raja *et al.*, 1994). Target cells for HIV are T helper cells, dendritic cells, including Langerhans' cells in the skin and in mucous membranes, and cells of the monocyte-macrophage lineage, including microglial cells in the brain. Dendritic cells present in the genital mucosa are now thought to be the first target cell in the host. They can transport the virus to lymph nodes and distribute it to contacting T cells possibly by circumventing co-receptor-dependent mechanisms (Hladik *et al.*, 1999). Moreover, dendritic cells lose their immunostimulatory functions upon infection, which is the first step to immunodeficiency (for a review, see Knight & Patterson, 1997).

Glycoprotein 120 expressed on the surface of macrophages may induce apoptosis in lymphocytes via co-receptor interactions, which eventually contributes to the destruction of these immune cells (Herbein *et al.*, 1998). In the CNS, receptors such as galactocerebroside (GalC; Bhat *et al.*, 1991, 1993; Harouse *et al.*, 1991) or co-receptors alone can interact with soluble gp120 and influence pathogenesis. Glycoprotein 41 has also been found to induce a proliferative inhibition in lymphocytes (for reviews, see Denner, 1998; Haraguchi *et al.*, 1995). Synthetic peptides containing 17 amino acids of the gp41 sequence inhibit the mitogen-stimulated and the IL-2-dependent proliferation of T cells, the mixed lymphocyte reaction, and the respiratory burst and chemotaxis of monocytes. Attempts to identify cellular receptors mediating the suppressive effects are in progress but the mechanism has not yet been elucidated.

Interestingly, a natural co-receptor mutation exists which directly influences the interaction with HIV and which is of pathogenetic relevance. A 32 bp deletion in CCR5, which abolishes the virus site of interaction, may confer partial resistance to infection with macrophage-tropic HIV-1 to individuals who carry the mutation (Huang *et al.*, 1996b; Liu *et al.*, 1996; Samson *et al.*, 1996). Haplotype analyses indicate that the mutated allele originated quite recently, approximately 700 years ago in northeastern Europe. The timing and distribution of the mutation suggest that a former epidemic, which exerted enormous selective pressure against CCR5, might have facilitated the rapid distribution of the 32 bp deletion (Libert *et al.*, 1998; Stephens *et al.*, 1998). It has been suggested that in addition to the reduced levels of CCR5, high levels of the chemokines MIP-1 α , MIP-1 β and RANTES may contribute to the clinical resistance or the slow progression of the disease in certain individuals. These findings may be exploited therapeutically by designing substances which block the co-receptor interaction with HIV, or by removing co-receptors by somatic gene therapy (Berger *et al.*, 1999). Viruses expressing the cellular receptors CD4 and CXCR4 as envelope proteins have also been engineered to eliminate gp120-positive infected cells (Mebatsion *et al.*, 1997; Schnell *et al.*, 1997). Viruses bearing these molecules interact with HIV-1-infected

cells in tissue culture and reduce HIV titres in infected T cell lines by a factor of 10000. However, the clinical application of such viruses appears questionable.

Competition for the same receptors: coxsackie viruses and adenoviruses

The non-enveloped capsids of picornaviruses can interact with a variety of cellular proteins (Table 1; Bergelson *et al.*, 1994; Kuhn, 1997; Shafren, 1998; Triantafilou *et al.*, 1999; Ward *et al.*, 1994). Following binding, picornaviruses usually undergo several conformational changes leading to virus entry and uncoating of the genome (Arita *et al.*, 1998; Dove & Racaniello, 1997; Kaplan *et al.*, 1990; Racaniello, 1996). The geometry of the picornavirus and adenovirus interaction with the target cell surface is quite different. Depressions on the icosahedral capsids of some picornaviruses, the so-called canyons, were found to interact with cellular receptors, whereas attachment of adenoviruses is mediated by fibres with globular knobs at their tips projecting from the virus capsids. In spite of these structural differences, some viruses of both families compete for the same receptor, CAR (coxsackie virus-adenovirus receptor; Bergelson *et al.*, 1997; Roelvink *et al.*, 1998). CAR is a 46 kDa transmembrane protein belonging to the immunoglobulin superfamily and containing two extracellular domains. When transfected into hamster cells, this molecule mediates both attachment and entry of coxsackie virus B3 and B4 and adenoviruses 2 and 5 (Bergelson *et al.*, 1997). The binding sites on the adenoviral fibre knobs for CAR have been identified recently, and might now be modelled to develop adenovirus vectors with altered tropism for gene therapy or as antiviral drugs (Bewley *et al.*, 1999; Roelvink *et al.*, 1999).

The attachment and uptake of serogroup C adenoviruses depends on two separate but co-operative events: the interaction of the fibre with an attachment receptor (CAR), and the interaction of the penton base with an internalization receptor, $\alpha_v\beta_3$ and $\alpha_v\beta_5$ integrins (Bergelson *et al.*, 1997; Roelvink *et al.*, 1998; Wickham *et al.*, 1993). The penton base of adenovirus 2 may also interact with β_2 -integrins as attachment receptors on the surface of haematopoietic cells (Huang *et al.*, 1996a). Thus, CAR or β_2 -integrins promote attachment of adenoviruses to cells, and α_v -integrins mediate their internalization via endosomes. Interestingly, some of the coxsackie virus B strains which use CD55 (decay-accelerating factor, DAF) as attachment receptor also require co-receptors of the integrin family for virus entry (Agrez *et al.*, 1997; Shafren *et al.*, 1995).

