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## Measles virus, immune control and persistence

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### Abstract

Measles remains one of the most important causes of child morbidity and mortality worldwide with the greatest burden in the youngest children. Most acute measles deaths are due to secondary infections that result from a poorly understood measles-induced suppression of immune responses. Young children are also vulnerable to late development of subacute sclerosing panencephalitis, a progressive, uniformly fatal neurologic disease caused by persistent measles virus (MeV) infection. During acute infection, the rash marks the appearance of the adaptive immune response and CD8<sup>+</sup> T cell-mediated clearance of infectious virus. However, after clearance of infectious virus, MeV RNA persists and can be detected in blood, respiratory secretions, urine and lymphoid tissue for many weeks to months. This prolonged period of virus clearance may help to explain measles immunosuppression and the development of lifelong immunity to re-infection, as well as occasional infection of the nervous system. Once MeV infects neurons, the virus can spread transynaptically and the envelope proteins needed to form infectious virus are unnecessary, accumulate mutations and can establish persistent infection. Identification of the immune mechanisms required for clearance of MeV RNA from multiple sites will enlighten our understanding of the development of disease due to persistent infection.

### Keywords

Subacute sclerosing panencephalitis; CD8<sup>+</sup> T cells; rhesus macaques; virus clearance; innate immunity; adaptive immunity

### Introduction

Measles remains one of the most important causes of child morbidity and mortality worldwide with the greatest burden in the youngest children (Moss & Griffin, 2006; Nandy et al., 2006; Wolfson et al., 2009). Measles is unique for childhood rash diseases in that it is associated with substantial mortality with a case fatality rate of 5–10% in Africa (Grais et al., 2007; Nandy et al., 2006) and up to 25% in refugee camps and virgin populations (Moss, 2007; Shanks et al., 2011). Mortality is highest in girls and most acute measles deaths are due to secondary infections that result from a poorly understood measles-induced suppression of immune responses (Beckford et al., 1985; Garenne, 1994; Shanks et al., 2011; Tamashiro et al., 1987). In addition to the risks of acute infection, children, particularly boys, under the age of 2 years are also vulnerable to development of subacute sclerosing panencephalitis (SSPE), a progressive, uniformly fatal neurologic disease associated with persistent measles virus (MeV) infection of the nervous system. SSPE has a

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long latent period and presents many years after the original MeV infection (Bellini et al., 2005; Cattaneo et al., 1986; Freeman et al., 1967).

A safe and efficacious live attenuated virus vaccine is available and recent strides have been made toward global measles control. However, logistical and financial difficulties in sustaining the current vaccination strategies in developing countries have led the World Health Organization to forecast an increase in the number of measles cases and deaths (Centers for Disease Control, 2009). Furthermore, complacency and concerns about safety, along with philosophical and religious objections to vaccination, have resulted in failure to control measles in many industrialized nations (Muscat et al., 2009; Richard & Masserey Spicher, 2009).

## Measles virus and virus replication

Measles virus is a negative-sense RNA virus with a non-segmented genome (Fig. 1b) and a lipid envelope that belongs to the morbillivirus genus of the family *Paramyxoviridae*. The 16kb genome encodes eight proteins and most likely evolved from rinderpest virus, a recently eradicated disease of cattle (Barrett, 1999; Furuse et al., 2010; Horzinek, 2011). Six proteins are found in the virion (Fig. 1a). The envelope has surface projections composed of the viral hemagglutinin (H) and fusion (F) glycoproteins with the matrix (M) protein lining the interior. The helical nucleocapsid is formed from the genomic RNA wrapped with the nucleocapsid (N) protein and is packed within the envelope in the form of a symmetrical coil with the phosphoprotein (P) and large polymerase (L) proteins attached. There are 2 nonstructural proteins, C and V, encoded within the P gene that regulate the cellular response to infection and modulate interferon (IFN) signaling (Bellini et al., 1985; Cattaneo et al., 1989). C is translated from an alternative start site by leaky scanning to produce a basic protein of 186 amino acids. V has the same N-terminus (231 amino acids) as P, but insertion of an additional guanine by RNA editing alters the reading frame to produce a unique 68 amino acid cysteine-rich zinc-binding C-terminal domain that is highly conserved amongst paramyxoviruses (Cattaneo et al., 1989; Liston & Briedis, 1994).

