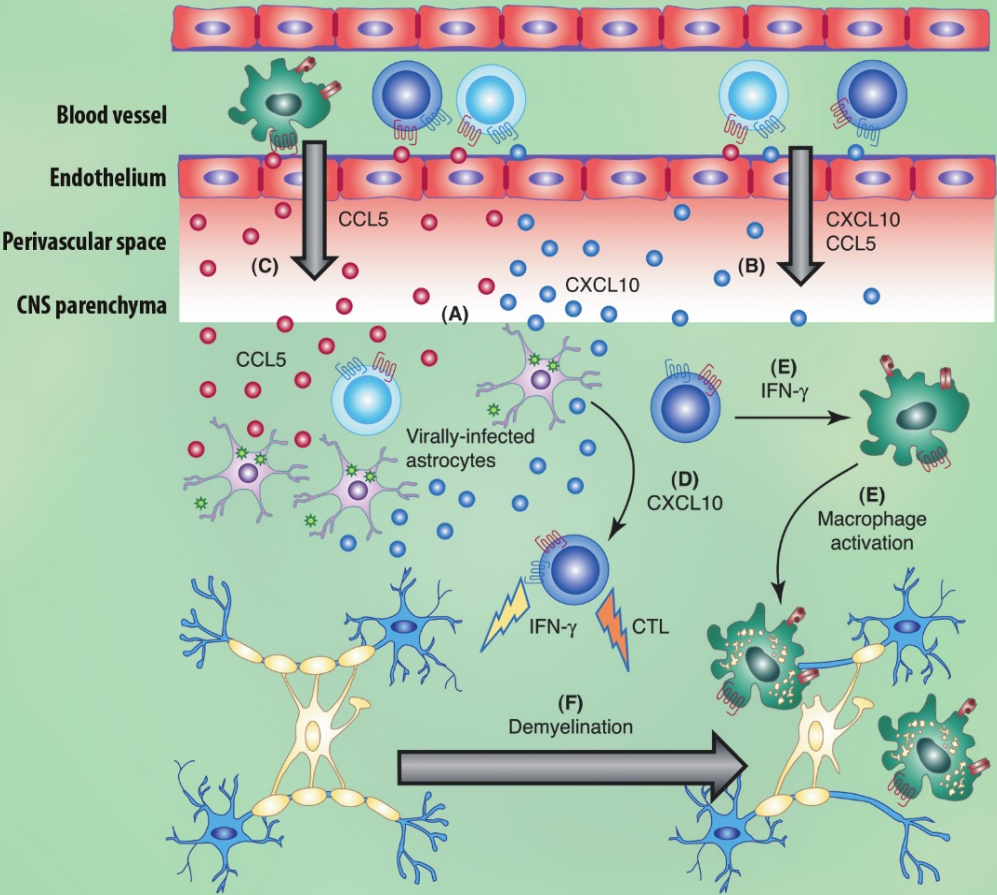


Chemokines and Viral Infection



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Chemokines and Viral Infection

With 14 Figures and 7 Tables

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Preface

Chemokines represent a family of over 40 small proteins that, for the most part, are secreted into the environment and function by binding to G protein-coupled receptors (GPCRs) that are expressed on numerous different cell types. When initially identified close to 30 years ago, these molecules were associated with various human inflammatory diseases and it was recognized that expression might be integral in leukocyte recruitment to inflamed tissue [1–3]. Within a relatively short period of time, early participants within the field determined that these proteins displayed distinct and conserved structural features and exerted potent chemotactic effects on defined lymphocyte subsets [4]. There are now four subfamilies of chemokines identified based on defined structural criteria relating to the positional location of conserved cysteine residues within the amino-terminus of the protein [4, 5]. Chemokines are now recognized as important in numerous biological processes ranging from maintaining the organizational integrity of secondary lymphoid tissue to participating in various aspects of both innate and adaptive immune responses following microbial infection [6, 7].

The host response to viral infection represents a well-orchestrated ballet consisting of numerous participants with diverse roles in defense but with the ultimate goal of generating virus-specific lymphocytes whose job is to control and eliminate the invading viral pathogen from infected tissues. Over the years, an emerging picture has developed that indicates that chemokines and their receptors are intimately involved in development of effective host responses to viral pathogens. Chemokine expression is now associated with all facets of defense against viral infection including linking innate and adaptive immune responses. Early chemokine expression in response to certain viruses such as murine cytomegalovirus (MCMV) is critical in recruiting into the liver natural killer (NK) cells that control viral replication [8]. Expression of chemokines following viral infection has also been demonstrated in tissues originally thought to be relatively immunologically inert such as the central nervous system (CNS). For example, infection of the CNS with either herpes simplex virus1 (HSV-1) or mouse hepatitis virus

(MHV) results in an orchestrated expression of chemokines whose function is to attract antigen-educated lymphocytes into the CNS that contribute to the control of viral replication [9, 10]. Paradoxically, chronic expression of certain chemokines during viral persistence in CNS tissue is also associated with immune-mediated pathology [11–13]. In the face of such a robust and effective immune response, viruses have evolved various ways to avoid or distract the immune response thus enabling the establishment of infection. Certain viruses have exploited the chemokine system to their benefit by either using specific chemokine receptors as coreceptors for efficient entry into host cells (HIV) to encoding receptors with homology to chemokine receptors (various herpes and poxviruses) that may function to subvert the immune system [14–17].

Clearly, the biological roles of chemokines in host defense and/or disease are constantly evolving. This volume of *Current Topics in Microbiology and Immunology* provides an opportunity to examine the relationship between chemokines and viruses with regards to host defense and disease. In addition, the potential of chemokines and their receptors as therapeutic targets for treatment and/or prevention of disease in response to viral infection is not overlooked.

Irvine, California, July 2005

Thomas E. Lane

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Functional Diversity of Chemokines and Chemokine Receptors in Response to Viral Infection of the Central Nervous System

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Abstract Encounters with neurotropic viruses result in varied outcomes ranging from encephalitis, paralytic poliomyelitis or other serious consequences to relatively benign infection. One of the principal factors that control the outcome of infection is the localized tissue response and subsequent immune response directed against the invading toxic agent. It is the role of the immune system to contain and control the spread of virus infection in the central nervous system (CNS), and paradoxically, this response may also be pathologic. Chemokines are potent proinflammatory molecules whose expression within virally infected tissues is often associated with protection and/or

pathology which correlates with migration and accumulation of immune cells. Indeed, studies with a neurotropic murine coronavirus, mouse hepatitis virus (MHV), have provided important insight into the functional roles of chemokines and chemokine receptors in participating in various aspects of host defense as well as disease development within the CNS. This chapter will highlight recent discoveries that have provided insight into the diverse biologic roles of chemokines and their receptors in coordinating immune responses following viral infection of the CNS.

1

Introduction

1.1

Biology and Biochemistry of *Coronaviridae*

Coronaviruses are classified on the basis of several fundamental characteristics, including nucleic acid type, a lipid envelope, and their distinctive morphology [42, 64, 79]. All members have characteristic petal-shaped proteins extending from the virion surface. Coronaviruses infect numerous vertebrate hosts including humans, chickens, pigs, and mice, causing a wide variety of disorders involving a number of different organ systems; however, there are specific tropisms for the CNS, lungs, gastrointestinal tract, and liver [42, 64, 79]. Receptor use among the varied coronaviruses is restricted to several well-defined proteins. Human coronavirus infections result in acute enteritis as well as 15% of common colds indistinguishable from those caused by other viruses [42, 64, 79]. More recently, a human coronavirus has been indicated to be the etiologic agent for severe acute respiratory syndrome (SARS). SARS is a potentially lethal disease and is recognized as a health threat internationally [43].

The first murine coronavirus strain (mouse hepatitis virus, MHV), was isolated in 1949 [12]. MHV is a pathogen of wild mice, and natural infection is due to horizontal transmission, resulting in acute hepatitis with death in young animals and a variable course of persistent gastrointestinal tract infection in adults [79]. MHV is not an endemic mouse virus, but infects mouse colonies sporadically. It is very closely related to some human coronaviruses both at the genomic and protein levels. For example, human sera often contain antibody reactive to MHV. Therefore, characterizing the immune response to murine coronaviruses may provide important insight to mechanisms of control and elimination which may have important implications with regards to understanding the immune response to human coronaviruses such as the SARS coronavirus.

Coronavirus genomes are single-stranded positive-polarity RNA molecules, larger than the size of any other known stable RNA, ranging from 27 kb for the avian infectious bronchitis virus, to 31 kb for murine coronaviruses [50]. Genomic RNA is infectious, contains a cap structure at the 5'-end and poly(A) at the 3'-end. The genome is organized into seven or eight genes, each containing one or more open reading frames (ORF) separated by intergenic sequences that contain the signals for the initiation of transcription of the subgenomic viral messenger (m)RNA species. Upon entry, the viral RNA encodes an RNA polymerase that transcribes the genome into a negative-stranded RNA [50]. The latter serves as templates for positive-sensed genomic RNA and subgenomic mRNAs. Important viral structural proteins include the envelope glycoproteins (S) that bind to receptors on cell membranes [42, 64, 79]. Analysis of monoclonal antibody neutralization escape variants demonstrated that the viral S protein controls cellular tropism *in vivo* and the role of the S protein in tropism has recently been confirmed using stable recombinant viruses in which all genes except the S protein gene were held constant [9, 82].

1.2

Immunity to MHV Infection

The protective immune response to MHV infection is characterized predominantly by cell-mediated immunity during acute infection. A number of unique aspects of CNS viral infection have been described by analysis of the interactions between MHV and the immune response. Antibody, although protective if administered prior to infection, is not present in the serum of infected mice until after the vast majority of virus has been cleared from the CNS [56, 84]. Following infection, neutrophils, macrophages, and NK cells are rapidly recruited into the CNS, followed by T cells and B cells [104]. Inflammation is accompanied by a progressive loss of blood–brain barrier (BBB) integrity that is apparent as early as 4 days post-infection. The initial influx of innate effectors is important in facilitating T cell infiltration, as well as regulating viral replication [104]. However, the ability to survive MHV infection appears to be predominantly due to an effective T cell-mediated response [103]. Recent data have confirmed that cell-mediated immunity is critical during acute infection [53, 55, 74, 76, 92]; however, the ability to prevent viral recrudescence is associated with the continued presence of plasma cells in the CNS secreting neutralizing antibody [56, 84].

The major effectors of anti-viral immunity are virus-specific CD8⁺ T cells. Cytotoxic T lymphocyte (CTL) induction following MHV infection of the CNS has been shown to require CD4⁺ T cell help [92]. Although the pre-

cise mechanism or mechanisms by which CD4⁺ T cells assist CD8⁺ T cells have yet to be completely determined, recent studies have demonstrated that CD4⁺ T cells are important in preventing apoptosis of CTL entering the CNS parenchyma [92]. In addition, the quality of the CTL response is CD4⁺ T cell-dependent [92]. An important concept derived from analysis of MHV infection is that although CD8⁺ T cells are the most prominent effectors for viral clearance during the acute infection, the mechanisms which control virus replication differ with the type of CNS cell infected. Cytolysis is important for the control of viral replication in microglia/macrophages and astrocytes while interferon (IFN)- γ is the critical effector responsible for control of virus replication in oligodendroglia [73]. The demonstration that CD8⁺ CTL suppresses viral replication by two separate effector mechanisms, which function within the CNS in a cell type-specific manner, is an important new concept.

1.3

Viral Persistence and Immune-Mediated Demyelination

Viral persistence in white matter tracts results in a chronic demyelinating disease in which foci of demyelination are associated with areas of viral RNA/antigen [51]. Clinically, mice develop loss of tail tone and a partial to complete hind-limb paralysis. As a result of the clinical and histologic similarities between MHV-induced demyelination and the human demyelinating disease multiple sclerosis (MS), the MHV system is considered a relevant model for studying the underlying immunopathologic mechanisms contributing to immune-mediated demyelinating diseases [51]. A variety of different mechanisms have been postulated to contribute to MHV-induced demyelination. Several studies suggest that MHV-induced demyelination involves immunopathologic responses against viral antigens expressed in infected tissues [30, 31, 37, 47]. Although virus-specific antibody is considered important in suppressing viral recrudescence [84, 85], it may also have a role in promoting demyelination [48]. MHV infection of immunosuppressed or immunodeficient mice results in high titers of virus within the CNS and death but not robust demyelination [53, 105]. Adoptive transfer of MHV-immune splenocytes results in demyelination to the infected recipients, suggesting a role for immune cells in amplifying demyelination [30, 31]. Additional evidence for T cells in contributing to demyelination is provided by Wu et al. [105] who demonstrated that both CD4⁺ and CD8⁺ T cells are important in mediating myelin destruction. In support of this are studies derived from our laboratory demonstrating that adoptive transfer of MHV-specific CD4⁺ or CD8⁺ T cells to MHV-infected RAG1^{-/-} mice results in demyelination [30, 31]. However, demyelination was more severe in recipients of CD4⁺ T cell

compared to CD8⁺ T cell recipients, and this supports a more important role for CD4⁺ T cells in amplifying demyelination in this model. Indeed, we have demonstrated that MHV-infected CD4^{-/-} mice displayed a significant reduction in the severity of demyelination compared to CD8^{-/-} and immunocompetent wildtype mice, suggesting an important role for CD4⁺ T cells in amplifying the severity of white matter destruction [53].

While T cells are generally considered important in driving demyelination in mice persistently infected with MHV, the mechanisms by which these cells participate in disease may vary and depend upon various factors including the ability to secrete interferon (IFN)- γ [80, 81]. While conventional CD4 and CD8 $\alpha\beta$ T cells are generally viewed as the primary T cell type important in disease, $\gamma\delta$ T cells have also been shown to participate in demyelination in MHV-infected athymic mice [16]. In addition, we and others have found that macrophages/microglia are also important in contributing to demyelination [29, 32, 53, 59, 105]. The collective evidence points to a role for inflammatory T cells in contributing to macrophage/microglial infiltration and activation which ultimately results in myelin destruction. Current evidence suggests that demyelination in MHV-infected mice is not the result of epitope spreading and induction of an immune response against neuroantigens as has recently been reported to occur during Theiler's virus-induced demyelination [69]. However, adoptive transfer of T cells from MHV-infected rats to naïve recipient's results in demyelination [100]. Whether a similar response occurs in MHV-infected mice and what the contributions are to demyelination is not clear at this time.

1.4

Chemokines and Chemokine Receptors

Chemokines represent a family of low molecular weight (7–17 kDa) proinflammatory cytokines that are divided into four subfamilies based on structural and functional criteria [14, 60, 94]. The two major subfamilies are the CXC and CC chemokines. The CXC subfamily is structurally characterized by two conserved cysteine residues that are separated by an amino acid, while the CC subfamily is structurally characterized by conserved cysteine residues adjacent to one another. Lymphotactin, the sole member of the C family, is chemotactic for T cells [44]. The CX₃C chemokine, fractalkine, is unique in that it is expressed on the surface of cells as well as being secreted into the surrounding environment [5].

Chemokines have been shown to selectively attract distinct leukocyte populations during periods of inflammation in various disease models. The CXC chemokines function primarily in attracting neutrophils, yet have a limited effect on T lymphocytes and monocytes [14, 60, 94]. However, there

are exceptions to this rule in that CXC chemokines that lack the glutamic acid-leucine-arginine (ELR) motif on the amino terminus are chemotactic for T cells. For example, the non-ELR chemokine CXCL10 is a potent chemoattractant for activated T cells and NK cells and functions by binding to CXCR3 expressed on the surface of these cells [40, 83, 102, 106]. However, CXCL10 does not exert a chemotactic effect on neutrophils [19]. The CC chemokines are thought to attract T cells, monocytes, and macrophages, but not neutrophils [14, 60, 94]. The CC chemokine ligand 5 (CCL5) is able to attract both T cells and macrophages by binding to one of several CC chemokine receptors including CCR1 and CCR5 [14, 60, 94]. Furthermore, there is increasing evidence that chemokines, such as CCL3, influence other immune system activities including T_H1/T_H2 development and T cell proliferation [46, 95]. Chemokines function by binding to seven-transmembrane-spanning G protein-coupled receptors. The chemokine receptors are divided into those that preferentially bind CXC and CC chemokines. In addition, CC and CXC chemokine receptors are capable of binding more than one CC or CXC chemokine, respectively. A variety of cell types including lymphocytes and macrophages, as well as resident cells of the CNS such as neurons, astrocytes, and microglia, express chemokine receptors [60, 94].

2

Orchestrated Expression of Chemokines and Chemokine Receptors Within the CNS Following Infection with MHV

Instillation of MHV into the CNS of susceptible mice results in a well-orchestrated expression of chemokine genes, and the expression pattern correlates with the level of inflammation and disease [52]. Early (~1–3 days) following infection, transcripts for CXCL10 and CCL3 are detected within the CNS, suggesting an important role in initiation of immune responses (see following section; Table 1). By day 6 post-infection (p.i.), virus has spread throughout the brain parenchyma, and a robust inflammatory response, characterized primarily by $CD4^+$ and $CD8^+$ T cells and macrophages, is established within the brain. Chemokines expressed at this time include CXCL9, CXCL10, CCL2, CCL3, CCL4, CCL5, and CCL7 (MIP-2) (Table 1). Analysis of chemokine receptor expression by both RNase protection assay (RPA), immunostaining, and flow cytometry reveals that CCR1, CCR2, CCR5, and CXCR3 are the prominent receptors expressed within the CNS at various stages of disease (Table 2).

Chemokine transcripts are detected almost exclusively in areas in which virus is present, indicating a localized response to infection and subsequent

Table 1 Chemokine gene expression following MHV infection of the CNS

Days post infection	Chemokine	Function (cells attracted)	Reference(s)
1–3	CXCL10	NK cells	97
	CCL3	Dendritic cells	96
7 and 12	CCL2	Macrophage	39, 52
	CCL3	Dendritic cells, T cells	95, 96
	CCL4		52
	CCL5	T cells, macrophage	52, 53
	CXCL9	T cells	58
≥21	CXCL10	T cells	18, 57
	CXCL10	CD4 ⁺ T cells	59
	CCL5	T cells, macrophages	32

Table 2 Chemokine receptors expressed within the CNS of MHV-infected mice

Days post infection	Receptor	Chemokine receptor expression	Reference(s)
1–3	CCR2	T cells, macrophages	13, 39
7 and 12	CCR2	T cells, macrophages	13, 39
	CCR5	T cells, macrophages	29, 30
	CXCR3	T cells	57
>21	CXCR3	T cells	59
	CCR5	T cells, macrophage	29

spread of the virus throughout the parenchyma. In situ hybridization indicates that astrocytes are the primary cellular source for many chemokines during the acute stage of disease [52]. Infection of primary cultures of mouse astrocytes with MHV and evaluating chemokine gene expression by RPA provide additional support for astrocytes as an important cellular source of chemokines in this model [52]. Moreover, viral replication appears to be a necessary prerequisite for inducing chemokine expression, as infection of astrocytes with inactivated virus results in a muted chemokine expression profile. Additional analysis revealed that both infected and noninfected astrocytes are capable of secreting chemokines following instillation of virus into the brain, indicating that viral infection is not required for chemokine gene synthesis by target cells. These data indicate that a factor or factors (possibly type I interferons) derived from infected cells are capable of functioning in both an autocrine and paracrine manner and regulate chemokine gene expression in response

to viral infection. Other cell types that may also secrete chemokines following MHV infection include resident microglia/inflammatory macrophages as well as neurons [52, 75].

By day 12 p.i., MHV-infected mice that have survived the acute stage of disease develop an immune-mediated demyelinating disease. Mice have cleared infectious virus (as determined by plaque assay) by 12 days, yet viral RNA and protein can be detected within white matter tracts for months after infection. As the level of CNS infiltration subsides following reduction of viral burden there is a corollary reduction in the expression of chemokine transcripts. Analysis of chemokine message expression within the brains and spinal cords of MHV-infected mice during the demyelinating phase of disease (days 12 and onward) indicates that CXCL10 and CCL5 are the two prominent chemokines expressed [52]. In situ hybridization for chemokine transcripts indicated expression was limited primarily to areas of viral persistence within white matter tracts undergoing active demyelination [52]. Similar to what was found during acute disease, astrocytes were determined to be the cellular source of CXCL10 at this stage of disease whereas inflammatory cells, presumably CD4⁺ T lymphocytes, expressed CCL5. More recent data now indicate that MHV-infected astrocytes treated with IFN- γ can also express CCL5 mRNA transcripts and protein (T.E. Lane, unpublished observations). Chemokine receptors expressed during chronic demyelination include CXCR3 and CCR5, which are capable of binding CXCL10 and CCL5, respectively. Indeed, we have recently determined that the majority (~90%) of infiltrating virus-specific CD4⁺ and CD8⁺ T cells express CXCR3 (T.E. Lane, unpublished observations).

3

Chemokines, Innate Immune Response, and MHV-Infection of the CNS

The presence of dendritic cells (DCs) within the CNS has been debated for quite some time. However, a series of recent studies clearly indicates that during induction of an autoimmune demyelinating disease, there exists the presence of cell types within the brain that clearly have characteristics of DCs [34, 65]. In addition, emerging evidence points to a previously unappreciated role for chemokines in activating and inducing the migration of differing populations of DCs in response to microbial infection of the CNS [22, 23]. These cells may be important in initiation and/or maintenance of disease by participating in the activation of T cells. Given the potential importance of this population of cells with regards to linking innate and adaptive immune responses following viral infection of the CNS, we investigated whether DC-

like cells were present within the CNS in response to MHV infection. In brief, our findings clearly indicate that a DC-like population of cells is detectable within the CNS as early as day 2 p.i. with MHV [96]. The activation/maturation of these cells as well as the ability to accumulate within the draining cervical lymph node (CLN) appeared to be dictated by localized expression of CCL3 [96]. Moreover, the ability of cultured DCs to secrete cytokines associated with the development of a T_H1 response such as interleukin (IL)-12 was profoundly altered in the absence of CCL3 [96]. The importance of CCL3 signaling and the evolution of an effective T cell response was further confirmed by the demonstration that in the absence of CCL3 signaling, robust anti-viral effector responses, e.g., cytokine production and CTL activity, were dramatically compromised following MHV infection of CCL3^{-/-} mice [95, 96]. Collectively, these studies highlight a previously unappreciated role for the importance of chemokine signaling and DC maturation/activation following MHV infection of the CNS. Moreover, these studies demonstrate that generation of effective T cell responses relies upon CCL3 signaling to successfully combat MHV infection.

4

Chemokines and Chemokine Receptors and Their Role in Acute Viral-Induced Encephalomyelitis

4.1

CCL3

CCL3 is a chemoattractant for both T cells and macrophages and has been implicated in host defense following infection with a wide variety of microbial pathogens. Mice deficient in CCL3 production exhibit increased susceptibility to disease following infection with paramyxovirus [17], influenza virus [15], and coxsackievirus, as well as other microbial pathogens [67, 72]. In all cases, alterations in an effective host response correlated with a paucity in leukocyte accumulation at sites of infection. Although originally thought to participate in defense by attracting effector cells to infected tissue, recent reports also suggest that CCL3 expression is important in coordinating a T_H1 response [46]. Numerous studies now indicate that DCs are capable of expressing various chemokines including CCL3 [21, 66, 77, 78]. Moreover, DC precursors express the CCL3 receptors CCR1 and CCR5 and are capable of responding to CCL3 *in vivo* and *in vitro* resulting in both mobilization and maturation [24, 108]. Indeed, Flesch and colleagues have demonstrated an important role for CCL3 in DC-dependent priming of CTL to viral antigens [24].

Using CCL3^{-/-} mice, we have demonstrated a role for CCL3 in regulating trafficking as well as antiviral effector functions following MHV infection of the CNS [95]. Specifically, our experiments revealed an important role for CCL3 signaling in tailoring T cell responses that allowed for egress out of draining cervical lymph nodes and trafficking into the CNS. Although generation of antigen-specific CD8⁺ T cells was not impaired following MHV infection of CCL3^{-/-} mice, a significant percentage of CD8⁺ T cells retained expression of lymph-node homing receptors CD62L (L-selectin) and the CC chemokine receptor 7 (CCR7) and did not display a dramatic increase in mRNA transcripts for either CXCR3 or CCR5, two receptors which are important in allowing MHV-specific T cells access to the CNS [95]. Moreover, adoptive transfer of CCL3^{-/-} CD8⁺ T cells into MHV-infected RAG1^{-/-} mice (which express CCL3 following MHV infection) resulted in homing back to secondary lymphoid organs, suggesting that lack of CCL3 imprinted on these cells carries an inability to remodulate surface tissue homing receptors. Analysis of antiviral effector functions also revealed that CCL3^{-/-} CD8⁺ T cells displayed overall muted cytolytic activity as well as expression of IFN- γ when compared to CCL3^{+/+} CD8⁺ T cells [95]. Collectively, these studies highlight that, in addition to chemotactic function, chemokines influence specific lymphocyte responses and ultimately effector functions that are required for optimal host defense against microbial pathogens.

4.2

CXCL9 and CXCL10

CXCL9 and CXCL10 attract activated T lymphocytes following binding to CXCR3. Analysis of CXCL9 and CXCL10 mRNA expression within the CNS of MHV-infected mice revealed that CXCL10 was clearly detectable by day 1 p.i. and was prominently expressed at days 7, 12, and 35 p.i. [52]. In contrast, CXCL9 transcripts were only detected at days 7 and 12 p.i. [58]. These data suggested that both CXCL9 and CXCL10 might be important in host defense by attracting antiviral T lymphocytes into the CNS. In support of this is the observation that administration of neutralizing antibodies specific for either CXCL9 or CXCL10 to MHV-infected mice during the acute stage of disease results in a dramatic increase in mortality [57, 58]. Additionally, this treatment also resulted in a significant decrease in numbers of CD4⁺ and CD8⁺ T lymphocyte infiltrating into the CNS which correlated with decreased expression of IFN- γ and increased levels of virus [57, 58]. MHV infection of CXCL10^{-/-} mice supported and extended our previous work on antibody-mediated neutralization of CXCL10 in that MHV-infected CXCL10^{-/-} mice displayed reduced T cell infiltration into the CNS accompanied by reduced IFN- γ

secretion and increased viral burden [18]. Therefore, the collective evidence points to pivotal roles for both CXCL9 and CXCL10 as important sentinel molecules in promoting a protective response following MHV infection of the CNS by attracting T cells into the CNS that participate in elimination of virus.

4.3

CCL5

CCL5 is a T cell and macrophage chemoattractant that has been shown to influence leukocyte migration during periods of inflammation. Upon MHV infection of the CNS of mice, CCL5 transcripts and protein are readily detected within the brain [52]. Initial studies in which CD4^{-/-} or CD8^{-/-} mice were infected with MHV indicated an overall reduction in CCL5 mRNA transcripts within the brains of CD4^{-/-} mice, suggesting that CD4⁺ T cells were either a primary cellular source for CCL5 and/or influenced the expression of CCL5 by resident and inflammatory cells [53]. We now know that both inflammatory CD4⁺ T cells as well as astrocytes are capable of expressing CCL5 following instillation of MHV into the CNS [32, 53]. Furthermore, treatment with neutralizing anti-CCL5 antisera results in diminished T cell and macrophage accumulation within the CNS, suggesting that in this model CCL5 is capable of regulating trafficking of these two populations of cells [32].

4.4

CCR5

CCR5 is a member of the CC chemokine receptor family that is expressed on various hematopoietic cells including lymphocytes and macrophages [86]. Chemokines that are capable of binding to CCR5 include CCL3, CCL4, and CCL5 [7, 68, 86]. Recent studies have clearly indicated that CCR5 expression correlates with leukocyte trafficking to sites of inflammation as well as regulating the immune response following microbial infection. For example, mice deficient in CCR5 (CCR5^{-/-}) exhibit altered T cell activity and impaired macrophage function [88, 109]. Furthermore, macrophage trafficking in response to antigen is impaired in CCR5^{-/-} mice, indicating that CCR5 is required for migration of this population of cells [45]. Given that both T cells and macrophages express CCR5 following MHV infection of the CNS and these cells clearly influence outcome in response to infection, we have defined the contributions of CCR5 to both host defense and disease in response to MHV infection. Using an adoptive transfer model in which virus-expanded T cells are transferred into MHV-infected RAG1^{-/-} mice, we have been able to examine how CCR5 expression influences trafficking of T cells into the CNS. Transfer of CCR5^{+/+}-derived CD4⁺ T cells to MHV-infected RAG1^{-/-} mice

resulted in CD4⁺ T cell entry into the CNS and a reduction in viral titers within the brain [30]. These mice also displayed robust demyelination correlating with macrophage accumulation within the CNS. Conversely, CD4⁺ T cells from CCR5^{-/-} mice displayed an impaired ability to traffic into the CNS of MHV-infected RAG1^{-/-} recipients, which correlated with increased viral titers, diminished macrophage accumulation, and limited demyelination. Analysis of chemokine receptor mRNA expression by M133–147-expanded CCR5^{-/-}-derived CD4⁺ T cells revealed reduced expression of CCR1, CCR2, and CXCR3, indicating that CCR5 signaling is important in increased expression of these receptors which aid in trafficking of CD4⁺ T cells into the CNS. Collectively these results demonstrate that CCR5 signaling is important to migration of CD4⁺ T cells to the CNS following MHV infection.

With regards to the role of CCR5 in CD8⁺ T cell trafficking, comparable numbers of virus-specific CD8⁺ T cells derived from immunized CCR5^{+/+} or CCR5^{-/-} mice were present within the CNS of MHV-infected RAG1^{-/-} mice following adoptive transfer, indicating that CCR5 is not required for trafficking of these cells into the CNS [30]. RAG1^{-/-} recipients of CCR5^{-/-}-derived CD8⁺ T cells exhibited a modest yet significant ($p \leq 0.05$) reduction in viral burden within the brain that correlated with increased cytolytic activity and IFN- γ expression. Histologic analysis of RAG1^{-/-} recipients of either CCR5^{+/+} or CCR5^{-/-}-derived CD8⁺ T cells revealed only focal areas of demyelination with no significant differences in white matter destruction. These data indicate that CCR5 signaling on virus-specific CD8⁺ T cells modulates antiviral activities but is not essential for entry into the CNS.

