

Pathogenetic Consequences of Cytomegalovirus-Host Co-evolution *

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Abstract: Co-evolution has been shown to result in an adaptive reciprocal modification in the respective behaviors of interacting populations over time. In the case of host-parasite co-evolution, the adaptive behavior is most evident from the reciprocal change in fitness of host and parasite-manifested in terms of pathogen survival versus host resistance. Cytomegaloviruses and their hosts represent a pairing of populations that has co-evolved over hundreds of years. This review explores the pathogenetic consequences emerging from the behavioral changes caused by co-evolutionary forces on the virus and its host.

Key words: Cytomegalovirus; Co-evolution; Pathogenesis

Co-evolution is the process of reciprocal, adaptive genetic change in two or more species (127, 140). It can occur between any interacting populations, but it is expected to be particularly important in host-pathogen systems because of the intimate nature of the association and the strong selective pressures that each can exert on the other (140). Cytomegaloviruses (CMV) and their hosts are thought to have co-evolved over hundreds of years (40). Recent data brought to light by studies on CMV pathogenesis provide an interesting glimpse on how the lengthy association between virus and host has shaped many of the viral pathogenetic features.

Human CMV (HCMV) is a ubiquitous human herpesvirus that infects a great majority of the world's population. The virus is a member of the β -group of herpesviruses characterized by their strict host specificity, comparatively large genome, and slow growth in culture (66, 80). Cells infected with the virus present a characteristic ballooned-cytopathology from which the name of the etiologic agent -"cytomegalovirus"- was derived (117, 118, 138). The linear double stranded viral DNA genome of 200-240 kbp encodes at least 150 proteins, many of which contribute to making the virus one of the most successful intracellular parasites in nature (25, 31, 81, 82, 98, 133).

The worldwide incidence of HCMV infection varies widely from 60%-100% (40, 122). Disparity in the incidence of the disease among population groups is influenced by prevailing health, hygiene, and socio-economic status (40, 86, 102, 122). Although the infection is mostly well tolerated by people with intact

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immune systems, it can be life threatening or severely debilitating for immunocompromised individuals such as AIDS patients, cancer patients, organ or tissue transplant recipients undergoing immunosuppressive therapy, infants, fetuses, and the elderly (1, 33, 34, 86, 87, 102, 129).

Like other herpesviruses, the CMV infectious cycle starts with an acute episode which progresses to a persistent stage that paves the way to the latent state (1, 49, 62, 66). Acute infection is usually precipitated by contact of virus with epithelial body surfaces but may also occur after organ transplant, blood transfusion, or as a result of congenital or perinatal infection (17, 24, 88, 104-106). It is characterized by robust viral replication at the site of primary infection and may become disseminated systemically via the lymphatic system then through cell-associated viremia. Terminal cases of acute CMV infection typically reveal widespread lesions of cellular cytomegaly in almost all organs of the body (94). The most common cell types found to be infected at autopsy are ductal epithelial cells, but other cell types also known to be infected are endothelial cells, smooth muscle cells, hepatocytes, granulocytes, monocytes, neurons, and glial cells (61, 65, 66, 93, 113, 129).

The persistent phase of CMV disease is characterized by low-level viral replication in infected organs. There is intermittent viral shedding in body fluids due to persistent infection of ductal epithelia. This stage usually presages latent infection wherein the infected host is negative for virus excretion but harbor the viral genome in a non-replicative form in some cells (49, 50, 99, 111, 112, 114). Latent virus may reactivate when the host is immunosuppressed or presumably, when the latently infected progenitor cell undergoes

differentiation into the mature phenotype (112, 114, 119, 120). The molecular mechanisms underlying viral reactivation from latency are not well understood. In the blood mononuclear cell lineage where data are most abundant, it has been shown that latently infected monocyte progenitor cells reactivate the virus in the course of terminal differentiation. Interestingly, reactivation appears to be associated with chromatin remodeling that accompanies cellular differentiation. Indeed, in one model, it has been shown that euchromatin formation resulting from acetylation of histone tails also loosens important regions in the latent viral DNA, notably the IE region, thereby allowing access of factors involved in initiating viral transcription that culminate in reactivation (101).

CMV disease is transmitted vertically from mother to offspring, or horizontally between individuals (1, 62, 87, 88). Vertical transmission can occur transplacentally, during birth, or through breast milk (5, 7, 17, 24, 57, 92, 109). Horizontal transmission can occur by direct exchange of body fluids, organ/tissue transplantation, or through contaminated materials as occurs in day care centers (32, 84, 142).