H interacts with the virus receptor for attachment and F interacts with H and with the same or an additional cellular protein for fusion and entry (Fig. 1c). Three receptors have been identified: membrane cofactor protein or CD46 (Dorig et al., 1993; Nanche et al., 1993), signaling lymphocyte activation molecule (SLAM) or CD150 (Tatsuo et al., 2000) and poliovirus receptor-related 4 (PVRL4) or nectin 4 (Muhlebach et al., 2011; Noyce et al., 2011). CD46 is a widely distributed human complement regulatory protein expressed on all nucleated cells (Riley-Vargas et al., 2004). It acts as a cofactor for the proteolytic inactivation of C3b/C4b by factor I (Riley-Vargas et al., 2004), but also induces proliferation and differentiation of regulatory T cells (Kemper et al., 2003). SLAM is a costimulatory molecule expressed on activated cells of the immune system (Sidorenko & Clark, 2003). The cytoplasmic domain has an immunoreceptor tyrosine-based switch motif that binds small SH-2 domain adaptor proteins important for cell signaling (Ohno et al., 2003; Yanagi et al., 2002). Nectin-4 is an adherens junction protein of the immunoglobulin superfamily expressed on epithelial cells (Shirogane et al., 2010; Sinn et al., 2002). The receptor binding regions on H are all found on the lateral surface of the head structure and are contiguous or overlapping (Colf et al., 2007; Hashiguchi et al., 2007; Hashiguchi et al., 2011; Masse et al., 2004; Santiago et al., 2002; Santiago et al., 2010; Schneider et al., 2002; Vongpunsawad et al., 2004). Both vaccine and wild type strains of MeV can use SLAM as a receptor, but wild type strains do not use CD46 efficiently (Erlenhofer et al., 2002; Ono et al., 2001; Yanagi et al., 2002). Differences in receptor usage may involve interactions with F as well as H (Koumou & Wild, 2002; Takeuchi et al., 2002).

MeV probably uses additional receptors. In acute infections endothelial cells, as well as epithelial and immune system cells, are infected (Andres et al., 2003; Esolen et al., 1995; Oldstone et al., 2002; Takeuchi et al., 2003) and in persistent infections neurons and glial cells are important targets for infection (McQuaid & Cosby, 2002; Shingai et al., 2003). The vaccine virus was attenuated by growth in chicken cells.

H and F cooperate to induce fusion of the viral envelope and cellular plasma membrane for entry. Infected cells expressing the viral glycoproteins at the cell surface can also fuse with uninfected cells to produce multinucleated giant cells followed by cell death. However, not all types of infected cells fuse to form syncytia. *In vivo*, giant cells are observed in the lung, skin and lymphatic tissue, but not the central nervous system (CNS). Cellular protein synthesis is relatively unaffected by MeV infection, but specific cellular proteins (e.g. cell surface receptors) and functional responses (e.g. signal transduction, expression of transcription factors) may be altered in a cell-type-specific manner (Bazarsky et al., 1997; Fishman et al., 1997; Indoh et al., 2007).

MeV replication is interferon (IFN)-sensitive (Leopardi et al., 1992; Naniche et al., 2000) and some IFN-stimulated proteins (e.g. MxA, ADAR1) inhibit MeV replication in a cell type-specific manner (Schneider-Schaulies et al., 1994; Schnorr et al., 1993; Ward et al., 2011). However, MeV effectively inhibits both induction of IFN synthesis and IFN signaling in infected cells and this property may play an important role in the ability of MeV to establish persistent infection. The C-terminal domain of the V protein prevents induction of type I IFN synthesis both through the toll-like receptor (TLR)/MyD88 and RNA helicase pathways (He et al., 2002). V binds IKK $\alpha$  and inhibits TLR7/9-mediated phosphorylation of IRF7 in plasmacytoid dendritic cells (DCs) (Pfaller & Conzelmann, 2008; Schlender et al., 2005). V also binds MDA5, but not RIG-I, to prevent activation and induction of IFN $\beta$  synthesis through the RNA helicase pathway (Andrejeva et al., 2004; Childs et al., 2009). Strains of MeV differ in V sequence and transient transfection studies indicate strain-dependent differences in function (Takaki et al., 2011).