Finally, MHV infection of CCR5^{-/-} mice resulted in a dramatic reduction in macrophage (defined as CD45^{high}F4/80⁺ dual-positive cells) accumulation within the brains, and this correlated with a significant reduction in the severity of demyelination compared to CCR5^{+/+} mice. Collectively, these data suggest that ligand binding, e.g., CCL5 and/or CCL3, and signaling via CCR5 results in macrophage migration and infiltration into the CNS. However, we have previously demonstrated that CCL3 is expressed only at low levels during acute disease and is not detectable during chronic demyelination, whereas robust expression of CCL5 is detected during both phases of disease, and this suggests that CCL5 is the primary CCR5 signaling chemokine in this model. This is supported by earlier studies that showed an important role for CCL5 in attracting macrophages into the CNS following MHV infection [53]. Therefore, the data presented in this study suggest that one mechanism by which CCL5 contributes to demyelination is via attracting macrophages into the CNS through CCR5-mediated signaling pathways. Additional evidence supporting this is provided by the observation that even in the presence of increased CCL5 expression at day 12 p.i., demyelination is reduced in CCR5^{-/-} mice.

4.5

CCL2 and CCR2

CCL2 is capable of regulating the pathobiology of various inflammatory diseases including MS and atherosclerosis [1, 8, 28, 33, 35, 61]. In addition to its potent chemoattractant effect on monocytes and macrophages, CCL2 also influences T_H2 polarization in response to certain antigenic challenge [36, 41, 46, 99]. The influence of CCL2 on T cell polarization may be due to the fact that CCL2 is constitutively expressed within secondary lymphoid tissue and would be capable of affecting cellular responses following exposure to antigen [36]. Thus, available evidence indicates that expression of CCL2 is capable of influencing both innate as well as adaptive immune responses by regulating monocyte and T cell responses, respectively.

Analysis of chemokine receptor expression following MHV infection reveals that CCR2 is expressed by endogenous cells of the CNS as well as by inflammatory T cells and macrophages, indicating a role for these receptors in regulating both the immune response and disease development [13, 31]. Indeed, MHV-infection of CCR2^{-/-} mice resulted in a dramatic increase in mortality and enhanced viral recovery from the brain that correlated with reduced T cell and macrophage entry into the CNS compared to viral infection of CCR2^{+/+} mice [13].

MHV infection of CCL2^{-/-} mice does not result in a similar disease phenotype as observed in CCR2^{-/-} mice. This was somewhat surprising as CCR2 is currently the only known functional receptor for CCL2. Specifically, CCL2^{-/-} mice were able to clear virus from the brain in a similar time frame as wild-type mice, and this correlated with the ability to generate antigen-specific T cells [39]. The deficiency in CCR2^{-/-} mice to clear virus from the brain is not the result of an inherent inability to generate an effective adaptive immune response to virus, as CCR2^{-/-} mice had a similar frequency of antigen-presenting cells (APC) and virus-specific T cells present within draining CLN compared to either CCL2^{-/-} or wildtype mice. Our findings from MHV infection of CCL2^{-/-} mice indicated that while CCL2 does influence leukocyte migration into the CNS in response to viral infection, CCR2 is clearly more influential in directing T cell trafficking into the CNS. In support of the role for CCL2 in promoting leukocyte migration into the CNS of MHV-infected mice are recent studies by Perlman and colleagues demonstrating that localized CCL2 expression within the CNS promotes macrophage infiltration [47]. These data highlight the possibility that ligand(s) other than CCL2 are important in signaling through the CCR2 receptor. Alternatively, it is possible that CCR2 signaling by either endothelial cells and/or astrocytes regulates the permeability of the BBB, as recently suggested by Stamatovic and colleagues [91].

5 Chemokines and Chronic Viral-Induced Demyelination

Expression of chemokines has been associated with demyelinating plaque lesions present in MS patients [3, 4, 26, 27]. Elevated levels of chemokines, notably CXCL10, were found in the cerebral spinal fluid (CSF) of MS patients during periods of clinical attack [25, 89]. Indeed, the concentration of CXCL10 within the CSF of MS patients correlated with numbers of inflammatory cells and the severity of clinical disease [2, 89, 90]. Moreover, when CXCL10 levels decreased, there was a corresponding decrease in inflammation and disease severity [89]. Astrocyte expression of CXCL10 has been reported in active plaque lesions present in MS patients, and the majority of T cells infiltrating into the CNS of MS patients express the CXCL10 receptor, CXCR3. Collectively, these studies highlight a potentially important role for CXCL10 in the pathogenesis of demyelinating diseases such as MS by attracting CXCR3-expressing T cells into the CNS and support targeting chemokines and their receptors for therapeutic intervention in the treatment of MS [10, 54, 70, 90].

Studies from animal models of MS support this notion by demonstrating that blocking of CXCL10 often results in diminished disease severity accompanied by a marked reduction in neuroinflammation. For example, several recent reports indicate that treatment with anti-CXCL10 neutralizing antibodies resulted in delayed disease onset and diminished neuroinflammation in mice with the autoimmune demyelinating disease experimental autoimmune encephalomyelitis (EAE) [20]. These studies support the idea that localized expression of CXCL10 within the CNS amplifies disease severity by attracting CXCR3-expressing T cells into the CNS. Once present, these cells enhance neuroinflammation by secreting additional chemokines as well as cytokines that can activate resident glia cells. Importantly, these studies also implicate CXCL10 as a potential therapeutic target and suggest that alternative CXCR3 ligands, e.g., CXCL9 and CXCL11, do not exert a prominent effect on T cell infiltration into the CNS. However, the role of CXCL10 in contributing to neurologic disease in EAE has been questioned by results indicating that CXCL10 may actually exert a protective effect in mice with EAE [49, 71]. Antibody-mediated neutralization following induction of EAE in rats resulted in increased disease severity, and this was associated with smaller draining lymph nodes and increased numbers of CD4⁺ T cells infiltrating into the CNS [71]. In addition, CXCL10^{-/-} mice exhibited increased clinical disease severity following immunization with myelin peptides, and this correlated with diminished lymph node sizes although T cell infiltration into the CNS was not dramatically altered when compared to wildtype mice [49]. In these

particular EAE models in which mice are immunized peripherally with antigen, CXCL10 expression within secondary lymphoid tissue is considered important in dictating disease outcome by serving to retain lymphocytes and tailoring T cell responses. Moreover, these findings highlight the different roles of CXCL10 in regulating cellular immune responses in different models of neuroinflammation and emphasize the need for a better understanding of how signaling by this chemokine regulates inflammation and disease.

As indicated, we have determined that MHV infection of the CNS results in an orchestrated expression of chemokine and chemokine receptor genes that are regulated, in large part, by the viral burden. Similar to MS patients, CXCL10 is expressed primarily by astrocytes in areas undergoing demyelination, suggesting an important role in the pathogenesis of demyelination by attracting CXCR3-expressing T cells into the CNS [52, 59]. Indeed, our laboratory was the first to demonstrate that treatment of mice with established demyelination and paralysis with anti-CXCL10 neutralizing antibody resulted in a significant reduction in CD4⁺—but not CD8⁺—T cells present within the CNS, and this correlated with improved motor skills and a reduction in the severity of demyelination [59]. Moreover, the dramatic regain of movement in anti-CXCL10-treated mice corresponded with more than 80% of previously demyelinated axons undergoing remyelination, indicating that removal of CXCL10 promoted an environment capable of remyelination. In addition to reduced numbers of CD4⁺ T cells within the CNS, there was a paucity of macrophage infiltration into the CNS of anti-CXCL10-treated mice that correlated with a dramatic reduction in the levels of the macrophage-chemoattractant CCL5. These data were consistent with previous studies indicating that CD4⁺ T cells were the major source for CCL5 in MHV-infected mice undergoing demyelination [53, 59]. The influence of CXCL10 in contributing to T cell responses was also examined. T cells isolated from secondary lymphoid tissue of mice treated with anti-CXCL10 displayed muted expression of IFN- γ in response to viral antigen when compared to T cells isolated from control mice, suggesting that CXCL10 also serves to influence T cell effector functions during chronic disease (T.E. Lane, unpublished observations).

We have previously determined that CCL5 mRNA transcripts and protein are present within the CNS of MHV-infected mice during chronic demyelination, indicating a potentially important role for this chemokine in promoting inflammation [52, 53]. In order to assess the functional role of CCL5 in participating in viral-induced immune-mediated demyelination, MHV-infected mice were treated via intraperitoneal (i.p.) injection with anti-CCL5 monoclonal antibody (mAb) following onset of clinical disease and demyelination. Such treatment resulted in a significant ($p \leq 0.05$) reduction in the severity of

clinical disease compared to mice treated with an isotype (IgG₁)-matched antibody [32]. Upon removal of anti-CCL5 treatment, clinical disease returned to mice such that there was no difference between the two experimental groups of mice. Immunophenotyping the cellular infiltrate of mice treated with anti-CCL5 revealed reduced T cell and macrophage infiltration into the CNS that is consistent with our earlier studies that CCL5 attracts these cells into the CNS of mice with chronic demyelination. Further, analysis of the severity of demyelination in experimental groups of mice indicated that anti-CCL5 treatment resulted in a significant ($p < 0.05$) reduction in the severity of demyelination compared to control-treated mice.

A picture is slowly evolving from our experiments designed to test the functional contributions of CXCL10 and CCL5 to chronic demyelination within MHV-infected mice. Antibody targeting of the T cell chemoattractant CXCL10 in MHV-infected mice selectively affects CD4⁺ T cell accumulation within the CNS accompanied by improved motor skills and a reduction in the severity of demyelination [59]. In contrast, CCL5 is capable of attracting both CD4⁺ and CD8⁺ T cells into the CNS. It is also important to emphasize that our data on CCL5 and CXCL10 inhibition with regards to T cell and macrophage trafficking are corollary and it is possible that alternative scenarios exist. For example, studies by Bergmann and colleagues suggest that during persistent MHV infection there is limited to no trafficking of T cells from the periphery into the CNS. Rather, upon entry during acute encephalomyelitis a certain percentage of CD4⁺ and CD8⁺ T cells is retained and participate in disease [62, 93]. In this instance, CXCL10 expression would not be functioning as a T cell chemoattractant but rather to influence specific biologic functions of T cells as well as potentiating the retention of T cells within the CNS. In support of this, it is possible that CXCL10 serves to enhance CD4⁺ T cell proliferation, as several recent studies indicate that CXCL10 is important in contributing to T cell proliferation [18, 71, 101].

It is unlikely that CXCL10 contributes to T cell survival, as CXCL10^{-/-} mice do not display any abnormalities with regards to T cell half-life nor do we see any increase in numbers of apoptotic T cells following anti-CXCL10 treatment. In addition, Narumi et al. [71] speculate that CXCL10 actually serves to retain CXCR3⁺ T cells within tissues and this influences disease severity. Therefore, the selective reduction in CD4⁺ T cells within the CNS of MHV-infected mice may not be the result of impaired trafficking. Rather, either CD4⁺ T cells are not undergoing a steady-state turnover or are actually migrating out of the CNS in the absence of signals specifying their retention.

In addition, recent studies indicate an important role for CXCL10 in imparting effector functions to T cells. For example, Salomon and colleagues demonstrated that anti-CXCL10 treatment improved joint swelling in a rodent

model of arthritis and this correlated in part with an altered T_H1/T_H2 balance, suggesting that CXCL10 expression promotes and maintains a T_H1 state in T cells in this model [87].

Similarly, we have shown that MHV-infection of CXCL10^{-/-} mice results in diminished IFN- γ expression by virus-specific T cells, supporting the idea that CXCL10 expression serves to maintain a T_H1 -like state in T cells [18] (T.E. Lane, unpublished observations). CCL5 signaling also modulates cytokine production by T cells following antigenic challenge. In support of this is our demonstration that inhibition of CCL5 signaling results in enhanced IFN- γ expression by virus-specific T cells, supporting the idea that CCL5 expression serves to regulate a T_H1 -like state in T cells [32]. Moreover, ablation of CCL5 signaling also modifies the cytolytic activity of MHV-specific CD8⁺ T cells [30].

6 Perspectives

This chapter highlights mechanisms by which chemokines participate in both host defense and disease progression in response to MHV infection of the CNS. An overview of the potential functional role for select chemokines in linking innate and adaptive immune responses in response to viral infection of the CNS is provided in Fig. 1. In brief, following MHV infection there is robust expression of chemokines by infected astrocytes including CCL3 that contribute to the maturation/activation of local DCs, which ultimately enables migration to draining cervical lymph nodes. Activated DCs present antigen to T cells as well as secrete chemokines such as CCL3 and CXCL10 that enhance polarization to a T_H1 response. In turn, MHV-specific T cells express chemokine receptors including CXCR3 and CCR5 that enable them to traffic into the CNS as a result of localized expression of ligands CXCL9 and CXCL10 (ligands for CXCR3) as well as CCL5 (ligand for CCR5). In addition, our contention is that expression of CCR2 by endothelial cells of the BBB is also important in increasing the permeability of this structure.

With regards to chronic disease, MHV persistence within the CNS results in chronic expression of CXCL10 and CCL5 which together contribute to the maintenance of a chronic inflammatory disease by attracting both T cells and macrophages (Fig. 2). Local secretion of CXCL10 and CCL5 may also contribute to demyelination by enhancing specific T cell effector functions including (1) secretion of IFN- γ that activates local inflammatory macrophage and resident microglia, as well as directly damaging oligodendrocytes and (2) increasing CTL activity by CD8⁺ T cells.

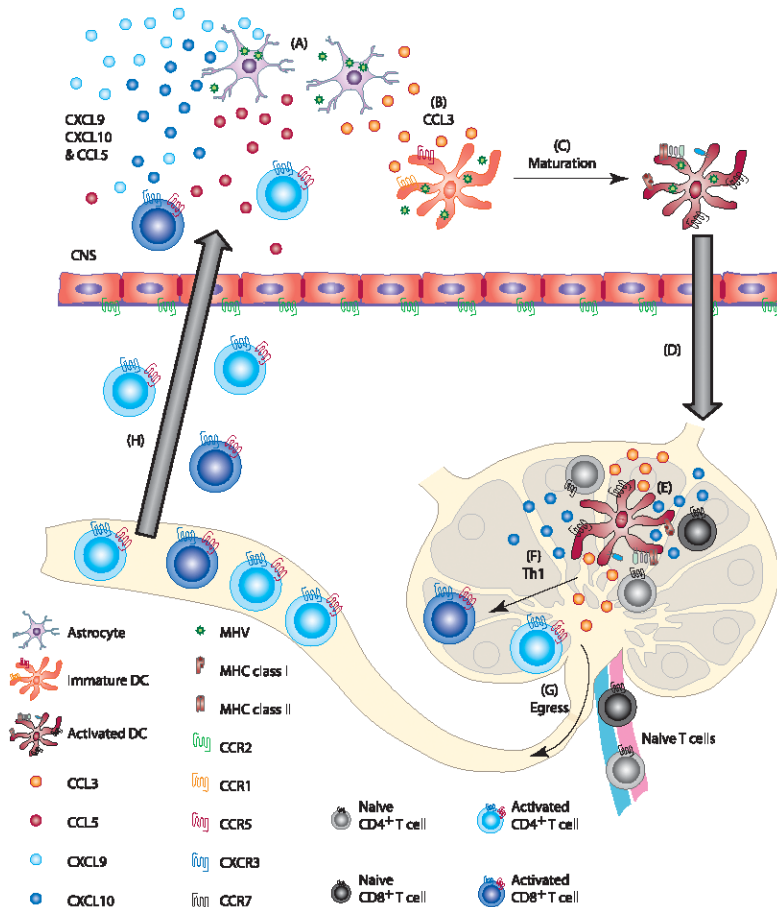


Fig. 1A–H Chemokines and innate/adaptive immune response following MHV infection of the CNS. Instillation of MHV into the CNS of susceptible mice results in infection of astrocytes that are an important source of chemokines including CXCL10, CCL5, and CCL3 (A). In addition, immature DC-like cells may also be susceptible to infection and secrete CCL3 (B) that functions in a paracrine and autocrine manner to bind to CCR1 expressed on immature DC-like cells. As a result of CCL3 signaling and MHV infection, the DC-like cells undergo maturation and activation (C) resulting in a remodulation of the plasma membrane characterized by decreased expression of CCR2 accompanied by increased expression of CCR1 as well as major histocompatibility complex (MHC) class I and II. CCR7-expressing, activated DCs home to the draining cervical lymph node (D). Upon entry, activated DCs express a variety of soluble factors including CCL3 and CXCL10 (E) that activate and enhance polarization of virus-specific T cells to a T_H1 phenotype (F). Activated T cells exit the lymph node via the efferent lymph (G), enter the blood stream, and migrate to the CNS via expression of the chemokine receptors CXCR3 and CCR5 (H)

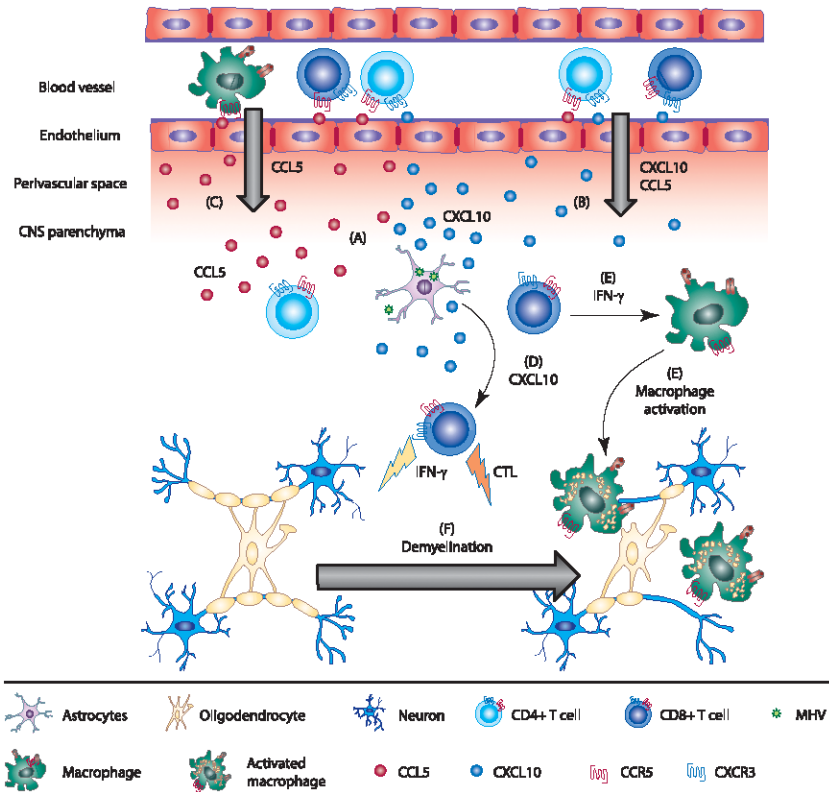


Fig. 2A–F Chemokines and MHV-induced demyelination. Persistent MHV infection within astrocytes leads to chronic CXCL10 and CCL5 expression (A) that serves to recruit CXCR3⁺ and CCR5⁺ T cells into the CNS (B). In addition, activated CD4⁺ T cells secrete CCL5 that enhances macrophage migration into the CNS (C). We believe that CXCL10 may also influence T cell effector functions within the CNS, including CTL activity (D) and IFN- γ secretion (E), leading to macrophage activation. Both IFN- γ production and CTL activity may enhance tissue destruction as well as macrophage activation that amplifies myelin destruction (F)

Clearly, these observations indicate that chemokine signaling is an integral component involved in eliciting protective immunity in response to viral infection of the CNS. Conversely, our studies also indicate that chronic localized secretion of select chemokines ultimately amplifies disease severity through maintaining inflammation within the CNS. Importantly, studies derived from the MHV system demonstrate that antibody targeting of select chemokines offers a powerful approach towards delineating the functional contributions

of these molecules in a model of immune-mediated demyelination. Further, these studies highlight the relevancy of such an approach in treating human neuroinflammatory and demyelinating diseases such as MS.

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Cytokine and Chemokine Networks: Pathways to Antiviral Defense

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Abstract The complex interplays between cytokines and chemokines are emerging as key communication signals in the shaping of innate and adaptive immune responses against foreign pathogens, including viruses. In particular, the virus-induced expression of cytokine and chemokine profiles drives the recruitment and activation of immune effector cells to sites of tissue infection. Under the conditions of infection with murine cytomegalovirus (MCMV), a herpesvirus with pathogenic potential, early immune functions are essential in the control of virus replication and virus-induced pathology. The coordinated MCMV-induced cytokine and chemokine responses promote effective natural killer (NK) cell recruitment and function, and ultimately MCMV clearance. The studies highlighted in this chapter illustrate *in vivo* pathways mediated by innate cytokines in regulating chemokine responses that are vital for localized antiviral defenses.

Abbreviations

MCMV	Murine cytomegalovirus
NK	Natural killer
MIP-1 α	Macrophage inflammatory protein 1 α
Mig	Monokine induced by interferon- γ
MCP-1	Monocyte chemoattractant protein-1
rIFN- α	Recombinant interferon- α

1**Introduction**

The host response to microbial pathogens necessitates the integrated action of both the innate and adaptive arms of the immune system. Innate immunity is largely dependent on granulocytes, macrophages, dendritic cells, and natural killer (NK) cells, whereas adaptive immune responses require T and B lymphocytes. It is becoming increasingly evident that an effective immune response requires crosstalk among the various immune cells for linkage of innate and adaptive immunity. This intercellular network of communication signals is mediated in part by cytokine and chemokine responses generated against infectious agents, including viruses.

Cytokines constitute a group of low molecular weight soluble proteins that modulate various immune functions upon induction by various stimuli, such as bacterial or viral components [10–12, 32, 92]. Virtually all cells produce these proteins, including leukocytes and infected or activated nonimmune cells such as fibroblasts, endothelial cells, and a variety of tissue parenchymal cells [10, 11]. Cytokines control the magnitude and kinetics of immune responses by inducing or inhibiting the activation, proliferation, and/or differentiation of various target cells, and they also regulate the production of antibodies and other cytokines including chemokines [1, 11, 54].

Chemokines are small heparin-binding secreted cytokines that are functionally appearing to be more diverse than used to be thought. Housekeeping chemokines are generally constitutively expressed under physiological conditions, and they function in development and homeostasis [20, 56, 73, 81, 95, 104]. Inducible inflammatory chemokines function in the directed trafficking and localization of effector leukocytes within tissue compartments during inflammation, infection, and trauma [5, 58, 73, 82, 91, 95, 104]. There is considerable evidence highlighting the importance of chemokine-mediated inflammatory responses to pathogens as being crucial to survival during infections [18, 53–55, 57, 77, 78, 80, 83]. Additionally, it has become evident that infiltrating leukocytes may sometimes play a role in disease pathogenesis [18,

54, 55, 83, 98]. Nevertheless, as chemokines are central to the routing of key immune cells, they have emerged as key players in host defense mechanisms [54–58, 62, 80, 95, 104]. These proteins mediate their biological effects through selective interactions with seven-transmembrane G protein-coupled receptors on the surface of target cells [7, 9, 59, 74, 90]. Inflammatory chemokines are selective for a broad range of receptors. Nonetheless, *in vivo* studies have demonstrated specific functions for various chemokines [18, 19, 21, 25, 27, 37, 58, 80, 93].

Protective immunity to viruses is dependent on the activation and interplay between cytokines and chemokines to enhance or regulate innate or adaptive (or both) effector functions. Studies have demonstrated that the cytokine milieu induced by pathogens may determine the cellular constituents that get activated, and thus the nature of the immune response, by selectively inducing specific chemokines in infected tissue compartments [18, 37, 55, 57, 77, 78, 80]. The murine cytomegalovirus (MCMV) model of infection in the liver has been used to demonstrate the coordinated effects of activated cytokine and chemokine responses on the recruitment of NK cells to sites of infection to maintain early control of virus replication. This chapter presents a brief overview of the role of NK cells in antiviral defense, the molecular mechanisms regulating the innate cytokine and chemokine networks promoting NK cell inflammation into liver, and the conceivable role of these pathways in promoting downstream adaptive responses for effective antiviral defense.

2

NK Cells and Antiviral Defenses

NK cells are innate effector cells that respond quickly to a variety of pathogens before the onset of adaptive immunity [11, 96, 103]. These cells originate from bone marrow precursors and predominate in peripheral blood and spleen. However, they can be induced to traffic into other compartments including the liver during infection [77, 99]. Classical NK cells are CD3⁻ and do not express rearranged antigen-specific receptors [11, 42, 71, 97, 103]. Instead, it is now widely accepted that NK cells express a complex repertoire of activating and major histocompatibility complex (MHC) class I-specific inhibitory receptors on their surfaces that interact with ligands on target cells [23, 101–103]. Engagement of activation receptors with ligands on infected cells permits NK cell-mediated killing and cytokine production, while the inhibitory receptors restrain NK cell activation [4, 23, 43, 101, 102]. The central role of NK cells as mediators of antiviral defenses has long been appreciated [11, 96].

Furthermore, viruses that evade immune detection by restricting the function of MHC class I T lymphocytes are more susceptible to NK cell-mediated protective responses [101–103]. These cells are quick to respond and can be activated to produce high levels of the cytokine interferon (IFN)- γ , as well as additional antiviral and immunoregulatory cytokines [11, 12]. NK cells have been demonstrated to mediate protection against a number of viral infections (reviewed in references [11, 12]), most notably is the extensive data documenting their importance in innate defenses against MCMV infection [6, 11, 15, 63, 64, 88].

2.1

NK Cell Responses in MCMV Infection

Resistance to MCMV infection is critically dependent on the activation of NK cells for early control of viral replication in target organs such as spleen and liver [11, 12, 14, 63, 77, 94], although T lymphocyte responses do get activated and contribute to viral clearance late in infection [35, 39, 69, 70]. The profound antiviral effects of NK cells against acute MCMV infection have been exemplified with a variety of experimental systems, including in vivo depletion of NK cells [14, 15, 63, 86], infection of beige mutant mice [66, 88], and most recently infection of mice deficient in NK cell, but not NKT or T cell, functions [50]. Together, these studies have demonstrated increased viral titers, liver pathology, and enhanced mortality upon elimination of functional NK cell responses. Conversely, resistance to MCMV infection has been demonstrated when NK cells were adoptively transferred into susceptible mice [16].

The mechanisms of NK cell-mediated defenses against MCMV infection in vivo have not been completely elucidated, although there is evidence that disparate NK cell responses are used in the spleen and liver for protection against MCMV infection. In the spleen, resistance seems to be mainly through perforin-dependent mechanisms, suggesting that NK cell-mediated cytotoxicity [94] and NK cell surface expression of an activating receptor [4, 23, 43, 101, 102], found on resistant strains of mice [4, 101], is required. In contrast, there is evidence that NK cell effector function in the liver is mediated through production of IFN- γ [52, 64, 77, 78, 94].

2.2

NK Cell Inflammatory Responses in Liver During MCMV Infection

The liver is a common target organ of MCMV infection [29, 61, 65, 87], and the rapid control of virus-induced disease is essential for survival [64, 65,

78, 80, 87]. As shown in Fig. 1a, the liver responds to MCMV infection by inducing a profound accumulation of inflammatory cells into the parenchyma that peaks between 48 and 72 h after infection of C57BL/6, 129SvEV, and T- and B cell-deficient C57BL/6-SCID mice [65, 77, 79]. Studies have identified NK cells as the major cellular constituents of the inflammatory foci [3, 22, 77]. As NK cells surround and sequester sites of MCMV antigen expression (Fig. 1b), it is highly conceivable that the inflammatory response limits the spread of infection to neighboring hepatocytes, thus minimizing virus-induced pathology. The precise effector mechanism used by inflammatory NK cells remains to be elucidated, although localization of IFN- γ within inflammatory sites ([77] and Sect.3) is critical to antiviral defense.

In vivo cell trafficking studies using fluorescently labeled bone marrow cells from either C57BL/6 or C57BL/6-SCID donor mice have demonstrated the rapid deployment and collective mobilization of NK cells between portal areas and central hepatic veins in MCMV-infected recipient mice [77]. Transfer studies using bone marrow donor cells from mice depleted of NK cell subsets using specific antibodies or from mice genetically deficient in NK cells and T lymphocytes demonstrated the accumulation of cells only in the liver sinusoids [77]. Thus, in vivo, NK cells are induced to migrate to sites in a pattern similar to the inflammatory foci observed in histological liver sections (see Fig. 1a).

