Review

Molecular mechanisms of measles virus persistence

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Abstract

As measles virus causes subacute sclerosing panencephalitis and measles inclusion body encephalitis due to its ability to establish human persistent infection, without symptoms for the time between the acute infection and the onset of clinical symptoms, it has been the paradigm for a long term persistent as opposed to chronic infection by an RNA virus. We have reviewed the mechanisms of persistence of the virus and discuss specific mutations associated with CNS infection affecting the matrix and fusion protein genes. These are placed in the context of our current understanding of the viral replication cycle. We also consider the proposed mechanisms of persistence of the virus in replicating cell cultures and conclude that no general mechanistic model can be derived from our current state of knowledge. Finally, we indicate how reverse genetics approaches and the use of mouse models with specific knock-out and knock-in modifications can further our understanding of measles virus persistence.

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Keywords: Measles virus; Persistent infection; Subacute sclerosing panencephalitis; Brain receptor; Mechanisms of persistence; Pathogenesis

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1. The scope of the review

Measles virus (MV) still provides one of the main paradigms of a long-term persistent infection by an RNA virus due to its involvement in the disease subacute sclerosing panencephalitis (SSPE), a progressive fatal neurological disease caused by high levels of neuronal infection by MV in the central nervous system (CNS). Hence, there has always been an interest in studying the underlying mechanisms of MV persistence. Initially, in the late 1960s and the 1970s, this was studied using cell cultures. However, with the advent in the 1980s and early 1990s of cDNA cloning and sequencing technology it became possible to examine virus genomes present in autopsy material obtained from the CNS of patients. This review will briefly recapitulate the main findings of the earlier studies and will then concentrate on setting out what has been found since the early 1990s. It will illustrate the utility of reverse genetic approaches and transgenic mouse studies and show how these, in the future, may further our understanding of viral persistence in a mechanistic sense. To date no study has been able to explain why the virus is able to persist. As such we use this review to highlight the most pertinent questions which remain to be addressed.

2. Subacute sclerosing panencephalitis and measles inclusion body encephalitis

The main impetus for the study of MV persistence has come from the discovery that MV was the cause of SSPE, a human CNS disease that manifests itself long after the acute infection with the virus. MV infection is associated with neurological complications in a small minority of cases. About 1:1000 cases will suffer post-infection encephalitis, which involves mainly perivascular demyelination (Litvak et al., 1943). This often fatal complication appears to be autoimmune in nature as no virus can be demonstrated in the brain of such patients. SSPE has been reported to occur in 1:300,000 cases. However, more recent data suggests that it is much more prevalent and can follow acute MV infection in 1:10,000 cases (Takasu et al., 2003). On average, symptoms present 8 years after the acute infection, but this ranges from 9 months to 30 years. Acute infection below the age of two is a risk factor in this disease, which, as yet inexplicably predominates in males at a 2.5:1 ratio (Halvey et al., 1980). The disease manifests itself in severe demyelination and profound infection of neurones. In the latter stages of SSPE small numbers of oligodendrocytes, astrocytes and endothelial cells have been shown to be affected (Kirk et al., 1991). This inevitably leads to severe neurological deficits and death of the patient. One of the longest recorded patients carried the persistent infection over three decades before the onset of symptoms. In terms of the duration of the symptomatic period, there is a report of a 52 years old who died 4 years after diagnosis (Tanaka et al., 1987). There is no evidence for a reduction in the cell-mediated immune responses to MV in SSPE patients. Furthermore, antibody responses lead to hyperimmunity with extremely high titres of neutralising antibody in both the serum and cerebrospinal fluid (CSF) of patients. The CSF contains oligoclonal bands specific to MV and it has been demonstrated that the antibodies present in these have undergone affinity maturation (Smith-Jensen et al., 2000).

In immuno-compromised patients, measles can give rise to an additional CNS infection, measles inclusion body encephalitis (MIBE) (ter Meulen et al., 1983). In contrast to SSPE, MIBE is not associated with a hyperimmune antibody response to measles proteins or oligoclonal bands in the CNS. Recently MIBE caused the death of a 13-year-old boy who had been treated for chronic granulomatous disease by stem cell therapy. Neither the patient nor the stem cell donor had apparent recent measles exposure or vaccination and neither had visited a region of the world where MV was endemic (Freeman et al., 2004). The simplest explanation may be persistence of the virus in either the donor or the recipient. Nevertheless repeat exposure cannot be ruled out in this case as the virus is highly infectious.

Other suggested sequelae of MV infection are multiple sclerosis, chronically active autoimmune hepatitis, Paget’s disease, osteorhoritis, Crohn’s disease and autism among many other diseases (e.g. Reddy et al., 1999). However, no confirmed evidence has been presented to substantiate these associations, let alone prove a causative relationship and as such discussion of these falls outside the scope of this review.

3. MV: the virus and its replication

In order to understand what is known of the molecular mechanisms of MV persistence it is first necessary to describe the molecular biology and pathology of MV.

3.1. Virus

MV is an enveloped RNA virus classified in the family Paramyxoviridae (Griffin, 2001) in the genus Morbillivirus
Fig. 1. Schematic representation of the virion membrane, genome organisation and the life-cycle of measles virus including the receptors used by the wild-type and vaccine viruses. Transcription units (TU), and messenger RNAs and proteins are not drawn to scale.