In order to investigate the internalization mechanism, the three-dimensional structure of soluble recombinant $\alpha_v\beta_5$ molecules bound to adenovirus has been determined. The results suggest a precise spatial arrangement of the five arginine, glycine, asparagine (RGD)-containing protrusions on the penton base promoting integrin clustering and signalling

Table 1. Viruses and cellular receptors discussed in this review

| Virus family (-group) virus* | Receptors | Distribution of receptors | Tropism of the virus | Associated diseases |
|--|---|--|---|--|
| <i>Adenoviridae</i> (subgroup A,C,D,E,F) adenovirus | CAR (Ig superfamily) $\alpha_5\beta_1$ - and $\alpha_3\beta_1$ -integrins $\alpha_4\beta_2$ -integrin | widely widely monocytes | epithelial cells, lymphoid cells | respiratory infection, lymphoid tissues |
| adenovirus C2 | | | | |
| <i>Arenaviridae</i> LCMV (mouse/human) | α -dystroglycan | widely | lymphoid tissue, brain, other tissues (mouse) | febrile disease, lymphocytic choriomeningitis, persistent infection (mouse) Lassa fever |
| LFV | α -dystroglycan | widely | lymphoid tissue reticuloendothelial system | |
| <i>Coronaviridae</i> (serogroup 1) HCoV-229E TGEV (pig) FIPV (cat) | hAPN pAPN fAPN | widely | respiratory tract enteric tract hepatocytes | common cold respiratory, enteric respiratory, enteric, hepatitis, neurologic enteric infection |
| CCV (dog) (serogroup 2) HCoV-OC43 MHV (mouse) | cAPN sialic acid Bgp (Ig superfamily) | widely widely | respiratory tract hepatocytes, brain | common cold respiratory, enteric, hepatitis, neurologic enteric infection |
| BCV (cow) (serogroup 3) IBV (chicken) | 9-O-acetyl-neuraminic acid ? | widely | | respiratory, hepatitis |
| <i>Filoviridae</i> Marburg virus | asialoglycoprotein receptor | hepatocytes | neutrophils, mononuclear cells, endothelial cells, hepatocytes | haemorrhagic fever |
| <i>Flaviviridae</i> dengue virus | heparan sulfate HAR Fc γ R ? | widely ? monocytes/macrophages | monocytes/macrophages | febrile illness, haemorrhagic fever, or shock syndrome |
| HCV | glycosaminoglycan (CD81 ?) | widely | hepatocytes | hepatitis, hepatocellular carcinoma |
| <i>Hepadnaviridae</i> HBV | (HBV-binding factor) | | hepatocytes, PBMC, other tissues | hepatitis, hepatocellular carcinoma |
| DHBV (duck) | carboxypeptidase D (gp180) | widely | | |
| <i>Herpesviridae</i> HSV-1, HSV-2 | mannose-6-phosphate R heparan sulfate HveA (TNFRSF14) HveB/C/D (PVR family) | macrophages, DC widely widely | epithelial cells, neurons | skin lesions, latent neuronal infection, encephalitis (rare) |
| EBV | CD21 (CCP family) second unknown receptor | B cells ? | B cells epithelial cells | infectious mononucleosis, Burkitt's lymphoma, epithelioid carcinoma |
| <i>Orthomyxoviridae</i> influenza A virus | sialic acid | widely | respiratory tract | influenza |
| <i>Paramyxoviridae</i> measles virus | CD46 (CCP family) second unknown receptor | widely ? | respiratory tract, mononuclear cells, endothelial and brain cells | acute measles, acute encephalitis, and SSPE (rare) |
| CDV (dog) | ? | | respiratory tract, lymphoid tissues, brain | distemper, encephalomyelitis |
| NDV (chicken) Sendai V (mouse) | sialic acid sialic acid | widely | epithelial cells | respiratory, enteric |
| <i>Picomaviridae</i> coxsackie virus (CV) A9 CV A13,18,21 CV B1,3,5 CV B | $\alpha_5\beta_1$ -integrin, β_2 -microglobulin ICAM-1 (CD54; Ig superfamily) DAF (CD55; CCP family), $\alpha_5\beta_1$ -integrin CAR (Ig superfamily) | widely widely widely widely | gastrointestinal tract, other tissues | enteric infections, febrile illness, meningitis |
| echovirus 1,8 echovirus 6,7,11,12,13, 20,21,29,33 | $\alpha_5\beta_1$ -integrin DAF (CD55; CCP family) | widely widely | gastrointestinal tract, other tissues | febrile illness, meningitis |
| HAV | HAVcr-1 (Ig superfamily, mucin-like) | widely | gastrointestinal tract, liver salivary gland, kidney, spleen, lymphocytes | hepatitis |
| rhinovirus | ICAM-1, -2 (Ig superfamily) | widely | respiratory tract | common cold |
| poliovirus | PVR (Ig superfamily) | widely | epithelial cells neurons | enteric infection, poliomyelitis (in 1-5% of infections) |
| <i>Retroviridae</i> HIV | CD4 (Ig superfamily) and chemokine receptors (TM7) GaiC (glycolipid) | macrophages, T cells, dendritic cells, microglia brain cells | CD4-positive cells, (m/T-tropic strains), few brain cells | lymphadenopathy, AIDS, encephalopathy |
| FIV (cat) | CXCR4 (TM7 family) | | | feline AIDS |

* Unless indicated in brackets, the viruses infect humans. For explanations of abbreviations see text of the review.

events required for virus internalization (Chiu *et al.*, 1999). The interaction of integrins with RGD-containing peptides can induce caspases and apoptosis (Ruoslahti & Reed, 1999 and references therein). It is not known whether viruses also induce such signals via interaction with integrins.

Adenoviruses have the ability to infect a wide range of tissues and have been identified as the cause of diseases such as respiratory infections, epidemic keratoconjunctivitis, pneumonia, cryptic enteric infection and gastroenteritis (Wadell, 1990). As suggested earlier, the different tropisms of the

adenoviruses probably result from differential receptor usage. Based on the recent findings, chimeric adenoviruses with exchanged fibres or fibre knobs have been constructed to target infections to certain tissues (Stevenson *et al.*, 1997).