CO-EVOLUTION AND CMV PATHOGENESIS

Reciprocal traits involved in pathogen-host co-evolution usually operate in opposite directions: what enhances fitness of the host diminishes the fitness of the pathogen, and vice-versa (140). In the context of CMV-host co-evolution, enhanced features of the virus include focused resources towards infecting a specific host species, striking evasive adaptability to the host's repertoire of antiviral strategies, and ability to perpetuate itself in the host. As such, CMVs, do not cross the species barrier (54, 108, 125), they have

developed cunning ways of evading the host immune response (9-12, 14-16, 19, 26, 29, 37, 48, 52, 56, 68, 69, 71, 79, 96, 135, 136), they code for functions that temper host perturbation (31) or delay apoptosis of infected cells (41, 42, 77, 115, 126), and most importantly- they can establish latency and subsequently reactivate when the conditions are right (100, 101, 111, 112, 114).

On the part of the virus' co-evolutionary partner- the host, the reciprocal loss of fitness is reflected in terms of pathogenetic manifestations that include prolonged persistence or life-long latent infection with recurrent disease episodes or periodic reactivation, autoimmune syndromes, inflammaging and immunosenescence.

Persistent or Life-long Latent Infection

The hallmark of all herpesvirus infections is prolonged persistence and latent infection. After an initial acute episode in which the virus goes through a burst of robust replication in various organ systems, the virus transitions into a low-level replication stage with intermittent shedding by the infected host. This is the persistent stage of CMV infection and it probably mirrors the shifting events between the host immune system and the viral replication machinery. At the host end, NK cells and other components of the cellular immune system are actively trying to root out infection; on the virus end, gene products are actively trying to subvert the host immune system in order to escape it.

Among the viral gene products reputed to modulate host immune function by interfering with natural killer (NK) cell activity are the gene products of UL40, pUL18, and UL16 of the human virus, and those of m155 and M157 of the mouse virus (MCMV).

UL40 gene product upregulates HLA-E expression for recognition by inhibitory NK cell receptors, pUL18 (MHC I heavy chain homologue) replaces host MHC I in infected cell surface and bind natural killer inhibitory receptors (KIRs) (21, 134), UL16 upregulates expression of UL-binding proteins (ULBPs) that sequester NKG2D ligands (22, 30, 124), m155 of MCMV downregulates expression of H60 which is a high affinity ligand for activating receptor NKG2D (70), M157 of MCMV binds to an inhibitory NK receptor in susceptible mice and to an activating receptor (Ly-49H) in resistant mice (4, 116).

The virus also tampers with the host immune function by interfering with MHC I gene expression and antigen processing. For example, US2 and US11 displace the heavy chain from the ER to the cytosol where it is degraded by proteasome (38, 139), US6 binds to TAP and prevents transport of peptides produced in the proteasome to the ER (3, 43, 67), and US3 promotes retention of assembled MHC molecules in the ER (2, 53).

The virus' repertoire for immune modulation also includes chemokine perturbation, exemplified as follows. HCMV encodes chemokine receptor homologues (e.g. US28) that can act as a chemokine sink-sequestering chemokines and preventing them from activating target effectors (97). The UL146 gene product also causes chemotaxis of cells harboring the homologous receptor, thus acting as a bait to propagate infection to other cells (97). UL111.5A, a homologue of IL-10 that functions to dampen host inflammatory response, has been found to be expressed during viral latency in granulocyte-macrophage progenitor cells (51); presumably, protecting infected cells from the influx of inflammatory cells.

One might question whether viral latency actually represents as much a triumph for the virus as it is for the host. It is clear that the host immune system is a factor in maintaining the viral latent state since immunosuppression elicits reactivation. Nevertheless, from the viral perspective, the latent state also allows for a relatively safe refuge in the host and freedom from immunologic threat and elimination. Moreover, the latent state provides the virus the opportunity to wait out a hostile environment and the chance to reactivate as soon as conditions become more favorable.

Autoimmune Syndromes

Because part of the viral armamentarium for survival consists of molecular mimics of host proteins, and because persistent CMV infection and its intermittent reactivation put constant immunological pressure on the host, it has been suggested that CMV infection predisposes the host to develop autoimmune disorders. Indeed, antibodies directed against some viral proteins have been found to cross-react with the host proteins that they resemble. Alternatively, sera from individuals suffering from autoimmune diseases have been shown to react with CMV viral antigens. Examples of autoimmune disorders with known or suspected links to CMV are rheumatoid arthritis (RA) (45, 76, 78, 121), Systemic Lupus Erythematosus (SLE) (27, 46, 110), Inflammatory Bowel Disease (IBD) (23, 28, 44, 47, 63, 103), Systemic Sclerosis (Ssc) (72-74, 83, 85), and vascular diseases such as atherosclerosis, restenosis, and transplant vascular stenosis (13, 72, 75, 123, 141).