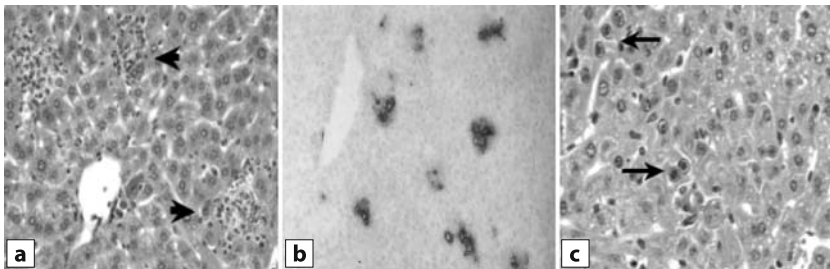


Fig. 1a–c Characterization of liver inflammatory foci during MCMV infection. **a** and **b** Paraffin-embedded or frozen livers sections were prepared from C57BL/6 mice infected with MCMV for 48 h and (a) stained with hematoxylin and eosin or (b) stained with immune serum antibodies to MCMV. Bound antibodies were detected with NBT/BCIP, followed by methyl green counterstain to highlight localization of inflammatory nuclei. *Arrowhead* denotes focus of inflammatory cells. **c** Paraffin-embedded liver sections were prepared from C57BL/6-MIP-1 α deficient mice infected with MCMV for 48 h and stained with hematoxylin and eosin. *Arrow* denotes cytomegalic inclusion bodies

3

CCL3/MIP-1 α : Primary Mediator of NK Cell Inflammation

To understand the key mechanisms governing the *in vivo* recruitment of NK cells to liver during MCMV infection, it is important to appreciate the chemokine expression profile. Of particular interest is the inflammatory chemokine CCL3 or macrophage inflammatory protein-1 α (MIP-1 α). Mice rendered genetically deficient in MIP-1 α (MIP-1 α knockouts) have been shown to exhibit reduced lung inflammation and delayed clearance of influenza virus when compared to control animals [19]. Moreover, MIP-1 α promoted pulmonary inflammation and antiviral defense in a model of paramyxovirus infection [24]. During MCMV infection, MIP-1 α messenger (m)RNA and protein can be detected in liver at times consistent with peak NK cell inflammation (48 h after infection) [77, 78]. Results obtained from *in vivo* cell trafficking studies demonstrated that the induction of NK cell inflammation in liver during MCMV infection was dependent on MIP-1 α , as NK cell trafficking is dramatically impaired in MIP-1 α knockout mice [77]. It is notable that monocyte and macrophage trafficking to liver is not affected in MIP-1 α knockout mice, suggesting that although other chemokines are induced in these mice, MIP-1 α responses are required for NK cell recruitment. Furthermore, MIP-1 α knockout mice lacked detectable inflammatory foci in liver sections by histological evaluation, and displayed a profound increase in the number of cytomegalic inclusion bodies, or MCMV-infected cells (Fig. 1c) [77]. Flow cytometric analysis demonstrated that in the absence of MIP-1 α function the absolute numbers of NK cells become significantly elevated in the blood but are dramatically reduced in the liver when compared to control mice [78]. These results imply that although NK cells get activated in response to infection, the communication signals directing their migration to tissue sites of virus replication are impaired in the absence of MIP-1 α . Collectively, these studies define a prominent and unique role for MIP-1 α in the initial influx of NK cells into the liver during MCMV infection.

3.1

MIP-1 α and Antiviral Defenses: The Cytokine and Chemokine Networks

As discussed above, NK cells are an essential source of IFN- γ production that is required for early antiviral defense in liver. During MCMV infection, this cytokine is maximally elevated in spleen and serum within 40 h but subsides by 48 h after viral challenge [75, 78]. It has been established that an essential function of the MIP-1 α -dependent NK cell inflammatory response is to sustain IFN- γ production in liver beyond the systemic kinetics of the cytokine, or further than 48 h [78]. MIP-1 α knockout mice, with their

inability to mount an effective NK cell inflammatory response, do not sustain sufficient levels of IFN- γ in the liver. The result is a profound elevation in spleen and liver viral titers followed by death on day 5 of MCMV infection. Interestingly, mice genetically deficient in interleukin (IL)-18 do not succumb to MCMV infection, although they are severely compromised in systemic, but not hepatic, IFN- γ responses [68]. Thus, MIP-1 α functions promote viral resistance by mediating the recruitment of NK cells and the delivery of IFN- γ in a localized site of infection.

3.2

The Type 1 Interferons (IFN- α/β) Association

Early infection with MCMV induces production of multiple innate cytokines including the type 1 interferons, IFN- α/β [1, 11, 12]. These cytokines are potent activators of antiviral pathways [12, 36, 46, 84, 50] as well as mediators of multiple immunomodulatory functions, including induction of MHC class I expression, activation of NK cell cytotoxicity, and modulation of cytokines and cytokine receptors, including regulation of other type 1 interferon genes [12, 84]. IFN- α/β expression has also been shown to affect leukocyte trafficking [33, 38, 76, 79]. During MCMV infection, bone marrow-derived macrophages and NK cells have been shown to migrate to secondary sites in response to IFN- α/β production [76]. Recent studies have demonstrated production of IFN- α/β in MCMV-infected livers [79]. Histological analysis of liver sections in mice unable to respond to functions induced by IFN- α/β as a result of mutation in the receptor for the cytokines (IFN- α/β R knockouts) illustrated the lack of inflammatory foci but the presence of extensive virus-induced pathology in liver [79]. Moreover, IFN- α/β R knockout mice had reduced levels of MIP-1 α protein in liver. Accordingly, IFN- α/β R knockout mice exhibit profound decreases in the accumulation of NK cells in liver. Furthermore, these mice exhibit mortality by day 5 of MCMV infection [79]. It is notable that NK cell accumulation is not significantly affected when uninfected MIP-1 α knockout mice are treated with recombinant IFN- α (rIFN- α), indicating that IFN- α/β mediate immunoregulatory events upstream of MIP-1 α .

In vivo cell trafficking studies demonstrated that leukocyte migration to the liver is dependent upon the effects of IFN- α/β , as only donor-derived fluorescent-labeled cells from immunocompetent—but not IFN- α/β R knockouts—accumulated extensively in liver [79]. Additionally, IFN- α/β mediated the recruitment of macrophage populations that were identified as a major source of MIP-1 α production [79]. Altogether, these studies identify IFN- α/β as key mediators in the production of MIP-1 α , and they define a cellular delivery mechanism driven by innate cytokines and chemokines for regulation of NK cell inflammation.

3.3

The CXCL9/Mig Association

One downstream consequence of the MIP-1 α -dependent NK cell inflammatory response is induction of the IFN- γ -inducible chemokine CXCL9/monokine-induced by interferon (Mig), a potent T cell chemoattractant [2, 47, 49, 100]. Mig production is severely reduced in MIP-1 α knockout mice when compared to control mice [78]. Furthermore, treatment of immunocompetent mice with immune serum against Mig resulted in highly significant increases in viral titers in both spleen and liver [78]. Consistent with results obtained using mice deficient in IFN- α/β and MIP-1 α functions, Mig was required for survival, as neutralization of the chemokine led to death by day 5 of infection [78]. Studies have identified a prominent T cell response in liver by day 5 after MCMV challenge [28, 39]. It is therefore plausible that early expression of MIP-1 α by MCMV-induced IFN- α/β recruits NK cells into the liver, and through localization of IFN- γ and subsequent Mig induction, these cytokine and chemokine networks provide an important link of innate and adaptive immune responses for overall antiviral defenses in tissue compartments. Ongoing studies in our laboratory are evaluating this likely scenario under the conditions of MCMV infection in the liver.

4

CCL2/MCP-1: The First Link

As discussed above, IFN- α/β clearly plays a role in promoting the recruitment of MIP-1 α -producing macrophages into liver, but the primary molecular mechanisms guiding this process have only recently been examined during MCMV infection. Studies have identified CCL2, or monocyte chemoattractant protein-1 (MCP-1), as a key intermediate of IFN- α/β activity for regulation of inflammatory responses in liver [30]. MCP-1 production can be induced at this site as early as 24 h after MCMV infection. Furthermore, MCP-1 production precedes that of MIP-1 α in a temporal fashion (Fig. 2) [30]. IFN- α/β R knockout mice show dramatic decreases in the levels of MCP-1 protein when compared to immunocompetent mice. In addition, the treatment of uninfected immunocompetent mice with rIFN- α results in a significant release of MCP-1 protein [30]. In vitro stimulation of naïve liver leukocytes obtained from immunocompetent mice with rIFN- α was shown to generate a dose-dependent induction of MCP-1. Together, these studies clearly establish that the induction of MCP-1 protein in liver is dependent on IFN- α/β -mediated functions.

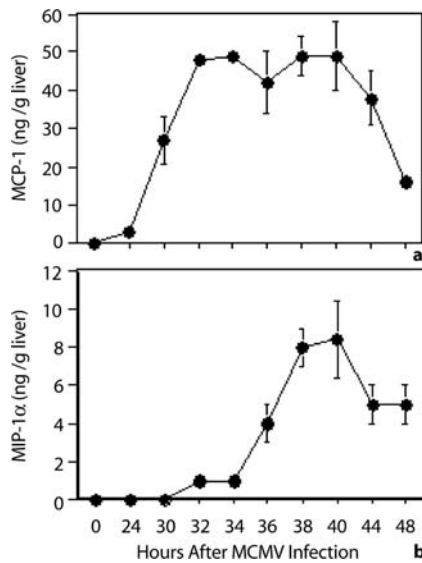


Fig. 2a, b Kinetics of MCP-1 and MIP-1 α during MCMV infection in liver. Infected intraperitoneally with 5×10^4 plaque-forming units (pfu) MCMV were 129 mice. Livers were harvested from uninfected (0 h) or infected mice at the indicated time points. MCP-1 (a) and MIP-1 α (b) protein levels in liver homogenates were determined by sandwich enzyme-linked immunosorbent assay (ELISA) [30]. The levels of detection were 0.08–0.2 and 0.02–0.05 ng/g liver for MCP-1 and MIP-1 α , respectively. Data are the means \pm SE ($n=3$ mice tested individually for each time point). (Figure used with permission from [30]. Copyright 2005. The American Association of Immunologists)

4.1

Resident Macrophages: MCP-1 Producers

In multiple models of hepatic injury, resident macrophages have been shown to contribute to MCP-1 production [8, 44, 72]. The experiments highlighted in Sect. 4) strongly suggest that naïve liver leukocytes can be stimulated to release MCP-1 in the presence of IFN- α/β . Additional studies using enriched F4/80-positive and F4/80-negative cell populations—F4/80 being a mouse macrophage-restricted marker [45]—from uninfected immunocompetent mice demonstrated a clear induction of MCP-1 protein following stimulation with r-IFN α [30]. A similar induction of MCP-1 protein was observed with enriched F4/80-positive, but not F4/80-negative, cell populations from immunocompetent mice infected with MCMV for 24 h [30]. Thus, resident macrophages are early responders to the effects of IFN- α/β and are major producers of MCP-1 protein in liver.

5 MCP-1 and Macrophage Recruitment

It has been clearly established that MCP-1 effectively promotes the mobilization of inflammatory macrophages to sites of tissue damage [17, 26, 31, 51, 72] by preferential binding to the chemokine receptor CCR2 [13, 34, 40, 41, 67]. Recent studies have shown a dynamic impairment in liver macrophage and NK cell accumulation in mice deficient in MCP-1 (MCP-1 knockout) or CCR2 (CCR2 knockouts)—when compared to control mice—during infection with MCMV. Furthermore, MCP-1 and CCR2 knockout mice have decreased levels of both MIP-1 α and IFN- γ proteins [30]. These results establish a central role for MCP-1 in promoting the recruitment of macrophages and NK cells. Moreover, they agree with previous observations that trafficking macrophages contribute to the initial release of MIP-1 α , and subsequently the delivery of NK cell-derived IFN- γ in the liver [79, 80]. As CCR2 knockout mice displayed comparable responses, the results define MCP-1 as a key factor in initiating critical innate inflammatory events.

5.1 MCP-1 and Antiviral Defenses

It is clear from previous studies that MCP-1 is an important innate chemokine because it is uniquely necessary for monocyte and macrophage migration and the establishment of host defense against various pathogens [13, 18, 51, 31, 34, 40, 41, 85]. During MCMV infection, MCP-1 knockouts exhibit a marked elevation in spleen and liver viral titers by day 4 that remains prominent into day 5 of infection [30]. Comparable results were evident in CCR2 knockout mice. Increased viral burden was associated with increases in the circulating levels of the liver enzyme alanine aminotransferase, indicating liver damage. Accordingly, histological evaluation of liver sections prepared from uninfected control, MCP-1 and CCR2 knockout mice, did not show variability in appearance within the groups of mice (Fig. 3a–c). In contrast, on day 5 post-MCMV infection, MCP-1 or CCR2 knockout mice revealed large areas of necrosis as well as numerous cytomegalic inclusion bodies (Fig. 3e and f). Mortality in these mice coincided with virus-induced liver disease, as they succumbed to infection by day 5. This marked pathology was not evident in control mice. Instead, control mice displayed evidence of intermittent clusters of inflammatory foci, viral clearance, and were remarkably similar to the liver sections from the uninfected mice (Fig. 3a and d). These studies define a role for MCP-1, through interactions with CCR2, in promoting antiviral defense and protection from virus-induced liver disease.

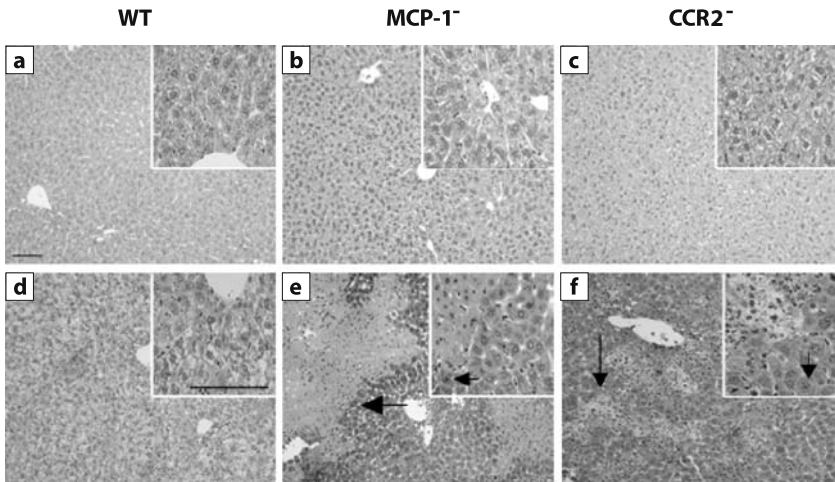


Fig. 3a–f Characterization of MCMV-induced liver damage in MCP-1- and CCR2-deficient mice. C57BL/6 (WT) (a and d) or mice genetically deficient in MCP-1 (MCP-1⁻) (b and e) or CCR2 (CCR2⁻) (c and f) were either uninfected (a–c) or infected with MCMV (5×10^4 PFU) for 5 days (d–f). Livers were harvested, paraffin was embedded, and they were sectioned for hematoxylin and eosin staining. Bar represents 100 μ m. Arrows indicate necrotic lesions. Arrows within insets indicate cytomegalyic inclusion bodies. Figure was used with permission from reference [30]. Copyright 2005. The American Association of Immunologists

6 Conclusions

The studies highlighted in this chapter define a network of cytokine and chemokine pathways that promote the activation, coordination, and shaping of the most effective immune response directed against a virus infection establishing itself in tissues. Specifically, the response elicits the migration of macrophages and NK cells by the selective induction of inflammatory chemokines (Fig. 4). The importance of chemokines to antiviral defense is underscored by the exploitation of the chemokine system by various human and mouse viruses, including herpesviruses, poxviruses, adenoviruses, and cytomegaloviruses [48, 53, 56, 60, 89]. Future *in vivo* studies dissecting the complex interactions between cytokines, chemokines, immune cell populations, and viruses will add to our understanding of immune regulation and perhaps the development of new therapeutic strategies for defense mechanisms against viral infections.

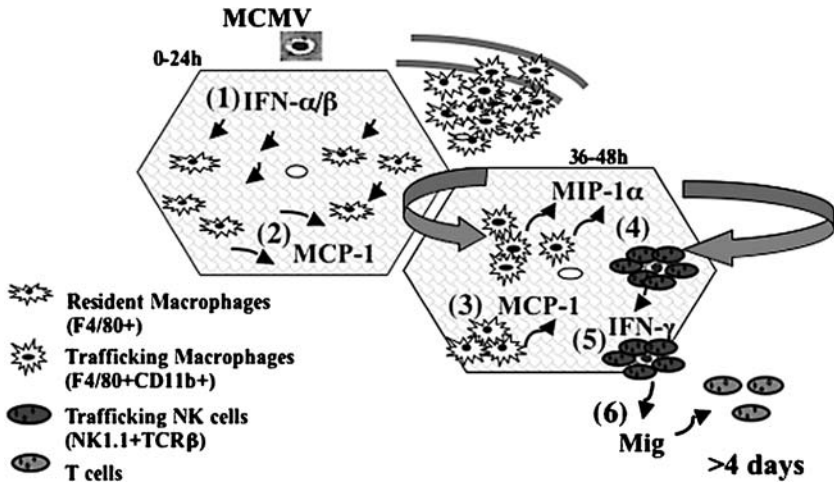


Fig. 4 Model of cytokine and chemokine interactions critical to antiviral defense during MCMV infection in liver. (1) The expression of the cytokine IFN- α/β is locally induced in response to MCMV challenge and (2) promotes the early release of MCP-1 from resident (F4/80+) macrophage populations. (3) MCP-1 initiates the recruitment of MIP-1 α -producing macrophages from the periphery to the liver. (4) Subsequently, MIP-1 α promotes the initial mobilization of NK cells from the periphery to the liver where they surround and sequester MCMV-infected cells to form characteristic clusters of inflammatory foci. (5) These events localize production of IFN- γ and (6) promote the induction of the IFN- γ -inducible chemokine Mig, a known potent chemoattractant of T lymphocytes. Together, these innate cytokine and chemokine interactions provide vital antiviral defenses in liver, and conceivably play a role in linkage of innate and adaptive immune responses

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Herpes Simplex Virus and the Chemokines That Mediate the Inflammation

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Abstract Herpes simplex viruses (HSV) are highly pervasive pathogens in the human host with a seroconversion rate upwards of 60% worldwide. HSV type 1 (HSV-1) is associated with the disease herpetic stromal keratitis, the leading cause of infectious corneal blindness in the industrialized world. Individuals suffering from genital herpes associated with HSV type 2 (HSV-2) are found to be two- to threefold more susceptible in acquiring human immunodeficiency virus (HIV). The morbidity associated with these infections is principally due to the inflammatory response, the development of lesions, and scarring. Chemokines have become an important aspect in understanding the host immune response to microbial pathogens due in part to the timing of expression. In this paper, we will explore the current understanding of chemokine production as it relates to the orchestration of the immune response to HSV infection.

Abbreviations

HSV	Herpes simplex virus
PMN	Polymorphonuclear cell
NK	Natural killer
HSK	Herpetic stromal keratitis
IL	Interleukin
DC	Dendritic cell
Th1	T helper 1 cell
TG	Trigeminal ganglion
IFN	Interferon
TNF	Tumor necrosis factor
TLR	Toll-like receptor
VEGF	Vascular endothelial growth factor

1**Introduction****1.1****General Properties of Herpes Simplex Viruses**

Herpes simplex virus type 1 (HSV-1) and type 2 (HSV-2) are neurotropic viruses that are members of the subfamily α -Herpesvirinae [42]. Both types of HSV are transmissible from person to person via infectious mucosal secretions that come in contact with mucosal epithelia that line surface apertures of the body [9, 42, 57]. Herpes simplex viruses can cause a variety of diseases including keratitis, cold sores, encephalitis, genital herpes, cutaneous herpes, and meningitis [12, 42]. HSV-1 and HSV-2 enter the epithelium of the host and initiate a lytic replicative cycle [18, 40–42, 57, 70]. HSV enters its target cell through a multistep process that includes envelope glycoproteins (g) that surround the viral particle [42, 64]. The initial interaction begins with the binding of gC and gB to heparin sulfate proteoglycans that are found on the surface of target cells [42, 64]. After the attachment of the viral particle to the host cell, another viral glycoprotein, gD, interacts with other host cell surface receptors, including herpesvirus entry mediator A, which is a tumor necrosis factor (TNF) receptor family member, and nectins, which allow for the fusion of the virion envelope to the cell's plasma membrane via gB, gD, gH, and gL [42, 64]. Local replication commences with transcription of viral lytic genes [18, 33, 40–42, 57, 64, 70]. Following a lytic replicative cycle, the virus enters sensory nerve endings in the basal aspect of the epithelium and undergoes retrograde transport to associated sensory ganglia [18, 42, 64, 70]. Within the sensory ganglia, HSV undergoes a second stage of lytic infection.

Depending on the extent of the infection, HSV may travel further to the central nervous system. Following acute infection of sensory ganglia, the virus establishes latency in a subpopulation of neurons [18, 42, 64, 70]. Periodic reactivation from latency during periods of stress or immune suppression results in the re-infection of the initial port of entry [18, 42, 70].

Clearance of the virus from the host is dependent on both the host's innate and adaptive immune responses. Polymorphonuclear cells (PMNs) are the first and most predominant cell type to infiltrate the area of infection, releasing a number of soluble factors including cytokines, chemokines, and tissue-degrading enzymes including matrix metalloproteinases [6, 22, 45, 96, 97]. Likewise, natural killer (NK) cells and subsequently, macrophages and T cells are recruited to the site of inflammation. Chemokine expression has become an interest in the scientific community as it relates to the immune response to infectious agents and the pathology that develops from this response.

1.2

Herpes Simplex Virus Type 1

The cornea is a transparent, avascular tissue composed of a surface epithelium, corneal stroma, and endothelium that covers the anterior portion of the eye [70]. It is the avascular nature of the cornea that preserves the visual axis, providing a translucent conduit for subsequent processing of an image by the lens and retina of the eye. However, experimental evidence suggests ocular HSV-1 can limit the visual axis through neovascularization and infiltration of leukocytes attracted to the site through the production of chemokines [103]. Experimental infection of the cornea initiates in the surface epithelium in the outermost squamous layer of cells. HSV-1 spreads from cell to cell in a polarized fashion to the next layer of cells, wing cells [70]. The virus is able to travel to the sensory nerve endings that can be found in the basal aspect of the epithelium [70].

One clinically significant disease that is caused by HSV-1 is herpetic stromal keratitis (HSK) an intense inflammatory response triggered by the viral infection of the corneal stroma [3, 45, 54]. If left untreated, the chronic inflammatory response leads to the formation of lesions, scarring, and eventually blindness.

1.3

Herpes Simplex Virus Type 2

HSV-2 is the causative agent of genital herpes of which approximately 500,000 new cases arise annually [33]. It has been estimated that 33% of the adult population is seropositive for this sexually transmitted disease, making HSV-2 the

most common sexually transmitted pathogen worldwide [33, 73, 78, 92]. Genital herpes infection can result in complications including urinary retention and meningoencephalitis [33, 73, 78, 92]. Approximately 3,500 births in the United States are impacted by HSV-2 infection, which can lead to fatal infant encephalitis [18]. Even though a relatively large percentage of the population is seropositive for HSV-2, only a small percentage is subjected to these complications. Hormones have been implicated in the susceptibility to infection in the female host [86]. Specifically, mice exposed to progesterone are rendered more susceptible to infection [37] whereas estradiol-treated mice are found to be resistant to infection [27]. Although the role of ovarian sex hormones in susceptibility to genital HSV-2 infection is not completely defined, immune suppression [27], changes in the vaginal epithelial thickness [72], and modulation of a cell membrane receptor, nectin-1- δ [48], may all influence the infectious process.

One common denominator in the recruitment process of leukocytes into the inflamed HSV-infected tissue is the expression of chemokines. Although a necessary process in attracting immune effector cells required to control replication and spread of the virus, chemokine expression and the ensuing inflammatory response has detrimental consequences to the host, especially when considering the eye. Understanding the sequential expression of chemokines relative to ocular HSV-1 infection is pertinent to the development of a strategy that will ultimately control local inflammation and the collateral damage without rendering increased susceptibility to the host.

2 HSV-1 Infection of the Eye

2.1 Innate Immune Response to Ocular HSV-1 Infection

After initial infection of the virus into the cornea, an innate immune response is triggered to clear the pathogen. Toll-like receptors (TLR), a family of pattern-recognition molecules, are known to respond to pathogens and serve as early warning molecules that induce the expression of proinflammatory molecules [5]. Of the twelve TLR subtypes found in the mouse, TLR2 and TLR9 are expressed by corneal epithelium [36]. HSV-1 stimulates TLR2 by unknown means resulting in the activation of nuclear factor (NF)- κ B and production of interleukin (IL)-6 [46]. HSV-1 which contains CpG motifs [106] is recognized by TLR9, resulting in the expression of type I interferon (IFN) [44]. In addition to the production of type I IFNs, the infected resident cells of the

cornea as well as neighboring cells (most probably through TLR signaling and NF- κ B activation) are known to release inflammatory cytokines including IL-1 α , IL-6, and TNF- α [34, 88]. The absence or hindrance of these cytokines has been linked to a significant reduction in the incidence of HSK [6, 22, 101]. It is thought that IL-1 α leads to the induction of IL-6 by resident corneal cells [6] that, in turn, elicit production of macrophage inflammatory protein-1 α (CCL3) and -2 (CXCL2) [22] ultimately recruiting PMNs into the infected tissue. PMNs infiltrate the stroma underlying the infected epithelial cells, contributing to clearance of the virus and limiting viral dissemination within 24 h postinfection [6, 96, 97]. PMNs are thought to be a rich source of inducible nitric oxide synthase (iNOS) and TNF- α [13], the latter of which upregulates intercellular adhesion molecule (ICAM)-1 expression [69] facilitating the adherence of leukocytes to the endothelium [89]. The administration of monoclonal antibody to ICAM-1 [15] or use of ICAM-1-deficient mice [67] has not been found to diminish the infiltration of cells or the clinical course of herpetic disease following corneal infection. However, ICAM-1 does play a key role in preventing herpetic encephalitis [15, 67], suggesting pathways independent of ICAM-1 expression are involved initially in the recruitment of cells into the cornea, whereas controlling virus spread in the central nervous system involves ICAM-1 expression. After the initial infiltration of neutrophils, macrophages and NK cells infiltrate the area but PMNs remain the predominant cell type residing in the inflamed cornea up to the first 96 h postinfection [93].

2.2

Chemokine Expression During the Innate Immune Response to Ocular HSV-1 Infection

Evidence for the expression of chemokines in the cornea following HSV-1 infection was first described using endpoint polymerase chain reaction (PCR) in which KC (CXCL1), CXCL2, IFN- γ -inducible protein 10 (CXCL10), monocyte chemoattractant protein-1 (CCL2), MIP-1 β (CCL4), and regulated upon activation, normal T cell expressed (CCL5) were observed [90]. While trauma to the cornea in the form of scarification induced the expression, continued expression of CCL2, CCL5, and CXCL10 were noted out to 72 h postinfection, whereas other chemokine messenger (m)RNA levels precipitously dropped in both BALB/c and outbred ICR mice [14, 90]. Of the chemokines noted above, CXCL1 and CXCL2 specifically target neutrophils principally through the receptor CXCR2 [11, 82, 99, 104]. Neutralization of CXCL2 with antibody leads to a reduction in polymorphonuclear neutrophil (PMN) infiltration into the cornea [54, 104]. Likewise, CXCR2 knockout mice infected with HSV-1 show

a minimal infiltration of PMNs into the cornea [3]. Even with a reduction in PMN influx, HSK still develops in the CXCR2-deficient mice, which is thought to be due to an increase in IL-6 expression driven by elevated virus titers ultimately facilitating angiogenesis [3]. Although evidence suggests IL-6 can drive neovascularization through vascular endothelial growth factor (VEGF) in the cornea, the kinetics of expression of VEGF during the infectious process in this model suggests other dynamics are involved including T cells that are known to contribute to HSK [16, 83] and are a source of VEGF [63].

Whereas CXCL2 is thought to be induced by IL-6 [57], another CXC chemokine, CXCL10, has been found to be the only chemokine that is constitutively expressed in the cornea as determined by PCR [14, 90] and enzyme-linked immunosorbent assay (ELISA) [10]. CXCL10 levels rapidly rise in the cornea following HSV-1 infection, and neutralization of the chemokine dramatically reduces corneal edema and infiltrating cells [10]. The lone receptor for CXCL10 is CXCR3 expressed by NK cells, macrophages, dendritic cells (DCs), and activated T cells [21, 23, 47, 77, 94]. However, CXCR3 knockout mice ocularly infected with HSV-1 show a transient suppression of PMN (Gr-1⁺CD11b⁺Mac-3⁻) recruitment into the cornea (D.J.J. Carr, unpublished observation), calling into question the role of CXCR3 and its ligands in PMN recruitment. However, other studies at different anatomical sites have described PMN infiltration as a result of CXCL10 expression [8, 105]. It is tempting to speculate that CXCL10 may upregulate CD11a on PMNs enhancing the adhesion to the endothelium as has been reported for Th1 cells [2] facilitating diapedesis into the stroma of the cornea. However, formal proof of this notion requires additional studies.

Of the CC chemokine ligands expressed during ocular HSV-1 infection, CCL2 is strongly expressed throughout the initial course of acute infection as measured by PCR [14, 90]. The role of CCL2 in the development of HSK may be peripheral to its effects on the recruitment of leukocytes into the cornea, since the administration of neutralizing antibody to CCL2 has no effect on the incidence of HSK in HSV-1-infected mice [99]. In contrast, the administration of anti-CCL3 antibody significantly reduces the severity of corneal opacity [99]. The kinetics of CCL3 expression suggest it is not a stimulus for the recruitment of leukocytes into the cornea until 7–10 days postinfection, a time that seems to correlate with the onset of HSK [99]. Consistent with this finding, mice deficient in CCL3 expression reportedly show little cellular infiltration in the cornea throughout the time course of infection with low to undetectable levels of T helper (Th)1 cytokines including IL-2 and IFN- γ [98] normally found during acute ocular infection [93]. Ironically, the CCL3 knockout mice clear the virus at the same time as wildtype control animals [99], which calls into question the mechanism of virus clearance. Since there is apparently

little leukocyte infiltration, including PMNs, that is known to control HSV-1 replication in the eye [97]—with a paucity of CD4⁺ T cells or IFN- γ present as well [99]—it is puzzling what mechanism(s) controls the virus.

Similar to CCL2, CCL5 is expressed throughout the course of acute HSV-1 infection [14]. CCL5, operating through its receptor CCR5, is a strong chemoattractant for T cells and NK cells [53, 80] but also influences PMN recruitment [71]. It is interesting to note that while HSV-1 tends to subvert immune activation, CCL5 is induced by HSV-1 through NF- κ B and IFN regulatory factor 3 pathways [56].