If IFN is produced by infected cells, the common N-terminal domains of the P and V proteins inhibit IFN-induced STAT1 activation (Caignard et al., 2009; Caignard et al., 2007; Palosaari et al., 2003) and the C-terminal domain of V inhibits STAT2 activation (Ramachandran & Horvath, 2010; Ramachandran et al., 2008). However, the role of type I IFN in natural MeV infection is unclear. There is little evidence that IFN $\alpha/\beta$  is induced *in vivo* and studies of IFN induction by MeV *in vitro* have been confounded by the frequent presence of defective interfering (DI) RNAs in virus stocks. DI RNAs are potent inducers of IFN and one mechanism used to establish cell lines persistently infected with MeV (Rima et al., 1977; Yount et al., 2008).

## Acute disease and tissue sites of replication

MeV is efficiently spread by the respiratory route and is highly infectious. Knowledge of measles pathogenesis comes from study of naturally infected humans and experimentally infected macaques, animals that develop measles very similar to that of humans. Infection is initiated in the respiratory tract followed by rapid spread of virus to local lymphoid tissue and then to multiple other organs (Moench et al., 1988). Wild type virus replicates efficiently in activated cells of the immune system that express SLAM (Condack et al., 2007; de Swart et al., 2007; Yanagi et al., 2006) and it is likely that immature pulmonary DCs or alveolar macrophages capture and transport MeV to regional lymph nodes where the immune response is initiated and spread of infection is facilitated (Kaiserlian & Dubois, 2001; Lemon et al., 2011; Schneider-Schaulies et al., 2002).

There is a latent period of 10–14 days and a 2–3 day prodrome of fever, coryza, cough, and conjunctivitis followed by the appearance of a characteristic maculopapular rash (Lessler et al., 2009). Multiple organs (*e.g.* liver, lung, thymus, spleen, skin) are infected and target cells include epithelial cells, endothelial cells, B lymphocytes, T lymphocytes, monocyte/macrophages and DCs (de Swart et al., 2007; Moench et al., 1988; Plaza & Nuovo, 2005), all cells that can be replaced if eliminated by the immune response during the process of virus clearance. Neurons and glial cells are not usually targets of acute infection (McQuaid et al., 1998; Moench et al., 1988), but infected CNS endothelial cells have been observed in autopsy specimens (Esolen et al., 1995).

The onset of the rash coincides with the appearance of the adaptive immune response and initiation of clearance of infectious virus (Auwaerter et al., 1999). After the rash has faded, infectious virus can rarely be recovered and this correlates with decreased transmission of infection (Pan et al., 2005; Permar et al., 2001; Van Binnendijk et al., 2003). However, viral RNA persists for many weeks (Fig. 2). Mechanisms of immune-mediated clearance of infectious virus and viral RNA from different types of cells may be distinct and occur at different rates.

## Immune response and clearance

Replication of MeV usually causes death of cells in culture, but this is not necessarily the case *in vivo*. Persistent non-cytopathic infection can be established *In vitro* and this is most easily accomplished in neuronal cells, but persistent infections in lymphoid, epithelial and glial cells have also been established (Miller & Carrigan, 1982; Rima & Duprex, 2005). Cellular factors that affect the ability of MeV to establish and maintain persistent infection include increased expression of heat shock proteins, IFN-inducible proteins and altered regulation of lipid metabolism (Miller & Carrigan, 1982; Rima & Duprex, 2005; Robinson et al., 2009; Schnorr et al., 1993; Takahashi et al., 2007). Antisense RNA can be used to cure persistently infected cells (Koschel et al., 1995).

If the cell survives infection, virus clearance will require immune-mediated elimination of the cell or of intracellular virus. For many virus infections, factors produced by the innate immune response directly in response to virus infection (*e.g.* IFN- $\alpha/\beta$ , TNF, IL-1, IL-6, IL-8) inhibit virus spread and set the stage for the adaptive immune response. However, the innate response to natural measles has not been well characterized. *In vitro* studies have shown that innate responses triggered by interaction of MeV RNA or proteins with pathogen recognition receptors at the cell surface or in the cytoplasm to activate signaling pathways involving transcription factors NF $\kappa$ B and IRF 3 differ with the strain of virus, are cell type-specific and are highly regulated by the viral P, C and V proteins (Bieback et al., 2002; Duhon et al., 2010; Helin et al., 2001; Katayama et al., 2000; Sato et al., 2008; Schuhmann et al., 2011; Tenover et al., 2002). MeV replication *in vitro* is sensitive to the inhibitory effects of IFN $\alpha/\beta$ . There is little evidence that type I IFN is produced *in vivo* during the acute phase of disease (Griffin et al., 1990; Leopardi et al., 1992; Schnorr et al., 1993; Tanabe et al., 2003; Yu et al., 2008) and this may be important for virulence as mutation of the V gene leads to virus attenuation (Devaux et al., 2011). IL-1 and IL-8 can be detected in plasma (Zilliox et al., 2007), but roles for these factors in control of MeV infection have not been identified.