CMV involvement in RA is thought to be related to production of rheumatoid factors (RFs) in the form of antiidiotypic antibodies to anti-viral Fc gamma-

binding proteins (FcBPs) of CMV and other herpesviruses (91, 128). In SLE, a large array of autoantibodies is produced that primarily target the whole chromatin (antinucleosome) and its individual components, dsDNA and histones (64). Apoptotic defects and impaired removal of apoptotic cells could contribute to an overload of autoantigens (and in particular of nucleosomes) in circulation or in target tissues that could become available to initiate an autoimmune response (20, 64, 74). Clinical evidence of CMV involvement in SLE is mounting (20, 46, 110).

The chronic mucosal inflammation in IBD is caused by hyperactivation of effector immune cells, which produce high levels of pro-inflammatory cytokines like tumor necrosis factor-alpha, interleukin-6 and interferon-gamma, resulting in colonic tissue damage (6). The nuclear transcription factor NF-kB was identified as one of the key regulators in this immunological setting. NF-kB activation is markedly induced in IBD patients and it strongly influences the course of mucosal inflammation through its ability to promote the expression of various pro-inflammatory genes. CMV genome is frequently found in IBD tissues, and epidemiologic studies strongly suggest association between the virus and the disease, although a definite causal relationship is yet to be established (23, 28, 95, 131).

Lunardi *et al* showed that in Ssc, endothelial cells undergo apoptosis following tetraspan novel antigen-2 (NAG-2) receptor binding by antibodies directed against the HCMV UL94 protein (73, 83). Moreover, they also showed that anti-HCMV antibodies not only caused endothelial cell activation and apoptosis but also activation of fibroblasts, which is a hallmark of the disease (74). The vascular endothelial injury,

with intimal proliferation and luminal narrowing in arteries and arterioles, excessive extracellular matrix accumulation, and fibroblast activation presumably leads to fibrosis of the skin and internal organs. Namboordiri *et al.* also showed significantly higher antibodies to HCMV UL83 among SSc patients, but could not detect any major Ssc autoantibody related to this protein (83).

In atherosclerosis, apoptosis and cytotoxic damage to endothelial cells have been attributed to binding of receptors and HSP 60 by antibodies directed to US28 and UL122 proteins resulting in plaque-formation and narrowing of involved blood vessel (8, 72, 75). Recently, HCMV infection has also been shown to result in increased endothelial cell proliferation, motility, and capillary tube formation (13). The observed HCMV-induced angiogenic response depended on viral binding to and signaling through the β 1 and β 3 integrins and the epidermal growth factor receptor, via their ability to activate the phosphatidylinositol 3- kinase and the mitogen-activated protein kinase signaling pathways.

Inflammaging and Immunosenescence

These terms have found their way into scientific literatures fairly recently as a result of growing consciousness for the health and welfare of the rapidly graying segment of the population. Inflammaging has been proposed to describe the low-grade, chronic, systemic inflammatory state that characterizes the aging process (39), while immunosenescence describes the decline in immunologic responsiveness due to adaptive remodeling of parts of the immune system that occurs with age (18, 36, 58). Both conditions are related to chronic antigenic exposure to a variety of antigens, especially to some viruses, and contribute significantly to age-associated morbidity and mortality

(35, 90). Presumably, the extended and sustained immunologic burden that occurs with chronic infections causes deterioration of clonotypic immunity, while innate immunity is largely preserved. There is accumulation of memory effector T-cells and exhaustion of naïve T-cells that is further exacerbated by the age-related involution of the thymus (18, 36). Emerging data suggest that CMV is a major contributor in inflammaging and immunosenescence because of its chronicity, widespread incidence, and immunogenicity (55, 107, 132, 137). Lifelong infection with CMV causes chronic antigenic stress resulting in the accumulation of anergic, apoptosis-resistant CD8 T-cells that burden the immune system (60, 89). Indeed, CMV seropositivity among the elderly is associated with oligoclonal expansion of T cells, especially CD8 cells of which as much as 10-14% carry receptors for just a single HCMV epitope (59, 130). Such a specific oligoclonal CD8 expansion, especially in the elderly, squanders limited immunologic space and is regarded to be a poor prognostic factor for survival in the elderly.

CONCLUSION

The co-evolution of CMV with its host has remarkably increased CMV's success in perpetuating itself in nature. As a result of its long-term intimate interaction with the host, CMV has acquired a complex array of functions to counterbalance the defensive repertoire of its host. In keeping with the principle that reciprocal traits involved in pathogen-host co-evolution operate in opposite directions, the enhanced viral fitness is mirrored by the diminished fitness of the host. Consequently, the host is overrun by a wide spectrum of diseases, many of which reflect the virus-host co-evolutionary struggle.

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