The plethora of chemokines and proinflammatory cytokines produced in the cornea during the innate immune response (i.e., 0–5 days postinfection) may be generated from several sources. With the exception of CXCL10, the chemokines CXCL1, CXCL2, CXCL9, CCL3, and CCL5 are not constitutively expressed in the cornea (Fig. 1). Analysis by confocal microscopy has found the endothelial layer of the cornea expresses very modest amounts of the CXCL10 in uninfected mice (D.J.J. Carr, unpublished observation). Consistent with previous results [90], scarification of the cornea (a process typically employed

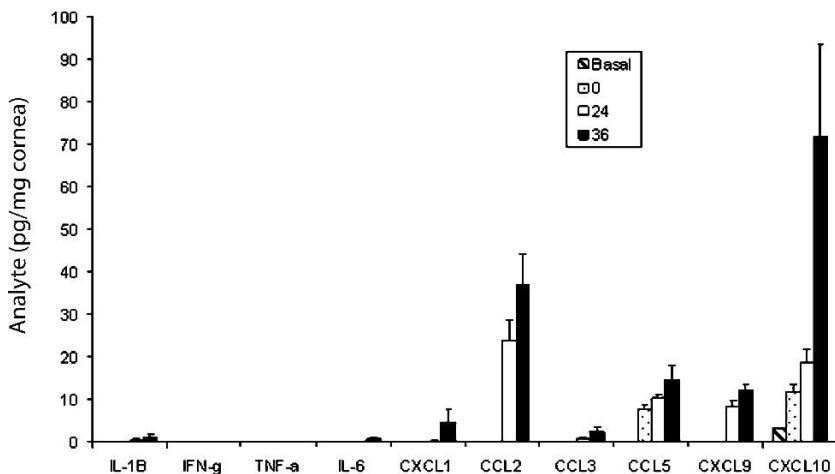


Fig. 1 Expression of inflammatory cytokines and chemokines in the cornea of HSV-1-infected mice. C57BL/6 female mice ($n=6$ /timepoint) were left alone (*basal*) or scarified (0) and infected with HSV-1 (McKrae strain), 1,000 plaque-forming units (pfu)/eye. The mice were euthanized 24–36 h postinfection, perfused, and the cornea was removed and homogenized in a buffer containing a cocktail of protease inhibitors. The supernatant was clarified (10,000 \times g, 5 min) and assayed for cytokine/chemokine content by ELISA. Bars represent mean \pm SEM for each analyte under measure. CCL2 basal levels were not measured

to infect mice) alone elicits a rise in CCL3, CCL5, and CXCL10 expression (Fig. 1). Following infection, CXCL1, CCL2, CCL5, CXCL9, and CXCL10 are induced or upregulated within 36 h. Analysis of CCL5 and CXCL10 expression by confocal microscopy show two different patterns of expression. CCL5 is expressed in the epithelial layers of the eye colocalizing with HSV-1 antigen as well as within the stroma of the cornea (D.J.J. Carr, J. Ash, T. Lane, and W. Kuziel, submitted). By comparison, CXCL10 expression chiefly colocalizes with HSV-1 antigen expression in the epithelial layers of the cornea with punctate staining in the endothelium (D.J.J. Carr, unpublished observation). The expression profile of CCL5 and CXCL10 suggests the resident population generates most if not all of the CXCL10 within the first 24 h postinfection, whereas CCL5 is produced principally by resident cells but may also be provided by the infiltrating PMNs that are found within the stroma 24 h postinfection (D.J.J. Carr, J. Ash, T. Lane, and W. Kuziel, submitted). It is likely that as the infection

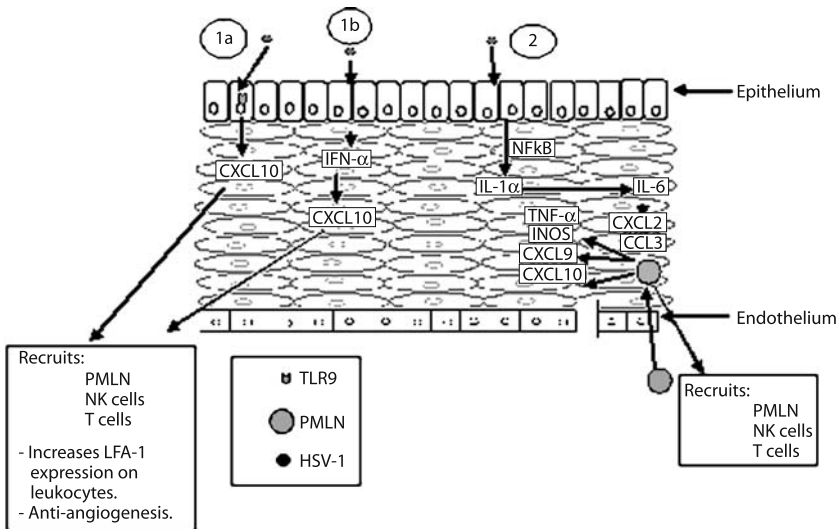


Fig. 2 Chemokine expression in the cornea following HSV-1 infection. Three different scenarios can operate in the production of chemokines within the cornea following ocular HSV-1 infection. In *1a*, HSV-1 DNA CpG motifs bind to the intracellular toll-like receptor (TLR)9 eliciting the production of CXCL10 through NF-κB activation. In *1b*, HSV-1 enters the epithelial cell and, following transcription, induces the production of IFN-α, which induces CXCL10 production. In *2*, HSV-1 activation of NF-κB stimulates IL-1α synthesis leading to IL-6 production, resulting in CXCL2 and CCL3 expression. These chemokines draw in PMNs and T cells. PMNs can secrete CXCL9 and CXCL10, which can recruit additional leukocytes including macrophages, DCs, NK cells, and T cells

spreads over the next several hours, chemokines generated including CCL2, CCL5, CXCL1, CXCL2, CXCL9, and CXCL10 are produced by multiple sources including the resident fibroblasts, epithelial, and endothelial cells as well as infiltrating PMNs, macrophages, NK cells, and DCs [11, 25, 82, 87, 100]. Collectively, the initial cascade of chemokine expression is complex but may be divided into two principal pathways involving CXCL10 and IL-6 (Fig. 2).

The delayed expression of CCL3 in the cornea is associated with a secondary wave of PMNs and some T cells into the stroma (day 10 postinfection) [99]. Since CCL3 targets monocytes, T cells, NK cells, basophils, eosinophils, DCs, and hematopoietic progenitors [11, 12, 82], it is currently unknown what events transpire to recruit the subsequent wave of cells. However, CCL3 is central to the effect since neutralizing this chemokine with antibody or suppressing expression with IL-10 reduces leukocyte recruitment into the cornea [99].

2.3

Adaptive Immune Response to Ocular HSV-1 Infection

Following the innate response to infection, preferential recruitment of Th1 CD4⁺ T cells into the cornea is observed [35, 65]. Although it is currently unknown why there is a preferential recruitment of CD4⁺ T cells into the cornea of HSV-1-infected mice, the expression of CXCR3 and CCR5 on activated T cells and the presence of CCL5 and CXCL9 in the cornea may influence the recruitment process [80, 81, 102]. The presence of CD4⁺ T cells is crucial in controlling local virus replication and spread [7, 26] as well as the development of HSK [25, 58]. However, bystander activation of CD4⁺ T cells in addition to virus antigen stimulation may also contribute to HSK development [24]. The continued expression of chemokines including CXCL2, CCL2, CCL3, CCL4, CCL5, and CXCL10 in the cornea would also provide the maintenance of leukocytes in the tissue recruited from the periphery and facilitate collateral damage to the cornea stroma [84]. Collectively, chemokines are instrumental in the initial trafficking of cells into the infected anterior segment of the eye as well as the development of HSK. Blocking their expression could preserve the visual axis, assuming local virus replication is controlled. A summary of chemokines expressed during the acute HSV-1 ocular infection is found in Table 1.

2.4

HSV-1 Latency in the Trigeminal Ganglion

After the successful infection of the cornea by HSV-1, a series of events occurs that can lead to a stable latent neuronal infection in the trigeminal ganglion

Table 1 Chemokine expression in the cornea during acute HSV-1 infection

Group	Name	Detection	Reference(s)
CXC	CXCL1	RT-PCR and ELISA	90, Fig. 1
	CXCL2	RT-PCR and ELISA	3, 6, 10, 22, 54, 90, 98, 104
	CXCL9	ELISA	10, Fig. 1
	CXCL10	RT-PCR and ELISA	10, 14, 90, Fig. 1
CC	CCL2	RT-PCR and ELISA	14, 90, 98, 99, Fig. 1
	CCL3	RT-PCR and ELISA	10, 22, 90, 98, 99, Fig. 1
	CCL5	RT-PCR and ELISA	10, 14, 90, Fig. 1

(TG) within 1–2 weeks postinfection [39, 41, 49]. Following an initial round of replication in the corneal epithelium, the virus is able to enhance its ability to access the axonal termini (via mechanisms that are not understood), and through retrograde axonal transport it enters the neuronal cell bodies in which another stage of lytic replication begins [49, 70]. After this brief replication cycle in the neuronal cell bodies, the lytic cycle genes are repressed and latency is established with minimal viral gene expression [49]. Infectious HSV-1 can consistently be detected in the TG out to approximately 10 days postinfection [12]. By day 30 postinfection, latency is established as defined by the lack of detectable infectious virions [12]. Even though infectious virions are not readily detected during latency, HSV-1 latency-associated transcripts (LATs) can be detected in the TG, and an associated local immune response is evident [28, 49]. With latency established, the immune system continually surveys the area with CD8⁺ T cells as the principal cell type that is thought to prevent reactivation [39]. Along these lines, CD8⁺ T cells are thought to control the infection through noncytolytic mechanisms using cytokines such as IFN- γ and TNF- α with minimal destruction to neurons [38, 50, 51, 95].

During latent infection, real time (RT)-PCR detection of CXCR3 and CCR5 expression has been reported [12]. Although unproven, it is likely these chemokine receptors are found on the CD8⁺ T cells present in the TG during latency [29, 38]. Although ligands for CXCR3 including CXCL9 and CXCL10 have not been evaluated during latency, one ligand for CCR5, CCL5, has been detected [28]. Exposing latently infected mice to the potent antiviral compound acyclovir has been found to reduce CCL5 expression in the TG. Yet, the continued presence of CD8 cells suggests additional signals provide a stimulus for retainment of these effector cells within the tissue [29].

2.5

Reactivation of HSV-1

Due to a variety of environmental cues including UV light, stress, and immunosuppression, the virus is able to reactivate in the latently infected neurons of the TG. Through antegrade transport, the virus can again be detected in the corneal epithelium and stroma [68, 70]. The reactivation cycle can be repeated eliciting chronic and episodic immune activation, which leads to progressive scarring of the cornea resulting in decreased vision, glaucoma, iritis, cataract, and necrotizing retinitis [70]. While there is experimental evidence to suggest regulatory T cells may control ocular pathogenesis [91], how these cells impact on local chemokine expression is not understood.

3

HSV-2 Infection of the Genitalia

3.1

Immune Response to Genital HSV-2 Infection

During initial infection of the mucosa of the vagina with HSV-2, the virus begins to replicate in the epithelium, typically restricted to the epidermis or cervicovaginal epithelium [43]. The initial host response to infection includes the induction of type I IFNs (i.e., IFN- α species) through TLR9 recognition of HSV-2 CpG motifs [52]. The IFN-responsive pathway, double-stranded RNA-dependent protein kinase but not 2',5'-oligoadenylate synthetases is essential for resistance to infection, as mice deficient in this pathway are highly susceptible to HSV-2-mediated mortality (D.J.J. Carr, L. Tomanek, R.H. Silverman, and B.R.G. Williams, manuscript in preparation). In addition to type I IFN production, IL-12, IL-15, IL-18, NK cells, and PMNs are important first lines of defense against HSV-2 replication and spread [1, 31, 59]. Current evidence suggests the resident populations of Langerhans cells [19] do not traffic to the inguinal/iliac lymph nodes with most migrating cells consisting of B lymphocytes [40]. T lymphocytes including $\gamma\delta$ T cells are essential components of the adaptive immune response in controlling genital infection with HSV-2 [55, 60, 66, 73]. CD4⁺ T cells produce the majority of IFN- γ in response to genital HSV-2 infection [32, 61]. Neutralization of IFN- γ leads to an increase in virus titer and a decrease in T cell recruitment into the vaginal tissue [61, 73]. B cell production of antibody is initiated in the draining lymph nodes and appears to have only a modest impact on HSV-2 titers, suggesting a limited role for B lymphocytes in the control of genital HSV-2 infection [17, 62, 75]. Manifestations of genital herpes include macules, papules, and vesicles resulting in the development of ulcers in the genital region [33]. Due to these

ulcerations, other pathogens are able to enter into the vaginal mucosa. Recent studies have shown that patients who are infected with HSV-2 have a higher risk of contracting HIV-1 than patients who are HSV-2 seronegative with a two- to threefold increase in susceptibility [79].

3.2

Chemokines and HSV-2

The recruitment of leukocytes into the vaginal tissue following HSV-2 infection appears to include IFN- γ induction of the adhesion molecules ICAM-1 and vascular cell adhesion molecule 1 [76] since neutralizing IFN- γ diminishes lymphocyte infiltration into the infected tissue [74]. The expression of IFN- γ has also been associated with CCL5 production [30] found in the vagina following HSV-2 infection [4, 33]. The role of CCL5 expression in recruiting leukocytes into the infected tissue has not been described. However, plasmid DNA containing CCL5 has been found to enhance survival of HSV-2-infected mice [85]. Manipulating local expression of selective chemokines including CXCL2 and CCL3 using plasmid DNA suggests these chemokines may also play a significant role in protection for the host during genital virus infection by facilitating CD4⁺ T cell immunity and elevating IFN- γ production by NK cells [20]. However, there are unresolved questions that remain as to those chemokines that initiate the inflammatory cascade as well as those that are critical for resistance to genital HSV-2.

4

Perspective

Chemokines are a significant group of soluble factors that contribute in the clearance of HSV-1 and HSV-2 pathogens from the host. Although necessary for an optimal immune response to the virus, chemokines initiate a frank inflammatory response that can result in a significant detrimental outcome to the host as it pertains to preservation of the visual axis. This chapter highlights the role of chemokines as they relate to the innate and adaptive immune response following ocular HSV-1 infection. Evidence suggests that curtailing expression of selective chemokines during HSV-1 infection of the eye may favor preservation of sight without consequences to controlling virus replication and spread. This observation suggests that while many chemokines are redundant in function and/or promiscuous in binding multiple receptors, selectivity in tissue expression of chemokines and targeting specific effector cells by those chemokines expressed in a given tissue may ultimately dictate

the inflammatory response of the host and outcome of the infection. Understanding this process will prove beneficial in developing antiinflammatory therapies for individuals experiencing chronic HSV reactivation.

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Influence of Proinflammatory Cytokines and Chemokines on the Neuropathogenesis of Oncornavirus and Immunosuppressive Lentivirus Infections

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Abstract Retroviral infection of the CNS can lead to severe debilitating neurological diseases in humans and other animals. Four general types of pathogenic effects with various retroviruses have been observed including: hemorrhage (TR1.3), spongiform encephalopathy (CasBrE, FrCasE, PVC211, NT40, Mol-ts1), demyelination with inflammatory lesions (HTLV-1, visna, CAEV), and encephalopathy with gliosis and proinflammatory chemokines and cytokines, usually with microglial giant cells and nodules [human immunodeficiency virus (HIV), feline immunodeficiency virus (FIV), simian immunodeficiency virus (SIV), Fr98]. This review focuses on this fourth group of retroviruses. In this latter group, proinflammatory cytokine and chemokine upregulation accompanies the disease process, and may influence pathogenesis by direct effects on resident CNS cells. The review first discusses the Fr98 murine polytropic virus system with particular reference to the roles of cytokines and chemokines in the pathogenic process. The Fr98 data are then compared and contrasted to the cytokine and chemokine data in the lentivirus systems, HIV, SIV, and FIV. Finally, various mechanisms are presented by which tumor necrosis factor (TNF) and several chemokines may alter the pathogenesis of retrovirus infection of the CNS.

Abbreviations

CAEV	Caprine arthritis encephalitis virus
CNS	Central nervous system
EIAV	Equine infectious anemia virus
GFAP	Glial fibrillary acidic protein
FIV	Feline immunodeficiency virus
FIV-E	FIV encephalitis
HAD	HIV-associated dementia
HIV	Human immunodeficiency virus
HTLV	Human T cell leukemia virus
IP	Intraperitoneal
LPS	Lipopolysaccharide
Mol-ts1	Moloney Ts1
NPSC	Neuroprogenitor stem cells
SIV	Simian immunodeficiency virus
SIV-E	SIV encephalitis

1

Retrovirus Infections of the CNS

1.1

Historical Perspective

In the initial years of the study of retroviruses the main emphasis was on the potential of these agents to induce neoplastic transformation of various tissues, especially muscle cells, fibroblasts, mammary glands, and bone marrow-derived hematopoietic cells. Subsequently non-neoplastic pathogenic effects of retroviruses were described, including anemia, arthritis, glomerulonephritis, immunodeficiencies, osteopetrosis, and neurological disorders. The studies of visna virus infection in sheep by Sigurdsson and colleagues in the 1950s demonstrated a slow CNS disease lasting several years (Sigurdsson et al. 1957, 1960). This long time course led ultimately to the name “lentiviruses” for the subgroup—including visna—of retroviruses with complex genomes. In the 1970s, Gardner and colleagues described a murine retrovirus from the oncornavirus subgroup (with simple genomes) which induced a slow neurological disease (Gardner et al. 1973). Since that time a large variety of other retroviruses from both subfamilies capable of inducing neurological disease in a variety of species including humans have been described (Table 1).

1.2

Diversity of Retrovirus-Induced Neurological Diseases

Retroviruses can cause several different types of neurological disease. Based on pathology and pathogenic effects, these can be divided into four groups (Table 1). These include: hemorrhage (TR1.3) (Park et al. 1993, 1994); spongiform encephalopathy (CasBrE, FrCasE, PVC211, NT40, Moloney-ts1) (Czub et al. 1995; Gardner 1988; Hoffman et al. 1992; Kai and Furuta 1984; Wong et al. 1985); demyelination with inflammatory lesions (HTLV-1, visna, CAEV) (Araujo and Hall 2004; Haase 1986; Jacobson 2002; Oaks et al. 2004); and encephalopathy associated with microgliosis, astrogliosis usually with microglial nodules, and giant cells and variable mononuclear cell infiltrates [human immunodeficiency virus (HIV), feline immunodeficiency virus (FIV), simian immunodeficiency virus (SIV), Fr98] (Glass et al. 1993, 1995; Kolson et al. 1998; Lackner et al. 1991; Portis et al. 1995; Robertson et al. 1997). Some viruses, such as SIV, appear to be able to induce more than one type of pathogenic process, depending on the viral strain used and/or the extent of immunosuppression (Lackner et al. 1991). In most models, infection of neurons is not observed and the mechanism of neuronal dysfunction is assumed to be indirect (Patrick et al. 2002; Portis 2001). In some systems, infection of

Table 1 Diversity of central nervous system pathological processes induced by retroviruses

Pathogenic effects	Virus	Species
Hemorrhage	TR1.3	Mouse
Spongiform encephalopathy	CasBrE	Mouse
	FrCasE	Mouse
	Mol-ts1	Mouse
	NT40	Rat
	PVC211	Rat
	TR1.3 ^a	Mouse
Demyelination with extensive mononuclear cell infiltrates	CAEV	Goat
	EIAV ^b	Horse
	HERV ^c	Human
	HTLV-1	Human
	HTLV-2 ^d	Human
	Visna	Sheep
Encephalopathy, gliosis, and upregulated proinflammatory cytokines and chemokines, with variable mononuclear cell infiltrates ^e	FIV	Cat
	Fr98	Mouse
	HIV	Human
	SIV	Monkey

^a TR1.3 has been reported to induce both hemorrhage and spongiform encephalopathy (Murphy et al. 2004)

^b Equine infectious anemia virus (EIAV) sporadically induces a brain inflammatory disease but demyelination was not noted (Oaks et al. 2004)

^c HERVs, human endogenous retroviruses, may be involved in multiple sclerosis (Christensen 2005)

^d HTLV-2 is believed to be associated with some rare cases of demyelinating encephalitis (Araujo and Hall 2004)

^e The extent of mononuclear cell infiltration in the lentiviral models (HIV, SIV, FIV) can vary considerably from prominent to minimal (Anthony et al. 2005; Gardner and Dandekar 1995; Kolson et al. 1998; Lackner et al. 1991). In the Fr98 neonatal mouse model mononuclear infiltration is minimal (Peterson et al. 2001; Robertson et al. 1997)

neurons has been noted, but this does not appear to account for the disease, because the infected cells are not present in the damaged areas (Lynch et al. 1991). Despite the diverse pathology, most retroviruses infect the same major target cells of microglia and macrophages in the brain (Patrick et al. 2002; Portis 2001). Brain capillary endothelial cells are often extensively infected in many murine models and may be in some primate systems (SIV). To a lesser extent, infection of astrocytes (Liu et al. 2004) and oligodendrocytes (Robertson et al. 1997) has also been observed with some retroviruses, but these types of infected cells may nevertheless play important roles in the pathogenesis.

1.3

Diversity of Retrovirus-Induced Pathogenic Mechanisms

Mechanisms of pathogenesis are not well understood in most of these retroviral systems. The simplest model appears to be the TR1.3 murine retrovirus, where infection of brain capillary endothelial cells leads to cell fusion and damaged and leaky blood vessels (Park et al. 1993, 1994). However, more recent data indicate that TR1.3 can also induce spongiform encephalopathy (Murphy et al. 2004). In some rodent spongiform encephalopathy models, such as PVC211, there is evidence that endothelial cell infection is important to pathogenesis probably by facilitating viral entry into the CNS (Hoffman et al. 1992; Kai and Furuta 1984). In other rodent spongiform encephalopathy models, such as FrCasE, Cas-Br-E, and Moloney ts1, there is growing evidence that viral envelope protein aggregation may lead to an endoplasmic reticulum stress response, which may in turn damage certain glial cells (Dimcheff et al. 2003, 2004; Kim et al. 2004a; Liu et al. 2004). However, the explanation for the very restricted spatial distribution of lesions in the face of widespread virus infection remains unclear. The demyelinating inflammatory viruses all appear to induce a very strong host inflammatory response involving lymphocytes and macrophages, and the cytokines and chemokines produced by infiltrating cells are believed to be important in demyelination and neuronal damage (Araujo and Hall 2004; Haase 1986; Jacobson 2002).

The immunodeficiency inducing lentiviruses, HIV, SIV, and FIV, as well as Fr98, a polytropic murine retrovirus, all induce a severe clinical CNS disease with minimal morphological neuronal damage and pathology. Multiple histopathological changes have been associated with HIV-associated dementia (HAD), including microglia nodules, astrogliosis, microgliosis, neuronal apoptosis, myelin pallor, and multinucleated giant cell formation (Anthony et al. 2005; Glass et al. 1995; Kolson et al. 1998). Many of these alterations have also been seen in animal models (Johnston et al. 2002; Lackner et al. 1991; Portis et al. 1995; Power et al. 2004; Robertson et al. 1997; Williams et al. 2001). The main pathological change-associated clinical neurological disease is the increased presence of activated macrophages and microglia in the brain (Anthony et al. 2005; Glass et al. 1995; Portis et al. 1995; Robertson et al. 1997; Williams et al. 2001). Virus infection does not generally induce extensive infiltration of inflammatory cells from outside the CNS (Anthony et al. 2005; Glass et al. 1995; Power and Johnson 1995, 2001; Robertson et al. 1997); however, there is evidence for a role for proinflammatory cytokines and chemokines in the pathogenesis of these viruses. The low level of inflammatory infiltrates in all of these models is likely related to the presence of severe immunosuppression induced by the virus (HIV, SIV, FIV) or the

neonatal state of the host (Fr98 infection). This review will focus on the role of proinflammatory cytokines and chemokines in the neuropathogenesis of this group of retroviruses with emphasis on the Fr98 mouse model and the use of knockout mice to study the contribution of cytokines and chemokines to retroviral pathogenesis.

2

Fr98 Polytopic Retrovirus Model of Neuropathogenesis

2.1

Use of a Mouse Model to Study Retroviral Neuropathogenesis








In human patients, it is difficult to distinguish cause versus effect in correlative studies of gene upregulation. Other animal models of retrovirus infection, including SIV infection of macaques and FIV infection of felines have this same limitation. Mouse models of retrovirus infection offer the unique advantage over other retrovirus systems in the ability to use knockout and transgenic animals to definitively determine whether specific proteins are necessary for disease development. The mouse model of polytopic retrovirus infection also allows the comparison between non-neurovirulent and neurovirulent retrovirus infections (Peterson et al. 2001, 2004b; Robertson et al. 1997). This permits the determination of whether a host response is specific to pathogenesis or is a general response to retrovirus infection. Additionally, the availability of inbred mouse strains, the short gestation period of mice, and the short incubation time of neurological disease induction in mice compared to humans or non-human primates allows for the kinetic and statistical analysis of the host response genes.

2.2

FMCF98 and Fr98 Polytopic Murine Leukemia Viruses

In 1990, during studies of retrovirus-induced leukemia using Friend murine leukemia virus (MuLV) inoculation of neonatal mice, a novel retrovirus was isolated which appeared to cause both a neurological disease and leukemia (Buller et al. 1990). After biological and molecular cloning, the causative virus, FMCF98, was found to have a polytopic host range, as it was capable of infecting cell lines from mice as well as from a variety of other species, and it caused the typical mink cell foci (MCF) associated with other polytopic mouse retroviruses (Portis et al. 1995). After intraperitoneal (IP) infection of susceptible mouse strains the infection expanded first in hematopoietic cells of bone marrow and spleen and then progressed via blood to the brain.

Table 2 Polytopic retroviruses

Virus	Viral genome	CNS disease	Virus load	Upregulation of cytokines and chemokines
FMCF98		Yes (6–24 weeks)	++	Not tested
FB29		No	+++++	No
Fr98		Yes (2–3 weeks)	+++	High ^a
Fr54		No	++	No
SE		Yes (3–8 weeks)	+++	High ^a
BE		Yes (3–8 weeks)	+++	High ^a
EC		Yes (3–8 weeks)	++	Low ^b

^a Genes upregulated: *Tnfa*, *Tnfb*, *IL-1 α* , *Ccl2*, *Ccl3*, *Ccl4*, *Ccl5*, *Cxcl10*

^b Expression of cytokine and chemokine mRNA not statistically different as compared to mock-infected controls in whole brain; however, some cytokines, such as TNF- α , are upregulated in the middle region of the brain including the hippocampus, thalamus, and hypothalamus

The neurological disease consisted of ataxia, hind limb weakness, tremors, seizures, and death occurred in nearly 80% of mice by 6 months. In genetic studies, IRW mice were highly susceptible and C57BL/10 were highly resistant and two uncharacterized host genes appeared to account for most of this resistance (Buller et al. 1990). Because studies of a disease taking 6–8 months were difficult, a virus with a more rapid phenotype was derived by cloning the envelope gene of FMCF98 into the backbone of a rapidly replicating retrovirus, FB29 (Table 2) (Portis et al. 1995). By 20–30 days postinfection with this virus, Fr98, mice had the same neurological symptoms and pathology as produced by FMCF98. Within the brain, endothelial cells and microglia were the main target cells of Fr98, although rare infection of oligodendrocytes was also detected (Robertson et al. 1997). The brain pathology consisted of prominent reactive astrogliosis and widespread white matter microglial infection with microgliosis and occasional microglial giant cells and nodules, and minimal vacuolation (Portis et al. 1995). Neuronal cell death was not a prominent feature (Portis et al. 1995).

2.3

Mapping of Neurovirulence Determinants in the Fr98 Genome

Since neurological disease was not induced by most murine retroviruses, it was of interest to determine which regions of the Fr98 genome were important for this brain disease. Fr98 was compared to Fr54, a non-neurovirulent chimeric polytropic retrovirus with a similar structure (Hasenkrug et al. 1996). Fr54 contained the envelope (*env*) gene of FMCF54 inserted into FB29, and differed from Fr98 by several amino acid residues in the polymerase (*pol*) and *env* genes. Fr54 was able to infect the same cell types in the brain as Fr98; however, no neurological symptoms were observed. The level of Fr54 virus infection was slightly lower than that of Fr98, but there was no clear difference in the neuropathology (Hasenkrug et al. 1996; Robertson et al. 1997). Thus the pathology appeared to be due to retroviral infection, independent of the disease induction, suggesting perhaps that the disease symptoms and death were due to biochemical abnormalities not represented by obvious morphological changes.

In order to determine which regions of the Fr98 genome were responsible for induction of the neurological disease, several chimeric recombinant viruses using sequences of either Fr98 or Fr54 were studied (Hasenkrug et al. 1996; Peterson et al. 2004b). These data indicated that there were two non-overlapping regions of the Fr98 genome which influenced neurovirulence, one from *SphI* to *EcoRI* (SE), and the other from *EcoRI* to *ClaI* (EC) (Table 2). Both these chimeras induced disease slower than Fr98, suggesting that they acted by different but complementary mechanisms. The EC region contained only *env* sequences, whereas the SE region contained both *pol* and *env* sequences. However, only *env* sequences were involved in neurovirulence because a chimera with Fr98 sequences from *BbsI* to *EcoRI* (BE), containing only *env*, was similar in virulence to SE (Peterson et al. 2004b) (Table 2). The BE region contains 11 *env* amino acid differences between Fr98 and Fr54, and current studies are investigating which residues are most important to disease induction (K. Peterson and B. Chesebro, in preparation). The EC region contained 17 *env* amino acid differences, and mutagenesis studies identified changes at two positions (residues 195 and 198) as being important for disease induction (Poulsen et al. 1998).

The mechanisms of disease induced by these two *env* regions are still unclear; however, some clues were provided by previous studies. Earlier data indicated that the SE/BE region appeared to influence the brain viral load and the kinetics of replication, and for these chimeras a high viral load was required for disease. In contrast, the EC region induced disease at a lower viral load, and thus appeared to generate neurotoxicity which did not require high virus replication (Poulsen et al. 1998).

2.4

Contribution of Virus Burden to Pathogenesis

A role for higher viral load influencing disease was also shown in studies using direct brain infection by intraventricular inoculation of virus-infected neural stem cells (Poulsen et al. 1999). In these experiments virus infection of brain endothelial cells was minimal, whereas infection of microglial cells was greatly increased for all viruses tested. Interestingly, with this method even the avirulent virus Fr54 was capable of inducing neurological disease, albeit considerably more slowly than Fr98. These data indicated that all the polytropic retroviruses studied had potential to induce neurological disease if expressed in the brain at a high enough level. Perhaps the role of the SE/BE *env* region is to elevate viral replication to these high levels even when the standard route of IP infection is used. In contrast, since the EC chimera induced disease even at lower viral loads, it would appear that the critical Fr98 amino acids at positions 195 and 198 in this chimera have a higher potential for disease induction than the comparable Fr54 residues.