Adaptive cellular immune responses are generally regarded as most important for clearance of MeV. Children with agammaglobulinemia recover from infection while those with defects in cellular immunity (*e.g.* HIV infection, congenital immune deficiency, transplant immune suppression, chemotherapy, etc) are prone to develop progressive infections of the lung (giant cell pneumonia) or CNS (inclusion body encephalitis) (Albertyn et al., 2011;

Enders et al., 1959; Good & Zak, 1956; McQuaid et al., 1998). MeV-specific antibody and T cell responses appear coincident with the onset of the rash and rash biopsies show infiltration of CD4<sup>+</sup> and CD8<sup>+</sup> T lymphocytes in regions of epithelial cell infection (Fig. 3).

Several lines of evidence suggest that CD8<sup>+</sup> T lymphocytes are particularly important for control and clearance of infectious virus. MeV-specific cytotoxic T lymphocytes are found in the blood during the rash and CD4<sup>+</sup> and CD8<sup>+</sup> T cells infiltrate sites of virus replication (Jaye et al., 1998; Mongkolsapaya et al., 1999; Myou et al., 1993; Polack et al., 1999) (Fig. 3). In monkeys, depletion of CD8<sup>+</sup> T cells, but not B cells, at the time of infection results in a higher and more prolonged viremia (Permar et al., 2004; Permar et al., 2003). *In vitro*, addition of CD8<sup>+</sup>, but not CD4<sup>+</sup>, T cells to MeV-infected B cells prevents spread to uninfected B cells (de Vries et al., 2010) and depletion of CD4<sup>+</sup> T cells does not affect virus titers in the lungs of infected cotton rats (Pueschel et al., 2007). Both cytotoxicity and IFN- $\gamma$  production have been implicated as effector mechanisms important for CD8<sup>+</sup> T cell-mediated MeV clearance. The relative importance of each is likely to differ depending on the target cell and tissue (Finke et al., 1995; Patterson et al., 2002; Stubblefield, Sr. et al., 2011; Tishon et al., 2006). For instance, IFN- $\gamma$ -induced indoleamine 2,3-dioxygenase is important for control of MeV replication in epithelial, endothelial and astroglial cells, but not in lymphoid or neuronal cells (Obojes et al., 2005).

In immunologically normal individuals, infectious virus cannot be recovered shortly after the rash fades (Fig. 2). Clearance of infectious virus and resolution of the accompanying rash are associated with clinical recovery in most children. However, clearance of infectious virus is only part of the story. Our studies of Zambian children with natural measles and of rhesus macaques experimentally infected with a wild type strain of MeV have shown that viral RNA persists in multiple locations long after infectious virus is no longer detectable (Fig. 2) (Pan et al., 2005; Permar et al., 2001; Riddell et al., 2007). In prospective studies of children hospitalized with measles, MeV RNA was detected in 62% of children from at least one site (peripheral blood mononuclear cells [PBMCs], urine or nasopharyngeal aspirates) at 1–2 months after discharge from the hospital and in 37% at 3–4 months after discharge (Permar et al., 2001; Riddell et al., 2007). These data indicate that clearance of MeV RNA after infection is a prolonged process.

Rhesus macaques infected with wild type MeV have provided additional information on clearance because they can be followed closely from the time of infection. Infectious virus appears in the blood 4–7 days after infection and is cleared by 14–18 days. However, MeV RNA can be detected in PBMCs for 4–6 months (Pan et al., 2005). Clearance of virus and viral RNA from PBMCs occurs in phases. After an initial peak of RNA coinciding with recovery of infectious virus, there is a period of rapid decline in viral RNA, followed by a rebound and then a slow decline to undetectable levels. In animals studied for longer periods of time, viral RNA may reappear in PBMCs after apparent elimination suggesting persistence in other tissues (Pan et al., 2005). The length of time required for clearance from lymphoid and other tissues is not known.