(Fig. 1). The lipid bilayer membrane is derived from the host cell and is decorated with a fringe of spikes formed by two viral glycoproteins, the fusion (F) and the haemagglutinin (H) proteins. In the virion the F (type I) glycoprotein oligomerises as a homotrimer whereas the H (type II) glycoprotein probably exists as a tetrameric dimer-of-dimers. The F protein is formed as an inactive precursor (F0), which is biologically activated by a proteolytic cleavage involving furin-like pro- teases (Maisner et al., 2000) to generate the F1 and F2 protein subunits, which are linked by a single disulphide bridge. In contrast to some other enveloped viruses, the proteolytic enzymes involved are so widespread that biological activation of the F glycoprotein does not appear to constitute a limiting factor in virus spread. The H and F glycoprotein homo-oligomers interact with each other to form the biologically active fusion complex (Wild et al., 1991). After binding of the H glycoprotein to cell surface receptor(s), it is likely that a structural change in the F protein is induced which activates the fusion process but the exact stoichiometry and molecular details are unknown. The inner leaflet of the virion membrane is “coated” with a hydrophobic protein called the matrix (M) protein (Fig. 1). This protein associates with both the short cytoplasmic tails of F and H and the helical ribonucleoprotein (RNP) nucleocapsid containing the genome. It plays a role in the budding of the virus from the plasma membrane.

3.2. Genome organisation

Measles virus RNP is 1 μm in length and 18–21 nm in diameter (Lund et al., 1984) and consists of the negative sense
viral genome and at least three associated viral proteins. A recent study has demonstrated that the virions can contain more than one RNP (Rager et al., 2002). The genome is a 15,894 nucleotide, non-segmented RNA molecule of negative polarity (Fig. 1). It contains six transcription units (TUs) which are separated by non-transcribed intergenic (Ig) sequences comprised of three nucleotides. The six TUs are preceded by a 3′ leader and are followed by a 5′ trailer (Fig. 1).

Mollivirus genomes are unique within the Paramyxoviridae in that they contain a very long non-coding region of nearly 1000 nucleotides between the M and F open reading frame (ORF). The region is GC rich and it is likely to fold into complex secondary RNA structures. The function of this region is not well understood. The intergenic sequence between the M and F genes is placed almost in the middle of this region.

The complete nucleotide sequence has been determined for several vaccine and wild-type strains of MV. The genome encodes at least eight proteins (Griffin, 2001) (Fig. 1). Three of these, the nucleocapsid (N), phospho-(P) and large (L) proteins, comprise the transcriptionally active RNP. At least two further non-structural proteins are generated from the gene encoding the P protein and as such this gene is sometimes designated P/V/C. The C protein is translated from an overlapping reading frame and is 186 amino acids in length. Whilst the function of the C protein is currently unknown, virus mutants lacking the protein have been propagated successfully in tissue culture (Radecke and Billeter, 1996) but they failed to replicate to a significant level in human thymus implants present in a SCID mouse model and spread within the animals (Radecke and Billeter, 1995). These stop/start events are mediated by a 3′ leader and are followed by a 5′ trailer (Fig. 1). It is probable that the viral RNA-dependent RNA polymerase (RdRp) not only consists of the P and L proteins but it may also involve unknown host cell proteins in addition to cytoskeletal components such as actin and tubulin (Moyer et al., 1990). The RdRp binds to the promoter sequences in the first 100 nucleotides at the 3′ end of the genomic RNA. Transcription terminates just before an intergenic trinucleotide at a gene end (GE) sequence (Fig. 1). For example, at the end of the N gene the RdRp encounters a consensus polyadenylation signal sequence of 3′-YYAU(U/C)/NNUUU-5′ which leads to polyadenylation of the mRNA by slippage on the U-rich template. The intergenic sequence (3′-GAA-5′) is not transcribed and transcription restarts at the 3′ end of the P/V/C gene at a consensus gene start (GS) sequence of 3′-UCCYY/N/UUCY/C/5′ (Radecke and Billeter, 1995). These stop/start events are repeated at the ends of the P, M, F, H and L genes. There is a finite chance that the RdRp will detach from the template at each intergenic junction and this gives rise to a gradient of gene expression in which the promoter proximal genes (i.e. N and P/V/C) are transcribed much more frequently into mRNA than the promoter distal genes (i.e. H and L).

During replication the nascent RNA molecule is immediately encapsidated by N protein and the GE, Ig trinucleotide and GS signals are ignored. This gives rise to an RNP containing the positive stranded RNA antigenome molecule. These have a strong promoter sequence at their 3′ end, which allows the generation of (−)RNP. These are transported to the cell membrane where they associate with viral M protein and the glycoproteins in lipid raft structures from which the RNPs bud to form new virus particles.

Development of systems during the last decade which permit the generation of recombinant MV, “virus rescue” (Radecke et al., 1995) has opened the door to mechanistic studies, not only of persistence and the role of specific genes in this process, but also dissection of the roles of individual genes in isolation or in combination with others.

### 3.3. Virus entry and cell surface receptors

Measles virus attaches to the host cell through the interaction of the viral glycoproteins with cellular receptors (Fig. 1). The H protein is probably the most important attachment protein but it is likely that the interaction of the complete fusion complex with receptors and possibly co-receptors is required for fusion of the viral envelope with the host cell membrane. CD46, also known as membrane cofactor protein, which plays a role in protecting cells from complement lysis, is a cellular receptor for some laboratory adapted MV vaccine strains (Dorij et al., 1993; Naanche et al., 1993). In cells infected with these MV strains (but not in those infected with wild-type strains), CD46 is down-regulated from the cell surface and this renders the cells more susceptible to complement lysis (Schneider-Schaulies et al., 1995b). Most wild-type viruses do not use CD46 but instead use CD150 (SLAM) as receptor (Erlenhöfer et al., 2001; Tatsuo et al., 2000). Fusion occurs in a pH independent manner at the cell membrane.