3

Cytokines and Chemokines in Fr98-Induced Neuropathogenesis

3.1

Analysis of Cytokine and Chemokine Gene Expression

Fr98-induced neurological disease is not associated with the widespread spongiform degeneration, intracerebral hemorrhaging, or extensive leukocyte infiltration associated with other neurovirulent murine retroviruses. Instead, the primary pathology associated with Fr98 infection is gliosis with increased presence of activated microglia, macrophages, and astrocytes in the brain (Portis et al. 1995; Robertson et al. 1997). As the pathology between Fr54 and Fr98 infection is similar (Portis et al. 1995; Robertson et al. 1997), the pathogenic mechanism by which Fr98 induces disease does not appear to cause distinctive morphological alterations. Possibly this pathogenesis acts at a molecular level through the regulation of gene expression. Molecular analysis of gene expression by RNase protection assay confirmed the lack of lymphocytic infiltration in the brain with no detectable increase in messenger (m)RNA for T cell- or B cell-specific genes or T cell-associated cytokines or cytokine receptors in brain tissue from Fr98-infected mice compared to mock-, Fr54-, or FB29-infected mice (Peterson et al. 2001). Additionally, no significant changes in gene expression were detected in the apoptosis-related genes, *Fas*, *Fasl*, *Fadd*, *Tradd*, *Bax*, *Bcl-X*, *Bcl-2*, and *Bcl-W*. Fr98 pathogenesis

was associated with a heightened proinflammatory response with increased mRNA expression of TNF(TNFSF1A,TNF α), TNFSF1B(TNF β , lymphotoxin A), IL1 β , CCL2(MCP-1), CCL3(MIP-1 α), CCL4(MIP-1 β), CCL5(RANTES), CXCL1(MIP-2), and CXCL10(IP-10) in the brain tissue of Fr98-infected mice (Peterson et al. 2001). Induction of cytokines and chemokines correlated with neurovirulence, not virus presence, as no significant mRNA upregulation of these genes was observed in FB29- or Fr54-infected mice. Protein levels of TNF(TNF α), CCL2(MCP-1), CCL3(MIP-1 α), CCL4(MIP-1 β), and CCL5(RANTES) were also increased in brain tissue from Fr98-infected mice (Fig. 1), indicating a correlation between the upregulation of cytokine and chemokine mRNA and protein expression. By in situ hybridization analysis, CCL2(MCP-1) and CXCL10(IP-10) mRNA was expressed by astrocytes, while CCL3(MIP-1 α), CCL4(MIP-1 β), and CCL5(RANTES) mRNA was expressed by uninfected cells, possibly microglia or macrophages (Peterson et al. 2004a; K. Peterson and B. Chesebro, unpublished observations).

Comparison of proinflammatory cytokine and chemokine expression following infection of the chimeric polytropic retroviruses indicated a corre-

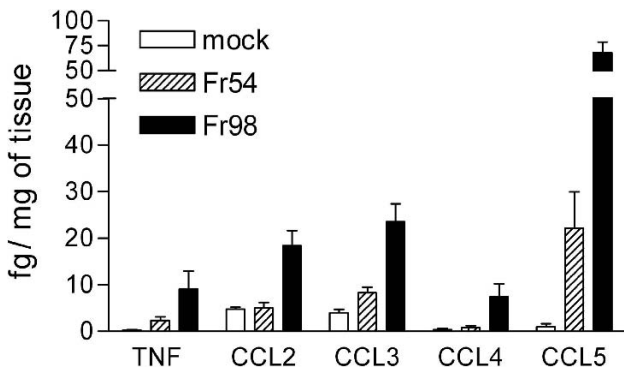


Fig. 1 Increased protein expression of TNF and chemokines in Fr98-infected mice. Enzyme-linked immunosorbent assay (ELISA) kits specific for the appropriate murine protein were purchased from R&D Systems (Minneapolis, MN). Brain tissue from Fr98-, Fr54-, or mock-infected mice were removed at 14 days postinfection, snap frozen in liquid nitrogen, and stored at -80°C until use. The samples were homogenized in 0.1 M Tris pH 7.4, 0.15 M NaCl, 0.5% NP40 with complete protease inhibitor (Roche Applied Science, Indianapolis, IN) to a final concentration of 30% w/v. Samples were incubated overnight at 4°C , and 50 μl per sample was added to duplicate wells for each protein-specific ELISA. Data are presented as femtograms of the protein of interest per milligram of brain tissue and are the mean \pm standard error of 4–8 samples per group. A significant increase ($p < 0.05$) in protein levels of brain tissue from Fr98-infected mice was observed for all proteins analyzed

lation between the SE/BE neurovirulent determinant of the Fr98 envelope and the induction of cytokine and chemokine mRNA expression (Peterson et al. 2001). Increased cytokine and chemokine expression was observed in the brain tissue of SE and BE-infected mice (Peterson et al. 2001, 2004b). In contrast, cytokine expression in EC-infected mice was more restricted, with localized upregulation of tumor necrosis factor (TNF) in the middle (hippocampus, midbrain, and thalamus) region of the brain (Peterson et al. 2001, 2004b). As Fr98, SE and BE replicate in the brain at a two- to threefold higher level than EC or Fr54 (Table 2) (Hasenkrug et al. 1996; Peterson et al. 2004b; Robertson et al. 1997), the upregulation of cytokine and chemokine expression may be due to the increased viral burden associated with these viruses. Alternatively, specific envelope determinants may be necessary for the induction of these proinflammatory factors.

3.2

Kinetics of Gene Expression

The correlation between increased proinflammatory cytokines and chemokines and retrovirus-induced neuropathogenesis suggests that these proinflammatory factors may induce pathogenesis or be induced as a result of pathogenic insult. One way to dissect the cause versus effect relationship of these events is the analysis of the timing of upregulation of cytokines and chemokines relative to disease onset. Kinetic analysis of gene expression is difficult in HIV, SIV, and FIV studies due to limitations in tissue sampling as well as the variation in disease progression and the incidence of disease. However, in the Fr98 mouse model, after infection with high virus doses, 100% of the animals develop neurological disease within 14 to 16 days postinfection (Peterson et al. 2001; Poulsen et al. 1999). An increase in mRNA expression of TNF, CCL2(MCP-1), CCL3(MIP-1 α), CCL4(MIP-1 β), CCL5(RANTES), CXCL1(MIP-2), and CXCL10(IP-10) was detected in pre-clinical mice, 3–4 days prior to the neurological disease, suggesting that these cytokines and chemokines might contribute to disease induction (Peterson et al. 2001). In contrast, increased expression of TNFSF1B(TNF β , lymphotoxin A) and interleukin (IL)-1 α mRNA was only consistently found in Fr98-infected mice with clinical disease, suggesting that these cytokines may be a response to disease rather than a cause of pathogenesis. Interestingly, mRNA expression of two additional chemokines, CCL7(MCP-3) and CCL12(MCP-5), was upregulated 3 to 4 days prior to clinical disease development, but returned to basal levels at the time of clinical disease (Peterson et al. 2004a). Similarly, CCL12(MCP-5)-positive cells were found in brain tissue of preclinical mice, but were difficult to detect in mice with clinical disease. Although

CCL7(MCP-3) and CCL12(MCP-5) are not upregulated at the time of disease, they could contribute to the early stages of disease development prior to the onset of clinical disease.

3.3

Studies with Knockout Mice

Knockout mouse and antibody blocking studies indicated a role for specific cytokines and chemokines in Fr98-mediated pathogenesis in the brain. Mice deficient in CCR2, the primary ligand for CCL2(MCP-1) and CCL12(MCP-5), had reduced incidence and kinetics of neurological disease following Fr98 infection, indicating that CCR2 stimulation was contributing to pathogenesis (Peterson et al. 2004a). Antibody blocking studies indicated that the CCR2 ligand CCL2(MCP-1), but not ligands CCL7(MCP-3) or CCL12(MCP-5), contributed to Fr98-induced disease. Thus, CCL2(MCP-1) stimulation of CCR2 appears to be a mechanism of Fr98-mediated neuropathogenesis. In contrast, CCR5 was not necessary for Fr98 pathogenesis as no decrease in neurovirulence was observed in CCR5-deficient mice, despite increased mRNA and protein expression of the CCR5 ligands CCL3(MIP-1 α), CCL4(MIP-1 β), and CCL5(RANTES) (Peterson et al. 2001, 2004a; Fig. 1).

In TNF-deficient mice, the rate of Fr98-induced disease progression was significantly delayed, demonstrating that TNF contributed to neuropathogenesis (Peterson et al. 2004b). Interestingly, the role of TNF in pathogenesis varied with different chimeric polytropic retroviruses. For example, the chimeric virus BE induced high levels of TNF mRNA in the brain, whereas the chimeric virus EC induced only localized production of TNF mRNA in the middle (midbrain, hippocampus, and thalamus) region of the brain. This correlation suggested that TNF deficiency might inhibit BE-induced disease and not EC-induced disease. However, paradoxically, the opposite was observed. TNF deficiency significantly inhibited EC-induced clinical disease, but had no detectable effect on BE-induced disease (Peterson et al. 2004b). This result demonstrated the danger of drawing conclusions strictly from correlative data.

EC-induced upregulation of the microglia and macrophage marker F4/80 was not observed in TNF-deficient mice, suggesting that TNF may contribute to disease by the activation or recruitment of microglia or macrophages (Peterson et al. 2004b). In contrast, TNF was not necessary for retrovirus-induced activation of astrocytes as measured by expression of glial fibrillary acidic protein (GFAP) mRNA. Further studies analyzing the responses of retrovirus infection in knockout mice should provide valuable information in regards to how cytokines and chemokines contribute to neuropathogenesis.

Increased TNF mRNA expression has also been associated with the spongiform degeneration and neurological disease induced by the FrCasE and Mol-ts1 murine retrovirus infections (Askovic et al. 2001; Choe et al. 1998; Peterson et al. 2004b). However, deficiencies in TNF or TNFR1 did not alter the pathogenesis of disease induced by FrCasE and Mol-ts1, respectively (Jolicoeur et al. 2003; Peterson et al. 2004b).

4

Cytokines and Chemokines in Immunosuppressive Lentivirus Pathogenesis

4.1

Correlation Between Gene Expression and Neurological Disease

Similar to the upregulation of cytokines and chemokines in the Fr98 model, several studies have demonstrated expression of proinflammatory cytokines and chemokines in HAD. Increased mRNA or protein expression of CCL2(MCP-1), CCL3(MIP-1 α), CCL4(MIP-1 β), CCL5(RANTES), CXCL10(IP-10), TNF(TNF α), interferon (IFN)- γ , and IL-1 have been observed in brain tissue or cerebrospinal fluid of HIV-infected patients with dementia (Conant et al. 1998; Kolb et al. 1999; McManus et al. 2000; Schmidtayerova et al. 1996; Tyor et al. 1992; Vago et al. 2001). A strong correlation was also observed between TNF mRNA expression and clinical signs of dementia (Glass et al. 1993), although, based on studies using TNF knockout mice in the Fr98 system, gene expression of TNF does not always correlate with a role of TNF in neuropathogenesis. The source of CCL2(MCP-1) expression in HAD patients was astrocytes (Conant et al. 1998), while CCL5(RANTES) was expressed by lymphocytes and uninfected microglia/macrophages (Vago et al. 2001) and TNF, IFN- γ , and IL-1 were produced by perivascular macrophages and endothelia (Tyor et al. 1992).

Increased cytokine and chemokine mRNA and protein expression also correlated with encephalitis induced by SIV or FIV infection. Increased cerebrospinal fluid levels of CCL2(MCP-1) was a strong indicator of SIV-induced encephalitis (Zink et al. 2001). Additionally, increased mRNA and/or protein expression of CCL3(MIP-1 α), CCL4(MIP-1 β), CCL5(RANTES), CCL7(MCP-3), CXCL10(IP-10), IL-1 β , IL-4, IL-6, IFN- γ , and TNF have been associated with encephalitis in the SIV model (Lane et al. 1996; Orandle et al. 2002; Sas-seville et al. 1996; Sopper et al. 1996; Sui et al. 2003), with TNF expression by macrophages in perivascular lesions (Orandle et al. 2002). Similarly, increased expression of TNF mRNA by microglia and astrocytes appears to be involved in the early stages of FIV-induced encephalitis in cats (Poli et al. 1999).

4.2

Effect of HIV Proteins on Cytokine and Chemokine Induction

In the Fr98 model, particular sequences in the viral envelope protein influenced the production of cytokines and chemokines, possibly through the regulation of virus levels in the brain (Peterson et al. 2001). In the SCID-HIVE model, increased expression of both CCL2(MCP-1) and CCL3(MIP-1 α) was associated with HIV-infected monocytes in the brain (Persidsky et al. 1999). Similar induction of cytokines and chemokines such as CCL2(MCP-1), CXCL10(IP-10), CXCL9(MIG), and IL-1 β were observed in mouse brain tissue following inoculation with HIV-1 provirus or a chimeric HIV virus with an ecotropic MuLV envelope protein (Potash et al. 2005; Wang et al. 2003). Both the Tat and Env protein of HIV appeared to contribute to the upregulation of cytokines and chemokines. HIV Tat stimulation of in vitro cultures of glial cell cultures induced the expression of several chemokines including CCL2(MCP-1) and CCL3(MIP-1 α) (McManus et al. 2000), while stimulation of astrocytes with HIV gp120 induced CXCL10(IP-10) expression (Asensio et al. 2001). A similar induction of CXCL10(IP-10) as well as CCL2(MCP-1) was observed in mice with transgenic expression of gp120 under the GFAP promoter (Asensio et al. 2001). Interestingly, no clinical signs of neurological disease were reported in these in vivo models, indicating that increased production of chemokines in the brain at the levels achieved in these experiments was not sufficient for the induction of neurological disease.

5

Potential Effects of Chemokines During Retrovirus Infection of the Brain

Polymorphism studies have suggested that certain alleles of TNF and CCL2(MCP-1) correlate with increased risk of the development of dementia in HIV-infected patients (Gonzalez et al. 2002; Quasney et al. 2001). Studies with the Fr98 mouse model also demonstrated that CCL2(MCP-1), its primary receptor, CCR2, and TNF contributed to retroviral pathogenesis in the brain (Peterson et al. 2004a, b). Comparison of wildtype and knockout mice in the Fr98 pathogenesis model as well as in vitro and in vivo studies with HIV, SIV, and FIV have indicated several mechanisms by which these proteins may contribute to pathogenesis.

5.1

Activation and Recruitment of Microglia and Macrophages

The lack of neurological disease in TNF-deficient mice following EC retrovirus infection was associated with a lack of increased expression of the microglia

and macrophage marker F4/80 (Peterson et al. 2004b). Thus, TNF may have an important role in the activation and/or recruitment of brain microglia and macrophages. Autopsy findings from HAD patients indicated a strong correlation between increased staining for activated macrophages and microglial cells in the brain and the severity of dementia (Glass et al. 1995). Similarly, an increase in activated macrophages and/or microglia has also been associated with encephalitis following SIV or FIV infection (Georgsson 1994; Lackner et al. 1991; Williams and Hickey 2002). Blood–brain barrier (BBB) permeability and tight junction disruption have been noted in cases of HIV and SIV infections (Boven et al. 2000; Luabeya et al. 2000), indicating that infected and uninfected peripheral macrophages may migrate to the brain and contribute to retroviral pathogenesis. In the SCID-HIVE mouse model, HIV-infected cells in the CNS were surrounded by murine macrophages, suggesting the migration of either peripheral or brain macrophages to the site of virus in the brain (Nukuna et al. 2004). TNF expression has been demonstrated to break down the BBB as well as induce microglia and macrophage activation and macrophage migration in vitro (Glabinski et al. 1998; Hurwitz et al. 1994).

Chemokines may play an important role in the migration of peripherally activated macrophages across the BBB. The term chemokine was coined to describe a family of chemoattractant cytokines that were involved in the recruitment and tissue extravasation of leukocytes during inflammation. The chemokine CCL2(MCP-1) induced monocyte migration across an endothelial cell/astrocyte co-culture model of the BBB (Eugenin and Berman 2003). Expression of CCR2, the primary receptor for CCL2(MCP-1), by macrophages was required for CCL2(MCP-1)-induced macrophage migration across a brain endothelial layer (Dzenko et al. 2005). Interestingly, CCR2 expression was also required on the brain microvessels, as neither CCR2⁺ nor CCR2⁻ macrophages could migrate across CCR2⁻ brain endothelial cells in response CCL2(MCP-1) stimulation (Dzenko et al. 2005). It is possible that CCL2(MCP-1) and TNF contribute to retroviral pathogenesis by the same mechanism, with both cytokines involved in the activation and/or migration of microglia and macrophages in the brain.

5.2

Lymphocyte Recruitment

Expression of cytokines and chemokines may also recruit CD3 lymphocytes to the brain (Dufour et al. 2002; Moser et al. 2004; Ransohoff 2002; Ransohoff and Tani 1998). Although a detectable increase in CD8⁺CD3⁺ lymphocytic infiltration is not observed in the Fr98 model, increased numbers of CD8⁺ lymphocytes in the CNS have been reported with both HIV-1 and SIV infec-

tions (Kim et al. 2004b; Miller et al. 2004; Petito et al. 2003). However, persistent depletion of CD8⁺ lymphocytes correlated with increased encephalitis in brains of SIV-infected macaques (Williams et al. 2001; Williams and Hickey 2002). Thus, rather than contributing to retroviral pathogenesis, CD8⁺ T cells may suppress the recruitment and trafficking of infected macrophages in the CNS, delaying the development of neurological symptoms.

5.3

Neuronal Apoptosis

Apoptotic neurons and neuronal dropout have been observed in brain tissue of HAD patients and animal models of retroviral neuropathogenesis, although there does not appear to be a direct correlation with the amount of neuronal apoptosis and clinical neurological disease (Ade-Biassette et al. 1999; Kolson et al. 1998). In contrast, no detectable increase in neuronal apoptosis was associated with Fr98 infection or disease (Peterson et al. 2004b; Portis et al. 1995), but lack of apoptosis might be due to the short disease course in this model. This result suggests that the severe clinical symptoms observed by Fr98 infection are not the result of neuronal death, but instead more likely represent neuronal dysfunction. In slower disease models, apoptosis may be the end result of neuronal damage induced by cytokines and chemokines, but this interpretation is not conclusive because these proinflammatory molecules can have opposing effects in different situations. For example, TNF has been directly implicated in inducing apoptosis through stimulation of TNFRI, but may be anti-apoptotic when stimulating through TNFRII (Saha and Pahan 2003). CCL2(MCP-1) inhibited neuronal apoptosis induced by either *N*-methyl-D-aspartate (NMDA) or HIV Tat in mixed glial cultures (Eugenin et al. 2003). Similar results were also observed by the addition of CCL5(RANTES), suggesting that the production of chemokines during retrovirus infection may provide protection from retrovirus-induced neuronal apoptosis and may, in some instances, decrease the pathogenesis of retrovirus infection. In vitro studies have shown that chemokines such as CCL5(RANTES), CXCL12(SDF1 α), and CCL22(MDC) can provide support for the survival of neuronal cultures in the absence of glial feeder cells (Meucci et al. 1998).

Retrovirus proteins including HIV-1 Tat and gp120 can induce apoptosis when added to neurons in vitro (Catani et al. 2000; Meucci et al. 1998; Zhang et al. 2003). HIV gp120-induced neuronal apoptosis was blocked by anti-CXCR4 or anti-CCR5 antibodies, indicating that HIV gp120 neurotoxicity may be mediated by chemokine receptor signaling (Zhang et al. 2003). CCL3(MIP-1 α), CCL4(MIP-1 β), CCL5(RANTES), and CXCL12(SDF1 α) inhibited gp120-induced apoptosis (Catani et al. 2000; Meucci et al. 1998), suggesting that the

expression of these chemokines during retrovirus infection may block the neurotoxic effects of gp120. Thus, the ratio of chemokine expression to virus envelope production and the levels of cytokines or chemokines produced may regulate the amount of neuronal apoptosis associated with retrovirus infection.

5.4

Direct Stimulation of Neurons

Chemokines may also contribute to retrovirus neuropathogenesis through the direct stimulation of neuronal subsets in the brain. Embryonic and adult neurons have been reported to express a number of chemokine receptors including CCR1, CCR2, CCR5, CXCR3, and CXCR4 (Meucci et al. 1998; Tran et al. 2004; Tran and Miller 2003). Studies with hippocampal neurons demonstrated functional chemokine receptors as stimulation of neurons with CCL3(MIP-1 α), CCL5(RANTES), CCL22(MDC), and CXCL12(SDF1 α) induced calcium signaling (Meucci et al. 1998). Although CCL2(MCP-1) did not induce calcium signaling in hippocampal neurons (Meucci et al. 1998), studies with Purkinje neurons indicated that CCL2 could enhance calcium signaling following glutamate receptor activation (van Gassen et al. 2005). Patch-clamp experiments of cultured hypothalamic neurons indicated that chemokines such as CXCL12(SDF1 α) might be directly involved in neuronal signaling (Guyon et al. 2005). Thus, the production of chemokines following retrovirus infection of the CNS may alter neuronal signaling patterns, leading to neurological disease.

5.5

Alteration or Inhibition of Neuroprogenitor Stem Cell Migration

Another mechanism by which CCL2(MCP-1)/CCR2 interactions may contribute to retroviral neuropathogenesis is through the alteration of neural progenitor stem cell (NPSC) migration in the brain or by effecting axonal growth and NPSC survival. This might be especially relevant in congenital HIV infection and also in the Fr98 mouse model, where mice are infected as neonates and the brain is still undergoing development. Abnormal brain development has not been reported in CCR1-, CCR2-, CCR3-, CCL2(MCP-1)-, or CXCL10(IP-10)-deficient mice, suggesting that these chemokines are not necessary for the normal migration of NPSC during development (Abbadie et al. 2003; Dufour et al. 2002; Humbles et al. 2002; Khan et al. 2001; Kuziel et al. 1997, 2003; Lu et al. 1998). However, CCL2(MCP-1) altered the migration of NPSC *in vitro* (Widera et al. 2004), suggesting that overexpression of chemokines may alter NPSC migration. Additionally, lipopolysaccharide

(LPS) was shown to inhibit NPSC migration patterns *in vivo*, possibly through the increased production of proinflammatory cytokines and chemokines in the brain (Monje et al. 2003). Chemokines have been shown to contribute to NPSC migration *in vivo*. Mice deficient in the chemokine receptor CXCR4, the receptor for the chemokine CXCL12(SDF1 α), have deformed cerebellum development and lack neuronal migration from the external granular layer (Lu et al. 2002). The loss of CXCL12(SDF1 α) also affects adult neurogenesis in the hippocampal dentate gyrus (Bagri et al. 2002). A decrease in migrating NPSC was detected in HIV-infected patients with dementia compared to those without, indicating that NPSC migration may influence disease (Krathwohl and Kaiser 2004). Alteration or suppression of NPSC migration could affect the development of the dentate gyrus and cerebellum and lead to the inhibition of memory and developmental skills associated with HIV infection in infants (Drapeau et al. 2003; Monje et al. 2003; Rola et al. 2004; Tran and Miller 2003).

5.6

Astrocyte Activation and Support Functions

Although most retroviruses do not productively infect astrocytes, reactive astrocytes as characterized by increased GFAP expression is commonly associated with neuropathogenesis induced by HIV, SIV, FIV, and Fr98, as well as other retroviruses (Kolson et al. 1998; Poli et al. 1997; Rausch et al. 1994; Robertson et al. 1997). Astrocytes are also the common source for CCL2(MCP-1) production during retrovirus infection and may contribute to pathogenesis by this mechanism (Conant et al. 1998; Peterson et al. 2004a; Zink et al. 2001). CXCL10(IP-10) production by retrovirus-stimulated astrocytes has also been detected (Asensio et al. 2001; Kutsch et al. 2000). Astrocytes express multiple functional chemokine receptors including CCR1, CCR2, CCR3, CCR5, CCR10, and CXCR4 (Andjelkovic et al. 2002; Croitoru-Lamoury et al. 2003; Dorf et al. 2000; Tanabe et al. 1997). Thus, the production of chemokines by astrocytes and other glial cells in the brain may affect the function of these cells.

Astrocytes play an important support function for neurons, by removing potentially neurotoxic glutamate from extracellular spaces and converting it to glutamine. Activated astrocytes express two glutamate receptors: SLC1A2 (solute carrier family 1–glial high-affinity glutamate transporter member 2, also known as GLT-1 or EAAT-2), which is found on astrocytes throughout the brain; and SLC1A3 (solute carrier family 1–glial high-affinity glutamate transporter member 3, also known as GLAST or EAAT-1), which can also be detected on neurons (Liberto et al. 2004). Trauma to cultured astrocytes results in increased mRNA and protein expression of both SLC1A2 and SLC1A3. Glutamate-ammonia ligase (GLUL, also known as glutamine synthase, GLNS),

which converts glutamate to the non-neurotoxic glutamine, can also be upregulated in activated astrocytes. Altered expression of SLCA3 or other glutamate regulatory genes has been associated with neuropathogenesis, including SIV infection of the brain (Chretien et al. 2002, 2004; Guo et al. 2003; Li et al. 1997; Martin et al. 2000). Chemokine activation of astrocytes may affect the regulation of the glutamine synthesis and lead to the build-up of neurotoxic glutamate.

5.7

Retrovirus Entry and Spread in the CNS

In the Fr98 model, the lack of CCR2, CCR5, or TNF did not influence virus burden in the brain (Peterson et al. 2004a, b). However, Fr98 has not been reported to use chemokine receptors as coreceptors for virus entry. In contrast, HIV and SIV utilize the chemokine receptors CXCR4 and CCR5 as coreceptors for infection of T cells and macrophages, respectively (Alkhatib et al. 1996; Feng et al. 1996; Oberlin et al. 1996). In addition, other chemokine receptors including CCR2b, CCR3, and CCR8 have been shown to contribute to HIV or SIV infection and are often referred to as minor coreceptors (Gorry et al. 2001; Margulies et al. 2001). HIV patients with a CCR5 allele containing a 32-bp deletion had reduced incidence of HIV encephalitis (HIV-E), indicating that CCR5 is an important contributor to retrovirus infection of macrophages and/or microglia in vivo (van Rij et al. 1999). Chemokine expression in the brain during HIV-1 infection could impact virus infection of brain macrophages or microglia. CCL3(MIP-1 α), CCL4(MIP-1 β), and CCL5(RANTES) are ligands for CCR5 and are detected at increased levels in patients with HAD (Schmidt-mayerova et al. 1996; Vago et al. 2001). The expression of these CCR5 ligands in the brain during HIV infection could block virus envelope binding of CCR5 molecules on macrophages and thus restrict the spread of HIV infection in the brain. Alternatively, stimulation of CCR5-positive macrophages by these ligands may induce increased expression of CCR5 on the cell surface, providing ample coreceptors for virus infection of brain macrophages.

5.8

Retroviral Protein Stimulation of Chemokine Receptors

As several retroviruses use chemokine receptors for virus entry, retroviral proteins may also contribute to pathogenesis by signaling cells through these chemokine receptors. For example, HIV-1 gp120-induced neuronal death can be inhibited by blocking or downregulating CXCR4 or CCR5 (Catani et al. 2000; Zhang et al. 2003; Zheng et al. 1999). CXCR4 expression has been detected on multiple cell types in the CNS including microglia, astrocytes, and

neurons (Bajetto et al. 1999; Catani et al. 2000; Flynn et al. 2003), while CCR5 appears to be expressed on glial cells (van der Meer et al. 2000; Bajetto et al. 1999). Although HIV-1 primarily infects microglia/macrophages in the brain, HIV gp120-induced stimulation of CCR5 or CXCR4 may alter the activation state of uninfected cells or induce apoptosis. Another retroviral protein, Tat, is also reported to mimic chemokines. Tat acts as a chemoattractant to leukocytes, can induce CCL2(MCP-1) expression by astrocytes, and can displace the binding of α -chemokines from their receptors (Albini et al. 1998; Conant et al. 1998). HIV Tat also binds to the chemokine receptor CCR1 with similar affinity to the chemokine CCL7(MCP-3) (Albini et al. 1998), indicating that high levels of Tat may mimic the production of this chemokine.

The xenotropic/polytropic receptor 1 (XPR1, RMC1) is the cellular receptor for polytropic retrovirus infection (Tailor et al. 1999; Yang et al. 1999). Based on the presence of an SPX domain and similarities to the yeast protein SYG1, the XPR1 protein is predicted to be involved in G protein-associated signal transduction and function as a phosphate sensor (Battini et al. 1999). It is possible that XPR1 is involved in signal transduction of chemokine receptors or other signal transduction pathways that lead to the cellular activation. Further studies that elucidate the function of XPR1 would determine if stimulation of this receptor contributes to neuropathogenesis.

6 Conclusions

The correlation between increased proinflammatory cytokines and chemokines and neuropathogenesis induced by Fr98, HIV, SIV, and FIV suggests that some proinflammatory factors contribute to the disease process. Furthermore, polymorphism studies in HAD patients and knockout mouse studies in the Fr98 mouse model indicate that the upregulation of both TNF and CCL2(MCP-1) contributes to Fr98 and HIV-induced retroviral neuropathogenesis. Other proinflammatory cytokines, such as IL-1 α or TNFSF1b(TNF β , lymphotoxin A) may be a host reaction to retrovirus-induced damage. Proinflammatory cytokines and chemokines are most commonly known for their ability to recruit lymphocytes and other immune cells to the sites of infection. However, the upregulation of cytokines and chemokines associated with neuropathogenesis induced by HIV-1, SIV, FIV, and Fr98 retrovirus infection is not associated with substantial lymphocyte infiltration, possibly due to the immunosuppressed nature of the host. The pathogenesis of cytokines and chemokines during retrovirus infection may be due to stimulation of resident CNS cells. Several mechanisms by which proinflammatory cytokines and

chemokines may contribute to the neuropathogenesis include the activation of perivascular macrophages and microglia, induction of neuronal apoptosis, interference with neuronal signal transduction, alteration of neuroprogenitor stem cell migration, and altering the activation and support functions of astrocytes. Further investigation is needed to determine the relative contribution of these mechanisms to the clinical neurological disorders associated with retrovirus infection. Additionally, it is important for possible therapeutic potential to determine whether certain chemokines might slow the progression of disease development as is suggested by some in vitro experiments.