Poliovirus: species tropism, but not tissue tropism, is determined by receptors

All three serotypes of poliovirus replicate initially in cells of the oropharyngeal and enteric tract. In the minority of cases (1–5%), virus then invades the CNS, destroys motor neurons and induces myelitis and paralysis. What role do cellular receptors have in the pathogenesis of the disease? The human poliovirus receptor (hPVR, CD155) belongs to the Ig superfamily. It contains three Ig-like extracellular domains and is expressed in four splice variants designated hPVR- α , - β , - γ , - δ (Bernhardt *et al.*, 1994; Koike *et al.*, 1990; Mendelsohn *et al.*, 1989). Domain 1 of hPVR is sufficient to bind the virus (for reviews, see Nomoto *et al.*, 1994; Racaniello, 1996; Wimmer *et al.*, 1994). The viral receptor-binding sites are amino acids located on the floor and at the rim of the canyon-like depressions in the capsid (Colston & Racaniello, 1994; Liao & Racaniello, 1997). It has been suggested that antibodies may not be able to recognize epitopes in this narrow cleft of the canyon and therefore the development of neutralizing antibodies is hampered (Chapman & Rosmann, 1993). Thus, the topography of the receptor-binding site may directly contribute to the pathogenicity.

In man, PVR proteins are expressed in many cells and tissues, including the small intestine, lung, liver, heart, neurons of the spinal cord and the motor end-plate of skeletal muscles (Freistadt, 1994; Leon-Monzon *et al.*, 1995; Nomoto *et al.*, 1994). Since liver, lung and heart are not normally considered to be replication sites of poliovirus, this observation indicates that the susceptibility of tissues to poliovirus is not determined merely by the distribution of PVR. The susceptibility of PVR-positive mononuclear cells in the blood may play a role in the eventual CNS invasion (Freistadt *et al.*, 1993). However, it remains to be investigated which of the PVR isoforms are expressed by which cell type and how the expression is correlated with infection during poliomyelitis. A mouse homologue of hPVR does not bind poliovirus, including those viruses adapted to mice. Thus, hPVR determines the species tropism of poliovirus (for a review, see Nomoto *et al.*, 1994).

In hPVR-transgenic mice, poliovirus induces neurological defects similar to those observed in man. This is a perfect animal model to test the neurovirulence of various poliovirus strains (Deatly *et al.*, 1999; Koike *et al.*, 1991; Ren *et al.*, 1990). Neurons, and not glial cells, were found to be infected and paralysis is caused by direct destruction of motor neurons. Interestingly, in both man and transgenic mice, the neurotropism of poliovirus cannot be explained solely by the tissue distribution of the receptor. Molecular determinants of neurovirulence and attenuation have been located in the 5'-proximal

1122 nucleotides of the viral genome (Macadam *et al.*, 1993). Most mutations in this part of the genome do not alter the receptor usage, but they influence the interaction with intracellular factors. The internal ribosomal entry site within the 5' non-coding region significantly contributes to host range specificity and neurovirulence (Gromeier *et al.*, 1999; Shiroki *et al.*, 1997).

Members of the poliovirus receptor family are also used by α -herpesviruses as cell entry mediators

Cell entry by α -herpesviruses, which have a double-stranded DNA genome of approximately 152 000 bp and encode more than 100 proteins is, in comparison to the smaller and simpler RNA viruses, a much more complex process. In most cases, five viral surface proteins (gB, gC, gD, gH and gL) interact with cellular receptors and mediate virus entry (for a review, see Spear, 1993). Several different cellular surface molecules have been identified as receptors which may act together, consecutively or independently, to effect the uptake of herpesviruses. These include heparan sulfate or chondroitin sulfate proteoglycans (Shieh *et al.*, 1992; Shukla *et al.*, 1999), mannose-6-phosphate receptors (Brunetti *et al.*, 1995) and the herpesvirus entry mediators (Hve) A, B, C and D (Geraghty *et al.*, 1998; Montgomery *et al.*, 1996; Takahashi *et al.*, 1999; Warner *et al.*, 1998). HveA belongs to the tumour necrosis factor receptor family (TNFRSF14), whereas HveB, -C and -D belong to the PVR family. Heparan sulfate appears to be a necessary surface component for virus entry into primary neuronal cells (Immergluck *et al.*, 1998). Is there a functional parallel between the receptor usage of poliovirus and α -herpesviruses resulting in the neurotropism of both viruses?

Heparan sulfate proteoglycans are used by several viruses as initial attachment receptors

The capacity of gD of α -herpesviruses to interact with a variety of receptors, including cell surface proteins of two different families and modified heparan sulfate, is astonishing. Why do these viruses use multiple receptors? Does it allow them to change their tropism in the course of an infection? Virus attachment to cells is normally mediated by gB and gC. However, gD is required for successful entry and is supposed to be involved in the activation of the fusogenic activity of the viral proteins gB and gH/gL. Wild-type strains of HSV-1 and -2 seem to be similar in the use of HveA or HveC for entry but they differ in the use of binding sites generated by sulfotransferases (3-OST-3) on heparan sulfate (Shukla *et al.*, 1999). While the clinical manifestations of disease caused by the two serotypes are indistinguishable, there are differences in their epidemiology and pathogenesis (Corey & Spear, 1986*a, b*; Lafferty *et al.*, 1987). HSV-1 is the usual cause of adult sporadic encephalitis, keratitis and oral mucocutaneous lesions,

whereas HSV-2 is more likely to cause genital lesions, meningitis and neonatal infections. This could be influenced by their differential receptor usage determined by the capacity of HSV-1 to interact with 3-OST-3-modified heparan sulfate (Shukla *et al.*, 1999).