### 3.4. Transcription, replication, assembly and virus budding

After fusion of the virion with the cell membrane, the (−)RNP is introduced into the cytoplasm where it acts as a template for both primary transcription of mRNAs and replication of the negative stranded genome RNA into positive antigenome RNA, which is concomitantly encapsidated to produce (+)RNP (Fig. 1). It is probable that the viral RNA-dependent RNA polymerase (RdRp) not only consists of the P and L proteins but it may also involve unknown host cell proteins in addition to cytoskeletal components such as actin and tubulin (Moyer et al., 1990). The RdRp binds to the promoter sequences in the first 100 nucleotides at the 3′ end of the genomic RNA. Transcription terminates just before an intergenic trinucleotide at a gene end (GE) sequence (Fig. 1). For example, at the end of the N gene the RdRp encounters a consensus polyadenylation signal sequence of 3′-YYAU(U/C)/NNUUU-5′ which leads to polyadenylation of the mRNA by slippage on the U-rich template. The intergenic sequence (3′-GAA-5′) is not transcribed and transcription restarts at the 3′ end of the P/V/C gene at a consensus gene start (GS) sequence of 3′-UCCYY/N/UUCY/C/5′ (Radecke and Billeter, 1995). These stop/start events are repeated at the ends of the P, M, F, H and L genes. There is a finite chance that the RdRp will detach from the template at each intergenic junction and this gives rise to a gradient of gene expression in which the promoter proximal genes (i.e. N and P/V/C) are transcribed much more frequently into mRNA than the promoter distal genes (i.e. H and L).

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in attenuation, virulence immunosuppression and interaction with the innate immune system.

4. Studies of MV persistence

Persistent infection in tissue culture cells by RNA viruses was a well studied topic in the 1960s and 1970s but became less fashionable, primarily because it was at that stage impossible to provide anything more than a description of very basic culture characteristics such as whether or not the cells produced virus and if so whether the virus had a mutant phenotype. Moreover, the paucity of discernable MV phenotypes hampered these important studies. Only when the viral proteins were delineated and when cloning and sequencing of the viral genome had been completed, was it possible to conceive of studies that would address mechanisms of persistence. Earlier reviews of persistent MV infections in cell cultures (Rima and Martin, 1976) and in the brain (Rima and Martin 1976; Schneider-Schaudies et al., 1995a) postulated roles for viral defective interfering (DI) particles, viral mutants, interferons, etc. However, no conclusive proposals for mechanisms for persistence emerged from these.

5. Persistence in cell culture

In this section and the next we review data obtained from the generation of persistently infected cell cultures and from sequencing material obtained from SSPE cases. What has been learnt from these experimental models of persistence and from clinical material is presented in a unified diagram (Fig. 2) in order to present the key alterations to the virus genome, in the virus life-cycle and to the host cell which have been associated with the persistent state in vitro and in vivo. When reviewing in vitro studies into persistence by RNA viruses it is important to distinguish between “carrier” cultures and “true” persistent infections. In “carrier” cultures persistent infection were constantly present due to the existence of a dynamic equilibrium between virus infected and uninfected cells. V ery occasionally transmissible infections developed after 6–9 weeks from these co-cultures indicating reversion of the virus to an independent fully infectious agent. Whether this involved back mutations is not known. Re-combination was also proposed as a possible mechanism for the reversion of the virus to an independent fully infectious agent. Whether this involved back mutations is not known. Re-combination was also proposed as a possible mechanism for the reversion of the virus to an independent fully infectious agent.

5.1. Generation of persistently-infected, non-neural cell lines

Early studies by Rustigian and co-workers (Rustigian, 1962, 1966a,b; Rustigian et al., 1979) and (Minagawa et al., 1976) demonstrated that it was relatively straightforward to establish “true” persistent infections with MV in tissue culture cells such as HeLa cells (Rustigian, 1962, 1966a,b). Others used Hep2 cells (Gould and Linton, 1975; McCullough, 1983; Rice and Wolff, 1978), monkey kidney cells (Burnstein et al., 1974; Crespi et al., 1988; Hummel et al., 1994; Rima et al., 1977; Wild and Dumge, 1978) or call kidney cells (Sorodoc et al., 1980) to produce similar cell lines. Such persistently infected cell lines were initially established using viruses derived from the original Edmonston isolate made by John Enders in 1954. These Edmonston strain derivatives were propagated many times and adapted to laboratory passage and form the basis of all MV vaccines. It was clear that MV could set up persistent infection in many human cell lines such as human amnion AV3 cells (Rapp and Robbins, 1981), leukocytes (Jacobson and McFarland, 1982; Joseph et al., 1975) and lymphoblastoid cells (Celma and Fernandez-Munioz, 1992; Cremer et al., 1979; Fernandez-Munioz and Celma, 1992; Juetal., 1980). In general one can draw the conclusion that such persistent infections allow the accumulation of viral mutants, e.g. temperature sensitive mutants, cold sensitive mutants (Rager-Zisman et al., 1984), small plaque mutants or non-syncytial mutants (McCullough, 1983) as well as mutants that were able to set up persistent infection more readily than the original virus.