Sequencing of RNA from late samples has identified no mutations in the variable regions of either the N or H genes (Riddell et al., 2007). These data suggest slow clearance as an explanation for the prolonged presence of MeV RNA after apparent recovery rather than mutation and escape from the immune response. A switch in the type of T cell response from type 1 to type 2 with production of regulatory T cells and cytokines may play a role in slowing clearance of viral RNA (Moss et al., 2002; Ward et al., 1991; Yu et al., 2008). Prolonged presence of viral RNA is highly relevant to the development of persistent infection and could explain the immunologic abnormalities that persist after the rash fades as well as the development of life-long immunity that characterizes the recovery from measles.

## Persistent infection

The frequency of failure of virus clearance from various tissues is not known, but clinically significant disease in immunologically normal individuals has only been convincingly linked to persistent infection of the CNS. Approximately 1 in 10,000 children (boys > girls) will develop SSPE as a late complication of measles (Bellini et al., 2005; Takasu et al., 2003). Both host and virus factors are likely to play a role in establishing persistence. SSPE is most likely to develop if the primary MeV infection occurs before the age of 2 years when the immune system is immature and residual maternal antibody may still be present (Bellini et al., 2005; Detels et al., 1973; Halsey et al., 1980; Jabbour et al., 1972; Miller et al., 1992; Modlin et al., 1977). In developing countries with high birth rates, measles often occurs in young infants (Grais et al., 2007; Halsey et al., 1980; Moss et al., 2008; Moss et al., 2002) and these countries appear to have a higher burden of SSPE (Saha et al., 1990; Takasu et al., 2003). This high burden is likely further exacerbated when there is a high prevalence of HIV infection because children of HIV-infected mothers are at increased risk to acquire measles at an early age (Embree et al., 1992; Moss et al., 2002) and animal models suggest that prior infection with an immunosuppressive virus increases the likelihood of persistent CNS infection (Oldstone et al., 2005).

Antibody to MeV may play a role in establishing persistent CNS infection either through alteration of the induction of the primary immune response at the time of initial infection or through modulation of infection once virus is in the nervous system (Endo et al., 2001; Fujinami & Oldstone, 1979; Rammohan et al., 1982). Passage of infected cells in the presence of antiviral antibody has been used to establish persistent infection *in vitro* (Rustigian, 1966). In small animals, treatment with antibody after intracerebral infection with MeV decreases acute disease, but increases the likelihood of persistent virus infection and subacute or chronic encephalitis (Liebert et al., 1990; Rammohan et al., 1981; Wear & Rapp, 1971). Cases of SSPE have been associated with passive transfer of immune globulin (Rammohan et al., 1982).

The average time to onset of SSPE after measles is 6–10 years, but ranges from 1 to 24 years (Campbell et al., 2007; Modlin et al., 1977). At the time that neurologic symptoms occur, neurons and glial cells contain nuclear and cytoplasmic MeV inclusion bodies and there is an extensive mononuclear inflammatory reaction in the CNS that includes CD4<sup>+</sup> and CD8<sup>+</sup> T cells, as well as monocytes and antibody-secreting B cells (Anlar et al., 2001; Brody et al., 1972; Dawson, 1934; Esiri et al., 1982; Herndon & Rubinstein, 1968). The antibody response to MeV is accentuated with significant production of MeV-specific antibody by plasma cells residing in the CNS (Burgoon et al., 2005). Thus, there is no evidence for a global defect in immune responses, but these immune responses are ineffective in clearing virus from the CNS.

Strains of MeV differ in ability to establish persistent infection in the same host cell *in vitro* (Fernandez-Munoz & Celma, 1992), but there is no clustering of SSPE cases to suggest that the wild type virus causing the initial infection is different from the virus causing uncomplicated disease. Sequence analysis of viral RNA from various parts of the brain shows that the virus is clonal (Baczko et al., 1993), implying that virus may have entered the brain during the original acute infection, perhaps by infecting endothelial cells (Dittmar et al., 2008; Esolen et al., 1995; Kirk et al., 1991; Ludlow et al., 2009), was not cleared and gradually spread throughout the nervous system. Once within neurons, virus can spread from neuron-to-neuron without the release of infectious particles (Ehrengruber et al., 2002) and it has been suggested that the MeV F protein interacts at the synapse with the substance P receptor neurokinin-1 to mediate trans-synaptic spread (Makhortova et al., 2007).