As well as α -herpesviruses, interaction with heparan sulfate has been demonstrated for HIV-1 (Mondor *et al.*, 1998), human cytomegalovirus (Compton *et al.*, 1993), foot and mouth disease virus (Jackson *et al.*, 1996), dengue virus (Chen *et al.*, 1997), Sindbis virus (Byrnes & Griffin, 1998), vaccinia virus (Chung *et al.*, 1998) and adeno-associated virus type 2 (Summerford & Samulski, 1998). It seems possible that heparan sulfate could help these viruses to adhere to a cell before further higher affinity receptors induce adhesion strengthening and mediate entry (Haywood, 1994). This model is supported by results obtained using the flaviviruses, dengue virus and TBEV. Dengue virus binds first to heparan sulfate and then to a high affinity receptor, which induces endocytosis and subsequent cell membrane fusion (Chen *et al.*, 1997; Hung *et al.*, 1999; Putnak *et al.*, 1997). Thus, heparan sulfate proteoglycans on the cell surface can be used as initial attachment receptors by several viruses.

The tropism of the γ -herpesvirus Epstein–Barr virus is mediated by alternative usage of the complement receptor CD21 and an unknown receptor

Epstein–Barr virus (EBV) glycoproteins gp350/220 mediate the attachment of virus to cellular receptors. These heavily glycosylated envelope proteins are the product of a single EBV gene, which is expressed as alternatively spliced RNAs (Beisel *et al.*, 1985). CD21, the human receptor for the complement protein C3dg, has been identified as a cellular receptor for EBV (Nemerow *et al.*, 1986; Nemerow & Cooper, 1992; Tanner *et al.*, 1987). CD21 is a single transmembrane protein of approximately 145 kDa containing 15 to 16 complement control protein (CCP) domains. The first two amino-terminal CCP domains of CD21 bear the virus-binding sites (Lowell *et al.*, 1989). CD21 is expressed by B cells, follicular dendritic cells and a subset of thymocytes. Electron microscopic studies, as well as biochemical studies, have shown that EBV enters human peripheral blood B cells via large uncoated endocytic vesicles. In contrast to the entry pathway in primary B cells, EBV can directly fuse with the plasma membrane of target cells such as the B cell line Raji. Fusion is mediated by the EBV envelope protein gp85 (Nemerow & Cooper, 1992).

Interestingly, binding of EBV, or beads bearing the viral envelope proteins gp350/220, induce the capping and endocytosis of CD21 (Tanner *et al.*, 1987; Tedder *et al.*, 1986). Thus, as found for viruses such as HIV and measles virus (MV), infection of cells with EBV leads to the downregulation of its receptor, CD21, from the cell surface. The normal function of

CD21 is not completely understood, but it certainly plays an important role in antigen-specific B cell activation and differentiation, processes which are disturbed by the interaction with EBV. After the binding of ligands, CD21 and the antigen receptor become associated in the B cell membrane. In addition, further cell surface molecules, such as CD19 and CD81, associate with CD21 and form a multimolecular complex, which is probably involved in signal transduction. Antigen localization and the generation of B memory cells are largely dependent on the presence of the complement protein C3, and soluble CD21 fragments can suppress the immune response in mice.

EBV, the causative agent of infectious mononucleosis, is closely associated with Burkitt's lymphoma and several benign and malignant lymphoproliferative diseases occurring in immunodeficient individuals. The cell tropism of EBV in these diseases can be explained by the use of CD21 as receptor. However, the EBV genome is also found in epithelial cell tumours such as nasopharyngeal and gastric carcinoma which do not express CD21. Therefore, the presence of a receptor other than CD21 on epitheloid gastric cells has been suggested (Hsu *et al.*, 1996; Kasai *et al.*, 1994; Kim *et al.*, 1998; Yoshiyama *et al.*, 1997). A very efficient mode of infection with EBV, much more efficient (up to 800-fold) than infection with cell-free virus, is direct cell-to-cell spread (Imai *et al.*, 1998).

Measles virus: also more than one receptor

MV is a monotypic negative-strand RNA virus causing acute measles accompanied by a transient immunosuppression, acute post-infectious encephalomyelitis and CNS diseases based on MV persistence (for a review, see Griffin & Bellini, 1996). The envelope glycoproteins haemagglutinin (H), as a tetramer, and the fusion protein (F), probably as a trimer, interact with receptors on the target cell surface (Langedijk *et al.*, 1997 and references therein). A complement regulatory protein containing four CCP domains, CD46, was identified as a receptor for vaccine strains of MV (for reviews, see Dörig *et al.*, 1994; Gerlier *et al.*, 1995). CD46 is expressed on almost all human cells except erythrocytes and cells in the CNS such as oligodendrocytes and a proportion of neurons and astrocytes (Johnstone *et al.*, 1993; Ogata *et al.*, 1997). Binding sites for MV H protein have been mapped to the first two extracellular CD46 domains (Buchholz *et al.*, 1997; Casasnovas *et al.*, 1999; Hsu *et al.*, 1997, 1999; Manchester *et al.*, 1997). MV infection of cells can result in the secretion of cytokines such as interferon- α/β , tumour necrosis factor- α , interleukin-1 and interleukin-6. Binding of MV to CD46 in the absence of infection can induce kinase-mediated signals in the contacted cells which contribute to the induction of cytokines (Ghali & Schneider-Schaulies, 1998; Wong *et al.*, 1997). In the presence of interferon- γ , the synthesis of nitric oxide by macrophages is enhanced through the cytoplasmic domain of CD46 in response to MV infection (Hirano *et al.*, 1999).