It has always been difficult to study the establishment phase as often the cultures did not show a consistent level of infection and underwent crises of cytopathology. This was especially the case in persistent infections in which DI particles had been involved and also in those in which a small number of cells that had survived a lytic infection were cultured (Rima et al., 1977). A number of studies were carried out in the 1970s that dealt with mechanisms of maintenance of stable persistent infections. Rustigian’s experiments of co-culture of his HeLa cells with V ero cells to address the nature of the blockage in K11A-HG-1 cells (Rustigian et al., 1979) demonstrated that the HeLa cells were infected by a defective MV which upon introduction into an adjacent V ero cell led to the formation of non-transmissible transient syncytia formation from a very small sub-fractin (0.2–0.4%) of the persistently infected cells. V ery occasionally transmissible infections developed after 6–9 weeks from these co-cultures indicating reversion of the virus to an independent fully infectious agent. Whether this involved back mutations is not known. Re-combination was also proposed as a possible mechanism for the reversion of the virus to an independent fully infectious agent. Whether this involved back mutations is not known. Re-combination was also proposed as a possible mechanism for the reversion of the virus to an independent fully infectious agent. Whether this involved back mutations is not known. Re-combination was also proposed as a possible mechanism for the reversion of the virus to an independent fully infectious agent. Whether this involved back mutations is not known. Re-combination was also proposed as a possible mechanism for the reversion of the virus to an independent fully infectious agent.
The appearance of mutants in persistently infected cultures was first demonstrated by comparison of serum responses in human convalescent and SSPE sera changes in patterns of antigenicity of the H protein (Robbins et al., 1991), N protein (Boriskin et al., 1986), the P or V protein (Bellini et al., 1986). Reduced amounts of M protein and altered processing of the H protein in persistently infected HeLa cell cultures were shown by difficult pulse-chase experiments (Young et al., 1985). Later the development of monoclonal antibodies to the different MV proteins made it much easier to study mutations and alterations in expression of specific MV proteins in persistence. Due to the lack of the M protein in particular, restriction of viral budding was offered as a mechanism of viral persistence. However, in a persistent infection of Vero cells with the hamster neurotropic (HNT) strain of MV restriction in the expression of the fusion protein was suggested as a mechanism for the maintenance of persistence (Hummel et al., 1994). The lack of F protein expression in these cells was attributed to the overabundance of M/F read-through transcripts (5:1 over F transcripts). Host factors involved in the control of persistent infection have been suggested to relate to elements of innate immunity such as oligo-2′,5′-adenylate synthetase (Fujii et al., 1988, 1990), interaction with heat shock proteins (Oglesbee et al., 1993) or altered lipid metabolism in the cells (Anderton et al., 1981, 1982, 1983a,b; Wild et al., 1981, 1986; Wild and Dugre,
M, F and H mRNAs are generated compared to the N mRNA derived material (see below). Lower relative amounts of the This gives rise to the transcription gradient, which has been confirmed by equivalent experiments in other systems, nevertheless these studies, which report the most extensive mechanisms and a number of cell lines based on MA106 cells.

5.2. Generation of persistently-infected, neural cell lines

More effort has been made to establish mechanistic parameters in persistently infected cells of neural origin. Persistent infections have been established in a number of rodent neural cell lines such as hamster brain cells (Vaivinopaia et al., 1982), in C6 rat brain glioma cells (Halbach and Koschel, 1979; Koschel and Muenzel, 1980) and mouse neuroblastoma cells (Gopas et al., 1992). Mechanistic studies in the C6 rat glioma cells demonstrated a loss of function in the endothelin signalling pathway by loss of its receptor (Heinssen and Koschel, 1995; Tas and Koschel, 1991) but this was not functionally linked to the phenomenon of persistence. The Rager–Zisman group established a persistent infection in a C1300 neuroblastoma cell clone called NS20Y (Rager-Zisman et al., 1984). These murine cells produced cold-sensitive mutant viruses and showed an increase in MHC-I expression. They also showed that a tyrosine residue of the N protein was phosphorylated in the persistently infected cells as opposed to in an acute infection, where only serine and threonine are phosphorylated (Segev et al., 1995). Many other aspects of these cells such as transcription regulation; interferon induc- tion and the expression levels of isoforms of protein kinase C were investigated (Fishman et al., 1997; Wolfson et al., 1989).

Nevertheless, these studies, which report the most extensive data on a specific MV persistently infected cell line, do not provide a coherent mechanistic explanation for persistence in vitro let alone in vivo. Furthermore the results have not been confirmed by equivalent experiments in other systems, for example persistently infected human neuronal cells, and this makes it at present impossible to use these observations to provide a generalised explanation of MV persistence.