However, the virus that is present in cell lines persistently infected with MeV and in the CNS at the time of onset of clinically apparent SSPE differs substantially from the original wild type virus. Although viral antigen and RNA are abundant in both inclusion body encephalitis of immune compromised individuals and in SSPE, the virus is difficult, if not impossible, to culture from CNS tissue. In fact, some viruses thought to be SSPE viruses have been discovered to be laboratory contaminants (Rima et al., 1995). Variants associated with persistent infection *in vitro* often display properties indicative of impaired replication such as temperature-sensitivity (Rager-Zisman et al., 1984; Takahashi et al., 2007), accumulation of intranuclear and intracytoplasmic nucleocapsids and decreased release of infectious virus (Robinzon et al., 2009). Some cell lines produce no infectious virus and persistent infection is maintained by passage of encapsidated viral RNA to daughter cells during cell division (Burnstein et al., 1974).

In SSPE, no virus is seen budding from the surface of infected cells. Nuclear inclusions are filled with “smooth” nucleocapsids that lack associated RNA and P protein (Dubois-Dalcq et al., 1974; Herndon & Rubinstein, 1968). The cytoplasm contains “fuzzy” nucleocapsids of N-encapsidated RNA decorated with P that extend into neuronal processes. Thus, virus can spread within the CNS by synaptic transmission of the ribonucleoprotein from cell to cell, a process that has been observed both *in vivo* and *in vitro* (Duprex et al., 2000; Ehrenguber et al., 2002; Lawrence et al., 2000; Sawaishi et al., 1999). Limited expression of viral proteins on the surface of persistently infected cells has led to the suggestion that defects in synthesis of viral envelope proteins or processing of F may be an important determinant of persistent infection (Menna et al., 1975; Young et al., 1985). Defects in glycoprotein expression may be due in part to limited production of mRNAs for these proteins associated with steep transcriptional gradients and an increase in bicistronic messages (Cattaneo et al., 1987). However, mutations in these genes are frequent and often lead to synthesis of proteins with altered expression or function.

Frequent U to C changes suggest that mutation of viral RNA by adenosine deaminase (biased or A/I hypermutation) is occurring in persistently infected cells (Cattaneo et al., 1988; Kuhne et al., 2006; Wong et al., 1991). Failure to recover infectious virus is likely due to the mutations that accumulate in the genes for the M, F, and H envelope proteins that interfere with assembly and budding of infectious virus (Baczko et al., 1986; Cattaneo et al., 1988; Cattaneo et al., 1989; Jin et al., 2002; Roos et al., 1981). In general, expression of M protein is low (Liebert et al., 1986) due either to lack of synthesis of M or instability of the synthesized protein (Sheppard et al., 1986; Stephenson et al., 1981) and this is accompanied by low levels of antibody to M (Hall et al., 1979). In addition, defects in the M protein hinder association of N with the viral glycoproteins and facilitate persistence (Patterson et al., 2001). Studies in transgenic mice have shown that a functional M protein is not needed for virus replication and spread in the CNS (Cathomen et al., 1998; Patterson et al., 2001). Truncations, mutations, and deletions in the cytoplasmic domain of F that interfere with virus budding are almost universal (Cattaneo & Rose, 1993; Schmid et al., 1992). H proteins are often defective in intracellular transport and protein-protein interactions important for cell-cell fusion (Cattaneo & Rose, 1993). It is not known whether these mutations facilitate spread within the CNS and are necessary to establish or perpetuate CNS infection or accumulate due to lack of selective pressure to maintain envelope functions during replication in the CNS because virus spread can occur transynaptically without production of infectious virus.

## Concluding remarks

The frequency of MeV RNA persistence in the absence of disease is unknown. MeV has been identified by RT-PCR or morphologic analysis in tissues from normal individuals

(Haase et al., 1984; Katayama et al., 1995; Katayama et al., 1998; Schneider-Schaulies et al., 1991). In addition to SSPE, MeV antigen or RNA has been described as present and postulated to be playing an etiologic role in a large number of chronic diseases of unknown etiology (*e.g.* multiple sclerosis, Paget's disease, otosclerosis, chronic active hepatitis, achalasia and Crohn's disease) (Friedrichs et al., 2002; Haase et al., 1981; Kawashima et al., 1996; Niedermeyer et al., 2007; Wakefield et al., 1993). None of these diseases has been convincingly linked to persistent MeV infection, but a better understanding of the immune mechanisms and their regulation necessary for clearance of virus and viral RNA and of how and where the virus or viral RNA persists could help to determine if a causative role is plausible.