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HIV-1 Coreceptors and Their Inhibitors

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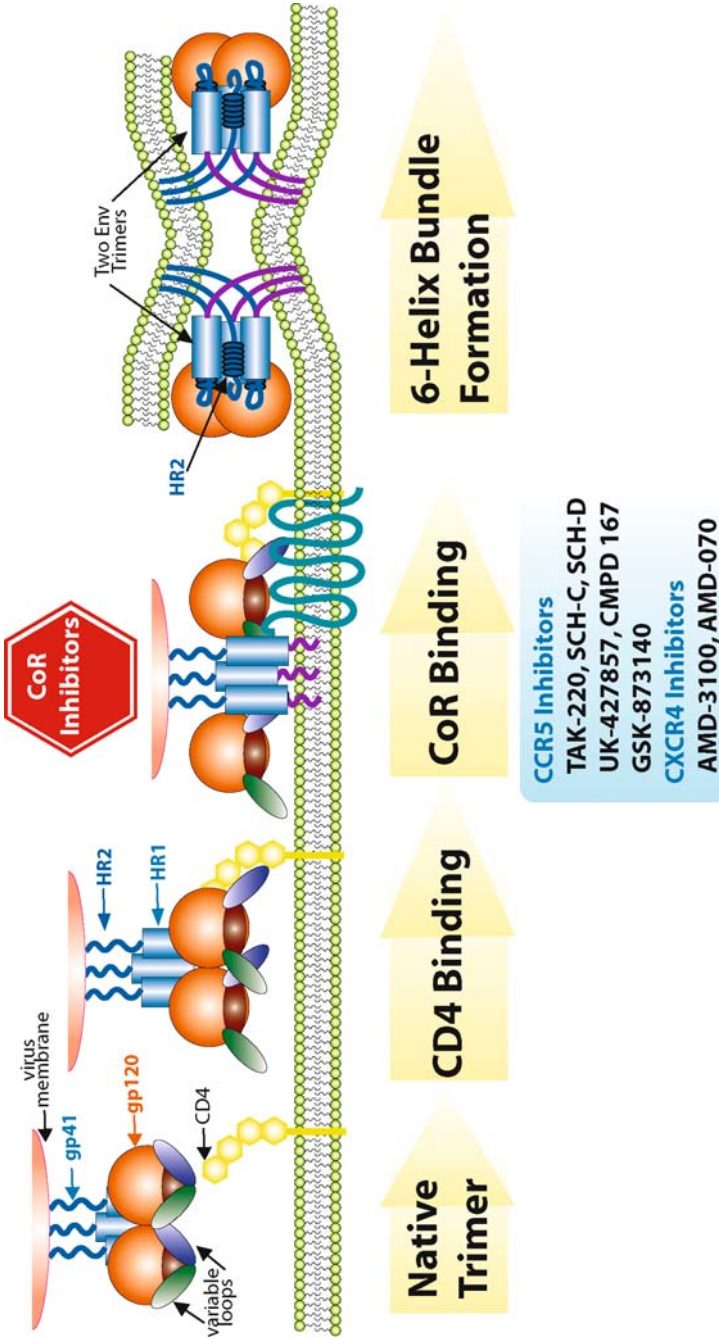
Abstract Entry of human immunodeficiency virus (HIV) into target cells is mediated by the viral Envelope glycoprotein (Env) and its coordinated interaction with a receptor (CD4) and a coreceptor (usually the chemokine receptors CCR5 or CXCR4). This review describes the identification of chemokine receptors as coreceptors for HIV-1 Env-mediated fusion, the determinants of chemokine receptor usage, and the impact of nonfunctional chemokine receptor alleles on HIV-1 resistance and disease progression. Due to the important role of chemokine receptors in HIV-1 entry, inhibitors of these coreceptors are good candidates for blocking entry and development of antiretroviral therapies. We discuss the different CCR5- and CXCR4-based antiretroviral drugs that have been developed thus far, highlighting the most promising drug candidates. Resistance to these coreceptor inhibitors as well as the impact of these drugs on clinical monitoring and treatment are also discussed.

1 Identification of Chemokine Receptors as Coreceptors for HIV-1 Env-Mediated Fusion

Human immunodeficiency virus (HIV) initiates infection by attaching and subsequently fusing its viral membrane to the plasma membrane of a target cell. As shown in Fig. 1, the process is mediated primarily by the viral Envelope protein (Env). Env is a glycoprotein, 160 kDa in size (gp160), that is proteolytically processed into a surface subunit (gp120) and a transmembrane subunit (gp41) by a host cell protease during transit to the cell surface. Each gp120 molecule interacts with one gp41 molecule to form a noncovalently linked complex, and the gp120–gp41 complexes then exist as trimers on the surface of HIV virions. These trimers bind with high affinity to CD4, the primary receptor for HIV on the target cell surface. The presence of CD4 is a prerequisite for efficient HIV infection and explains the tropism of HIV for CD4-positive T cells and macrophages.

Three main lines of evidence derived from experiments reported in the mid-1980s and early 1990s, however, brought into question the role of CD4 as the only receptor for HIV. First, studies with recombinant human CD4 demonstrated the ability of this molecule to render cells susceptible to Env-mediated fusion and virus entry, but only when expressed in human cell types [20, 61]. Further work with cell hybrids pointed toward the existence of an essential coreceptor, specific to human cells, in the absence of which CD4 was unable to support Env-mediated fusion [4, 14]. Second, in the late 1980s, different HIV-1 isolates were shown to display distinct tropisms for various

Fig. 1 Model of HIV entry. The Env glycoprotein of HIV mediates fusion of viral and cellular membranes. Env is a homotrimeric protein (*first panel*) in which each subunit is composed of surface gp120 and membrane-spanning gp41 proteins. Binding to CD4 is mediated by the gp120 subunit, and CD4 binding induces conformational changes in gp120 that result in the exposure of a conserved region that is important for coreceptor binding (*second panel*). In the native trimer, this conserved region is hidden in part by variable loops that are thought to undergo conformational changes and consequent repositioning after CD4 binding. Following CD4 binding, gp120 binds to a seven-transmembrane domain coreceptor (CoR; *third panel*). Coreceptor binding can be inhibited by a number of CCR5 and CXCR4 inhibitors such as TAK-220, SCH-C, SCH-D, UK-427857, CMPD 167, GSK-873140, AMD-3100, and AMD-070. The hydrophobic fusion peptide at the N terminus of gp41 becomes exposed and inserts into the cell membrane. Ultimately, coreceptor binding leads to the formation of a six-helix bundle in which the helical HR2 domains of each gp41 subunit fold back and bind to the triple-stranded HR1 domains (*fourth panel*), bringing the fusion peptide and transmembrane domain of gp41, and their associated membranes, into close proximity



CD4-positive human cell types *in vitro*. Some isolates are able to infect CD4-positive T cell lines but not primary macrophages, whereas others showed the opposite tropism and were able to infect primary macrophages much better than T cell lines ([71] and citations therein). The former were designated T cell-line tropic (T-tropic) and the latter macrophage tropic (M-tropic). Isolates that efficiently infected both T cell lines and macrophages were called dual-tropic. Soon after, it was also reported that viral isolates from peripheral blood of recently infected individuals are primarily M-tropic [85, 91, 116] and as the infection progresses to acquired immunodeficiency syndrome (AIDS), T-tropic viruses can be isolated in most patients [23, 91, 102]. Again, cell hybrid experiments indicated that these specific tropisms were likely resulting from the requirement for an additional coreceptor in the susceptible cells rather than the presence of an inhibitor in the nonsusceptible cells. Finally, the identity of the putative coreceptor became apparent from studies with the chemokines macrophage inflammatory protein (MIP)-1 α , MIP-1 β , and RANTES (regulated on activation, normal T-expressed and secreted), which were shown to block HIV-1 infection [21].

The first coreceptor was identified using a functional complementary DNA (cDNA) cloning strategy based on the ability of a cDNA library to render a CD4-expressing murine cell susceptible for fusion with cells expressing Env from a T-tropic strain [43]. This strategy allowed the isolation of a single cDNA; sequence analysis revealed that the encoded protein was a member of the superfamily of the seven-transmembrane domain G protein-coupled receptors. The protein was first named “fusin” for its role in HIV fusion, and later CXCR4 when it was shown to be a chemokine receptor for the CXC chemokines stromal cell-derived factor (SDF)-1 α and SDF-1 β [11, 78]. Importantly, CXCR4 did not function as a coreceptor for M-tropic virus isolates. However, at around the same time, the chemokine receptor CCR5 was shown to bind MIP-1 α , MIP-1 β , and RANTES, the same chemokines that had been shown to block infection by some HIV-1 strains [21]. Shortly thereafter, CCR5 was shown to be the major coreceptor for M-tropic HIV-1 strains [3, 19, 32, 37, 39]. CCR5-using (R5-tropic) HIV-1 strains tend to be transmitted between individuals, whereas strains using CXCR4 (X4-tropic) emerge in a subset of HIV-1-infected individuals at later stages of infection [25, 96]. In addition to the two main coreceptors for HIV-1, other chemokine receptors as well as some orphan receptors have been shown to be capable of mediating virus fusion. These alternative coreceptors include CCR2b, CCR3, CCR8, CCR9, CXCR6 (STRL33/Bonzo), CX₃CR1, ChemR23, GPR15 (BOB), and APJ (reviewed in [8, 95]). A subset of these alternative coreceptors, such as CCR3, CCR8, and CXCR6, are used efficiently by some HIV-1 isolates to infect cell lines over-expressing these proteins [7, 86, 114]. Certain minor coreceptors

(CXCR6 and GPR15) are expressed in the placenta and colon and could conceivably play a role in mother-to-child or homosexual transmission [33], while CCR8 is expressed on thymocytes and so could play a role in virus infection in the thymus. However, with only a handful of exceptions [93, 110, 115], infection of human macrophages and peripheral blood mononuclear cells (PBMCs) by HIV-1 strains is dependent upon the presence of either CCR5 or CXCR4 in conjunction with CD4. Most of the alternative coreceptors are either not expressed on CD4-positive cells at detectable levels, or are expressed at levels that are below that needed for efficient virus infection. Thus, at present there is no compelling evidence to indicate that receptors other than CCR5 or CXCR4 are important for HIV-1 infection *in vivo*.

2

Determinants of Tropism and Chemokine Receptor Usage

The *env* genes from different HIV-1 isolates display significant sequence heterogeneity in specific regions of gp120. There are five variable regions in gp120 (V1–V5) that are separated by five constant regions (C1–C5). Studies involving Env chimeras between M- and T-tropic isolates identified the V3 loop as the primary determinant of viral tropism [17, 18, 28, 51, 94, 101] and coreceptor usage [19, 22, 85, 98, 99]. Although even single amino acid changes in the V3 loop have been shown to be sufficient to alter tropism [27], many of the mutations observed in this region that alter tropism have strain-specific effects, and no single amino acid has emerged as crucial. In general, however, an increase in the net positive charge (i.e., more basic residues) in the V3 loop has been demonstrated in viral isolates from HIV-positive patients over time and correlates with conversion to T cell tropism and CXCR4 usage [9, 19, 22, 27, 49, 94]. Moreover, the specific nature of the V3 loop, based on whether it is from an R5 or X4 strain, is the primary determinant of direct Env chemokine receptor binding and Env-mediated inhibition of chemokine and monoclonal antibody binding to chemokine receptors [22, 105, 112].

3

Impact of Nonfunctional Chemokine Receptor Alleles on HIV-1 Resistance and Disease Progression

A mutation in the CCR5 open reading frame results in the premature truncation and a consequent 32-bp deletion in the protein (CCR5 Δ 32). Although this mutation is relatively common in the Caucasian population, with an allele frequency of 15–20%, it was found to be significantly underrepresented

in the HIV-1 infected groups [30, 88], and individuals homozygous for the mutation are only rarely infected with HIV [10, 45, 70, 77, 103]. In fact, in a group of people at high risk, two individuals that remained uninfected despite repeated exposure, were found to be homozygous for the same $\Delta ccr5$ mutation [60]. Lymphocytes from these individuals are resistant in vitro to M-tropic strains but permissive for T-tropic strains of HIV-1 [79]. In addition, HIV-1-infected individuals who are heterozygous for the $\Delta ccr5$ mutation have around a 2-year delay in their progression to AIDS compared to wildtype controls [30, 50, 69, 117]. These findings highlight the importance of CCR5 as a coreceptor in HIV-1 entry in humans.

In addition to the $\Delta ccr5$ mutation, other genetic polymorphisms have been found in certain chemokine receptors and their corresponding ligands. The CCR2-64I polymorphism causes a conservative valine to isoleucine mutation in CCR2. This mutation does not impact initial HIV transmission. However, individuals harboring this polymorphism progress to AIDS significantly slower (by 2–3 years) as compared to CCR2^{+/+} HIV-1 seroconverters [55, 74, 84, 97]. Moreover, seropositive individuals who carry this allele in combination with the $\Delta ccr5$ allele experience an additive delay in the progression to symptomatic disease [55, 97]. The mechanism for this protective effect is not clear, as CCR2 does not appear to function as a coreceptor for HIV entry on primary cells, and CCR2-64I appears to have normal receptor function [57].

Another notable coreceptor polymorphism is the CCR5 59029 G/A single-nucleotide polymorphism. Both alleles, either G or A at position 59020 in the CCR5 promoter, are very common across racial groups. In one study, individuals selected for the absence of CCR5 $\Delta 32$ or CCR2-64I had a mean time to AIDS for 59029 G/G that was 3.8 years longer ($p=0.004$) than for 59029 A/A individuals [67]. In reporter gene assays, promoter fragments differing in sequence only at 59029 G versus A had differential activity, with the 59029 A promoter being more active than the 59029 G promoter [67], suggesting that 59029 G/G individuals might have decreased transcription and consequently lower expression of CCR5. This is consistent with the observation that CCR5 $\Delta 32$ heterozygotes progress to AIDS more slowly in the absence of therapy, strongly suggesting that CCR5 levels are rate-limiting for HIV infection in vivo.

The SDF-1 3'A allele is a G to A transition at position 809 of the 3'-untranslated region (UTR) of the messenger RNA (mRNA) encoding one of the two chemokine ligands for CXCR4, SDF-1 β . In one report based on pooled seroconverters from three cohorts, a strong association was described between the 3'A/3'A genotype and delayed onset of AIDS [111]. However, in several subsequent reports, no association was found between homozygosity for the SDF-1 3'A allele and retarded progression to disease [13, 47, 66, 68, 74, 107].

Moreover, in an international meta-analysis study, the SDF-1 3'A allele was shown to not be predictive of disease outcome or progression [53].

Finally, individuals whose *CCL3L1* (*MIP1 α P*) gene copy number is above the population median have a reduced risk for acquiring HIV with each stepwise increase in copy number of this gene [44]. Moreover, a gene dose lower than the overall cohort median or the population-specific median is associated with a dose-dependent increased risk of progressing rapidly to AIDS or death. Since *CCL3L1* is a potent ligand for CCR5, it stands to reason that increasing *CCL3L1* copy number leads to a reduction in the proportion of CD4-positive CCR5-expressing T cells and a consequent diminution in the risk of acquiring HIV as well as the rate of progression to AIDS.

4 Coreceptor-Based Antiretroviral Therapy

Since the discovery of chemokine receptors as coreceptors for HIV-1 entry, a significant focus of antiretroviral drug development has been directed toward antagonists of these receptors and their interactions with HIV-1 Env. The structures of some of the important coreceptor inhibitors discussed below are shown in Fig. 2. The HIV coreceptors are especially attractive drug targets, particularly CCR5, which is used by most primary HIV-1 strains. The strongest evidence for the importance of CCR5 in HIV-1 transmission and pathogenesis is the profound resistance to HIV-1 infection of individuals encoding two copies of a nonfunctional *ccr5* gene [60, 88]. The lack of serious immunological defects in humans homozygous for the inactivating 32-bp deletion (CCR5 Δ 32) suggests that CCR5 may be a good therapeutic target.

4.1 CCR5-Based Antiretroviral Therapy

Early attempts at blocking CCR5 involved altered versions of the natural CCR5 ligands, MIP-1 α , MIP-1 β , and RANTES. These protein-based inhibitors blocked CCR5-mediated HIV-1 infection by competing with gp120 for the receptor-binding site, downregulation of receptor expression, and induction of receptor signaling events that altered cellular differentiation and susceptibility to HIV-1. Thus far, the poor pharmacokinetics and bioavailability of these drugs have prevented their development as candidates for antiretroviral therapeutics. However, the newer derivatives of RANTES (such as PSC-RANTES) might have potential as components of microbicides, as they can block vaginal transmission of virus in a rhesus macaque model [56].

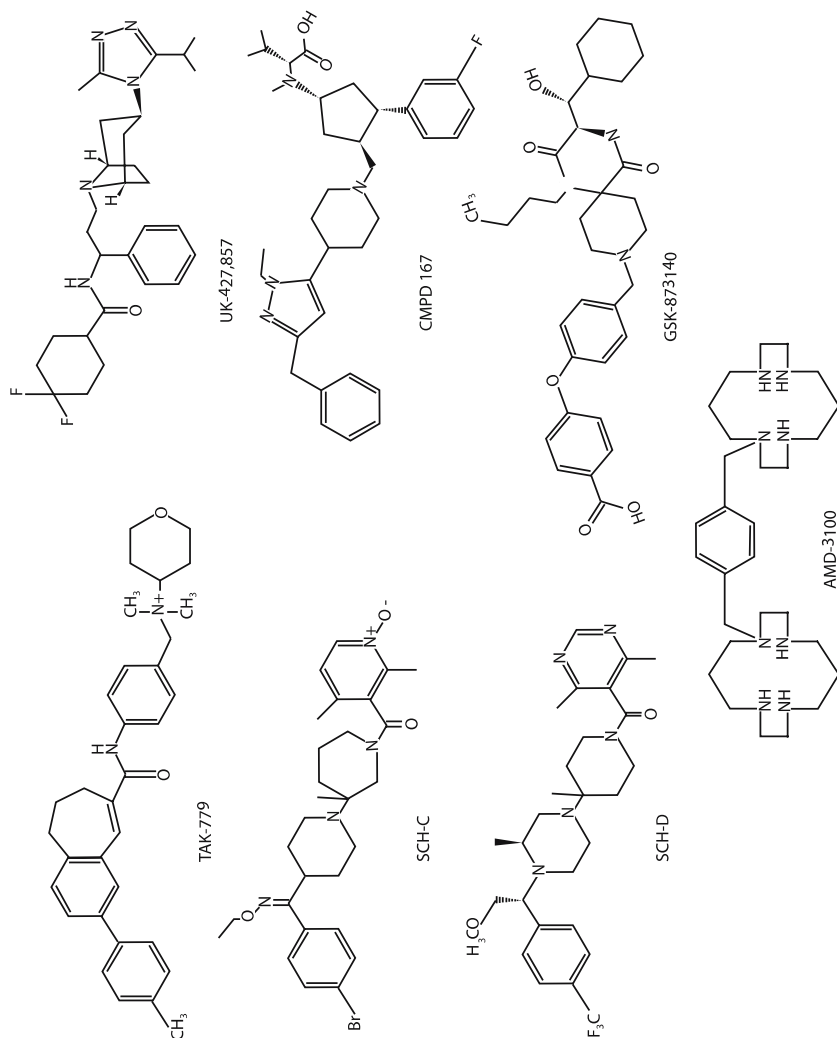


Fig. 2 Structures of CCR5 and CXCR4 inhibitors

4.1.1

TAK-779, TAK-220, and TAK-652

Small molecule inhibitors of CCR5 have proved to have significant potential as anti-HIV-1 therapy. TAK-779 was the first described small-molecule CCR5 inhibitor. This compound blocks CCR5-mediated signaling at nanomolar concentrations without any effects on CCR5 expression [6, 40]. Accordingly,

the compound can block infection by R5- but not X4-tropic HIV-1 strains by interfering in the interaction between gp120 and CCR5. TAK-779 can also block binding to CCR2, which shares sequence homology with CCR5. Therefore, TAK-779 is able to block infection by simian immunodeficiency virus (SIV)_{rcm}, which uses CCR2 as its major coreceptor [113]. Despite its potent antiviral capacity, further development of TAK-779 was abandoned because it was not orally bioavailable and caused irritation at the site of injection [52].

However, a derivative of TAK-779, termed TAK-220, is orally bioavailable and is capable of blocking HIV-1 replication in PBMCs in the low nanomolar range. Specifically, TAK-220 can inhibit R5 HIV-1 isolates with IC₅₀ and IC₉₀ values of 1.1 nM and 13 nM [52, 104]. When administered orally to fasting rats and monkeys at a dose of 5 mg/kg, the bioavailability of TAK-220 was 9.5% and 28.9%, respectively [52]. TAK-220 also inhibits the binding of RANTES and MIP-1 α to CCR5-expressing cells, but does not block binding of MIP-1 β . Owing to its potent activity and favorable pharmacokinetics, TAK-220 is a candidate for clinical development.

Recently, another TAK-779 derivative, TAK-652, was described [5]. TAK-652 selectively inhibited R5 HIV-1 but not X4 HIV-1 replication. This compound was able to potently inhibit the replication of six R5 HIV-1 clinical isolates, including reverse transcriptase- and protease inhibitor-resistant mutants, with mean IC₅₀ and IC₉₀ values of 0.061 nM and 0.25 nM, respectively. In addition, all recombinant HIV-1 strains with seven different subtype (A to G) Env proteins were equally susceptible to TAK-652 with a mean IC₅₀ of 1.0 nM. Single oral doses of TAK-652 (25–100 mg) were safe and well tolerated. TAK-652 showed good oral absorption, and its plasma concentration at 24 h after administration (25 mg) was 8.8 nM.

4.1.2

SCH-C and SCH-D

SCH-C is another small, non-peptide CCR5 antagonist that inhibits ligand binding to CCR5. SCH-C has broad and potent antiviral activity in vitro against primary R5-using HIV-1 isolates, with mean IC₅₀ values between 0.4 and 9 nM [100]. High doses of SCH-C are also able to slightly inhibit ligand binding to CCR2. SCH-C can strongly inhibit replication of an R5-using HIV-1 isolate in vivo in severe combined immunodeficiency (SCID)-hu Thy/Liv mice [100]. The compound has also shown favorable pharmacokinetics in rodents and primates, with an oral bioavailability of 50%–60% and a serum half-life of 5–6 h. Clinical data obtained from an early human trial where SCH-C monotherapy was administered (25 mg twice daily) to HIV-

infected adults for 10 days demonstrated viral load reductions between 0.5 and 1.0 \log_{10} [83]. However the same study found a prolongation of the QT_c interval, suggesting possible adverse cardiac effects at high doses, resulting in cessation of further development of this compound.

SCH-D, a derivative of SCH-C, was shown to have greater potency in vitro and in vivo [92]. In a phase I clinical trial, SCH-D monotherapy with escalating doses of 10–50 mg twice daily over 14 days, no adverse effects were seen. A dose-dependent reduction in plasma viremia was observed, with mean reductions of up to 1.62 \log_{10} [92].

4.1.3

UK-427857 (Maraviroc)

Another CCR5 inhibitor, UK-427857 (recently termed maraviroc), potently blocks cell entry of a range of lab-adapted and primary R5-tropic HIV-1 isolates in vitro ($IC_{90} < 10$ nM) [38]. Despite its potency against R5-tropic isolates, the compound is specific and remains inactive against X4-tropic isolates [38]. UK-427857 blocks gp120 and chemokine ligand binding to CCR5, but does not induce intracellular signaling or trigger receptor internalization [38]. UK-427857 is orally bioavailable, has favorable pharmacokinetics, and did not have any serious adverse effects on healthy volunteers [2]. In a study evaluating the effects of short-term (10 days) UK-427857 monotherapy on HIV viral load in HIV patients, subjects received 25 mg of the drug once a day, 100 mg twice daily, or a placebo for 10 days. The mean CCR5 receptor saturation at the 100-mg dose was in excess of 90% and the mean decrease in viral load was 1.42 \log_{10} from baseline to day 11 [80]. At the 25-mg dose, the mean receptor saturation fell to less than 80% by day 10 and the mean decrease in viral load was 0.42 \log_{10} [80]. The absence of any severe adverse effects combined with the potent antiviral properties of UK-427857 make it an attractive candidate for further development.

4.1.4

CMPD 167

CMPD 167 is a cyclopentane-based compound that can cause rapid and significant decline in plasma viremia in rhesus macaques chronically infected with SIV [108]. Moreover, vaginal application of gel-formulated CMPD 167 prevented vaginal SIV transmission in 2 out of 11 animals, and reduced early viral replication in all 11 animals receiving the drug compared to control-treated animals. These results provide a proof of principle for the use of small-molecule CCR5 inhibitors as a component of a topical microbicide to

prevent HIV-1 sexual transmission. However, CMPD 167 is no longer being developed as an anti-HIV-1 therapeutic agent.

4.1.5

Spirodiketopiperazine-Based Inhibitors

The first spirodiketopiperazine (SDP) derivative, E913, was described in 2001. E913 was active against R5-tropic HIV-1 in vitro, with IC_{50} values of 30–60 nM in PBMCs [64]. Subsequently, a more potent SDP derivative, AK602/GSK-873140, was described [31, 62]. In vitro, AK602 had potent antiviral activity against a wide range of laboratory and primary R5 HIV-1 isolates, including multidrug-resistant strains, with IC_{50} values ranging from 0.1 to 0.6 nM. The variability of this antiviral activity was low (similar to zidovudine), probably owing to the high potency of AK602 as compared with E913 or TAK-779. AK602 binds with high affinity to CCR5 ($K_d=2.9\pm 1.0$) and specifically blocks binding of MIP-1 α even though it preserves RANTES and MIP-1 β binding and their functions, including CC chemokine-induced chemotaxis and CCR5 internalization. In a nonobese diabetic SCID mouse model, AK602 elicited a 2.0 \log_{10} decline in plasma viremia in R5 HIV_{JREFL}-infected mice [63]. In a phase I clinical trial involving multiple-dose escalation in healthy subjects, AK602 was well tolerated and had no severe adverse effects. A phase II clinical trial of AK602 is currently underway.

4.2

CXCR4-Based Antiretroviral Therapy

As mentioned earlier, CXCR4 is the other major coreceptor commonly involved in HIV-1 infection in vivo [43]. CXCR4 is expressed on most CD4-positive lymphocytes as well as on many cell types that lack CD4 [58]. In some but not all individuals who progress to AIDS, viruses evolve to use CXCR4 for entry either in addition to or in place of CCR5 [25]. While this coreceptor switch is not required for disease progression, it does result in expanded viral tropism, since CXCR4 is more commonly expressed on CD4-positive T cells than is CCR5 [12].

4.2.1

Small Molecule CXCR4 Inhibitors

Inhibitors of CXCR4 are also under development, but these drugs may be more difficult to field because CXCR4, and its ligand SDF-1 α , are essential for normal development in the mouse [118]. AMD-3100 is a bicyclam compound that disrupts the interaction of gp120 and CXCR4 and is capable of blocking

replication of CXCR4 utilizing strains *in vitro* and in murine models [34, 48, 90]. AMD-3100 is very specific for CXCR4 and does not interact with any other known CXC- or CC-chemokine receptor [26]. An orally bioavailable AMD-3100 derivative, AMD-070, is currently in clinical trials. Several other CXCR4 antagonists have been described including polyphemusin analogs T22, T134, and T140, as well as a D-Arg peptide referred to as ALX40-4C [36, 75]. ALX40-4C was well tolerated in a phase I clinical trial, suggesting but not proving that CXCR4 inhibition may be tolerated in adults [35].

5

Resistance to Coreceptor Inhibitors

HIV-1 can acquire resistance to coreceptor inhibitors either by changing the mechanism or dynamics of coreceptor engagement or by switching coreceptor usage. The former could involve usage of the same coreceptor in a drug-bound form, increased affinity of the virus for the coreceptor leading to competitive removal of bound inhibitor molecules, or easier triggering of Env trimers resulting in membrane fusion even at low coreceptor density. For R5-tropic viruses, in particular, coreceptor switching (from R5 to X4) is a matter of concern because the presence of X4-tropic viruses is associated with advanced stages of disease and poor prognosis. Many of the studies addressing selection of viruses resistant to coreceptor inhibitors have used cell lines that express only one coreceptor [1, 29, 54, 65, 89]. Consequently, the resistant viruses selected in these studies did not have display coreceptor switching, but rather had alterations in how the virus bound to the original coreceptor.

In cells expressing both CCR5 and CXCR4, coreceptor switching of viruses passaged in the presence of coreceptor antagonists has been observed [73, 106]. For instance, when an R5 virus was passaged in the presence of AD101 (a CCR5 antagonist), the virus evolved to use CCR5 via an inhibitor-independent mechanism [106]. Similar results were observed with SCH-C, another CCR5 inhibitor [72, 106]. Finally, when X4 and R5X4-tropic viruses were passaged in the presence of the CXCR4 antagonist AMD-3100, R5 viruses expanded in the cultures [41, 46]. When CCR5 viruses persisted in the presence of AD101, the selected variants had various amino acid changes in Env, did not use CXCR4 for entry, and were able to replicate efficiently in PBMCs in a CCR5-dependent manner [106]. Despite their newly acquired resistance, these variants used CCR5 with reduced efficiency for entry into cell lines, implying that resistance might be associated with a loss in viral fitness [106].