Since rodents are not natural hosts for any of the known morbilliviruses studies of persistence and replication of MV in human cells of neuronal origin are possibly more relevant to in vivo persistence. Sybille Schneider-Schaulies and her colleagues have demonstrated differences in MV transcription and translation in six human glioma cell lines (D-54, D-32, U-251, U-105, U-373 and U-138) (Schneider-Schaulies et al., 1993ab, 1994). These cells are permissive for MV replication, but overall levels of transcription and replication are lower than in equivalently infected HEL or Vero cells. As mentioned above there is a finite chance that the RdRp will dissociate from the template at each intergenic junction. This gives rise to the transcription gradient, which has been shown to be steeper in rat astroglial cells and in SSPE patient derived material (see below). Lower relative amounts of the M, F and H mRNAs are generated compared to the N mRNA than in acutely infected non-neural cells. However, this effect on the transcription gradient was only observed in three of the six cell lines tested (D-54, D-32 and U-251) indicating that there are cell specific factors that regulate transcription attenuation in the other cell lines. One such factor may be the interferon inducible protein MxA. After in vitro differentia- tion of cells by the treatment with papaverine (a membrane permeable analogue of cyclic AMP), cells such as D-54 and U-251 or TE671 (Miller and Carrigan, 1982), showed a selective reduction in the rate of synthesis of MV proteins. In the case of D-54 and U-251 cells the reduced synthesis was specific to viral mRNAs as general protein synthesis was not affected, nor was the translatability of the viral mRNAs af- fected in vitro. In general these studies showed that in cells of neuronal origin, cell specific factors and differentiation state may affect the expression of viral proteins. The relevance of these observations to mechanisms of in vivo persistence has not been determined.

5.3. Utilisation of “SSPE” derived viruses

It is important to distinguish between persistently infected cell cultures which have been established by co-culture of non-neural cell lines with brain material obtained from SSPE patients that harbour defective viruses such as the Biken virus in HEL cells and those set up after infection with so called “replication competent” SSPE isolates such as the Hallé, Lec, Mantooth and Horta-Barbosa virus strains. We have shown earlier that based on their similarity in gene se- quences to the Edmonston strain the latter most likely repre- sent laboratory contaminants (Rima et al., 1995) and as such these cultures are not further discussed here. A number of cell lines have been established by co-culture such as Lu106 cells, a human embryo lung fibroblast cell line persistently infected with a SSPE derived virus, the Biken–Vero cells used by the Hirano group for a number of studies of persistence mecha- nisms and a number of cell lines based on MA106 cells.

In the SSPE IP-3-Ca cell line Sheppard et al. (1985) demonstrated that the defect in viral budding was not due either to a decrease in the stability of the M gene mRNA or in the efficiency of its translation. Restriction occurred as a result of abnormally rapid post-translational degradation of the M protein. The mechanistic basis of this instability has never been established. Nevertheless, it provides a reason- able explanation for the defect in viral replication in the cells and it correlates with the lack of M expression noted earlier (Lin and Thomson, 1980). In contrast budding and fusion of the cells was reduced in HNT-Vero cells and Lu106 cells due to a restriction in F protein (Hummel et al., 1994; Sheshber- alaran et al., 1985). In MA SSPE cells (Sheshberadaran et al., 1985), it was clear that it was a cellular factor that was important as these cells also failed to form syncyta on acute infection of the Edmonston virus in the cells. The Biken/HEL cell line that was derived from co-culture of SSPE brain tis- sue (Ueda et al., 1975) has been studied extensively. This persistent infection has been transferred into CV-1 cells by
co-culture. Sequencing analysis showed that all envelope-associated viral antigens had undergone mutations which led to the appearance of novel phenotypes. For example, in the H protein it was observed that haemadsorption was lost compared to the Nagahata strain, which is the wild-type precursor virus (Breschkin et al., 1979). Delayed activation of F0 was not associated with mutations found at the furin cleavage site or the lack of the C terminal pentadecapeptide but appeared related to mutations in F1 (Watanabe et al., 1995). However, the main emphasis has been on the study of the M protein which was shown to be unstable after translation and to have an eight amino-acid carboxy terminal extension and 20–22 mutations in the ORF (Ayata et al., 1989; Enami et al., 1989). The changes were later shown to be associated with biased hypermutation as they arose from uridine (U) to cytidine (C) mutations (Wong et al., 1991). The M protein has been shown not to have the normal RNP binding activity (Hirano et al., 1993). Reverse genetics was used to demonstrate that, when this M gene was inserted into the Edmonston genetic background, the resulting recombinant virus was infectious in CD46 transgenic mice following in intracerebral (i.c.) infection. The virus was also able to infect primary neuronal cultures from the transgenic mice in vitro (Patterson et al., 2001). Interestingly the Biken SSPE virus appears to out-compete wild-type MV in mixed infections of CV-1 (Hirano, 1992). Biken virus also out-competed the Edmonston strain better than the related Nagahata wild-type strain. Several mechanisms such as the presence of DI particles, or competition for interacting host or viral proteins were proposed to explain this. Nevertheless, it is clear that the resident Biken virus is at a selective advantage which could explain the accumulation of mutants and the replacement of wild-type viruses in SSPE. However, the mechanisms were unfortunately not further investigated.

Biken CV-1 cells do not normally form syncytia (Hirano et al., 1996). However, fusogenic c.p.e. was inducible by transfecting the cells with a plasmid DNA expressing human CD46. Replacing the transmembrane and cytoplasmic domains of CD46 with a glycosylphosphatidylinositol anchor did not prevent cell-to-cell fusion but abrogated the normal receptor down-regulation observed in persistently infected cells. The down-regulation of CD46 is determined by the presence of a so-called “late domain” (YXXL) in the cytoplasmic domain of CD46 (Yant et al., 1997). These late domains govern interactions with cellular proteins that regulate degradation and trafficking of proteins within the cell. Mutations in CD46 that prevented down-regulation enhanced syncytium formation indicating the role of the delicate balance between H and CD46 surface expression in controlling fusion in this system.