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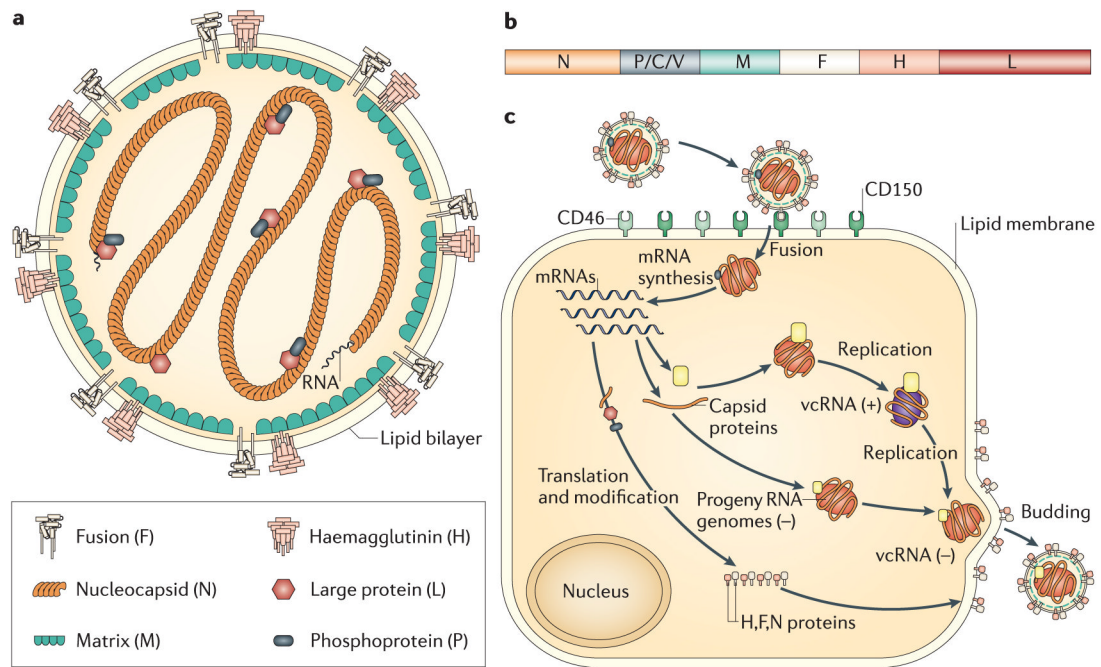
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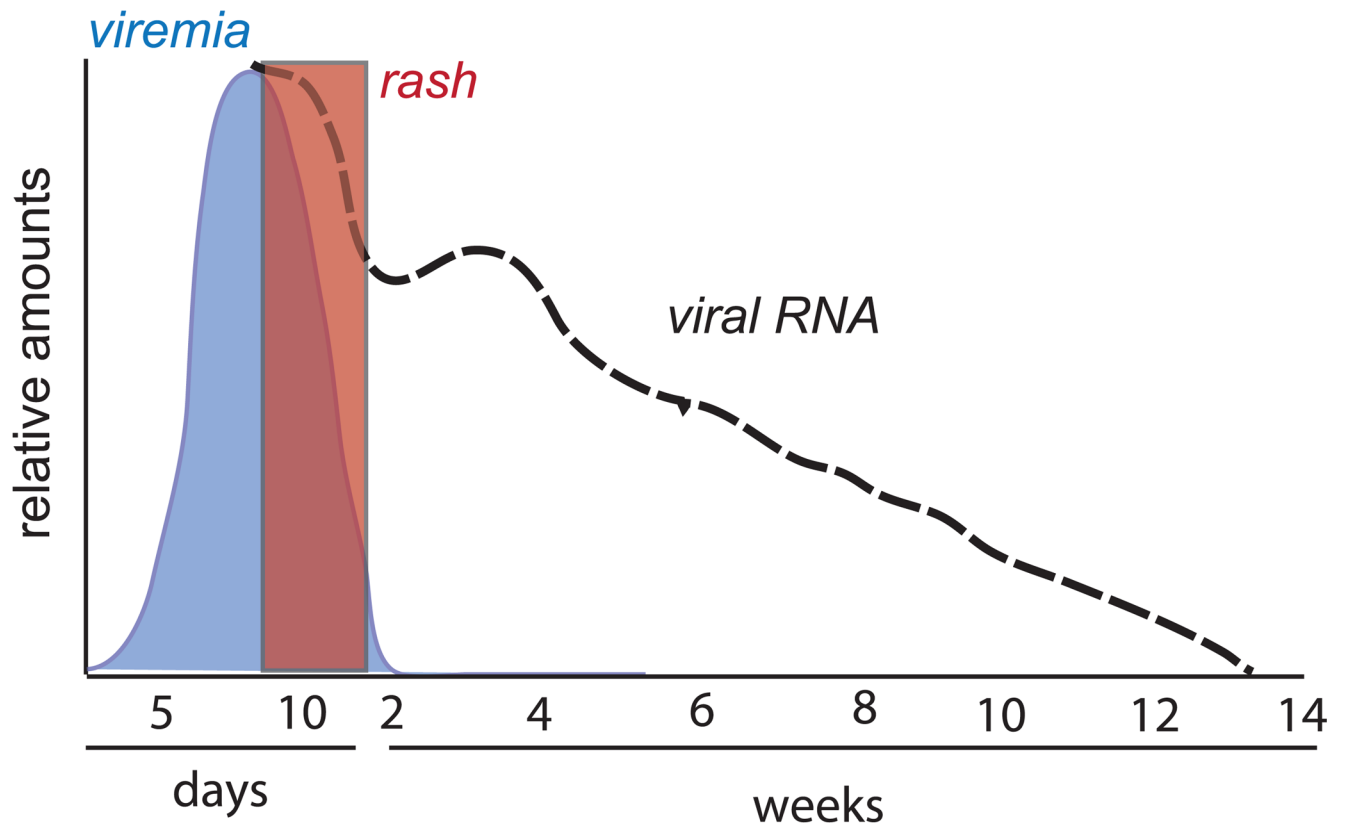
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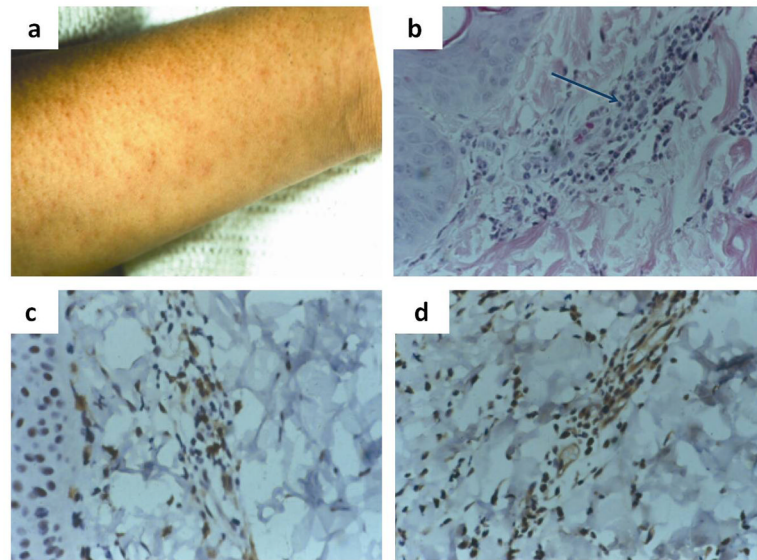
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**Figure 1.** Schematic diagrams of the measles virion (a), genome (b) and intracellular replication cycle (c). (a) The enveloped virion has 6 proteins: 2 surface glycoproteins, haemagglutinin (H) and fusion (F); a matrix (M) protein; a nucleocapsid (N) protein that surrounds the negative sense RNA and 2 replicase proteins, the phosphoprotein (P) and large (L) polymerase protein. (b) The P gene also encodes 2 host cell response regulatory proteins, V and C. (c) The H protein interacts with one of several MeV receptors resulting in F-mediated fusion with the plasma membrane. Replication occurs in the cytoplasm and assembled virions bud from the plasma membrane. (Moss & Griffin, 2006)



**Figure 2.** Schematic diagram showing the time course of the clearance of infectious measles virus (blue) and viral RNA (dashed black line) from blood in relationship to the appearance and clearance of the rash (red box).



**Figure 3.**

The measles virus rash (a) is indicative of the immune response and results from the infiltration of leukocytes (b), including CD4<sup>+</sup> (c) and CD8<sup>+</sup> (d) T lymphocytes into sites of virus replication in the skin. Histological examination of a biopsy of a measles skin rash lesion shows (a) an accumulation of mononuclear cells (arrow) that have infiltrated an area of infected epithelial cells (hematoxylin and eosin stain). Immunoperoxidase staining (brown) of the biopsy for CD4<sup>+</sup> (c) and CD8<sup>+</sup> (d) T cells shows that many of the infiltrating mononuclear cells are T lymphocytes (Polack et al, 1999).