As in the case of EBV and HIV, MV can induce the down-regulation of its receptor from the cell surface after infection or after the extracellular contact of cells with MV H protein (Krantic *et al.*, 1995; Naniche *et al.*, 1993; Schneider-Schaulies *et al.*, 1996). Since the natural function of CD46 is to act as a co-factor for the cleavage of the complement factors C3b and C4b, and to protect cells from lysis by autologous complement (for a review, see Liszewski *et al.*, 1991), CD46-modulation by MV enhances the sensitivity of cultured cells to complement (Schnorr *et al.*, 1995). *In vivo*, this may cause a rapid clearing of infected cells and thus contribute to the attenuation of such downregulating MV strains. Different MV isolates vary considerably in their capacity to interact with CD46. In contrast to vaccine strains, a number of recent wild-type isolates do not downregulate CD46 (Schneider-Schaulies *et al.*, 1995*a, b*). This capacity is closely related to amino acids at positions 451 and 481 in the H protein (Bartz *et al.*, 1996; Lecouturier *et al.*, 1996).

Recently, B cell lines have been used to isolate a number of MV strains which obviously do not interact with CD46 (Bartz *et al.*, 1998; Hsu *et al.*, 1998; Tanaka *et al.*, 1998). MV isolates that do not interact with CD46 have a preferred tropism for lymphoid cells. Studies using recombinant MVs (Radecke *et al.*, 1995) with defined envelope proteins have confirmed these findings (Johnston *et al.*, 1999). It remains to be seen whether MVs present during the acute disease *in vivo* interact with CD46, and what consequences the differential receptor usage might have for the pathogenicity of acute and persistent MV infections.

The most intriguing question at present is how cellular receptors are involved in MV-induced immunosuppression. During immunosuppression, the number of peripheral blood lymphocytes is reduced and activated T cells are depleted from the circulation (Nanan *et al.*, 1999; for reviews, see Griffin, 1995; Schneider-Schaulies & ter Meulen, 1999). *Ex vivo*, the proliferative response of peripheral blood lymphocytes to antigens or mitogens is strongly inhibited. The MV-induced immunosuppression is a multi-factorial process which may be influenced by soluble factors such as IL-12 (Karp *et al.*, 1996) and the direct contact of the viral H-F glycoprotein complex and the surface of lymphocytes (Schlender *et al.*, 1996). The contact requirements for the proliferative inhibition of lymphocytes have been defined by using recombinant viral glycoproteins and recombinant viruses, and CD46 appears not to be required (Niewiesk *et al.*, 1997*a*; Schlender *et al.*, 1996). Recent data indicate that although a native H-F complex is obligatory, the process of membrane fusion is not required for inhibition of T cell proliferation (Weidmann *et al.*, 2000). As in the case of HIV gp41, cellular receptors involved in the proliferative inhibition of lymphocytes have not yet been identified.

MV-induced CNS diseases and the mechanisms supporting virus persistence have been studied extensively (for a review, see Schneider-Schaulies *et al.*, 1999). The influence of the virus attachment protein H on neurovirulence was investigated

using antibody escape mutants in rats (Liebert *et al.*, 1994) and in a mouse model using a recombinant MV in which the H gene of the Edmonston strain was replaced by the H gene of the rodent-adapted neurovirulent MV strain CAM (Duprex *et al.*, 1999*a*). After intracerebral injection into suckling mice only the recombinant virus bearing CAM-H, and not the virus with the Edmonston-H, induced a neurological disease. However, the neurovirulence of the recombinant virus was reduced compared to the wild-type CAM strain, indicating that other viral genes also contribute to CAM-induced pathogenicity.

Recently, CD46-transgenic mice have been used to define the role of the cellular receptor for the neurotropism and virulence of MV. In such animals the normally apathogenic Edmonston strain is able to cause widespread neuronal infection and death in neonates, and scattered infection of neurons of adult mice (Rall *et al.*, 1997). These findings clearly demonstrate that expression of a suitable receptor on neurons can mediate neurovirulence. However, in the periphery of adult CD46-transgenic mice or rats, receptor expression did not lead to a significant increase of susceptibility for MV, suggesting an intracellular block of virus replication (Blixenkron-Moller *et al.*, 1998; Horvat *et al.*, 1996; Niewiesk *et al.*, 1997*b*). In contrast, a different line of CD46-transgenic mice seems to be more generally susceptible to MV infection (Oldstone *et al.*, 1999). Clearly, these differences in the susceptibility of different CD46 transgenic mice need to be further investigated. In interferon- α/β -receptor-deficient mice expressing a CD46 transgene, intracerebral inoculation of adult animals with low doses of MV caused encephalitis (Mrkic *et al.*, 1998). These findings underline the importance of the interferon system and associated intracellular factors for the virulence of this virus.

Receptor interactions of lymphocytic choriomeningitis virus (LCMV) strains determine pathogenesis

Infection of mice with LCMV has been extensively studied as a model system for virus persistence, immune-mediated pathology and immunosuppression (Borrow *et al.*, 1995). LCMV is the prototype arenavirus with a single-stranded, ambisense RNA genome of two segments, 7220 and 3376 nucleotides, containing four open reading frames. The receptor-interacting envelope glycoprotein G is cleaved to an external G1 and a transmembrane G2 glycoprotein. LCMV enters rodent target cells via receptor-mediated endocytosis and pH-dependent fusion (Borrow & Oldstone, 1994). A cellular receptor for LCMV has recently been identified (Borrow & Oldstone, 1992; Cao *et al.*, 1998 and references therein). Interestingly, several strains of LCMV and other arenaviruses, including Lassa, Oliveros and Mobala fever virus, bound to the same protein, namely α -dystroglycan. Dystroglycan is encoded by a single gene and processed into α - and β -chains, which form a complex. The dystroglycan complex is

expressed in a wide variety of tissues and cells, and mediates interactions of cells with the extracellular matrix.