Another possible mechanism by which HIV-1 could evolve resistance to CCR5 or CXCR4 inhibitors would be to acquire the ability to use alternative

coreceptors for virus entry. Switching to alternative coreceptors has not yet been observed. However, in an experimental setting where CCR5-negative peripheral blood lymphocytes (PBLs) were infected with an R5/X4/CXCR6-tropic HIV-1 isolate in the presence of AMD-3100, CXCR6-positive PBLs were preferentially infected [93]. This suggests that CXCR6 can be used as a coreceptor by HIV-1 on primary cells, and further that in the presence of CCR5 and CXCR4 inhibitors, variants using CXCR6 (or other minor coreceptor) might arise *in vivo* in tissues that express high amounts of minor coreceptors. It is also worth noting that SIV strains isolated from red-capped mangabeys often use CCR2 as their major coreceptor, perhaps because many red-capped mangabeys are CCR5-negative due to a naturally occurring polymorphism in the CCR5 open reading frame [16]. This represents an example of novel coreceptor use in the face of strong selective pressure. Theoretically, this could also occur in humans, though based on the expression patterns and levels of alternative coreceptors in humans we feel that resistance to CCR5 inhibitors in humans will likely involve either altered use of CCR5 by virus, or by coreceptor switching to CXCR4.

6 Impact of Chemokine Receptor Inhibitors on Clinical Monitoring and Treatment

Accurate and timely clinical monitoring is an integral part of any effective antiretroviral therapeutic regimen. Viral genotyping to determine specific resistance-associated mutations is increasingly becoming part of the clinical monitoring process. In the context of coreceptor antagonists, it will be particularly important to assess the relative proportions of R5, R5X4, and X4 viruses in individuals prior to initiating treatment. CCR5 inhibitors may not be beneficial to patients with X4 viruses and vice versa for CXCR4 inhibitors. Moreover, the possibility of coreceptor switching (from R5 to X4) will have to be carefully monitored. Monitoring host factors that might impact CCR5 expression could also prove useful in predicting treatment success, since CCR5 levels can influence the efficacy of coreceptor antagonists [81]. At present, phenotyping tests on cell lines expressing CCR5 or CXCR4 along with CD4 are used to measure the relative levels of coreceptor use on patient samples. However, it is not clear how results from these *in vitro* tests translate to coreceptor use *in vivo*.

As various entry inhibitors move through clinical development, it will be important to determine if particular combinations of entry inhibitors should be used. Coreceptor inhibitors effectively reduce the levels of coreceptor avail-

able to virus. As a result, virus entry is either inhibited or the rate of virus entry is slowed. As a consequence of slower fusion rates, virus becomes more susceptible to the fusion inhibitor T-20 (enfuvirtide) [81]. Enfuvirtide binds to a region on gp41 that becomes exposed as a result of CD4 binding, but that is lost once coreceptor binding triggers membrane fusion [15]. Slower coreceptor binding causes the T-20 binding site to be exposed for a longer period of time, resulting in synergistic inhibition of virus fusion [81, 82]. This finding provides a strong theoretical basis for using coreceptor inhibitors in conjunction with T-20. Moreover, since T-20 can inhibit both R5- and X4-tropic viruses, the use of T-20 in conjunction with a CCR5 inhibitor may limit the evolution of X4-tropic virus strains.

It is also possible that particular combinations of coreceptor inhibitors could be used together effectively, much like nucleoside and nonnucleoside reverse transcriptase inhibitors that are used in combination. In fact, a recent study reported greater synergism of the CCR5 inhibitor AK602/GSK-873140 with CXCR4 inhibitors (such as AMD-3100) than with other classes of anti-HIV drugs [76]. Another recent study indicates that virus resistance to some CCR5 inhibitors may not result in resistance to other CCR5 inhibitors. Specifically, a virus resistant to UK-427857 remained sensitive to CCR5 inhibitors with a different structure [109]. As a result, it may be possible to apply different classes of CCR5 inhibitors in combination—or sequentially—should resistance to one inhibitor arise. In conclusion, coreceptor antagonists constitute an important and valuable new class of drugs, and with careful monitoring and synergistic use, they can be successfully incorporated into an efficacious antiretroviral regimen.

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A Viral Conspiracy: Hijacking the Chemokine System Through Virally Encoded Pirated Chemokine Receptors

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Abstract Several herpesviruses and poxviruses contain genes encoding for G protein-coupled receptor (GPCR) proteins that are expressed on the surface of infected host cells and/or the viral envelope. Most of these membrane-associated proteins display highest homology to the subfamily of chemokine receptors known to play a key role in the immune system. Virally encoded chemokine receptors have been modified through evolutionary selection both in chemokine binding profile and signaling capacity, ultimately resulting in immune evasion and cellular reprogramming in favor of viral survival and replication. Insight in the role of virally encoded GPCRs during the viral lifecycle may reveal their potential as future drug targets.

1 Chemokine System

The chemokines and their cognate receptors play a key role in the immune system during homeostasis and inflammation by coordinating leukocyte migration, activation, degranulation, and differentiation. In addition, the chemokine system is involved in organogenesis, angiogenesis, and directing metastasis and growth of tumor cells (Murphy et al. 2000). The mammalian chemokine system (e.g., human, mouse, and rat) constitutes of approximately 45 chemokine ligands and 20 chemokine receptors (Murphy 2002).

Chemokines are a family of small proteins that adopt a similar tertiary folding, even in cases of low overall sequence identity (varying from 20% to 95%). They are characterized by a flexible amino-terminal domain, followed by a conserved core region consisting of a so-called N-loop, three anti-parallel β -strands, and a carboxyl-terminal α -helix, stabilized by disulfide bonds between four conserved cysteine residues (Mizoue et al. 1999). Four subclasses of chemokines (i.e., CC, CXC, CX3C, and XC) have been recognized on the basis of the number and sequential spacing of the first two conserved cysteine residues that are situated near the amino terminus (Zlotnik and Yoshie 2000). In addition, chemokines can be functionally classified into inducible (inflammatory) and homeostatic (constitutively expressed) chemokines, mediating inflammation-directed or basal (homing) leukocyte trafficking, respectively (Proudfoot 2002).

Recruitment of specific leukocyte populations by chemokines is essentially determined by the spatiotemporal expression of selected chemokine receptors, which belong to the membrane-associated G protein-coupled receptor (GPCR) family. Chemokine receptors are classified (i.e., CCR1–11, CXCR1–6, CX3CR1, and XCR1) according to their ability to bind a specific subclass of chemokines (Murphy 2002). Chemokine receptors are not only expressed on leukocytes but also on endothelial, smooth muscle, epithelial, stromal, and neural cells (Onuffer and Horuk 2002). Interestingly, most inflammatory chemokines display a high level of promiscuity by binding several chemokine receptor subtypes, and vice versa. In contrast, homeostatic chemokines are generally more specific, each interacting with a single chemokine receptor subtype (Proudfoot 2002). Given the prominent role of chemokine receptors in regulating intracellular signaling in response to chemokine ligands, these receptors are the most promising targets for immunomodulatory therapeutic interventions (Onuffer and Horuk 2002; Gao and Metz 2003). Interestingly, such receptors are also employed by several viruses in order to subvert the immune system and/or redirect intracellular signaling for their own benefit (Alcami 2003).

2

Viral Immune Evasion

Viruses are small, infectious, parasitic pathogens that (ab)use the host cell metabolism and “consume” cellular biomolecule resources for their replication. An important strategy which enables viruses to replicate efficiently in a host cell is to interfere with recognition and subsequent elimination of the infected cell by the immune system. To this end, distinct viruses have employed different strategies. For instance, large double-stranded DNA viruses, such as herpesviruses and poxviruses, encode viral mimics of host cytokines and chemokines, as well as their soluble binding proteins and/or membrane-associated receptors, to subvert the immune system (Alcami 2003). The viral genes encoding these proteins have probably been derived from the genomes of the viral host during evolution. Of particular interest are the viral genes that code for membrane-associated GPCRs, as these proteins are localized at the boundary of the extracellular and intracellular milieu, and transmit signals from the outside to the inside of the cell. The amino acid sequences of the virally encoded GPCRs (vGPCRs) are generally highly diverged between and within virus subfamilies. This suggests that these GPCRs have distinct and specialized functions that are optimized for different biological properties of each virus. Nonetheless, the majority of vGPCRs display highest sequence similarity to the subfamily of chemokine receptors (Fig. 1, Tables 1 and 2). Some vGPCRs are indeed responsive to chemokines, whereas for others no endogenous ligands have been identified and remain “orphan”. Importantly, in contrast to their cellular homologs, a number of vGPCRs signal ligand-independently (i.e., constitutively). Constitutive GPCR signaling is of major significance as revealed by several pathologies associated with activating GPCR mutations (Seifert and Wenzel-Seifert 2002). This constitutive activity of many vGPCRs, together with the current awareness that chemokines and their receptors play prominent roles in inflammatory pathologies and tumor metastases (Proudfoot 2002), suggests that vGPCRs may be key players in virus-associated diseases.

3

Herpesvirus-Encoded GPCRs

Herpesviruses have been isolated from a wide variety of vertebrates and are generally characterized by their strict specificity for a single host species (Davison 2002). Herpesviruses have been classified into three subfamilies, the α -, β -, and γ -herpesvirinae, on the basis of their biological properties,

Table 1 Herpesvirus-encoded GPCRs

Subfamily	Genus	Species		vGPCR	Cellular homolog ^a	% ^b	
α-Herpesvirinae	<i>Simplexvirus</i>	<i>Human herpesvirus 1</i>	HHV-1	-	-	-	
		<i>Human herpesvirus 2</i>	HHV-2	-	-	-	
		<i>Human herpesvirus 3</i>	HHV-3	-	-	-	
β-Herpesvirinae	<i>Varicellovirus</i>	<i>Cercopithecine herpesvirus 8</i> (Rhesus cytomegalovirus)	CeHV8	UL33	CCR10	20	
				UL78	CXCR1	14	
	<i>Cytomegalovirus</i>				Rh214	CCR5	22
					Rh215	CXCR1	22
					Rh216	CCR1	21
					Rh218	CXCR3	22
					Rh220	CX3CR1	34
					ORF3	CCR4	22
					ORF4	CCR3	25
					ORF5	CCR2	22
				ORF6	CXCR1	21	
				ORF7	CXCR6	21	
				UL33	CCR3	20	
				UL78	CXCR1	13	
				US27	CXCR3	23	
				US28	CX3CR1	38	
				UL33	CCR10	21	
				UL78	Somatostatin R3	12	
				US27	CXCR3	23	
				US28	CX3CR1	36	

Table 1 (continued)

Subfamily	Genus	Species	MCMV	vGPCR	Cellular homolog ^a	% ^b
γ -Herpesvirinae	<i>Roseolovirus</i>	<i>Murid herpesvirus 1</i> (Mouse cytomegalovirus)	MCMV	M33	CCR10	21
		<i>Murid herpesvirus 2</i> (Rat cytomegalovirus)	RCMV	M78	Opiate R-like 1	13
		<i>Tupaia herpesvirus 1</i> (Tupaia herpesvirus)	TCMV	R33	CCR10	23
		<i>Human herpesvirus 6a</i>	HHV-6a	R78	CCR10	15
		<i>Human herpesvirus 6b</i>	HHV-6b	T33	CCR10	23
		<i>Human herpesvirus 7</i>	HHV-7	T78	Formyl peptide R-like	12
		<i>Human herpesvirus 7</i>	HHV-7	U12	CCR10	19
	<i>Lymphocryptovirus</i>	<i>Callitrichine herpesvirus 3</i>	CaHV3	U51	Cysteinyl leukotriene R2	16
		<i>Human herpesvirus 4</i> (Epstein-Barr virus)	CeHV15	U12	CCR10	19
		<i>Human herpesvirus 4</i> (Epstein-Barr virus)	HHV-4	U51	Cysteinyl leukotriene R2	16
		<i>Alcelaphine herpesvirus 1</i>	AHV1	U12	CX3CR1	20
		<i>Porcine lymphotropic herpesvirus 1</i>	PLHV1	U51	CCR2	16
		<i>Porcine lymphotropic herpesvirus 2</i>	PLHV2	ORF6	CXCR5	13
<i>Rhadinovirus</i>	<i>Porcine lymphotropic herpesvirus 3</i>	PLHV3	BILF1	CXCR4	14	
	<i>Bovine herpesvirus 4</i>	BHV4	BILF1	CXCR4	15	
	<i>Cercopithecine herpesvirus 17</i>	CeHV17	A5	CCR3	15	
	<i>Human herpesvirus 8</i> (KS-associated herpesvirus)	HHV-8	A5	CXCR2	14	
	<i>Human herpesvirus 8</i> (KS-associated herpesvirus)	HHV-8	A5	CXCR2	15	
	<i>Human herpesvirus 8</i> (KS-associated herpesvirus)	HHV-8	A5	CCR10	13	
	<i>Human herpesvirus 8</i> (KS-associated herpesvirus)	HHV-8	-	-	-	
	<i>Human herpesvirus 8</i> (KS-associated herpesvirus)	HHV-8	ORF74	CXCR1	24	
<i>Human herpesvirus 8</i> (KS-associated herpesvirus)	HHV-8	ORF74	CXCR2	26		

Table 1 (continued)

Subfamily	Genus	Species		vGPCR	Cellular homolog ^a	% ^b
		<i>Macaca fuscata rhadinovirus</i>	MFRV	ORF74	CXCR1	24
		<i>Murid herpesvirus 4</i>	MuHV4	ORF74	CCR4	20
		<i>Saimiriine herpesvirus 2</i> (<i>Herpesvirus saimiri</i>)	HVS2	ORF74	CXCR2	24
		<i>Equid herpesvirus 2</i>	EHV2	ORF E1	CCR3	51
				ORF E6	CCR10	16
				ORF74	CXCR5	22
				ORF E1	CCR3	51

^a Nearest cellular homologs are identified by basic local alignment search tool (BLAST) analysis of each vGPCR on the human protein sequence reference database at NCBI, subsequently followed by ClustalW analysis

^b Percentage amino acid identity

Table 2 Chordopoxvirus-encoded GPCRs

Genus	Species		vGPCR	Cellular homolog ^a	% ^b
<i>Avipoxvirus</i>	<i>Fowlpox virus</i>	FPV	FPV021	GPCR1	32
			FPV027	GPCR1	29
			FPV206	EBV-induced GPCR2	35
<i>Canarypox virus</i>	CNPV		CNPV039	GPCR1	34
			CNPV045	GPCR1	70
			CNPV277	EBV-induced GPCR2	36
			CNPV315	Chemokine-like R1	28
<i>Capripoxvirus</i>	<i>Goatpox virus</i>	GTPV	-	-	-
		<i>Sheeppox virus</i>	SPPV	CCR8	40
		<i>Lumpy skin disease virus</i>	LSDV	CCR8	39
<i>Molluscipoxvirus</i>	<i>Molluscum contagiosum virus</i>	MOCV	-	-	-
<i>Orthopoxvirus</i>	<i>Camelpox virus</i>	CMPV	-	-	-
	<i>Cowpox virus</i>	CPV	-	-	-
	<i>Ectromelia virus</i>	ECT	-	-	-
	<i>Monkeypox virus</i>	MPV	-	-	-
	<i>Vaccinia virus</i>	VV	-	-	-
	<i>Variola virus</i>	VAR	-	-	-
<i>Parapoxvirus</i>	<i>Bovine papular stomatitis virus</i>	BPSV	-	-	-
	<i>Orf virus</i>	ORFV	-	-	-
<i>Suipoxvirus</i>	<i>Swinepox virus</i>	SPV	SPV146	CCR8	34
<i>Yatapoxvirus</i>	<i>Yaba monkey tumor virus</i>	YMTV	7L, 145R	CCR8, CCR8	51, 39
	<i>Yaba-like disease virus</i>	YLDV	7L, 145R	CCR8, CCR8	53, 44
Unclassified	<i>Mule deer pox</i>	DPV83	gp013, gp162	CCR8, CCR4	42, 32

^a Nearest cellular homologs are identified by basic local alignment search tool (BLAST) analysis of each vGPCR on the human protein sequence reference database at NCBI, subsequently followed by ClustalW analysis

^b Percentage amino acid identity

genome organization, and deduced amino acid sequence similarity between conserved gene orthologs (McGeoch et al. 2000). About 43 genes are shared between most members of the three herpesvirus subfamilies (Davison et al. 2002). These so-called core genes encode proteins that contribute to universal processes such as viral DNA replication and packaging into the viral capsid. During the course of coevolution with their host, individual herpesvirus subtypes acquired unique genes through pirating or gene duplication. Among these so-called accessory genes are genes that allow the virus to subvert the host immune response.

3.1

β -Herpesvirinae

The β -Herpesvirinae subfamily comprises two genera, namely *Roseolovirus* and *Cytomegalovirus* (CMV). Hitherto, four members of the *Roseolovirus* genus have been isolated, three of which are found in man. In contrast, host-specific cytomegaloviruses have been isolated from a wide variety of mammals from the orders Rodentia (e.g., mouse and rat), Scandentia (e.g., tree shrew), and Primates (e.g., rhesus macaque, African green monkey, chimpanzee, and human). CMV genomes are the largest of all herpesviruses (195–241 kb), whereas genomes of roseoloviruses are somewhat smaller (153–162 kb). The genomes of roseoloviruses and CMVs, share extensive characteristics, including position and orientation of large blocks of genes (Neipel et al. 1991; Gompels et al. 1995; Nicholas 1996; Weir 1998).

3.1.1

Roseoloviruses

Three distinct species of *Roseolovirus* have been isolated from peripheral blood of humans. Human herpesvirus (HHV)-6A was first isolated from peripheral blood mononuclear cells derived from adults with acquired immunodeficiency syndrome (AIDS) and displaying lymphoproliferative disorders (Salahuddin et al. 1986). In addition, a second highly related variant of HHV-6, sharing an overall nucleotide sequence identity of 90% (Dominguez et al. 1999), but displaying distinct biological properties, was formally recognized and named HHV-6B. The third human roseolovirus, HHV-7, is highly related to the HHV-6 variants with respect to genome organization as well as sequence, with HHV-6 and HHV-7 genes sharing deduced amino acid identities between 22% and 75% (Nicholas 1996; Dominguez et al. 1999).

Primary infection with HHV-6B occurs between 6 and 12 months of age, whereas infection with HHV-7 occurs at a later time, though often within

the first 4 years of childhood (De Bolle et al. 2005). The time of HHV-6A infection is still unknown, but is thought to occur following infection with HHV-6B. As a consequence, roseoloviruses are ubiquitously spread in the general adult population, usually reaching a seroprevalence of greater than 95%. Primary infection with HHV-6b or HHV-7 results in an acute febrile illness that is in some cases followed by the appearance of a mild skin rash on the face and trunk (i.e., exanthem subitum or roseola infantum; Yamanishi et al. 1988; Tanaka et al. 1994). Interestingly, infection with HHV-6A is usually asymptomatic (Dewhurst et al. 1993; Stodberg et al. 2002; Freitas et al. 2003). Clinical complications of (primary) HHV-6 and -7 infections include febrile seizure, but also meningoencephalitis, encephalopathy, and multiple sclerosis (for a review see De Bolle et al. 2005). Importantly, primary HHV-7 infection can reactivate HHV-6 (Frenkel and Wyatt 1992; Katsafanas et al. 1996; Tanaka-Taya et al. 2000). In contrast, reactivation of HHV-6 in healthy children has been reported to occur usually without clinical consequences (Caserta et al. 2004).

Roseoloviruses are (T-)lymphotropic and replicates most efficiently in vitro CD4⁺ T lymphocytes (Takahashi et al. 1989), but can also infect various other cell types in vitro (De Bolle et al. 2005). HHV-6B and HHV-7 replicate predominantly in salivary glands, with viral shedding into saliva being the major route of virus transmission (Harnett et al. 1990). After primary infection, roseoloviruses persist latently in the host in monocytes and early bone marrow progenitor cells (De Bolle et al. 2005). In healthy individuals, the pathogenic potential of roseoloviruses is kept under control by the immune system. However, both HHV-6 and HHV-7 can reactivate under immunosuppressive conditions (e.g., in AIDS patients and transplant recipients).

The genome of roseoloviruses contains two GPCR-encoding genes, i.e., *U12* and *U51*. The *U12* and *U51* genes are situated on similar positions and have a similar orientation as the *UL33* and *UL78* genes of CMVs, respectively. The *U12* and *U51* genes of HHV-6 are expressed with similar late and early kinetics (Isegawa et al. 1998; Menotti et al. 1999). Temporal expression profiles of the HHV-7-encoded GPCRs have not been reported yet, but are presumably similar to those observed for the HHV-6- and CMV-encoded receptors.

U12 and *U51* display the highest amino acid sequence identity to human chemokine receptors. Although the shared sequence identity between these virally encoded receptors and the cellular receptors is rather limited (<20%), both *U12* and *U51* are highly responsive to a variety of CC chemokines. HHV-6B *U12* displays high binding affinity for CCL5, CCL4, and CCL2, and lower affinity for CCL3 (Fig. 2). Moreover, these CC chemokines induce *U12*-mediated increases in intracellular Ca²⁺ levels in stably transfected K562 cells, via pertussis toxin-insensitive signaling pathways (Isegawa et al. 1998). In-

terestingly, the HHV-7-encoded U12 displays a different chemokine binding profile than HHV-6B U12 and induces intracellular Ca^{2+} signaling in stably transfected K562 cells in response to CCL17, CCL19, CCL21, and CCL22 (Fig. 2), but not CCL1, CCL2, and CCL5 (Nakano et al. 2003; Tadagaki et al. 2005). In addition, expression of HHV-7 U12 in Jurkat cells induces chemotaxis of these cells towards CCL19 and CCL21 (Tadagaki et al. 2005). Interestingly, CCL17 and CCL22 are unable to attract U12-expressing Jurkat cells. Hence, besides CCR7 and its cognate ligands, U12 expression on the surface of HHV-

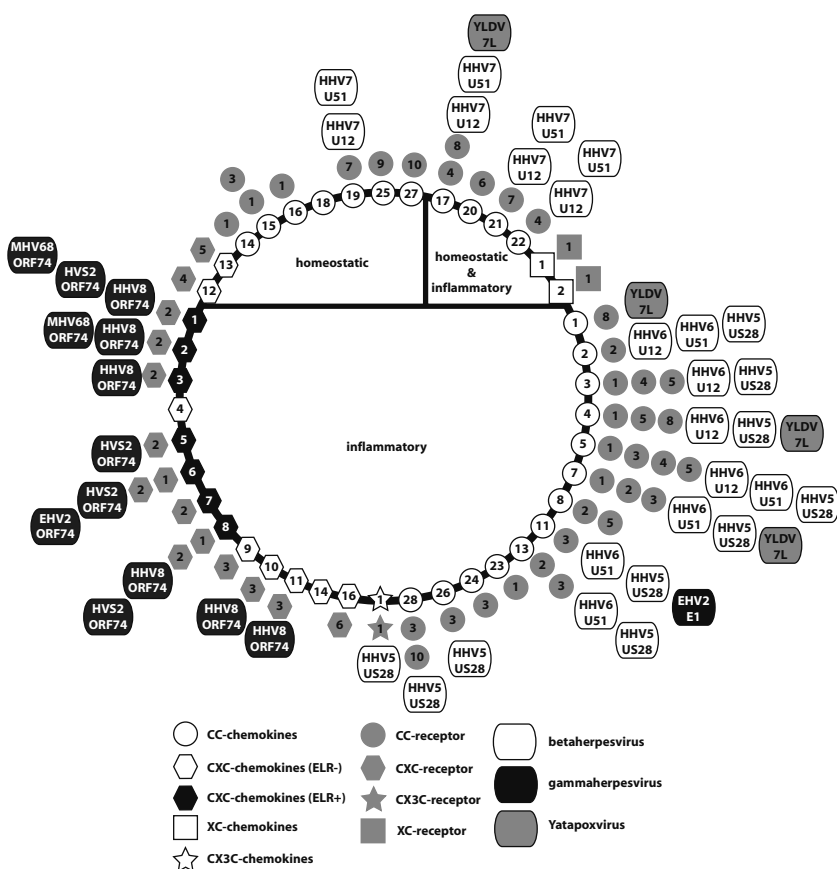


Fig. 2 Chemokine binding of vGPCRs. Homeostatic as well as inflammatory chemokines bind a specific subset of herpesvirus-encoded GPCRs. Chemokines are depicted on the *inner circle*. Their cognate chemokine receptors are displayed next to them, followed by vGPCRs from the β -herpesvirus, γ -herpesvirus, and yatapoxvirus families that were shown to bind the respective chemokines

7-infected T lymphocytes may also support homing of these cells into lymph nodes, which may contribute to viral dissemination.

Despite its low sequence similarity with chemokine receptors, the HHV-6-encoded U51 displays an overlapping chemokine binding profile with HHV-6 U12. This protein binds CCL5 and CCL2 with high affinity, but is unable to bind CCL3. In addition, HHV-6 U51 efficiently binds CCL7, CCL11, CCL13, and HHV-8-encoded viral macrophage inflammatory protein (vMIP)-II (Milne et al. 2000). Interestingly, when transfected into adherent cells (HEK293 or 143tk cells), HHV-6 U51 accumulates predominantly intracellularly in the endoplasmic reticulum and cannot be detected on the cell surface. In contrast, U51 is readily detectable on the cell surface of transfected T lymphocytic cell lines as well as on HHV-6-infected cord blood mononuclear cells *in vitro* (Menotti et al. 1999). Hence, expression of U51 at the cell surface appears to be cell type-specific, and requires trafficking functions that are apparently present in activated T cells and monocytes, but not in adherent cell types. Interestingly, stable expression of HHV-6 U51 in epithelial cells results in morphological alterations consisting of increased spreading and flattening of the cells and downregulation of CCL5 expression and secretion (Milne et al. 2000). The latter may contribute to immune evasion of the infected cells. The mechanism(s) by which U51 modulates epithelial cell functioning remains to be elucidated, but may include constitutive and/or autocrine U51-mediated signaling as observed for other vGPCRs (Milne et al. 2000). Moreover, in view of the impaired trafficking of U51 to the cell membrane as observed in some adherent cell lines, U51 cell membrane expression needs to be confirmed in epithelial cells.

Despite the low amino acid sequence identity between HHV-7 U51 and U12, these proteins induce intracellular Ca^{2+} elevation in response to the same chemokines (Tadagaki et al. 2005). In contrast, however, U51-expressing Jurkat cells were not able to migrate towards any of the tested chemokines (Tadagaki et al. 2005).

3.1.2

Cytomegaloviruses

Human CMV (HCMV) or HHV-5 is a widely spread virus, with a seroprevalence ranging from 50% to 80%, and it is able to persist lifelong in a latent form. Primary infection of immunocompetent hosts is usually asymptomatic. In contrast, primary infection or reactivation of the virus in immunocompromised hosts, such as the developing fetus, transplant recipients, or AIDS patients, can have severe implications and be fatal (Zhou et al. 1996). Common complications after HCMV infection include damage of liver, brain, retina,

and lung (interstitial pneumonitis; Landolfo et al. 2003). Coinfection of HCMV with *human immunodeficiency virus* (HIV) has been shown to accelerate progression to AIDS and dementia in HIV patients (Webster 1991; Kovacs et al. 1999). Increasing evidence suggests that HCMV may also contribute to the development of vascular diseases, e.g., atherosclerosis, restenosis, and vascular allograft rejection (Zhou et al. 1995; Burnett 2001).

CMV primarily infects monocytes, smooth muscle cells, and endothelial and epithelial cells of the upper gastrointestinal, respiratory, or urogenital tracts (Landolfo et al. 2003), and disseminates throughout the body by latently infected monocytes in the blood (Streblow and Nelson 2003). Allogenic stimulation of these monocytes induces differentiation into macrophages, which in latently infected cells is accompanied by reactivation of HCMV leading to the release of infectious virions (Streblow and Nelson 2003). CMV, like other β - and γ -herpesvirus subfamilies, appears to have “pirated” genes encoding key regulatory cellular proteins, showing highest homology to chemokine receptors (Murphy 2001; Sodhi et al. 2004b). HCMV encodes four GPCRs referred to as US27, US28, UL33, and UL78 (Chee et al. 1990). Two GPCR-encoding genes, i.e., *UL33* and *UL78*, are conserved with respect to position and orientation in the genomes of all sequenced β -herpesviruses. Possibly, these genes have been captured from an ancient host species by an ancestral β -herpesvirus. Interestingly, except for the intronless *UL33* genes of rhesus macaque CMV (RhCMV or *cercopithecine herpesvirus 8*) and rat CMV (RCMV), all *UL33* genes consist of two exons interrupted by a single intron. CMV-encoded *UL33* orthologs are fairly well conserved and display deduced amino acid sequence identities varying from 35% to 68% (Fig. 1). In contrast, amino acid sequences have diverged considerably between the *UL78* orthologs of individual CMV species (12%–54% sequence identity), suggesting a reduced selective pressure on this protein during the course of evolution.

Intriguingly, CMVs infecting host species of the primates (i.e., human, chimpanzee, African green monkey, and rhesus macaque) have pirated an additional GPCR-encoding gene cluster compared with CMVs that infect species from the Glires (i.e., mouse and rat) or Scandentia (i.e., tree shrew) orders. This gene cluster is located in the unique short (US) region of the CMV genome, which is not present in nonprimate CMV genomes, and consists of two adjacent genes in HCMV and chimpanzee CMV (CCMV) (*US27* and *US28*), and five juxtaposed genes in RhCMV and simian CMV (SCMV) (Table 1). Interestingly, the divergence in sequence and number of genes in this gene cluster parallels the coevolution of primate CMVs with two different host species families, with HCMV and CCMV infecting members of the Hominidae family (human and chimpanzee, respectively) and RhCMV and SCMV infecting Old World monkeys (rhesus macaque and African green

monkey, respectively). In addition, the highest amino acid sequence identities within proteins encoded by this gene cluster as well as common chemokine binding profiles are observed between rh220, cUS28, and hUS28 (34%–71%), suggesting that these genes have emerged through duplication and rapid diversification of an ancestral US28-like gene.