6. Persistence in the patient

SSPE has been shown to be caused by a persistent MV infection (Connolly et al., 1967, 1971). MV specific inclu-
cell lines (Cattaneo et al., 1987b) it was found that the RdRp with brain material that established the Y amagata and the MF (Sidhu et al., 1994). They have been shown to be present in measles vaccines (Belloq et al., 1990) but it is unclear whether their presence affects the phenotype of the virus.

One further unexplored finding in MV persistence in cell culture and SSPE that is mirrored in cell culture studies into persistent infections using other paramyxoviruses, is a high degree of self-hybridisation when genome length RNA extracted from cultures or brain material was analysed (Hall and ter Meulen, 1976). This has been interpreted as indicative of a higher ratio of antigenome to genome RNP. The potential mechanism that underlies this observation, e.g. mutations in the promoters at genome ends have not been explored.

6.2. Altered transcription of measles virus in SSPE

Expression of the M protein can also be reduced by two transcriptional mechanisms. The first involves the generation of read-through transcripts of the P and M transcription units. In at least three SSPE patients, e.g. RNA derived from brain samples of case K (Cattaneo et al., 1986), and co-cultures with brain material that established the Yamagata and the MF cell lines (Cattaneo et al., 1987b) it was found that the RdRp RNA derived from brain samples of case K (Cattaneo et al., 1986), and co-cultures with brain material that established the Yamagata and the MF cell lines (Cattaneo et al., 1987b) it was found that the RdRp was unable to recognise the signals in the GE sequences at the end of the P/V/C gene and GS sequences at the start of the M genes meaning that all M transcripts were in the form of P/M read-through RNAs. In these transcripts is unlikely that a scanning ribosome would get as far downstream as this to translate the third ORF and thereby synthesize M protein. Interestingly in both SSPE patients (cases K and MF), there were no changes in the GE, Ig and GS sequences and hence mutations leading to the altered properties of the transcriptional control mechanisms should lie elsewhere genome. In the case of the persistent infection with the Yamagata strain, a change in the intergenic sequence could explain the accumulation of P/M read-through RNAs (Yoshikawa et al., 1990). Osaka viruses have well delineated changes in GS/GE sequences (Ayata et al., 2002).

The second transcriptional control mechanism affects the gradient of gene expression. The gradient varies from one host cell type to another and appears especially steep in MV infection in the human CNS. For example, in SSPE the gradient of gene expression is so steep that little F and H protein is produced, which may aid the virus in escaping detection by the immune system and would lead to a defect in budding (Cattaneo et al., 1987a,b). The reduction in transcripts of the L gene may or may not affect the level of viral RNA synthesis depending on whether the concentration of L protein is the rate-limiting step in transcription and/or replication. The effects of transcription attenuation could be further enhanced if the respective promoter distal M, F and H mRNAs were less stable. However, to date there has been no evidence presented that reports a greater degree of instability of any specific MV mRNA. On the contrary, all data, although limited, so far argues for similar half lives of all viral mRNAs (Ogura et al., 1989).

Hyper-mutation and read through transcription both lead to viruses that are defective in M protein expression. Re-combinant viruses that have the M protein gene deleted are highly fusogenic and though they are able to penetrate the brain parenchyma of CD46-expressing interferon α/β receptor knockout mice deeply after i.c. infection, they cause less mortality (Cathomen et al., 1998b).

6.3. Mutations in the fusion protein in SSPE and MIBE

Other consistent alterations that occur in all SSPE cases lead to the loss of the carboxy-terminal pentadecapeptide of the F protein. This sequence is strictly conserved in all morbilliviruses and hence is assumed to have a specific, albeit as yet unknown function in viral budding. This region contains a tyrosine residue shown to be important as a basolateral sorting signal (Maisner et al., 1998) and it is also assumed that the cytoplasmic tail of F is involved in targeting the protein to lipid rafts and interaction with the M protein. This was confirmed by generating a recombinant MV which has the F and H proteins replaced by the G protein of vesicular stomatitis virus (Spiehler et al., 1998). The resulting virions did not contain the M protein, illustrating that the protein is not absolutely required for virus assembly, although viral titer are significantly reduced. Viruses that lacked the F protein tail were found to be highly fusogenic in cell culture. Cathomen et al. constructed recombinant viruses that had deletions in both the F and H tails and tested these in i.c. infection of transgenic CD46-expressing interferon α/β receptor knockout mice (Cathomen et al., 1998a). Similarly to viruses that expressed no M protein, these “tailless” mutants were found to be less lethal than the standard virus and to penetrate more deeply in the brain parenchyma (Cathomen et al., 1998b). Mutations that remove the conserved pentadecapeptide include the introduction of premature stop codons and as well as frame shift mutations that lead to carboxy-terminally extended or truncated F proteins. Deletion of a specific A nucleotide has been observed in a number of cases (Schmid et al., 1992). Mutants and wild-type sequences have been found in the same brain. The mechanism of this deletion is not known but it could be similar to that observed in human respiratory syncytial virus where deletions in stretches of A residues can alter the reading frame for the G protein leading to large scale differences in immunoreactivity of the protein (Garcia-Barreno et al., 1994).