Persistent infection of C3H/St mice with certain clones of LCMV strain WE can cause growth hormone deficiency syndrome (GHDS). Reassortant studies indicate that a single amino acid exchange at position 153 in the viral envelope protein G1 is sufficient to allow infection of the growth hormone-producing cells and cause GHDS (Teng *et al.*, 1996). It is not yet known whether this change in the virus tropism and pathogenicity is due to alterations in receptor usage of such clones. Another pair of LCMV strains, strain Armstrong and clone 13, have been found to cause differential immunosuppressive effects in mice (Borrow *et al.*, 1995). Mice infected with LCMV Armstrong rapidly clear the infection, whereas mice infected with clone 13 develop a generalized immunosuppression associated with loss of interdigitating dendritic cells and failure to stimulate the proliferation of T cells. These two strains differ in only two amino acids, at positions 260 in the G1 protein and 1079 in the RNA polymerase. A difference in the tropism of the two strains has been found, which is probably caused by a stronger binding affinity of clone 13 to the LCMV receptor. This could enable clone 13 to infect cells expressing limited amounts of α -dystroglycan, or to infect cells more effectively than the Armstrong strain. These findings suggest an association between receptor usage and pathogenicity.

Coronaviruses: receptors determine the host range

Coronaviruses are a group of enveloped, positive-strand RNA viruses. The closely related human coronavirus (HCV) 229E, porcine transmissible gastroenteritis virus (TGEV), feline infectious peritonitis virus (FIPV) and canine coronavirus (CCV) belong to serogroup 1 and are antigenically and genetically distinct from the so-called haemagglutinating coronaviruses, such as HCV-OC43, murine hepatitis virus (MHV) and bovine coronavirus (BCV), which belong to serogroup 2, and the avian infectious bronchitis virus (IBV), which comprises serogroup 3 (Table 1; for a review, see Siddell, 1995). The envelopes of all coronaviruses contain a spike protein (S), which binds to receptors on the target cell membrane. Some viruses in serogroup 2 have in addition a haemagglutinin esterase, which binds to cell membrane molecules bearing 9-O-acetylated neuraminic acid.

Coronaviruses of serogroup 1 interact species-specifically with aminopeptidase-N (APN) as the attachment receptor (Delmas *et al.*, 1992; Kolb *et al.*, 1996; Yeager *et al.*, 1992). APN is a type II transmembrane glycoprotein and belongs to the family of membrane-bound metalloproteinases (Ashmun *et al.*, 1992). The protein is found in large amounts on the microvillar membrane of the small intestine and is also present on renal proximal tubule epithelium, synaptic membranes of the CNS and cells of the granulocytic and monocytic lineage (Delmas *et al.*, 1994; Look *et al.*, 1989; Olsen *et al.*, 1988). Human APN

(CD13) is used as a receptor by HCV 229E not only for infection of lung fibroblasts but also for infection of neuronal and glial tissue culture cells (Lachance *et al.*, 1998). Interestingly, the host range of coronaviruses is associated with receptor usage, while the disease type is not (Hegyi & Kolb, 1998; Tresnan & Holmes, 1998).

The receptor for MHV was initially identified as the biliary glycoprotein Bgp1^a, a member of the carcinoembryonic antigen (CEA) family of cell surface proteins (Dveksler *et al.*, 1991; Williams *et al.*, 1991). Bgp1^a consists of four immunoglobulin-like extracellular domains, a transmembrane domain, and either a long or a short cytoplasmic tail. It is expressed at the sites of virus entry such as the apical membranes of respiratory and intestinal epithelial cell layers, the luminal surfaces of endothelial cells, on hepatocytes, B lymphocytes and macrophages (Coutelier *et al.*, 1994; Godfraind *et al.*, 1995). In the liver, Bgp1^a expression correlates with infection of hepatocytes and endothelial cells, leading to the development of hepatitis. However, other cells expressing this molecule, such as endothelial cells of the CNS, are not infected (Godfraind & Coutelier, 1998). Although the molecular basis for this observation is not known, it may explain how the blood-brain barrier prevents dissemination of MHV A59 into the brain.

MHV A59 binds only to Bgp1^a on intestinal brush border membranes of susceptible mice, and not to membranes from humans, cats, dogs, pigs, cows, rabbits, rats, cotton rats or chickens (Compton *et al.*, 1992). Other members of the CEA family in addition to Bgp1^a, namely Bgp1^b (Dveksler *et al.*, 1993a, b; Yokomori & Lai, 1992), Bgp2 (Nedellec *et al.*, 1994) and brain CEA (Chen *et al.*, 1995) may also serve as receptors, with different binding efficiencies (Zelus *et al.*, 1998). Bgp1^a is the major receptor for MHV in susceptible mice, whereas Bgp1^b, which is used less efficiently as a receptor, is expressed homozygously by resistant SJL mice (Williams *et al.*, 1990).

A change of receptor usage may be associated with the transition of the host range of coronaviruses from one species to the other. Conversely, experimental interspecies transfer of MHV also changed the receptor usage (Hensley *et al.*, 1998). The S protein of MHV has recently been exchanged by targeted RNA recombination for the S protein of FIPV (Kuo *et al.*, 2000). The resulting chimeric virus acquired the ability to infect feline cells and lost the ability to infect murine cells, supporting the view that the host range of coronavirus infections is mainly determined by receptor usage.

Do the known receptors for hepatitis viruses explain their liver tropism?