The genes encoding US28 and UL78 are expressed with early kinetics, whereas US27 and UL33 genes are transcribed with late kinetics (Mocarski 1996). The late and early expression kinetics of UL33 and UL78, respectively, are similar to those of their corresponding U12 and U51 counterparts in *Roseolovirus*. In addition, CMV-encoded GPCRs are constituents of the virion, with UL33 (Margulies et al. 1996), UL78 (Oliveira and Shenk 2001), US28, rhUS28.5 (Penfold et al. 2003), and presumably US27 being expressed on the viral envelope. Colocalization of US28 (Fraile-Ramos et al. 2001), US27, and UL33 (Fraile-Ramos et al. 2002) with two major HCMV envelope glycoproteins, i.e., glycoprotein B and H, on virus-wrapping membranes of endocytotic vesicles in transfected or HCMV-infected cells, indicates that these GPCRs are incorporated in the viral envelope.

Although expression of CMV-encoded receptors seems not to be essential for infection of permissive cells in vitro, deletion of either R33/M33 (Davis-Poynter et al. 1997; Beisser et al. 1998) or R78/M78 (Oliveira and Shenk 2001; Kaptein et al. 2003) has significant impact on viral dissemination in vivo. A reduced replication in salivary glands and a lower mortality in infected animals is apparent in in vivo studies using recombinant RCMV and mouse CMV (MCMV) strains, lacking the corresponding UL33 and UL78 genes (see Vink et al. 2001 for references), underlining the importance of these receptors in the pathogenesis of infection.

The HCMV-encoded receptor US28 is so far the best characterized HCMV-encoded GPCR. It possesses a large spectrum chemokine-binding profile, including binding of a number of inflammatory CC as well as CX3CL chemokines (Gao and Murphy 1994; Kuhn et al. 1995; Kledal et al. 1998; Penfold et al. 2003; Fig. 2). This broad-spectrum binding profile suggests that US28 could act as a chemokine scavenger and thereby aid in subversion of the immune system (Kuhn et al. 1995; Kledal et al. 1998). CC chemokines, which are shown to bind to US28, induce increasing levels of intracellular calcium, activation of mitogen-activated protein kinase (MAPK) and focal adhesion kinase (FAK). Interestingly, infection of smooth muscle cells with CMV leads a US28-dependent migration. Hence, activation of the former signaling pathways by US28 may provide a molecular basis for the involvement of HCMV in the progression of atherosclerosis. These effects appear to be primarily $G\alpha_{12/13}$ mediated and involve activation of tyrosine kinase-linked signaling pathways (Streblov et al. 2003).

Despite the sequence similarity to chemokine receptors and US28, US27 does not seem to interact with chemokines. Therefore, this receptor is still classified as an orphan receptor. Interestingly, US28 is able to alter cellular signaling in a constitutive manner when expressed in COS-7 cells and after HCMV infection (Casarosa et al. 2001; Casarosa et al. 2003a). US28 is considered a versatile signaling device since it is able to activate multiple signaling networks in a constitutively active manner via activation of effectors and transcription factors within infected cells [i.e., InsP production, nuclear factor (NF)- κ B, cAMP-response element (CRE), and nuclear factor activated T cell (NFAT)]. US28 shows promiscuous G protein coupling, through primarily G_q , G_s , and G_{12} proteins (Casarosa et al. 2001; Waldhoer et al. 2002; Casarosa et al. 2003a; Minisini et al. 2003). The chemokine receptor homologs, on the other hand, do not display—or display only limited—ligand-independent signaling and activate primarily $G_{i/o}$ proteins (Offermanns 2003). Interestingly, US28-mediated, constitutive signaling potentiates chemokine-induced signaling of the G_i -coupled CCR1 (Bakker et al. 2004). Since HCMV primarily infects leukocytes, smooth muscle, and endothelial cells—in which chemokine receptors play prominent roles—HCMV-encoded receptor expression may alter ligand-induced signaling via these receptors and contribute to the CMV-induced pathology.

US28-mediated signaling (constitutive or ligand-dependent) is accompanied by G protein receptor kinases (GRK)-mediated phosphorylation of the C-terminal tail, which is followed by a rapid constitutive, agonist-independent endocytosis into perinuclear endosomes and recycling of the receptor US28. The observed internalization of US28 is not dependent on the constitutive activity but involves the C-terminal tail, which serves as a docking site for β -arrestins as well as other scaffolding proteins (Brady and Limbird 2002; Heydorn et al. 2004; Lefkowitz and Shenoy 2005). Binding of these proteins appears important for intracellular signaling and/or receptor trafficking. Interestingly, however, US28 internalization via clathrin-coated pits or lipid rafts is independent of β -arrestins but requires AP-2 adaptor complex proteins and dynamin (Fraile-Ramos et al. 2003; Droese et al. 2004).

CC chemokines do not modulate the constitutive signaling of US28 in the InsP, NF- κ B, and CRE assays (Casarosa et al. 2001; McLean et al. 2004), while CX3CL1 acts as inverse agonist in these assays (Casarosa et al. 2001). When US28 loses its capacity to constitutively internalize upon deletion of its C-terminal tail, the CC chemokines, as well as CX3CL1, activate these signaling pathways instead (Waldhoer et al. 2003). Thus, differential modulation of constitutive US28 internalization kinetics and the cellular context in which US28 is expressed determine the efficacy of chemokines acting at this receptor.

The broad chemokine binding profile in combination with rapid and constitutive internalization kinetics (Fraile-Ramos et al. 2001) allows US28 to sequester inflammatory chemokines efficiently from the environment of HCMV-infected cells. As a consequence, the recruitment of leukocytes—and therefore the inflammatory response—may be hampered (Fig. 3; Bodaghi et al. 1998; Billstrom et al. 1999; Randolph-Habecker et al. 2002).

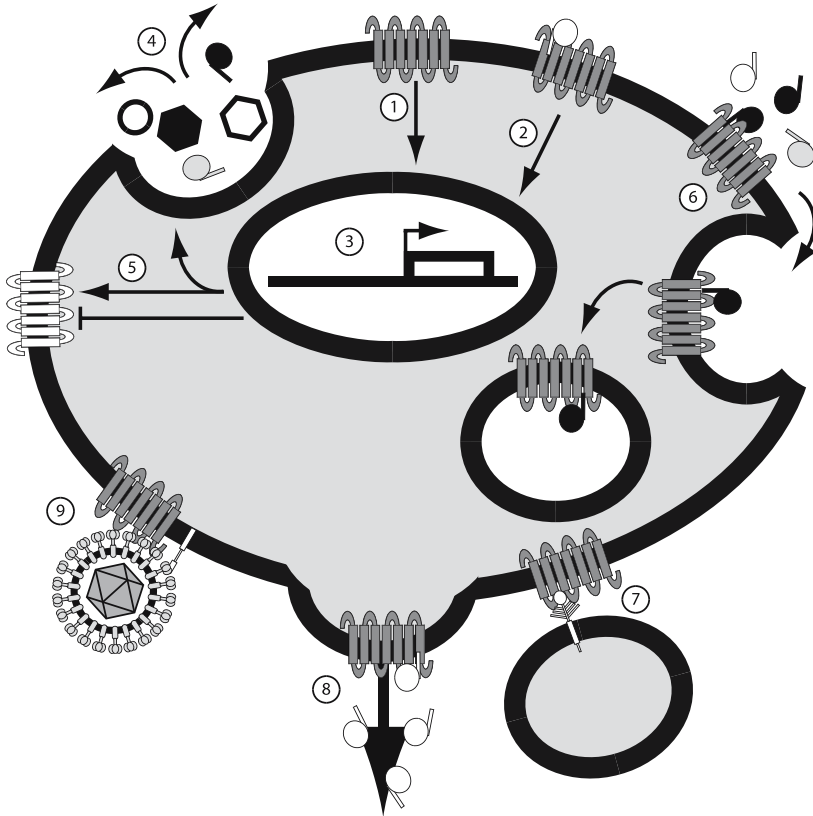


Fig. 3 Suggested roles for vGPCRs. Constitutive (1) or ligand-dependent signaling (2) of a vGPCR results in up-/downregulation of gene expression (3), including autocrine and/or paracrine (angiogenic) factors (4) as well as cellular GPCR proteins (5). Due to their broad-spectrum chemokine binding profile, vGPCRs may serve as chemokine decoy receptors by internalizing bound chemokine, thereby limiting the immune response (6). Binding of vGPCRs (US28) to membrane-associated CX3CL1 facilitates cell-cell adhesion (7). vGPCR-mediated chemotaxis in response to chemokine stimulation may increase viral dissemination and other pathogenesis (8). In addition, vGPCRs may act as HIV coreceptor (9)

The constitutive activity of US28 can be inhibited by a small nonpeptidergic inverse agonist VUF2274 (Casarosa et al. 2003b) derived from a CCR1 antagonist (Hesselgesser et al. 1998). VUF2274 dose-dependently inhibits US28-mediated constitutive activation of phospholipase C in both transfected and HCMV-infected cells, and US28-mediated HIV entry. Importantly, VUF2274 inhibits CCL5 binding in a noncompetitive manner, thus acting as an allosteric modulator. Although a gain in affinity is required, these inverse agonists will serve as valuable tools to further determine the role of (constitutive activity of) US28 in CMV infection.

For UL33, like US28, constitutive signaling has been reported in transfected and infected cells, while no signaling has been detected for UL78 (Casarosa et al. 2003a). Both UL33 and UL78 still remain orphan. In addition, R33 and M33 are able to signal in a constitutively active manner (Gruijthuijsen et al. 2002; Waldhoer et al. 2002). The constitutive signaling of R33 differs from that of UL33 in that R33 is only able to couple to $G_{i/o}$ and G_q , while UL33 shows activation of the G_q , $G_{i/o}$, and G_s classes.

Taken together, CMVs may effectively use their virally encoded receptors to orchestrate multiple signaling networks within infected cells. Importantly, the immediate-early (IE) promoter of HCMV, constituting the genetic switch for progression of viral infection and reactivation, contains four consensus CRE and four NF- κ B binding sites. Binding of cognate transcription factors to these sites is required for efficient transactivation of the immediate early promoter (Hunninghake et al. 1989; Keller et al. 2003; DeMeritt et al. 2004; Lee et al. 2004). Moreover, NF- κ B is a ubiquitously expressed transcription factor that plays a critical role in the regulation of inducible genes in immune response and inflammatory events associated with e.g., atherosclerosis (Chen et al. 1999). NFAT is an important regulator of immune responses, developmental processes, and angiogenesis (Horsley and Pavlath 2002). It is suggestive to propose that US28 and UL33, through constitutive activation of these transcription factors, induces expression of viral IE proteins and cellular proteins, leading to alteration of the immune response in favor of viral survival and spreading and may contribute by this means to the onset, progression, or enhancement of inflammatory disorders. Further studies in cellular systems more relevant to HCMV infection are required to elucidate the role of these receptors in CMV pathology.

3.2

γ -Herpesvirinea

The γ -Herpesvirinea family is subdivided into the *Lymphocryptovirus* and *Rhadinovirus* genera (Table 1). Although γ -herpesviruses have cell transform-

ing potential, their associated malignancies are mostly seen in the context of immune suppression, such as HIV coinfection or iatrogenic immune suppression, suggesting these viruses are normally “controlled” by the immune system.

3.2.1

Rhadinoviruses

Hitherto, about 48 species of the *Rhadinovirus* genus have been isolated from a wide variety of mammals, of which 8 genomes have been fully sequenced. HHV-8, also known as Kaposi’s sarcoma-associated herpesvirus (KSHV), is the only human rhadinovirus identified to date, and was first discovered in Kaposi’s sarcoma (KS) skin lesion of an AIDS patient (Chang et al. 1994; Cesarman et al. 1995; Renne et al. 1996). In contrast to the ubiquitous (and infectious) dissemination of most other herpesviruses within their natural host populations, HHV-8 displays a rather low infectivity rate and is unevenly distributed among geographically disparate human populations (Hayward 1999). HHV-8 seroprevalence is low (<5%) in the general population of most European, Asian, and American countries, but can range from 10% to 40% in some Mediterranean countries (Hayward 1999) and 40% to 100% in African countries (Dedicoat and Newton 2003). In addition, HHV-8 seropositivity is highly prevalent among homosexual men (Verbeek et al. 1998). HHV-8 establishes lifelong, latent infections in pre- and post-germinal center B cells and endothelial precursor cells (Dupin et al. 1999), which is characterized by the expression of only a limited number of viral genes (Jenner et al. 2001).

While HHV-8 infection of healthy individuals is usually without severe pathogenic consequences, immune suppression (e.g., in AIDS or transplant recipients) can result in impaired control of HHV-8, leading to multifocal angioproliferative KS lesions (Sturzl et al. 1997) and/or lymphoproliferative diseases (primary effusion lymphomas, multimeric Castleman’s disease).

Like other herpesviruses, HHV-8 has captured a cellular gene from its hosts, *ORF74*, which resembles chemokine receptors. The *ORF74* receptor shows significant similarity with the human chemokine receptor CXCR2, known to play an important role in angiogenesis, embryonic development, wound healing, and tissue regeneration. Importantly, constitutive expression and signaling of *ORF74* induce focus formation in stably transfected NIH3T3 cells, which is accompanied by an increased production and secretion of vascular endothelial growth factor (VEGF), a major angiogenesis activator (Bais et al. 1998). Moreover, these *ORF74*-expressing cells form highly vascularized tumors that resemble KS when injected into nude mice (Bais et al. 1998). Likewise, transgenic mice expressing HHV-8-encoded *ORF74* in hematopoietic or

vascular endothelial cells develop angioproliferative KS-like lesions (Yang et al. 2000; Guo et al. 2003; Sodhi et al. 2004c).

ORF74 can constitutively couple to G proteins of the $G_{q/11}$, $G_{i/o}$, and G_{13} classes, thereby modulating a multitude of intracellular signaling pathways, including phospholipases, adenylyl cyclases, kinases, and small G proteins (Arvanitakis et al. 1997; Rosenkilde et al. 1999; Couty et al. 2001; Montaner et al. 2001; Shepard et al. 2001; Smit et al. 2002). Importantly, HHV-8 ORF74-mediated (constitutive) signaling is (partially) increased by angiogenic chemokines [containing a Glu-Leu-Arg (ELR) amino acid motif in the N-terminus]. CXCL8 (ligand for CXCR2) acts as a low-potency partial/neutral agonist (Rosenkilde et al. 1999; Rosenkilde and Schwartz 2000; Couty et al. 2001; Smit et al. 2002; McLean et al. 2004), while the non-ELR, angiostatic chemokines CXCL10 and CXCL12 (ligands of CXCR3 and CXCR4, respectively) and HHV-8-encoded vMIP-II decrease constitutive ORF74 signaling, thus acting as inverse agonists (Fig. 2). Importantly, constitutive signaling by HHV-8 ORF74 as well as chemokine modulation of this constitutive activity are prerequisites for the oncogenic potential of ORF74 in vivo (Holst et al. 2001; Sodhi et al. 2004c). ORF74-mediated modulation of intracellular signaling networks leads to increased transcription of cellular gene and paracrine factors regulating a range of cellular processes including transformation, proliferation, and immortalization (Bais et al. 1998, 2003). HHV-8-ORF74-mediated upregulation and secretion of proangiogenic growth factors and chemokines by lytic cells recruits neighboring cells that can be subsequently infected by released virions (Sodhi et al. 2004a).

Examination of biopsies of KS lesions from AIDS patients revealed high phosphorylated (activated) Akt (PKB) levels, suggesting a critical role for this antiapoptotic serine-threonine kinase in the onset and progression of KS pathology (Sodhi et al. 2004c). Moreover, inhibition of the PI3K/PDK1/Akt pathway prevented proliferation and survival of ORF74-expressing endothelial cells in vitro, and inhibited their tumorigenic potential upon allografting into nude mice (Sodhi et al. 2004c). ORF74 activates Akt by stimulating PI3K through $G\beta\gamma$ -subunits of both pertussis toxin-sensitive and -insensitive G proteins (Montaner et al. 2001), but also via phospholipase C (PLC)-dependent protein kinase C and p44/42 MAPK activation (Smit et al. 2002). In addition, ORF74 activates Akt indirectly in an autocrine manner by upregulating both the expression of VEGF (Bais et al. 1998; Sodhi et al. 2000) and its cognate receptor KDR2 (Bais et al. 2003). Upregulation of growth factors, chemokines, and cytokines in even a few ORF74-expressing cells drives angioproliferative tumor formation by paracrine stimulation of neighboring cells that are latently infected with HHV-8 (Montaner et al. 2003; Jensen et al. 2005). Despite its oncogenic potential, ORF74 is not sufficient for inducing KS in immuno-

competent individuals as indicated by one case of KS in every 17,000 HHV-8 infections. ORF74 is primarily expressed during (early) lytic replication, which occurs in about 3% of the spindle-shaped tumor cells within KS lesions (Kirshner et al. 1999; Sun et al. 1999), whereas the majority of cells in KS lesions are latently infected with HHV-8 (Staskus et al. 1997). Moreover, continuous expression of HHV-8-ORF74 appears to be essential for the progression of KS (Jensen et al. 2005). In this respect, it is puzzling how transient expression of HHV-8-ORF74 in lytic cells can cause KS. However, dysregulated expression of ORF74 under certain circumstances—such as HIV-1 coinfection, inflammation, or aborted lytic cycle progression—has been hypothesized to result in non-lytic (continuous) expression of ORF74 in a fraction of KS tumor cells (Sodhi et al. 2004a). In fact, the KS incidence increases about 10,000-fold in HIV-1-infected man, and 100,000-fold in HIV-1-infected homosexual men (Gallo 1998; Reitz et al. 1999), whereas HHV-8-infected transplant recipients have a 500-fold increased risk in developing KS (Cathomas 2003).

In contrast to the ability of HHV-8-ORF74 to constitutively activate a multitude of signaling pathways by coupling to G_q , G_i , and $G_{12/13}$ proteins (Bais et al. 1998; Munshi et al. 1999; Rosenkilde et al. 1999; Sodhi et al. 2000), the ORF74 proteins encoded by nonhuman rhadinoviruses activate a narrower range of G proteins in a ligand-independent manner. Herpesvirus saimiri-encoded ORF74 (i.e., HVS-ORF74 or ECRF3) signals constitutively via G_i and $G_{12/13}$ proteins, but not through coupling to G_q (Rosenkilde et al. 2004). The ORF74 protein encoded by equid herpesvirus 2 (i.e., EHV2-ORF74) only activates G_i -mediated pathways in a constitutive manner (Rosenkilde et al. 2005), whereas ORF74 of murine γ -herpesvirus 68 (i.e., MHV68-ORF74), also known as *murine herpesvirus 4* (MuHV4), is devoid of any constitutive activity (Verzijl et al. 2004). Both constitutive (G_i and $G_{12/13}$) and non-constitutive (G_q) HVS-ORF74-mediated signaling pathways can be stimulated by CXCL1 and CXCL6, whereas CXCL5 and CXCL8 act as neutral antagonists (Rosenkilde and Schwartz 2004). Interestingly, the non-ELR CXC chemokines that act as inverse agonists on the HHV-8-ORF74, do not bind the HVS-ORF74. Likewise, both human and mouse CXCL1 and CXCL2 stimulates MHV68-ORF78-mediated activation PLC, NF- κ B, p44/p42 MAPK, and Akt, as well as the inhibition of cAMP formation, whereas non-ELR CXC, CC, and CX3C chemokines were ineffective (Verzijl et al. 2004). In contrast to the broad chemokine binding profile of HHV-8-, EHV2-, and MHV68-ORF74, only a single chemokine (CXCL6) binds to EHV2-ORF74, resulting in a further increase of its constitutive G_i -mediated signaling (Rosenkilde et al. 2005).

Despite the apparent lack of constitutive activity, MHV68-ORF74 expression in NIH3T3 cells induces focus formation by these cells (Wakeling et al. 2001). This transforming potency of MHV68-ORF74 may result from consti-

tively signaling through yet-unidentified signaling pathways (Verzija et al. 2004). Alternatively, autocrine secretion of mouse CXCL1 (i.e., KC) by NIH3T3 cells (Bosio et al. 2002) may activate the MHV68–ORF74 that is expressed on the cell surface of these cells. In fact, MHV68–ORF74-mediated signaling in response to mouse CXCL1 enhances in vitro viral replication in permissive NIH3T3 cells (Lee et al. 2003). In contrast, disruption of the MHV68–ORF74 gene did not affect in vitro replication of MHV68 in infected NIH3T12 cells, or in vivo replication in spleen and lungs (Moorman et al. 2003). Interestingly, MHV68–ORF74 appeared to be essential for efficient reactivation of MHV68 from latency (Lee et al. 2003; Moorman et al. 2003). Like other ORF74 genes, *MHV68–ORF74* is an early lytic gene but is also expressed in latently infected cells (Kirshner et al. 1999; Sun et al. 1999; Wakeling et al. 2001).

Interestingly, ORF74-encoding genes are absent in two rhadinoviruses: the *bovine herpesvirus 4* and *alcelaphine herpesvirus 1*. In contrast to other members of the *Rhadinovirus* genus that are sequenced to date, the EHV2 genome contains three additional vGPCR-encoding ORFs adjacent to the conserved ORF74 (Telford et al. 1995). Interestingly, the hitherto uncharacterized ORF E6 displays highest sequence identity to the A5 receptors of *alcelaphine herpesvirus 1* and the lymphotropic porcine herpesviruses 1–3. Moreover, this subfamily of rhadinovirus-encoded GPCRs is homologous to the lymphocryptovirus-encoded BILF1 receptors (see the next section). The other two ORFs are gene duplicates that encode the E1 protein. These ORFs are located in the terminal direct repeat elements on both ends of the genome. E1 displays highest sequence identity to members of the cellular CC chemokine receptor family (30%–51%) and poxvirus-encoded CC chemokine receptors (25%–30%). Despite the relatively high sequence identity with a variety of CC chemokine receptors, only the CCR3-specific chemokine CCL11 was able to induce an E1-mediated increase in intracellular Ca^{2+} levels and chemotaxis (Camarda et al. 1999; Fig. 2).

3.2.2

Lymphocryptoviruses

In contrast to other herpesviruses, lymphocryptoviruses (LCV) have only been isolated from “higher primate” species of the infraorder Simiiformes. Hitherto, about 44 distinct LCVs have been identified (Ehlers et al. 2003). The LCV genomes which have been sequenced include those infecting man [i.e., HHV-4 or Epstein-Barr virus (EBV)], common marmoset [(i.e., *calitrichine herpesvirus 3* (CalHV3)], and rhesus macaques [i.e., *cercopithecine herpesvirus 15* (CeHV15)] have been fully sequenced (Table 1).

LCVs are ubiquitous (>90%) B lymphotropic viruses that establish life-long, generally asymptomatic, persistent infections in memory B lymphocytes (Wang et al. 2001). However, the potency of LCV to transform B lymphocytes can result in acute infectious mononucleosis, as well as malignant lymphomas, such as Hodgkin's and Burkitt's lymphomas, and post-transplant/AIDS-associated lymphomas (Middeldorp et al. 2003; Thorley-Lawson and Gross 2004). In addition, EBV has been directly associated with nasal natural killer (NK)-T cell lymphoma, nasopharyngeal and gastric carcinoma, oral hairy leukoplakia, and leiomyosarcoma (Middeldorp et al. 2003; Thompson and Kurzrock 2004). Such lymphomas are thought to arise from proliferating, infected B cells that are blocked in the transition from naïve to memory B cells, and/or are not efficiently eliminated by cytotoxic T cells. Hence, individuals with deficiencies in T cell-mediated immunity (e.g., post-transplant immunosuppression and AIDS) are in particular risk of developing EBV-associated lymphoproliferative diseases (Rivailler et al. 2004; Thorley-Lawson and Gross 2004).

The genome of LCVs contains one gene coding for a vGPCR, which is transcribed in various EBV-positive tumor cells (Beisser et al. 2005). LCV-encoded GPCRs show very limited amino acid sequence identity (<15%) to any cellular GPCR (Table 1). Nevertheless, functional analysis revealed that the EBV BILF1 protein is a functional membrane-associated GPCR that constitutively activates NF- κ B and CRE signaling pathways—both implicated in cell proliferation—in a G_{i1} -dependent manner (Beisser et al. 2005; Paulsen et al. 2005). In addition, BILF1 constitutively inhibits phosphorylation of the RNA-dependent protein kinase, which is important for antiviral responses (Beisser et al. 2005). Hitherto, BILF1 is still considered an “orphan” receptor, and information on its biological relevance is yet unknown.

4

Poxvirus-Encoded GPCRs

The Poxviridae is a family of large, brick-shaped, double-stranded DNA viruses. A characteristic of these viruses is that they replicate in the cytoplasm of infected cells, independent of the host nuclear machinery. Poxvirus infections are characterized by acute febrile illness accompanied by skin lesions that blister and form pockmarks. Infections are often self-limiting. Some species of poxvirus, however, can cause life-threatening infections in certain hosts (e.g., *variola virus* or smallpox infections in human). Most poxviruses are epitheliotropic and transmitted by direct contact or via the respiratory tract (Diven 2001). Many poxviruses are able to infect a range of host species.

Poxviruses may reside in a reservoir host in which viral infection results in mild, subclinical conditions. However, transfer of the virus to a zoonotic host often causes more severe pathologies (McFadden 2005).

The poxvirus family is divided into the Entomopoxvirinae and Chordopoxvirinae subfamilies, which infect insects or vertebrates, respectively (Table 2). Genome analysis and phylogenetic analysis of multiple deduced amino acid sequences divide the *Chordopox* genera in four (to five) main subgroups (Gubser et al. 2004; see Table 2). Interestingly, the genomes of avipoxviruses, capripoxviruses, suipoxvirus, and yatapoxviruses contain one or more putative GPCR-encoding genes (see Table 2).

4.1

Yatapoxviruses, Suipoxviruses, and Capripoxviruses

The *Yaba-like disease virus* (YLDV) contains two genes, *7L* and *145R*, encoding for membrane-associated proteins that display 53% and 44% amino acid sequence identity with CCR8 (Lee et al. 2001). YLDV-encoded 7L protein, but not 145R, displays a similar chemokine binding profile to CCR8, and binds hCCL1, hCCL7, hCCL4, hCCL17, vMIP1, and vMIP2, but not by mCCL1 (Najarro et al. 2003). In addition, 7L couples to G proteins and induces p44/p42 MAPK phosphorylation in response to CCL1 stimulation. Protein expression analyses of YLDV-infected cells revealed that 7L is expressed as early as 2 h postinfection and its expression increases with time. Blocking late gene expression using a viral DNA replication inhibitor resulted in a 26% decrease in 7L protein expression, suggesting that 7L displays both early and late gene expression kinetics.

The mechanism by which 7L exactly interferes with the CCR8-mediated adaptive and innate immune response has not yet been determined. However, considering the upregulation of CCL1 secretion by dendritic cells, mast cells, and dermal endothelial cells in certain skin inflammations (Gombert et al. 2005), resulting in the recruitment of CCR8-expressing T cells and Langerhans-type dendritic cells, it is tempting to speculate that 7L may sequester CCL1 from the environment of infected cells to impair the immune response. In fact, CCR8 appears to be a vulnerable target for viral hijacking, as several viruses specifically target this receptor by mimicking its ligands (e.g., HHV-8-encoded vMIP-I and vMIP-II, and the molluscum contagiosum virus-encoded vMCC-1) or expressing membrane-associated CCR8 mimics. Alternatively, 7L-mediated signaling in response to CCL1 may also activate anti-apoptotic as well as migratory signaling pathways, as observed for CCR8 (Haque et al. 2001; Louahed et al. 2003; Spinetti et al. 2003; Haque et al. 2004), thereby increasing cell survival and viral dissemination.

Genomes of sui- and capripoxviruses contain a single GPCR gene, of which the deduced amino acid sequences display highest sequence identity to CCR8 (Table 2). However, no pharmacological data are yet available for these receptors.

4.2

Avipoxviruses

The genomes of the fowlpox and canarypox viruses of the Avipoxvirus genus contain 3 and 4 ORFs encoding for vGPCRs. These vGPCRs share about 24% sequence identity with some members of CXC chemokine receptor family, but share more identity with GPCR1 and EBV-induced GPCR2. Nevertheless, this unique cluster of avipoxvirus-encoded GPCRs still awaits functional characterization.

5

Conclusions

Exploitation of the chemokine receptor system through molecular mimicry appears to be an effective means to assist viruses in evading immune surveillance, thus contributing to viral dissemination and virus-induced pathology (Fig. 3). Infection of cells and consequent expression of viral chemokine receptors enables them to respond to a broad spectrum of chemokines, evading the immune response or facilitating viral dissemination to areas with increased chemokine expression (Figs. 2 and 3). The ability of the viral chemokine receptors to signal in a constitutively active manner via promiscuous G protein coupling turns them into versatile signaling devices that modulate cellular signaling networks, thereby reprogramming the cellular machinery to modulate cellular function after infection.

Although many attractive roles have been attributed to this class of receptors, little is known about their (patho)physiological potential. The biological significance of ORF74 and the members of the UL33 and UL78 family in the pathogenesis of HHV-8 and CMV infections has been demonstrated *in vivo*. Mouse models and studies using recombinant rodent CMVs that carry a disrupted gene or lack the respective gene (Davis-Poynter et al. 1997; Bais et al. 1998; Beisser et al. 1998, 1999; Yang et al. 2000; Oliveira and Shenk 2001; Guo et al. 2003; Kaptein et al. 2003; Sodhi et al. 2004c; Streblov et al. 2005) indicate a role for these viral receptors in pathophysiology. GPCRs constitute a highly drugable class of membrane-associated proteins, accounting for about 50% of protein targets for therapeutic interventions. In addition, the

awareness that chemokines and their cognate receptors play a prominent role in numerous pathophysiological processes urges the quest for bioavailable small-molecule antagonists that specifically block viral chemokine receptor functioning (Onuffer and Horuk 2002). Small nonpeptidergic compounds inhibiting US28 constitutive signaling can be considered as tools to investigate the role of US28 in CMV pathology and may serve as promising therapeutics for clinical antiviral intervention. Also for the other viral chemokine receptors, however, specific (pharmacological or RNA interference) inhibitors or antibodies targeting these viral chemokine receptors is essential to elucidate the contribution of viral chemokine receptors to viral pathogenesis and reveal their potential as a future drug target.

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