6.4. Only wild-type virus sequences have been found in SSPE

Measles virus is a monotypic virus and the virus exists as a single serotype. Infection with one strain of measles appears...
to provide life-long protection from the disease. With the development of RT-PCR and DNA sequencing techniques it has become clear that virus isolates vary in their nucleotide sequences especially in those encoding the last 150 amino acids of the N protein and the entire H protein (Rima et al., 1997; Rota et al., 1992, 1994; Taylor et al., 1991). During the last decade sequences of over 250 strains have been determined and these show that at least 21 genotypes exist which belong to eight different groups or clades. Although these viruses may once have been geographically restricted in their distribution, the increase in travel by children, who are the prime reservoir for virus replication, has now allowed worldwide distribution of most of the genotypes. Some of the clades appear to be extinct as no recent isolates have been made, but it is difficult to be certain about this as global measles surveillance is inadequate. In the USA and the UK, it has been possible to link the origin of the imported strain with travel by specific index cases (Rota et al., 2004). Thus the different genotypes have made it possible to establish transmission chains for a number of outbreaks.

The description of specific clades and genotypes of MV has allowed the evaluation of mutations found in the MV RNA sequences from SSPE brain material against wild-type (clades B–G) viruses. All the vaccine viruses are derived from the Edmonston strain (clade A) but no clade A virus has been found in SSPE brain material. The sequences found in SSPE brain are related to the wild-type viruses circulating at the time of initial infection of the child, appears to persist and SSPE is not due to a super-infection by viruses circulating during the onset of symptoms (Jin et al., 2002; Rima et al., 1995; Rota, personal communication). To the best of the authors’ knowledge no vaccine virus, genotype A, sequences have been obtained from SSPE cases. SSPE has been vastly reduced in incidence after successful control of measles by vaccination (Dyken et al., 1989). In contrast, vaccine strains have been identified in MV infections in immuno-compromised patients who died in SSPE (Bitun et al., 1999) and giant cell pneumonia (Mawhinney et al., 1971).

7. In which tissues does measles virus reside before to onset of symptoms of SSPE?

Detection of MV RNA in the CNS of SSPE and MIBE cases is pathognomonic and without exception. However, the question has been raised as to where the virus persists in the patient prior to the onset of symptoms. Brown et al. (1989) documented finding MV in CNS and peripheral tissues obtained from SSPE patients by immunostaining for protein and in situ hybridisation for RNA. This study used the same in situ MV probe that was used by Fournier in his studies (Basle et al., 1986). It should be noted that this probe has been used extensively in both initial and ongoing in situ hybridisation studies of a variety of diseases, for example Paget’s disease. However, in none of the diseases have the results been confirmed by others and the fact that 70% of leukocytes were infected with MV in SSPE patients is at variance with all other data (Schneider-Schaulies et al., 1991). The most comprehensive search for the presence of MV virus outside the brain is reported in the Brown et al. study (1989). However, no clear picture emerges from this study as the findings vary between the cases to case and the results of in situ hybridisation and immunocytochemistry give are inconsistent. Several laboratories have examined other tissues isolated from SSPE patients and have not been able to find evidence of MV outside the brain. None of these studies have been reported in the literature due to the well-known bias against the publication of negative results. There is no question that SSPE is caused by persistent MV infection and it has been generally assumed that MV resides in the CNS before the onset of symptoms. However, there is no direct evidence to support this hypothesis. It would be difficult to obtain conclusive evidence either way, as these studies are made post mortem, hence present late stages of the disease and therefore cannot answer questions about the site of persistence before the onset of symptoms. Once again this emphasises why in vitro studies in non-neural cell lines are still very useful. The fact that in MIBE there are all the hallmarks of MV hypermutation and spread of the virus over the entire brain but with a much shorter symptomless period between the acute infection and the manifestation of CNS infection could be seen as an argument against the persistence of MV in the CNS in SSPE cases. It appears that once the virus sets up neuronal infection it is difficult to stop and even though there is large variation in the length of time between onset of symptoms and death in SSPE, it is invariably fatal. Thus it is the level of the replication in the periphery that might be the controlling factor that determined the length of symptomless persistence. The alternative explanation may be that the virus has been in the CNS all along but has been controlled by the immune system. Until recently it was assumed that the CNS was subjected to no or at least lower levels of immune surveillance than many other organs and hence was a place where a virus such as measles could maintain itself, even though as an RNA virus it requires constant gene expression and low level replication in order to persist, which would, in any other tissue make it visible to the immune system. It is now clear that the CNS is under immune surveillance (McGavern et al., 2002). At one time the life-long immunity to measles virus demonstrated in Panum’s island studies of 1846 was considered to be evidence for life-long persistence of the antigen (Panum, 1938). However, it is difficult to accept life-long persistence of measles virus RNA or protein in the absence of viral replication and low level gene expression. Indeed intracellular non-replicating MV nucleocapsids are inactivated within 3 days (Mottet et al., 1990). Hence the life-long immunity was considered evidence for viral persistence and SSPE cases might have been considered to occur whether the normal mechanisms to check this persistent infection had broken down. However, with the discovery of slow cycling memory
Fig. 3. Immunoreactivity and autofluorescence in primary mouse neurones infected with a recombinant measles virus which expresses EGFP and the H protein of a rodent-brain adapted strain of MV (CAM/RB). Cells were infected with the virus at a multiplicity of infection of 0.01. Cells were fixed using paraformaldehyde and examined by confocal scanning laser microscopy for autofluorescence and immunoreactivity. Photomicrographs represent an 8–10 μm composite optical section. Images were obtained in double excitation mode. The MV H glycoprotein (red) was detected and visualised by indirect immunofluorescence using a monoclonal antibody and a CY3 secondary antibody whilst EGFP (green) was detected by virtue of its autofluorescence. Two representative interconnected cells are shown. (A) EGFP autofluorescence, (B) H glycoprotein and (C) EGFP/H overlay. Magnification ×40.