A cellular receptor for hepatitis A virus (HAV) has been identified by screening a cDNA expression library of African green monkey kidney cells with an infection-inhibiting antibody (Kaplan *et al.*, 1996). The HAV cellular receptor 1 (HAVcr-1) is a class I integral mucin-like membrane glycoprotein of unknown function (Kaplan *et al.*, 1996; Thompson

et al., 1998). As shown for other picornaviruses, low pH during the uptake of HAV by receptor-mediated endocytosis induces conformational changes in its capsid which may be the first step to uncoating the HAV genome (Bishop, 1999). huHAVcr-1 is expressed in all human organs, with higher levels in the kidney and testis (Feigelstock *et al.*, 1998). Since extrahepatic sites of HAV replication were found in the gastrointestinal tract, liver, salivary glands, kidney, spleen and lymph nodes of experimentally infected primates, the liver-specific pathogenesis of HAV cannot easily be explained (Asher *et al.*, 1995). The detection of HAV in various organs may correlate with the expression of HAVcr-1. However, it is likely that unknown co-receptors or intracellular factors are required to render cells fully susceptible to HAV infection.

Human hepatitis B virus (HBV), an enveloped hepadnavirus with a partially double-stranded DNA genome of approximately 3200 nucleotides in length, binds to a 50 kDa binding factor (HBV BF) present in serum and on the surface of cells (Budkowska *et al.*, 1993). HBV BF is a neutral metalloproteinase which shares substrate specificity with a family of membrane-type matrix metalloproteinases. Treatment of HBV with the metalloproteinase results in cleavage of the N-terminal part of the pre-S2 envelope protein, and probably induces a conformational change in the pre-S1 domain that enables cell membrane attachment and virus entry into T lymphocytes (Budkowska *et al.*, 1997). Since an inhibitor of the metalloproteinase blocked both processes, the host-dependent proteolytic activation of the envelope proteins seems to be essential for HBV entry into cells. The tissue tropism of HBV may be determined by this process of envelope activation and not by cellular receptors, which might be expressed ubiquitously (Budkowska *et al.*, 1997; Köck *et al.*, 1996).

An interesting mechanism has been proposed for the specific uptake of duck hepatitis B virus (DHBV) into hepatocytes using carboxypeptidase D (gp180) as a cellular receptor (Breiner *et al.*, 1998; Kuroki *et al.*, 1995; Tong *et al.*, 1999; Urban *et al.*, 1998). This peptidase is a Golgi-resident protein which is found only to a limited extent at the external cell surface. It cycles to and from the plasma membrane and in doing so, it may function as a carrier leading to the endocytosis of DHBV (Breiner *et al.*, 1998). In spite of the high affinity binding of the DHBV surface protein to gp180, expression of gp180 in heterologous cells did not render them permissive to infection, suggesting that a species-specific co-receptor or co-factor is required for virus entry (Breiner *et al.*, 1998). The highly specific infection of the liver by DHBV does not correlate with the ubiquitous gp180 expression, suggesting other mechanisms for targeting the virus to the liver.

Suramin, a polyanionic compound similar to heparin, was found to block HCV binding to human hepatoma cells at a concentration similar to that reported to be effective against dengue virus, suggesting an interaction of HCV with glycosaminoglycans on the cell surface (Chen *et al.*, 1997; Garson *et al.*, 1999). In addition, it was recently found that the

E2 glycoprotein of HCV binds specifically to CD81, a transmembrane protein of the tetraspanin family (Pileri *et al.*, 1998). It is not yet clear whether CD81 acts as a cellular receptor for attachment and entry of HCV into target cells. CD81 is involved in a number of biological responses including cell adhesion, proliferation and differentiation of T and B lymphocytes (Levy *et al.*, 1998). Interestingly, the HCV E2 protein, after binding to CD81, induced aggregation of lymphoid cells and inhibited the proliferation of a B cell line (Flint *et al.*, 1999). This might have important consequences for the pathogenesis of HCV. Since glycosaminoglycans and CD81 are expressed by a wide variety of cells, additional specific factors must determine the liver tropism of HCV.

Taken together, there is no obvious common receptor-mediated pathway for hepatic viruses and none of the cellular receptors known so far can explain the specific liver tropism and pathogenesis caused by these viruses. Interestingly, a receptor for Marburg virus, the asialoglycoprotein, is expressed specifically on liver cells, although this virus has a quite different tropism (Becker *et al.*, 1995). Marburg and Ebola viruses infect a wide spectrum of cells including neutrophils, mononuclear cells, endothelial cells, fibroblasts and hepatocytes, and cause fulminant haemorrhagic fevers. Thus, this liver-specific receptor is used by a virus with a much broader tropism. The viral glycoprotein gene encodes three forms of the G protein: two secreted soluble forms, sGP and GP1, and the membrane bound GP1/2, which are involved in the virus-specific pathogenesis (for a review, see Klenk *et al.*, 1998). The asialoglycoprotein receptor on hepatocytes may serve as a liver-specific receptor for Marburg virus, thereby explaining its liver tropism. However additional receptor molecules on other target cells must be postulated. The asialoglycoprotein receptor might be an attractive tool to target recombinant viruses as chemotherapeutic agents to the liver (Bitzer *et al.*, 1997).

Cell-to-cell spread of viruses contributes to pathogenesis, but may not depend on cellular receptors

It was observed in the late 1960s that the MV ribonucleoprotein complex spreads in the CNS in the virtual absence of the viral envelope proteins and infectious particles. Cell-to-cell spread of MV was demonstrated *in vivo* and in tissue culture. It most likely involves localized fusion events at cell contact points, but CD46 is not required (Allen *et al.*, 1996; Duprex *et al.*, 1999b; Firsching *et al.*, 1999; Lawrence *et al.*, 2000; McQuaid *et al.*, 1998; Meissner & Koschel, 1995; Urbanska *et al.*, 1997). The velocity of virus spread also depends on the cytoplasmic parts of the viral glycoproteins and considerably contributes to pathogenesis (Cathomen *et al.*, 1998a, b). In the case of canine distemper virus (CDV), another morbillivirus, antibodies to the cellular transmembrane molecule CD9 inhibit the CDV-induced formation of syncytia (cell-cell fusion), but not binding and uptake of virus (virus-cell

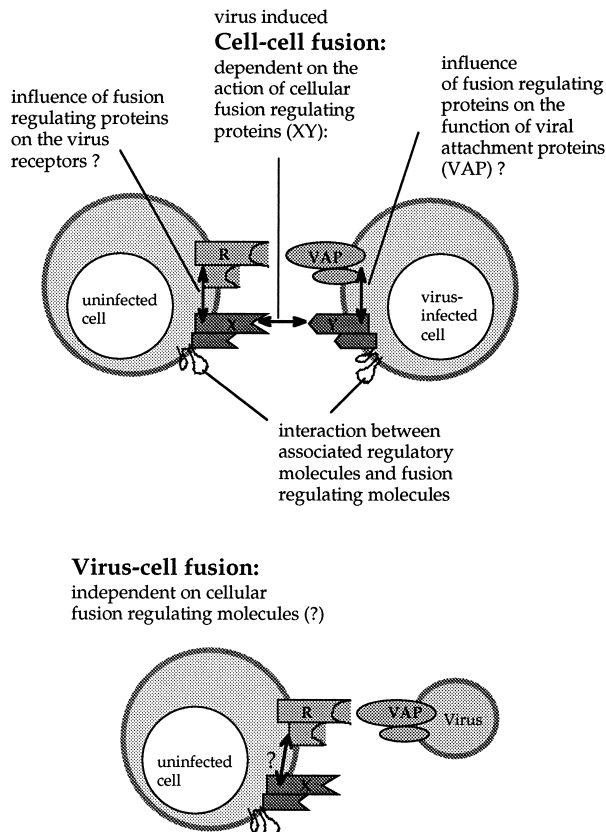


Fig. 2. Differences between cell–cell and virus–cell fusion. When an infected cell fuses with an uninfected cell, cellular surface molecules (XY) on both cells play a role in regulating the fusion, while in the case of virus–cell fusion, such molecules are not present on the virion.

fusion; Löffler *et al.*, 1997; Schmid *et al.*, 2000). In contrast, it has been demonstrated for feline immunodeficiency virus (FIV) that antibodies to CD9 block the assembly or release of the virus (De Parseval *et al.*, 1997; Willett *et al.*, 1997). Obviously cell-to-cell spread and the infection of cells with extracellular virus involve different mechanisms and different cell surface molecules, as hypothetically presented in Fig. 2.

The involvement of viral proteins in the infection of cells via exogenous virus particles in comparison to the cell-to-cell transmission is an important facet of the herpesvirus infection. The viral glycoproteins gE and gI of HSV play a role in cell-to-cell spread across junctions formed between fibroblasts and neurons, whereas mutants lacking both glycoproteins can infect fibroblasts as extracellular virus (Balam *et al.*, 1984; Dingwell *et al.*, 1994). In addition, the modification of glycoproteins with mannose-6-phosphate and mannose-6-phosphate receptors influences the virus plaque size (Brunetti *et al.*, 1995). Similar results have been described with another α -herpesvirus, pseudorabies virus (Karger *et al.*, 1998; Klupp *et al.*, 1999). These data show that the process by which HSV spreads from cell to cell is mechanistically different from virus entry into cells and requires the presence of different cellular receptor molecules.

The cellular fusion-regulating proteins (FRP)-1 and -2 play a role in cell–cell fusion. These proteins were initially found with monoclonal antibodies that stimulate the Newcastle disease virus (NDV)-induced cell–cell fusion (Ito *et al.*, 1987, 1992; Ohgimoto *et al.*, 1995). Interestingly, antibodies to FRP-1 stimulate NDV-induced and inhibit parainfluenza virus-induced cell fusion (Okamoto *et al.*, 1997). Recent data indicate that HIV-induced cell fusion is also regulated by FRP-1, integrins and the activation of tyrosine kinases (Ohta *et al.*, 1994; Tabata *et al.*, 1998). In addition, HIV DNA may also spread from cell to cell in a CD4-independent fashion via apoptotic bodies (Spetz *et al.*, 1999). Also, the syncytium formation of human T cell leukaemia virus type 1 is regulated in a cell-type-specific manner by ICAM-1, ICAM-3 and VCAM-1 and can be inhibited by antibodies to integrin β_2 or β_7 (Daenke *et al.*, 1999).

Conclusions

Infection of cells by cell-free virus and virus spread from cell to cell are different processes which may depend on the presence of different cellular surface molecules. In infected organs, the cell-to-cell spread contributes significantly to the pathogenesis of a viral disease. Underlying mechanisms are not well understood and require more research in the future. There are several viruses for which the host-specificity depends on their cellular receptors, whereas a specific organ or cell tropism appears often to be influenced by still unknown factors. Experiments are being undertaken to define the potential of certain viruses to change their host ranges. These are necessary steps in determining biosafety in xenotransplantation and gene therapy. Signal transduction as a consequence of a virus binding to its receptor is an important mechanism that influences virus cytopathogenicity and the immune response. A major impact on pathogenesis is due to the immunosuppressive capacity of many viruses which in part can also be exerted via cell surface receptor interactions. The increasing number of systems in which recombinant viruses can be applied will help to further investigate such virus–receptor interactions and to define the consequences of these interactions for tropism, virulence and pathogenesis.

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