CD8+ T cells it is no longer necessary to invoke the idea that life-long immunity equates to viral persistence (Wherry and Ahmed, 2004).

8. Is there a specific brain receptor for measles virus?

The role of the currently identified receptors in the spread of MV within the brain of SSPE patients is unclear. CD46 has not been detected on a differentiated neuronal cell line (McQuaid et al., 1998) and it has been shown that the virus can spread between contacting hippocampal neurones in the absence of CD46 expression without extracellular virus production (Lawrence et al., 2000). The utility of recombinant viruses which express fluorescent proteins is evident in studies which aim to investigate the mechanism of MV cell-to-cell spread in vitro and a MV which expresses enhanced green fluorescent protein (EGFP) from an additional promoter proximal transcription unit has been used to infect astrocytoma, oligodendroglioma and neuroblastoma cell lines (Duprex et al., 1999a, 2000; Plumb et al., 2002). The recombinant MV (MVegFP) has also been used to infect ex vivo hippocampal brain slices in which the virus was observed to spread unidirectionally, in a retrograde manner from CA1 to CA3 pyramidal cells and from there to the dentate gyrus (Ehrengruber et al., 2002). MVegFP has also been used to infect CD46-expressing interferon α/β receptor knockout transgenic mice by the i.c. route. Animals showed clinical signs of infection and EGFP was detected in discrete focal regions of the brain, in ependymal cells and neuroblasts and deep into the parenchyma (Duprex et al., 2000). Molecular determinants of neuropathogenesis have been mapped by generating a recombinant virus which expresses a rodent-brain adapted H glycoprotein in an Edmonston vaccine background (Duprex et al., 1999a). We have recently generated an equivalent virus which expresses EGFP (Duprex et al., unpublished) and have been able to infect dissociated non-transgenic mouse neurones in vitro. It is clear that this virus can spread transneuronally in the absence of CD46 in these cultures, reinforcing the suggestion that there are MV neuronal receptors. Furthermore, it is clear that although H is predominantly localised in the neuronal cell body it can also be detected in the long interconnecting axonal processes (Fig. 3). Collectively, these results suggest that the virus spreads transneuronally although this has not been formally proven. Recombinant viruses which express EGFP within the L protein (Duprex et al., 2002) or at the carboxy terminus of the P protein (Devaux and Cattaneo, 2004) of MV could help resolve this question as these viruses permit the visualisation of RNP.

9. Future perspectives

Forty years after the initial electron microscopy studies (Tellez-Nagel and Harter, 1966) and the identification of the link between MV and SSPE (Connolly et al., 1967; Payne et al., 1969) it is clear that much has been learnt about the plethora of alterations which occur in the genome which drive the virus to an intracellular existence. As such MV exemplifies long-term persistence of an RNA virus which
must continually replicate in the host and evade immune detection. Nevertheless, many questions remain unanswered. Now that SLAM has been identified as a MV receptor, and since SLAM expression appears to be limited to dendritic cells and activated T and B lymphocytes as well as monocytes (Minagawa et al., 2001) two new questions arise: First: how does the virus transfer from the cells of the lymphoreticular system to the CNS, endothelia and epithelia? In vitro persistent infection models in SLAM expressing cells may help us gain understanding of this process. The second question is: how do cells of the lymphoreticular system enter the CNS? A Trojan horse mechanism has been proposed for the related morbillivirus canine distemper virus (Appel et al., 1981) and since it is now accepted that lymphocytes and macrophages traffic into the CNS, such a mechanism would no longer be controversial or problematic. The studies reviewed here also show that host factors play a role in the maintenance of MV persistence. In terms of CNS infection these may simply reflect the fact that neurons are less prone to generate innate immune responses so as to avoid cytotoxicity due to the generation of an inflammatory cytokine milieu in the CNS.

Some very basic questions also remain about the cell biology of a MV infection in the neuron in SSPE. If microfusion occurs at the synaptic membrane and if this involves an interaction between viral glycoproteins and receptors then what are the receptors and are both H and F involved; are there specific fusion receptors; how do the viral glycoproteins localise to the synaptic membrane; does this involve local protein synthesis, or are excretory vesicles containing viral glycoprotein transported to the synapse in a retrograde or anterograde pathway, using dynein or kinesin? It is unlikely that glycoproteins traffic from the cell membrane of neuron cell body along the axonal membranes to the synapse by simple diffusion. These questions are now answerable, at least in part by combined in situ hybridisation and immunocytochemistry, for cellular and viral proteins using multicolour fluorescent probes and viruses which express fluorescent proteins.

Finally, it is clear from the recent report on the generation of MIBE in a stem cell recipient (Freeman et al., 2004) that we need to take cognisance of the existence of persistent viruses when such medical interventions are performed. Another example of this is the potential difficulties porcine endogenous retroviruses (PERVs) may cause in xenotransplantation approaches (Magre et al., 2003). Indeed, widening the scope of PERVs to include endogenous retrovirus-like elements may help us gain understanding of the mechanisms of MV persistence that may help if and when such agents are identified.

10. Conclusions

Much has been learned about mutations that accumulate during persistence especially in SSPE but it has not been possible to assess the functional significance of these mutations. New approaches using reverse genetics will now allow us to introduce selective mutations in vaccine and wild-type viruses and to assess whether they alter the phenotype of the virus in such a way as to aid persistence of the virus.

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